

RAxML version 8: a tool for phylogenetic analysis and p

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Citation Report

#	ARTICLE	IF	CITATIONS
14	Global Diversification at the Harsh Sea-Land Interface: Mitochondrial Phylogeny of the Supralittoral Isopod Genus <i>Tylos</i> (Tylidae, Oniscidea). PLoS ONE, 2014, 9, e94081.	1.1	18
15	Phylogenetic Species Identification in <i>Rattus</i> Highlights Rapid Radiation and Morphological Similarity of New Guinean Species. PLoS ONE, 2014, 9, e98002.	1.1	14
16	A Phylogeographic Survey of the Pygmy Mouse <i>Mus minutoides</i> in South Africa: Taxonomic and Karyotypic Inference from Cytochrome b Sequences of Museum Specimens. PLoS ONE, 2014, 9, e98499.	1.1	7
17	Molecular and Phenotypic Data Support the Recognition of the Wakatobi Flowerpecker (<i>Dicaeum</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 1.1	1.1	14
18	Prevalence of HPV 16 and HPV 18 Lineages in Galicia, Spain. PLoS ONE, 2014, 9, e104678.	1.1	25
19	High Local Diversity of <i>Trypanosoma</i> in a Common Bat Species, and Implications for the Biogeography and Taxonomy of the <i>T. cruzi</i> Clade. PLoS ONE, 2014, 9, e108603.	1.1	38
20	Updating the description and taxonomic status of <i>Brachionus sessilis</i> Varga, 1951 (Rotifera): Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 507 345-70.	0.2	7
21	Diversification at the narrow sea-land interface in the Caribbean: phylogeography of endemic supralittoral <i>Ligia</i> isopods. <i>Frontiers in Ecology and Evolution</i> , 2014, 2, .	1.1	15
22	The transcriptome of the bowhead whale <i>Balaena mysticetus</i> reveals adaptations of the longest-lived mammal. <i>Aging</i> , 2014, 6, 879-899.	1.4	62
23	Analyzing Phylogenetic Trees with Timed and Probabilistic Model Checking: The Lactose Persistence Case Study. <i>Journal of Integrative Bioinformatics</i> , 2014, 11, 17-31.	1.0	1
24	Linking genetic diversity and morphological disparity: biodiversity assessment of a highly unexplored family of harvestmen (Arachnida : Opiliones : Neopilionidae) in New Zealand. <i>Invertebrate Systematics</i> , 2014, 28, 590.	0.5	6
25	Nemertean Toxin Genes Revealed through Transcriptome Sequencing. <i>Genome Biology and Evolution</i> , 2014, 6, 3314-3325.	1.1	22
26	<i>Heligmosomoides neopolygyrus</i> Asakawa & Ohbayashi, 1986, a cryptic Asian nematode infecting the striped field mouse <i>Apodemus agrarius</i> in Central Europe. <i>Parasites and Vectors</i> , 2014, 7, 457.	1.0	12
28	The Extracellular Heme-binding Protein HbpS from the Soil Bacterium <i>Streptomyces reticuli</i> Is an Aquo-cobalamin Binder. <i>Journal of Biological Chemistry</i> , 2014, 289, 34214-34228.	1.6	8
29	Genome analysis of a major urban malaria vector mosquito, <i>Anopheles stephensi</i> . <i>Genome Biology</i> , 2014, 15, 459.	3.8	119
30	Whole-genome enrichment and sequencing of <i>Chlamydia trachomatis</i> directly from clinical samples. <i>BMC Infectious Diseases</i> , 2014, 14, 591.	1.3	71
31	Pogo-like Transposases Have Been Repeatedly Domesticated into CENP-B-Related Proteins. <i>Genome Biology and Evolution</i> , 2014, 6, 2008-2016.	1.1	38
32	Use of whole genome sequences to develop a molecular phylogenetic framework for <i>Rhodococcus fascians</i> and the <i>Rhodococcus</i> genus. <i>Frontiers in Plant Science</i> , 2014, 5, 406.	1.7	29

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33	Collapse of Amphibian Communities Due to an Introduced Ranavirus. <i>Current Biology</i> , 2014, 24, 2586-2591.	1.8	182
34	ExaBayes: Massively Parallel Bayesian Tree Inference for the Whole-Genome Era. <i>Molecular Biology and Evolution</i> , 2014, 31, 2553-2556.	3.5	423
35	A new genus of soft coral (Cnidaria, Octocorallia) from the Republic of Congo (Pointe-Noire Region). <i>ZooKeys</i> , 2014, 462, 1-10.	0.5	0
36	Inteins as indicators of gene flow in the halobacteria. <i>Frontiers in Microbiology</i> , 2014, 5, 299.	1.5	24
37	A New Record of <i>Penicillium antarcticum</i> from Marine Environments in Korea. <i>Mycobiology</i> , 2014, 42, 109-113.	0.6	13
38	The Finding of a Group IIE Phospholipase A2 Gene in a Specified Segment of <i>Protobothrops flavoviridis</i> Genome and Its Possible Evolutionary Relationship to Group IIA Phospholipase A2 Genes. <i>Toxins</i> , 2014, 6, 3471-3487.	1.5	8
39	Protocols for Investigating the Microbiology of Drilling Fluids, Hydraulic Fracturing Fluids, and Formations in Unconventional Natural Gas Reservoirs. <i>Springer Protocols</i> , 2014, , 133-156.	0.1	1
40	Functional analysis of COP1 and SPA orthologs from <i>Physcomitrella</i> and rice during photomorphogenesis of transgenic <i>Arabidopsis</i> reveals distinct evolutionary conservation. <i>BMC Plant Biology</i> , 2014, 14, 178.	1.6	44
41	<i>vanG</i> Element Insertions within a Conserved Chromosomal Site Conferring Vancomycin Resistance to <i>Streptococcus agalactiae</i> and <i>Streptococcus anginosus</i> . <i>MBio</i> , 2014, 5, e01386-14.	1.8	39
42	Highly Recombinant <i>VGI</i> <i>Cryptococcus gattii</i> Population Develops Clonal Outbreak Clusters through both Sexual Macroevolution and Asexual Microevolution. <i>MBio</i> , 2014, 5, e01494-14.	1.8	81
43	Detection of Zoonotic Pathogens and Characterization of Novel Viruses Carried by Commensal <i>Rattus norvegicus</i> in New York City. <i>MBio</i> , 2014, 5, e01933-14.	1.8	310
44	Phylogenetics and morphological evolution of coral-dwelling barnacles (Balanomorpha: Tj ETQq1 1 0.784314 rgBT/Overlock_10 Tf 503	0.7	21
45	<i>Aureoscheda</i> , a new genus of marine Pelagophyceae from the Bahamas, Caribbean Sea. <i>Phycologia</i> , 2014, 53, 513-522.	0.6	9
47	Evolution of substrate specificity in bacterial AA10 lytic polysaccharide monoxygenases. <i>Biotechnology for Biofuels</i> , 2014, 7, 109.	6.2	69
48	Chloroplast phylogenomic analysis resolves deep-level relationships within the green algal class Trebouxiophyceae. <i>BMC Evolutionary Biology</i> , 2014, 14, 211.	3.2	107
49	Taming the wild: resolving the gene pools of non-model <i>Arabidopsis</i> lineages. <i>BMC Evolutionary Biology</i> , 2014, 14, 224.	3.2	61
50	S ² ance: reference-based phylogenetic analysis for 18S rRNA studies. <i>BMC Evolutionary Biology</i> , 2014, 14, 235.	3.2	8
51	Pan-African phylogeny of <i>Mus</i> (subgenus <i>Nannomys</i>) reveals one of the most successful mammal radiations in Africa. <i>BMC Evolutionary Biology</i> , 2014, 14, 256.	3.2	75

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52	Correlation between the genomic <i>o454-nlpD</i> region polymorphisms, virulence gene equipment and phylogenetic group of extraintestinal <i>Escherichia coli</i> (ExPEC) enables pathotyping irrespective of host, disease and source of isolation. <i>Gut Pathogens</i> , 2014, 6, 37.	1.6	6
53	History of Plastid DNA Insertions Reveals Weak Deletion and AT Mutation Biases in Angiosperm Mitochondrial Genomes. <i>Genome Biology and Evolution</i> , 2014, 6, 3210-3221.	1.1	57
54	A Systematic Computational Analysis of Biosynthetic Gene Cluster Evolution: Lessons for Engineering Biosynthesis. <i>PLoS Computational Biology</i> , 2014, 10, e1004016.	1.5	164
55	Contrasting patterns in the evolution of the Rab GTPase family in Archaeplastida. <i>Acta Societatis Botanicorum Poloniae</i> , 2014, 83, 303-315.	0.8	15
56	Genomic analysis of <i>Pseudomonas aeruginosa</i> PA96, the host of carbapenem resistance plasmid pOZ176. <i>FEMS Microbiology Letters</i> , 2014, 356, 212-216.	0.7	9
57	Stick Insect Genomes Reveal Natural Selection's Role in Parallel Speciation. <i>Science</i> , 2014, 344, 738-742.	6.0	386
58	Diversification and asymmetrical gene flow across time and space: lineage sorting and hybridization in polytypic barking frogs. <i>Molecular Ecology</i> , 2014, 23, 3273-3291.	2.0	78
59	Phylogenomics of the carrot genus (<i>Daucus</i> , Apiaceae). <i>American Journal of Botany</i> , 2014, 101, 1666-1685.	0.8	42
60	Wild Sex in Zebrafish: Loss of the Natural Sex Determinant in Domesticated Strains. <i>Genetics</i> , 2014, 198, 1291-1308.	1.2	282
61	Phosphate absorption across multiple epithelia in the Pacific hagfish (<i>Eptatretus stoutii</i>). <i>American Journal of Physiology - Regulatory Integrative and Comparative Physiology</i> , 2014, 307, R643-R652.	0.9	18
62	Editing on tRNAs: Biochemical, biological and evolutionary implications. <i>FEBS Letters</i> , 2014, 588, 4279-4286.	1.3	113
63	Phylogeny of the freshwater crabs of the Western Ghats (Brachyura, Gecarcinucidae). <i>Zoologica Scripta</i> , 2014, 43, 651-660.	0.7	9
64	Genomic atolls of differentiation in coral reef fishes (<i>Hypoplectrus</i> spp.). <i>Trends in Ecology and Evolution</i> , 2014, 29, 101-109.	2.0	50
65	Integration of Clustering and Multidimensional Scaling to Determine Phylogenetic Trees as Spherical Phylograms Visualized in 3 Dimensions. <i>PLoS ONE</i> , 2014, 9, e101111.		7
66	Genomic and transcriptomic analysis of <i>Laccaria bicolor</i> CAZome reveals insights into polysaccharides remodelling during symbiosis establishment. <i>Fungal Genetics and Biology</i> , 2014, 72, 168-181.	0.9	81
67	Variability of the transporter gene complement in ammonia-oxidizing archaea. <i>Trends in Microbiology</i> , 2014, 22, 665-675.	3.5	81
68	Genomic Analysis of the Pacific Oyster (<i>Crassostrea gigas</i>) Reveals Possible Conservation of Vertebrate Sex Determination in a Mollusc. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 2207-2217.	0.8	81
69	<i>Kentomonas</i> gen. n., a New Genus of Endosymbiont-containing Trypanosomatids of Strigomonadinae subfam. n.. <i>Protist</i> , 2014, 165, 825-838.	0.6	63

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70	A putative β -1-pyrroline-5-carboxylate synthetase involved in the biosynthesis of proline and arginine in <i>Leptinotarsa decemlineata</i> . <i>Journal of Insect Physiology</i> , 2014, 71, 105-113.	0.9	10
71	Phylogeny, identification and nomenclature of the genus <i>Aspergillus</i> . <i>Studies in Mycology</i> , 2014, 78, 141-173.	4.5	835
72	Understanding the spectacular failure of <i>cpDNA</i> barcoding in willows (<i>Salix</i>): Does this result from a trans-specific selective sweep?. <i>Molecular Ecology</i> , 2014, 23, 4737-4756.	2.0	109
73	Shotgun assembly of the assassin bug <i>Brontostoma colossus</i> mitochondrial genome (Heteroptera, TJ ETQq1 1 0.784314 rgBT /Overl	1.0	41
74	Phylogenomic analyses uncover origin and spread of the <i>Wolbachia</i> pandemic. <i>Nature Communications</i> , 2014, 5, 5117.	5.8	121
75	Mitochondrial genomes of <i>Trichinella</i> species and genotypes – a basis for diagnosis, and systematic and epidemiological explorations. <i>International Journal for Parasitology</i> , 2014, 44, 1073-1080.	1.3	40
76	Application of RAD-based phylogenetics to complex relationships among variously related taxa in a species flock. <i>Molecular Phylogenetics and Evolution</i> , 2014, 80, 137-144.	1.2	69
77	Gene Transfers Shaped the Evolution of De Novo NAD + Biosynthesis in Eukaryotes. <i>Genome Biology and Evolution</i> , 2014, 6, 2335-2349.	1.1	17
78	Cellulolytic <i>Streptomyces</i> Strains Associated with Herbivorous Insects Share a Phylogenetically Linked Capacity To Degrade Lignocellulose. <i>Applied and Environmental Microbiology</i> , 2014, 80, 4692-4701.	1.4	70
79	Not Only for Egg Yolk – Functional and Evolutionary Insights from Expression, Selection, and Structural Analyses of <i>Formica</i> Ant Vitellogenins. <i>Molecular Biology and Evolution</i> , 2014, 31, 2181-2193.	3.5	78
80	Determination of coleopteran insects associated with spore dispersal of <i>Cryptoporus volvatus</i> (Polyporaceae: Basidiomycota) in Korea. <i>Journal of Asia-Pacific Entomology</i> , 2014, 17, 647-651.	0.4	9
81	Transcriptome Analysis Reveals the Same 17 <i>S-Locus F-Box</i> Genes in Two Haplotypes of the Self-Incompatibility Locus of <i>Petunia inflata</i> . <i>Plant Cell</i> , 2014, 26, 2873-2888.	3.1	84
82	Complete genome of a nonphotosynthetic cyanobacterium in a diatom reveals recent adaptations to an intracellular lifestyle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 11407-11412.	3.3	121
83	Phylogenomic Analysis of Spiders Reveals Nonmonophyly of Orb Weavers. <i>Current Biology</i> , 2014, 24, 1772-1777.	1.8	127
84	An Introduction to Supertree Construction (and Partitioned Phylogenetic Analyses) with a View Toward the Distinction Between Gene Trees and Species Trees. , 2014, , 49-76.		10
85	Phylogenomics Resolves a Spider Backbone Phylogeny and Rejects a Prevailing Paradigm for Orb Web Evolution. <i>Current Biology</i> , 2014, 24, 1765-1771.	1.8	204
86	Out of the deep: Cryptic speciation in a Neotropical gecko (Squamata, Phyllodactylidae) revealed by species delimitation methods. <i>Molecular Phylogenetics and Evolution</i> , 2014, 80, 113-124.	1.2	57
87	Mitogenomic phylogeny of the Percichthyidae and Centrarchiformes (Percomorphaceae): comparison with recent nuclear gene-based studies and simultaneous analysis. <i>Gene</i> , 2014, 549, 46-57.	1.0	25

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88	The changing face of the molecular evolutionary clock. <i>Trends in Ecology and Evolution</i> , 2014, 29, 496-503.	4.2	110
89	Molecular phylogenetic analysis of Western Australian troglobitic chthoniid pseudoscorpions (Pseudoscorpiones : Chthoniidae) points to multiple independent subterranean clades. <i>Invertebrate Systematics</i> , 2014, 28, 386.	0.5	30
90	BorreliaBase: a phylogeny-centered browser of Borrelia genomes. <i>BMC Bioinformatics</i> , 2014, 15, 233.	1.2	40
91	The complete mitochondrial genomes of sixteen ardeid birds revealing the evolutionary process of the gene rearrangements. <i>BMC Genomics</i> , 2014, 15, 573.	1.2	45
92	Differential retention and expansion of the ancestral genes associated with the paleopolyploidies in modern rosid plants, as revealed by analysis of the extensins super-gene family. <i>BMC Genomics</i> , 2014, 15, 612.	1.2	13
93	Genome-wide survey and expression analysis of the bHLH-PAS genes in the amphioxus <i>Branchiostoma floridae</i> reveal both conserved and diverged expression patterns between cephalochordates and vertebrates. <i>EvoDevo</i> , 2014, 5, 20.	1.3	12
94	Deep global evolutionary radiation in birds: Diversification and trait evolution in the cosmopolitan bird family Rallidae. <i>Molecular Phylogenetics and Evolution</i> , 2014, 81, 96-108.	1.2	74
95	Transmission of Methicillin-Resistant <i>Staphylococcus aureus</i> via Deceased Donor Liver Transplantation Confirmed by Whole Genome Sequencing. <i>American Journal of Transplantation</i> , 2014, 14, 2640-2644.	2.6	41
96	Multiple independent colonization of the Canary Islands by the winged grasshopper genus <i>Sphingonotus</i> Fieber, 1852. <i>Molecular Phylogenetics and Evolution</i> , 2014, 81, 174-181.	1.2	24
97	Marine-derived <i>Penicillium</i> in Korea: diversity, enzyme activity, and antifungal properties. <i>Antonie Van Leeuwenhoek</i> , 2014, 106, 331-345.	0.7	34
98	Toward a stable classification of genera within the Entolomataceae: a phylogenetic re-evaluation of the <i>Rhodocybe</i> - <i>Clitopilus</i> clade. <i>Mycologia</i> , 2014, 106, 1127-1142.	0.8	40
99	Dramatic expansion of the black widow toxin arsenal uncovered by multi-tissue transcriptomics and venom proteomics. <i>BMC Genomics</i> , 2014, 15, 366.	1.2	93
100	The MADS-Box Gene Family of the Basal Eudicot and Hybrid <i>Aquilegia coerulea</i> 'Origami' (<i>Ranunculaceae</i>). <i>Annals of the Missouri Botanical Garden</i> , 2014, 99, 313-322.	1.3	8
101	Molecular systematics and biogeography of <i>Logania</i> R.Br. (<i>Loganiaceae</i>). <i>Molecular Phylogenetics and Evolution</i> , 2014, 78, 324-333.	1.2	7
102	Reisolation and redescription of <i>Balantidium duodeni</i> Stein, 1867 (Litostomatea, Trichostomatia). <i>Parasitology Research</i> , 2014, 113, 4207-4215.	0.6	43
103	<i>Ptolemeba</i> n. gen., a Novel Genus of Hartmannellid Amoebae (Tubulinea, Amoebozoa); with an Emphasis on the Taxonomy of <i>Saccamoeba</i> . <i>Journal of Eukaryotic Microbiology</i> , 2014, 61, 611-619.	0.8	5
104	Balticidins A-D, Antifungal Hassallidin-Like Lipopeptides from the Baltic Sea Cyanobacterium <i>Anabaena cylindrica</i> Bio33. <i>Journal of Natural Products</i> , 2014, 77, 1287-1296.	1.5	37
105	A chloroplast tree for <i>Viburnum</i> (<i>Adoxaceae</i>) and its implications for phylogenetic classification and character evolution. <i>American Journal of Botany</i> , 2014, 101, 1029-1049.	0.8	56

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106	Global Genomic Diversity of Human Papillomavirus 6 Based on 724 Isolates and 190 Complete Genome Sequences. <i>Journal of Virology</i> , 2014, 88, 7307-7316.	1.5	33
107	Expanding the Mimiviridae family using asparagine synthase as a sequence bait. <i>Virology</i> , 2014, 466-467, 112-122.	1.1	21
108	A new colorful species of <i>Pristimantis</i> (Anura: Craugastoridae) from the eastern flank of the Cordillera Central in Colombia. <i>Zootaxa</i> , 2014, 3900, 223-42.	0.2	9
109	Antibacterial gene transfer across the tree of life. <i>ELife</i> , 2014, 3, .	2.8	66
110	On the systematic position of the genus <i>Timmiella</i> (Dicranidae, Bryopsida) and its allied genera, with the description of a new family Timmiellaceae. <i>Phytotaxa</i> , 2014, 181, 151.	0.1	25
111	RNA interference-aided knockdown of a putative saccharopine dehydrogenase leads to abnormal ecdysis in the brown planthopper, <i>Nilaparvata lugens</i> (Stål) (Hemiptera: Delphacidae). <i>Bulletin of Entomological Research</i> , 2015, 105, 390-398.	0.5	4
112	<i>Epiphloea</i> belongs to Collemataceae (Lecanoromycetes, lichenized Ascomycota). <i>Lichenologist</i> , 2015, 47, 369-378.	0.5	8
113	Phylogeny of tremellomycetous yeasts and related dimorphic and filamentous basidiomycetes reconstructed from multiple gene sequence analyses. <i>Studies in Mycology</i> , 2015, 81, 1-26.	4.5	133
114	Near full-length HIV type 1M genomic sequences from Cameroon. <i>Evolution, Medicine and Public Health</i> , 2015, 2015, 254-265.	1.1	15
115	Lineage-specific gene radiations underlie the evolution of novel betalain pigmentation in Caryophyllales. <i>New Phytologist</i> , 2015, 207, 1170-1180.	3.5	152
116	<i>Miconia abscondita</i> (Melastomataceae: Miconieae), A New Species from the Massif De La Hotte, Haiti: Rediscovered in Herbaria After Being Hidden for Nearly Nine Decades. <i>Rhodora</i> , 2015, 117, 317-341.	0.0	6
117	Characteristics of Plant Essential Genes Allow for within- and between-Species Prediction of Lethal Mutant Phenotypes. <i>Plant Cell</i> , 2015, 27, 2133-2147.	3.1	91
118	Two new <i>Trechispora</i> species from La Réunion Island. <i>Mycological Progress</i> , 2015, 14, 1.	0.5	11
119	Rethinking phylogeographic structure and historical refugia in the rufous-capped babbler <i>Cyanoderma ruficeps</i> in light of range-wide genetic sampling and paleodistributional reconstructions. <i>Environmental Epigenetics</i> , 2015, 61, 901-909.	0.9	5
120	Origin and higher-level diversification of acariform mites – evidence from nuclear ribosomal genes, extensive taxon sampling, and secondary structure alignment. <i>BMC Evolutionary Biology</i> , 2015, 15, 178.	3.2	57
121	Extensive genetic diversity and endemism across the global range of the oceanic copepod <i>Pleuromamma abdominalis</i> . <i>Progress in Oceanography</i> , 2015, 138, 77-90.	1.5	31
122	Towards an integrated phylogenetic classification of the <i>Tremellomycetes</i> . <i>Studies in Mycology</i> , 2015, 81, 85-147.	4.5	393
123	<i>Wolbachia</i> distribution in selected beetle taxa characterized by PCR screens and MLST data. <i>Ecology and Evolution</i> , 2015, 5, 4345-4353.	0.8	19

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124	Assessing biodiversity and endemism using phylogenetic methods across multiple taxonomic groups. <i>Ecology and Evolution</i> , 2015, 5, 5177-5192.	0.8	29
125	Molecular operational taxonomic units as approximations of species in the light of evolutionary models and empirical data from Fungi. <i>Molecular Ecology</i> , 2015, 24, 5770-5777.	2.0	63
126	What is the origin of the Scottish populations of the European endemic <i>Cherleria sedoides</i> (Caryophyllaceae)? <i>New Journal of Botany</i> , 2015, 5, 13-25.	0.2	4
127	Extracting phylogenetic signal and accounting for bias in whole-genome data sets supports the Ctenophora as sister to remaining Metazoa. <i>BMC Genomics</i> , 2015, 16, 987.	1.2	134
128	Exogenous selection rather than cytonuclear incompatibilities shapes asymmetrical fitness of reciprocal <i>A</i> hybrids. <i>Ecology and Evolution</i> , 2015, 5, 1734-1745.	0.8	27
129	Comparative genomic analyses of freshly isolated <i>Giardia intestinalis</i> assemblage A isolates. <i>BMC Genomics</i> , 2015, 16, 697.	1.2	55
130	Contrasting genetic structure between mitochondrial and nuclear markers in the dengue fever mosquito from Rio de Janeiro: implications for vector control. <i>Evolutionary Applications</i> , 2015, 8, 901-915.	1.5	36
131	Microfluidic PCR-based target enrichment: A case study in two rapid radiations of <i>Commiphora</i> (Burseraceae) from Madagascar. <i>Journal of Systematics and Evolution</i> , 2015, 53, 411-431.	1.6	22
132	<i>Toxoplasma gondii</i> Toc75 Functions in Import of Stromal but not Peripheral Apicoplast Proteins. <i>Traffic</i> , 2015, 16, 1254-1269.	1.3	36
133	Population Structure of Endomicrobia in Single Host Cells of Termite Gut Flagellates (“ <i>Trichonympha</i> spp.). <i>Microbes and Environments</i> , 2015, 30, 92-98.	0.7	29
134	Distribution and Evolution of Nitrogen Fixation Genes in the Phylum “Bacteroidetes“. <i>Microbes and Environments</i> , 2015, 30, 44-50.	0.7	67
135	The making of a branching annelid: an analysis of complete mitochondrial genome and ribosomal data of <i>Ramisyllis multicaudata</i> . <i>Scientific Reports</i> , 2015, 5, 12072.	1.6	34
136	Evidence for horizontal transfer of mitochondrial DNA to the plastid genome in a bamboo genus. <i>Scientific Reports</i> , 2015, 5, 11608.	1.6	62
137	Marine amoebae with cytoplasmic and perinuclear symbionts deeply branching in the Gammaproteobacteria. <i>Scientific Reports</i> , 2015, 5, 13381.	1.6	36
138	The genomics of ecological vicariance in threespine stickleback fish. <i>Nature Communications</i> , 2015, 6, 8767.	5.8	115
139	Comparative genomics <i>Lactobacillus reuteri</i> from sourdough reveals adaptation of an intestinal symbiont to food fermentations. <i>Scientific Reports</i> , 2015, 5, 18234.	1.6	65
140	Exploring molecular variation in <i>Schistosoma japonicum</i> in China. <i>Scientific Reports</i> , 2015, 5, 17345.	1.6	33
141	Phylogenetic and genomic diversity in isolates from the globally distributed <i>Acinetobacter baumannii</i> ST25 lineage. <i>Scientific Reports</i> , 2015, 5, 15188.	1.6	93

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142	Phylogenetic relationships and a new sectional classification of Croton (Euphorbiaceae) in Australia. Australian Systematic Botany, 2015, 28, 219.	0.3	6
143	Red clover (<i>Trifolium pratense</i> L.) draft genome provides a platform for trait improvement. Scientific Reports, 2015, 5, 17394.	1.6	136
144	Phylogenetic analysis of Ascidae <i>sensu lato</i> and related groups (Acari: Mesostigmata: Gamasina) based on nuclear ribosomal DNA partial sequences. Systematic and Applied Acarology, 2015, 20, 225.	0.5	6
145	Multiple conversion between the genes encoding bacterial class-I release factors. Scientific Reports, 2015, 5, 12406.	1.6	1
146	Highly Pathogenic Avian Influenza A(H5N1) Virus Struck Migratory Birds in China in 2015. Scientific Reports, 2015, 5, 12986.	1.6	47
147	A new predatory leech from Vietnam (Hirudinida : Arhynchobdellida : Salifidae): its phylogenetic position with comments on the classification of the family. Invertebrate Systematics, 2015, 29, 473.	0.5	4
148	De Novo Assembly and Characterization of Four Anthozoan (Phylum Cnidaria) Transcriptomes. G3: Genes, Genomes, Genetics, 2015, 5, 2441-2452.	0.8	74
149	<i>Inocybe griseorubida</i> , a new species of <i>Pseudosperma</i> clade from tropical India. Phytotaxa, 2015, 221, 166.	0.1	12
150	Phylogenetic placement and new data on macro and micro morphology of <i>Nopalxochia phyllanthoides</i> (Cactaceae), an endangered species from Mexico. Phytotaxa, 2015, 222, 241.	0.1	1
151	<i>Opuntia delafuentiana</i> (Cactaceae: Opuntioideae), a new cactosperma from central Mexico. Phytotaxa, 2015, 231, 230.	0.1	6
152	Infrageneric treatment of <i>Phalaris</i> (Canary grasses, Poaceae) based on molecular phylogenetics and floret structure. Australian Systematic Botany, 2015, 28, 355.	0.3	10
153	How Many Genes are Needed to Resolve Phylogenetic Incongruence?. Evolutionary Bioinformatics, 2015, 11, EBO.S26047.	0.6	6
154	Chimeric adaptor proteins translocate diverse type VI secretion system effectors in <i>Vibrio cholerae</i> . EMBO Journal, 2015, 34, 2198-2210.	3.5	132
155	A maximum pseudo-likelihood approach for phylogenetic networks. BMC Genomics, 2015, 16, S10.	1.2	164
156	Distribution of Mitochondrial Clades and Morphotypes of Baboons <i>Papio</i> spp. (Primates). PLoS One, 2015, 10, e0122100.	0.6	22
157	Unnoticed in the tropics: phylogenomic resolution of the poorly known arachnid order Ricinulei (Arachnida). Royal Society Open Science, 2015, 2, 150065.	1.1	34
158	Root sepsis associated with insect-dwelling <i>Sebaldella termitidis</i> in a lesser dwarf lemur (<i>Cheirogaleus medius</i>). Antonie Van Leeuwenhoek, 2015, 108, 1373-1382.	0.7	7
159	Phylogenetic analysis of HIV sub-epidemics in Mochudi, Botswana. Epidemics, 2015, 13, 44-55.	1.5	22

#	ARTICLE	IF	CITATIONS
160	Middle East Respiratory Syndrome Coronavirus Outbreak in the Republic of Korea, 2015. <i>Osong Public Health and Research Perspectives</i> , 2015, 6, 269-278.	0.7	218
161	Interisland variegation of venom [Lys49]phospholipase A2 isozyme genes in <i>Protobothrops</i> genus snakes in the southwestern islands of Japan. <i>Toxicon</i> , 2015, 107, 210-216.	0.8	3
162	Molecular phylogenetics reveals convergent evolution in lower Congo River spiny eels. <i>BMC Evolutionary Biology</i> , 2015, 15, 224.	3.2	23
163	Chloroplast phylogenomic analysis of chlorophyte green algae identifies a novel lineage sister to the Sphaeropleales (Chlorophyceae). <i>BMC Evolutionary Biology</i> , 2015, 15, 264.	3.2	69
164	<i>Escherichia coli</i> O157:H7 strains harbor at least three distinct sequence types of Shiga toxin 2a-converting phages. <i>BMC Genomics</i> , 2015, 16, 733.	1.2	47
165	Comparative genomics of <i>Fructobacillus</i> spp. and <i>Leuconostoc</i> spp. reveals niche-specific evolution of <i>Fructobacillus</i> spp.. <i>BMC Genomics</i> , 2015, 16, 1117.	1.2	53
166	<i>Drosophila</i> innate immunity: regional and functional specialization of prophenoloxidases. <i>BMC Biology</i> , 2015, 13, 81.	1.7	146
167	A synopsis of <i>Soyauxia</i> (Peridiscaceae, formerly Medusandraceae) with a new species from Liberia. <i>Plant Ecology and Evolution</i> , 2015, 148, 409-419.	0.3	31
168	Phylogenetic classification of yeasts and related taxa within <i>Pucciniomycotina</i> . <i>Studies in Mycology</i> , 2015, 81, 149-189.	4.5	202
169	The Utility of Genome Skimming for Phylogenomic Analyses as Demonstrated for Glycerid Relationships (Annelida, Glyceridae). <i>Genome Biology and Evolution</i> , 2015, 7, 3443-3462.	1.1	55
170	SoTree: An Automated Phylogeny Assembly Tool for Ecologists from Big Tree. , 2015, , .		2
171	A dengue outbreak on a floating village at Cat Ba Island in Vietnam. <i>BMC Public Health</i> , 2015, 15, 940.	1.2	11
172	Ultra-large alignments using phylogeny-aware profiles. <i>Genome Biology</i> , 2015, 16, 124.	3.8	113
173	Negligible nuclear introgression despite complete mitochondrial capture between two species of chipmunks. <i>Evolution; International Journal of Organic Evolution</i> , 2015, 69, 1961-1972.	1.1	88
174	Body size evolution under character release in the ground beetle <i>Carabus japonicus</i> . <i>Journal of Biogeography</i> , 2015, 42, 2145-2158.	1.4	10
175	Revival of the genus <i>Tropicoperdix</i> Blyth 1859 (Phasianidae, Aves) using multilocus sequence data. <i>Zoological Journal of the Linnean Society</i> , 2015, 175, 429-438.	1.0	10
176	Complete Genome Sequence of <i>Curtobacterium</i> sp. Strain MR_MD2014, Isolated from Topsoil in Woods Hole, Massachusetts. <i>Genome Announcements</i> , 2015, 3, .	0.8	3
177	The Gap Procedure: for the identification of phylogenetic clusters in HIV-1 sequence data. <i>BMC Bioinformatics</i> , 2015, 16, 355.	1.2	17

#	ARTICLE	IF	CITATIONS
178	Alternative translation initiation codons for the plastid maturase MatK: unraveling the pseudogene misconception in the Orchidaceae. <i>BMC Evolutionary Biology</i> , 2015, 15, 210.	3.2	18
179	The Perchlorate Reduction Genomic Island: Mechanisms and Pathways of Evolution by Horizontal Gene Transfer. <i>BMC Genomics</i> , 2015, 16, 862.	1.2	39
180	Phylogenetic patterns of gene rearrangements in four mitochondrial genomes from the green algal family Hydrodictyaceae (Sphaeropleales, Chlorophyceae). <i>BMC Genomics</i> , 2015, 16, 826.	1.2	11
181	Transcription analysis of neonicotinoid resistance in Mediterranean (MED) populations of <i>B. tabaci</i> reveal novel cytochrome P450s, but no nAChR mutations associated with the phenotype. <i>BMC Genomics</i> , 2015, 16, 939.	1.2	59
182	Exploring the genomic traits of fungus-feeding bacterial genus <i>Collimonas</i> . <i>BMC Genomics</i> , 2015, 16, 1103.	1.2	57
183	The <i>Listeria monocytogenes</i> Core-Genome Sequence Typer (LmCGST): a bioinformatic pipeline for molecular characterization with next-generation sequence data. <i>BMC Microbiology</i> , 2015, 15, 224.	1.3	33
184	Prospective function of FtsZ proteins in the secondary plastid of chlorarachniophyte algae. <i>BMC Plant Biology</i> , 2015, 15, 276.	1.6	9
185	Diversification of non-visual photopigment parapinopsin in spectral sensitivity for diverse pineal functions. <i>BMC Biology</i> , 2015, 13, 73.	1.7	38
186	Phylogenetically typing bacterial strains from partial SNP genotypes observed from direct sequencing of clinical specimen metagenomic data. <i>Genome Medicine</i> , 2015, 7, 52.	3.6	38
187	Russulaceae Associated with Mycoheterotroph <i>Monotropa uniflora</i> (Ericaceae) in Tlaxcala, Mexico: A Phylogenetic Approach. <i>Cryptogamie, Mycologie</i> , 2015, 36, 479-512.	0.2	16
188	Validation of <i>Polytomella piriformis</i> nomen nudum (Chlamydomonadaceae): a Distinct Lineage Within a Genus of Nonphotosynthetic Green Algae. <i>Journal of Eukaryotic Microbiology</i> , 2015, 62, 840-844.	0.8	5
189	Not all are free-living: high-throughput <i>scp</i> DNA metabarcoding reveals a diverse community of protists parasitizing soil metazoa. <i>Molecular Ecology</i> , 2015, 24, 4556-4569.	2.0	116
190	Inferring speciation history in the Andes with reduced representation sequence data: an example in the bay-backed antpittas (Aves; Grallariidae; <i>Grallaria hypoleuca</i> s. l.). <i>Molecular Ecology</i> , 2015, 24, 6256-6277.	2.0	28
191	Knocking down a putative ¹ -pyrroline-5-carboxylate dehydrogenase gene by RNA interference inhibits flight and causes adult lethality in the Colorado potato beetle <i>Leptinotarsa decemlineata</i> (Say). <i>Pest Management Science</i> , 2015, 71, 1387-1396.	1.7	23
192	Anthracoze Fungi with Curved Conidia, & Colletotrichum spp. belonging to Ribosomal Groups 9-13, and Their Host Ranges in Japan. <i>Japan Agricultural Research Quarterly</i> , 2015, 49, 351-362.	0.1	14
193	Biogeography of the land snail genus <i>Allognathus</i> (Helicidae): middle Miocene colonization of the Balearic Islands. <i>Journal of Biogeography</i> , 2015, 42, 1845-1857.	1.4	21
194	A revised classification of the genus <i>Matrona</i> Selys, 1853 using molecular and morphological methods (Odonata: Calopterygidae). <i>Zoological Journal of the Linnean Society</i> , 2015, 174, 473-486.	1.0	6
195	Phylogenetic relationships of the ubiquitous coral reef crab subfamily Chlorodiellinae (Decapoda.) <i>Tj ETQq1 1 0.784314 rBT /Overl</i>	0.7	14

#	ARTICLE	IF	CITATIONS
196	Which came first: The lizard or the egg? Robustness in phylogenetic reconstruction of ancestral states. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2015, 324, 504-516.	0.6	57
197	Rock, Paper, Scissors: Harnessing Complementarity in Ortholog Detection Methods Improves Comparative Genomic Inference. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 629-638.	0.8	10
198	Dynamics of <i>Wolbachia pipientis</i> Gene Expression Across the <i>Drosophila melanogaster</i> Life Cycle. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 2843-2856.	0.8	55
199	Terrestrial fishes: rivers are barriers to gene flow in annual fishes from the African savanna. <i>Journal of Biogeography</i> , 2015, 42, 1832-1844.	1.4	56
200	Sterol Composition and Biosynthetic Genes of <i>Vitrella brassicaformis</i> , a Recently Discovered Chromerid: Comparison to <i>Chromera velia</i> and Phylogenetic Relationship with Apicomplexan Parasites. <i>Journal of Eukaryotic Microbiology</i> , 2015, 62, 786-798.	0.8	2
201	Particle-association lifestyle is a phylogenetically conserved trait in bathypelagic prokaryotes. <i>Molecular Ecology</i> , 2015, 24, 5692-5706.	2.0	113
202	Stepwise and lineage-specific diversification of plant <i>RNA</i> polymerase genes and origin of the largest plant-specific subunits. <i>New Phytologist</i> , 2015, 207, 1198-1212.	3.5	32
203	Of flowers and twigs: phylogenetic revision of the plant-mimicking praying mantises (<i>Mantodea</i> : <i>Eumantodea</i> and <i>Hymenopodidae</i>) with a new suprageneric classification. <i>Systematic Entomology</i> , 2015, 40, 789-834.	1.7	34
204	Draft Genome Sequence of the <i>Pandoraea apista</i> LMG 16407 Type Strain. <i>Genome Announcements</i> , 2015, 3, .	0.8	5
205	Phylogenetics of <i>Eulophiinae</i> (Orchidaceae: <i>Epidendroideae</i>): evolutionary patterns and implications for generic delimitation. <i>Botanical Journal of the Linnean Society</i> , 2015, 179, 43-56.	0.8	12
206	Sky island diversification meets the multispecies coalescent – divergence in the spruce-fir moss spider (<i>Microhexura montivaga</i> , <i>Araneae</i> , <i>Mygalomorphae</i>) on the highest peaks of southern Appalachia. <i>Molecular Ecology</i> , 2015, 24, 3467-3484.	2.0	82
207	Using RAxML to Infer Phylogenies. <i>Current Protocols in Bioinformatics</i> , 2015, 51, 6.14.1-6.14.14.	25.8	215
208	Human legacies differentially organize functional and phylogenetic diversity of urban herbaceous plant communities at multiple spatial scales. <i>Applied Vegetation Science</i> , 2015, 18, 513-527.	0.9	52
209	The complete mitochondrial genome of the endemic and highly specialized South African bee species <i>Rediviva intermixta</i> (Hymenoptera: Melittidae), with a comparison with other bee mitogenomes. <i>Biological Journal of the Linnean Society</i> , 2015, 116, 940-953.	0.7	11
210	Historical introgression among the American live oaks and the comparative nature of tests for introgression. <i>Evolution; International Journal of Organic Evolution</i> , 2015, 69, 2587-2601.	1.1	193
211	Simultaneous depletion of <i>Atm</i> and <i>Mdl</i> rebalances cytosolic Fe cluster assembly but not heme import into the mitochondrion of <i>Trypanosoma Brucei</i> . <i>FEBS Journal</i> , 2015, 282, 4157-4175.	2.2	15
212	Genetic and Physiological Diversity in the Diatom <i>Nitzschia inconspicua</i> . <i>Journal of Eukaryotic Microbiology</i> , 2015, 62, 815-832.	0.8	35
213	Geographic variation in the Pine Barrens Treefrog (<i>Hyla andersonii</i>): concordance of genetic, morphometric and acoustic signal data. <i>Molecular Ecology</i> , 2015, 24, 3281-3298.	2.0	17

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214	The <i>Casuarina</i> <i>NIN</i> gene is transcriptionally activated throughout <i>Frankia</i> root infection as well as in response to bacterial diffusible signals. <i>New Phytologist</i> , 2015, 208, 887-903.	3.5	87
215	<i>Trilobodrilus itoi</i> sp. nov., with a Re-Description of <i>T. nipponicus</i> (Annelida: Dinophilidae) and a Molecular Phylogeny of the Genus. <i>Zoological Science</i> , 2015, 32, 405.	0.3	7
216	Genomic sequencing reveals historical, demographic and selective factors associated with the diversification of the fire-associated fungus <i>Neurospora discreta</i> . <i>Molecular Ecology</i> , 2015, 24, 5657-5675.	2.0	32
217	Some answers: Application of a layered barcode approach to problems in ant taxonomy. <i>Molecular Ecology Resources</i> , 2015, 15, 1262-1274.	2.2	10
218	Visual system evolution and the nature of the ancestral snake. <i>Journal of Evolutionary Biology</i> , 2015, 28, 1309-1320.	0.8	72
219	The interacting proteins <i>HLH010</i> , <i>HLH089</i> and <i>HLH091</i> are redundantly required for <i>Arabidopsis</i> anther development and transcriptome. <i>Plant Journal</i> , 2015, 83, 976-990.	2.8	136
220	Pyrolocin A, a 3-Decalinoyltetramic Acid with Selective Biological Activity, Isolated from Amazonian Cultures of the Novel Endophyte <i>Diaporthe</i> sp. E6927E. <i>Natural Product Communications</i> , 2015, 10, 1934578X1501001.	0.2	3
221	Phylogenetic Position of the Queer, Backward-bent Entoproct <i>Loxosoma axisadversum</i> (Entoprocta: Tj ETQq1 1 0.784314 rgBT / Over 0.1	0.1	4
222	Four New Species of <i>Amanita</i> in Inje County, Korea. <i>Mycobiology</i> , 2015, 43, 408-414.	0.6	10
223	Middle East Respiratory Syndrome in 3 Persons, South Korea, 2015. <i>Emerging Infectious Diseases</i> , 2015, 21, 2084-2087.	2.0	22
224	Taxonomic Study of the Genus <i>Abundisporus</i> in Korea. <i>Mycobiology</i> , 2015, 43, 225-230.	0.6	4
225	Phylogenomics of H5N1 Highly Pathogenic Avian Influenza in Europe, 2005–2010: Potential for Molecular Surveillance of New Outbreaks. <i>Viruses</i> , 2015, 7, 3310-3328.	1.5	18
226	Genetic Diversity and Selective Pressure in Hepatitis C Virus Genotypes 1–6: Significance for Direct-Acting Antiviral Treatment and Drug Resistance. <i>Viruses</i> , 2015, 7, 5018-5039.	1.5	59
227	Sequence and Structure Analysis of Distantly-Related Viruses Reveals Extensive Gene Transfer between Viruses and Hosts and among Viruses. <i>Viruses</i> , 2015, 7, 5388-5409.	1.5	16
228	Phylogeny of the Vitamin K 2,3-Epoxy Reductase (VKOR) Family and Evolutionary Relationship to the Disulfide Bond Formation Protein B (DsbB) Family. <i>Nutrients</i> , 2015, 7, 6224-6249.	1.7	12
229	Against the flow: evidence of multiple recent invasions of warmer continental shelf waters by a Southern Ocean brittle star. <i>Frontiers in Ecology and Evolution</i> , 0, 3, .	1.1	26
230	Taxon-rich multigene phylogeny of the photosynthetic euglenoids (Euglenophyceae). <i>Frontiers in Ecology and Evolution</i> , 2015, 3, .	1.1	30
231	Phylogenomics of <i>Xanthomonas</i> field strains infecting pepper and tomato reveals diversity in effector repertoires and identifies determinants of host specificity. <i>Frontiers in Microbiology</i> , 2015, 6, 535.	1.5	156

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232	The link between independent acquisition of intracellular gamma-endosymbionts and concerted evolution in <i>Tremblaya princeps</i> . <i>Frontiers in Microbiology</i> , 2015, 6, 642.	1.5	18
233	Novel molecular markers for the detection of methanogens and phylogenetic analyses of methanogenic communities. <i>Frontiers in Microbiology</i> , 2015, 6, 694.	1.5	31
234	Genetic determinants of heat resistance in <i>Escherichia coli</i> . <i>Frontiers in Microbiology</i> , 2015, 6, 932.	1.5	105
235	Multiple adaptations to polar and alpine environments within cyanobacteria: a phylogenomic and Bayesian approach. <i>Frontiers in Microbiology</i> , 2015, 6, 1070.	1.5	81
236	Genomic Reconstruction of an Uncultured Hydrothermal Vent Gammaproteobacterial Methanotroph (Family Methylothermaceae) Indicates Multiple Adaptations to Oxygen Limitation. <i>Frontiers in Microbiology</i> , 2015, 6, 1425.	1.5	36
237	Microbial Communities on Seafloor Basalts at Dorado Outcrop Reflect Level of Alteration and Highlight Global Lithic Clades. <i>Frontiers in Microbiology</i> , 2015, 6, 1470.	1.5	72
238	Identification of dopamine receptors across the extant avian family tree and analysis with other clades uncovers a polyploid expansion among vertebrates. <i>Frontiers in Neuroscience</i> , 2015, 9, 361.	1.4	13
239	Two new species of <i>Cyrtodactylus</i> (Squamata: Gekkonidae) from the Southern Bukit Barisan Range of Sumatra and an estimation of their phylogeny. <i>Zootaxa</i> , 2015, 4020, 495-516.	0.2	28
240	New Light on the Systematics of Fungi Associated with Attine Ant Gardens and the Description of <i>Escovopsis kreiselii</i> sp. nov.. <i>PLoS ONE</i> , 2015, 10, e0112067.	1.1	18
241	Transient Changes in Bacterioplankton Communities Induced by the Submarine Volcanic Eruption of El Hierro (Canary Islands). <i>PLoS ONE</i> , 2015, 10, e0118136.	1.1	22
242	Complete Genome Sequence of <i>Borrelia afzelii</i> K78 and Comparative Genome Analysis. <i>PLoS ONE</i> , 2015, 10, e0120548.	1.1	16
243	In or Out-of-Madagascar? Colonization Patterns for Large-Bodied Diving Beetles (Coleoptera: Tj ETQq1 1 0.784314 rgBT / Overlock 17	1.1	17
244	Hepatitis B Virus Genotype Distribution and Genotype-Specific BCP/preCore Substitutions in Acute and Chronic Infections in Argentina. <i>PLoS ONE</i> , 2015, 10, e0121436.	1.1	25
245	Coalescent-Based Species Delimitation Approach Uncovers High Cryptic Diversity in the Cosmopolitan Lichen-Forming Fungal Genus <i>Protoparmelia</i> (Lecanorales, Ascomycota). <i>PLoS ONE</i> , 2015, 10, e0124625.	1.1	61
246	Novel Detection of Insecticide Resistance Related P450 Genes and Transcriptome Analysis of the Hemimetabolous Pest <i>Erthesina fullo</i> (Thunberg) (Hemiptera: Heteroptera). <i>PLoS ONE</i> , 2015, 10, e0125970.	1.1	3
247	Duplicated Leptin Receptors in Two Species of Eel Bring New Insights into the Evolution of the Leptin System in Vertebrates. <i>PLoS ONE</i> , 2015, 10, e0126008.	1.1	31
248	Ancestral Chromatin Configuration Constrains Chromatin Evolution on Differentiating Sex Chromosomes in <i>Drosophila</i> . <i>PLoS Genetics</i> , 2015, 11, e1005331.	1.5	36
249	Genotypic Diversity Is Associated with Clinical Outcome and Phenotype in Cryptococcal Meningitis across Southern Africa. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003847.	1.3	94

#	ARTICLE	IF	CITATIONS
250	ApiAP2 Factors as Candidate Regulators of Stochastic Commitment to Merozoite Production in <i>Theileria annulata</i> . PLoS Neglected Tropical Diseases, 2015, 9, e0003933.	1.3	29
251	A Genomic Approach to Resolving Relapse versus Reinfection among Four Cases of Buruli Ulcer. PLoS Neglected Tropical Diseases, 2015, 9, e0004158.	1.3	14
252	Shaking the Tree: Multi-locus Sequence Typing Usurps Current Onchocercid (Filarial Nematode) Phylogeny. PLoS Neglected Tropical Diseases, 2015, 9, e0004233.	1.3	96
253	Pathways of Amino Acid Degradation in <i>Nilaparvata lugens</i> (Stål) with Special Reference to Lysine-Ketoglutarate Reductase/Saccharopine Dehydrogenase (LKR/SDH). PLoS ONE, 2015, 10, e0127789.	1.1	18
254	Glycosyltransferase Family 43 Is Also Found in Early Eukaryotes and Has Three Subfamilies in Charophycean Green Algae. PLoS ONE, 2015, 10, e0128409.	1.1	30
255	The Complete Mitochondrial Genome of <i>Corizus tetraspilus</i> (Hemiptera: Rhopalidae) and Phylogenetic Analysis of Pentatomomorpha. PLoS ONE, 2015, 10, e0129003.	1.1	50
256	The Plastid Genome of the Cryptomonad <i>Teleaulax amphioxeia</i> . PLoS ONE, 2015, 10, e0129284.	1.1	30
257	Thriving in the Cold: Glacial Expansion and Post-Glacial Contraction of a Temperate Terrestrial Salamander (<i>Plethodon serratus</i>). PLoS ONE, 2015, 10, e0130131.	1.1	16
258	Phylogeography of the Coastal Mosquito <i>Aedes togoi</i> across Climatic Zones: Testing an Anthropogenic Dispersal Hypothesis. PLoS ONE, 2015, 10, e0131230.	1.1	11
259	Molecular and Morphological Species Boundaries in the Gorgonian Octocoral Genus <i>Pterogorgia</i> (Octocorallia: Gorgoniidae). PLoS ONE, 2015, 10, e0133517.	1.1	14
260	The Evolution of the Secreted Regulatory Protein Progranulin. PLoS ONE, 2015, 10, e0133749.	1.1	53
261	Identification of Habitat-Specific Biomes of Aquatic Fungal Communities Using a Comprehensive Nearly Full-Length 18S rRNA Dataset Enriched with Contextual Data. PLoS ONE, 2015, 10, e0134377.	1.1	62
262	Diversification of the Genus <i>Anopheles</i> and a Neotropical Clade from the Late Cretaceous. PLoS ONE, 2015, 10, e0134462.	1.1	29
263	Evidence of Positive Selection of Aquaporins Genes from <i>Pontoporia blainvillei</i> during the Evolutionary Process of Cetaceans. PLoS ONE, 2015, 10, e0134516.	1.1	9
264	Transcriptome Analysis of the Emerald Ash Borer (EAB), <i>Agrilus planipennis</i> : De Novo Assembly, Functional Annotation and Comparative Analysis. PLoS ONE, 2015, 10, e0134824.	1.1	9
265	Inaccessible Biodiversity on Limestone Cliffs: <i>Aster tianmenshanensis</i> (Asteraceae), a New Critically Endangered Species from China. PLoS ONE, 2015, 10, e0134895.	1.1	7
266	The Mitochondrial Genomes of <i>Aquila fasciata</i> and <i>Buteo lagopus</i> (Aves, Accipitriformes): Sequence, Structure and Phylogenetic Analyses. PLoS ONE, 2015, 10, e0136297.	1.1	21
267	Population Genomics of the Euryhaline Teleost <i>Poecilia latipinna</i> . PLoS ONE, 2015, 10, e0137077.	1.1	19

#	ARTICLE	IF	CITATIONS
268	The LysE Superfamily of Transport Proteins Involved in Cell Physiology and Pathogenesis. PLoS ONE, 2015, 10, e0137184.	1.1	25
269	Evolution of a Novel Antiviral Immune-Signaling Interaction by Partial-Gene Duplication. PLoS ONE, 2015, 10, e0137276.	1.1	9
270	Acinetobacter baumannii Virulence Is Mediated by the Concerted Action of Three Phospholipases D. PLoS ONE, 2015, 10, e0138360.	1.1	85
271	Biodiversity, Anti-Trypanosomal Activity Screening, and Metabolomic Profiling of Actinomycetes Isolated from Mediterranean Sponges. PLoS ONE, 2015, 10, e0138528.	1.1	58
272	New Type of Papillomavirus and Novel Circular Single Stranded DNA Virus Discovered in Urban Rattus norvegicus Using Circular DNA Enrichment and Metagenomics. PLoS ONE, 2015, 10, e0141952.	1.1	14
273	Seven New Complete Plastome Sequences Reveal Rampant Independent Loss of the ndh Gene Family across Orchids and Associated Instability of the Inverted Repeat/Small Single-Copy Region Boundaries. PLoS ONE, 2015, 10, e0142215.	1.1	131
274	TGS-TB: Total Genotyping Solution for Mycobacterium tuberculosis Using Short-Read Whole-Genome Sequencing. PLoS ONE, 2015, 10, e0142951.	1.1	77
275	Mitochondrial Haplotype Diversity in Zambian Lions: Bridging a Gap in the Biogeography of an Iconic Species. PLoS ONE, 2015, 10, e0143827.	1.1	8
276	Genomic Patterns of Positive Selection at the Origin of Rust Fungi. PLoS ONE, 2015, 10, e0143959.	1.1	20
277	Genomic Epidemiology of an Endoscope-Associated Outbreak of Klebsiella pneumoniae Carbapenemase (KPC)-Producing K. pneumoniae. PLoS ONE, 2015, 10, e0144310.	1.1	75
278	Inter-Seasonal Influenza is Characterized by Extended Virus Transmission and Persistence. PLoS Pathogens, 2015, 11, e1004991.	2.1	25
279	Using targeted enrichment of nuclear genes to increase phylogenetic resolution in the neotropical rain forest genus Inga (Leguminosae: Mimosoideae). Frontiers in Plant Science, 2015, 6, 710.	1.7	147
280	On the paraphyly of Homaloptera (Teleostei: Balitoridae) and description of a new genus of hillstream loaches from the Western Ghats of India. Zootaxa, 2015, 3926, 57.	0.2	12
281	A new species of Ptychochromis from southeastern Madagascar (Teleostei: Cichlidae). Zootaxa, 2015, 4044, 79.	0.2	8
282	Genetic differentiation among species of the genus Thermophilus (Serpentes, Colubridae) and comments on T. shangrila. Zootaxa, 2015, 4028, 102.	0.2	1
283	Molecular phylogenetics, systematics and host-plant associations of the Bruchidius albosparsus (Fåhræus) species group (Coleoptera, Chrysomelidae, Bruchinae) with the description of four new species. Zootaxa, 2015, 3931, 451.	0.2	5
284	Description of a new genus for Euptychia hilara (C. Felder & R. Felder, 1867) (Lepidoptera: Tortricidae). Zootaxa, 2015, 4028, 17.	0.2	17
285	Review of the aphid genus Aspiphorodon Verma, 1967 with descriptions of three new species from China (Hemiptera: Aphididae: Aphidinae). Zootaxa, 2015, 4028, 551.	0.2	3

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286	A revision of the genus <i>Conicofrontia</i> Hampson (Lepidoptera, Noctuidae, &Apameini,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 74 molecular data. <i>Zootaxa</i> , 2015, 3925, 56-74.	0.2	8
287	&strong&Molecular and morphological assessment of &em&Delma&/em& &em&australis&/em& Kluge (Squamata: Pygopodidae), with a description of a new species from the biodiversity "hotspot"™ of southwestern Western Australia&/strong&. <i>Zootaxa</i> , 2015, 3946, 301.	0.2	5
288	&strong&Molecular systematics and undescribed diversity of Madagascan scolecophidian snakes (Squamata: Serpentes)&/strong&. <i>Zootaxa</i> , 2015, 4040, 31.	0.2	16
289	<p>A new species of bright-eyed treefrog (Mantellidae) from Madagascar, with comments on call evolution and patterns of syntopy in the Boophis ankaratra complex</p>. <i>Zootaxa</i> , 2015, 4034, 531.	0.2	7
290	<p class="HeadingRunIn">Revision of the hillstream lizard loaches, genus Balitoropsis (Cypriniformes: Balitoridae)</p>. <i>Zootaxa</i> , 2015, 3962, 206.	0.2	4
291	Chromerid genomes reveal the evolutionary path from photosynthetic algae to obligate intracellular parasites. <i>ELife</i> , 2015, 4, e06974.	2.8	198
292	Identification and Biological Characterization of <i>Leishmania</i> (<i>Viannia</i>) <i>guyanensis</i> Isolated from a Patient with Tegumentary Leishmaniasis in GoiÃs, a Nonendemic Area for This Species in Brazil. <i>BioMed Research International</i> , 2015, 2015, 1-11.	0.9	5
293	The Evolutionary History of Daphniid Î±-Carbonic Anhydrase within Animalia. <i>International Journal of Evolutionary Biology</i> , 2015, 2015, 1-11.	1.0	7
294	Comparative Genomics of Amphibian-like Ranaviruses, Nucleocytoplasmic Large DNA Viruses of Poikilotherms. <i>Evolutionary Bioinformatics</i> , 2015, 11s2, EBO.S33490.	0.6	7
295	Population structure of <i>Neisseria gonorrhoeae</i> based on whole genome data and its relationship with antibiotic resistance. <i>PeerJ</i> , 2015, 3, e806.	0.9	67
296	Species Tree Inference Using a Mixture Model. <i>Molecular Biology and Evolution</i> , 2015, 32, 2469-2482.	3.5	13
297	Similarity-Based Codes Sequentially Assigned to Ebola Virus Genomes Are Informative of Species Membership, Associated Outbreaks, and Transmission Chains. <i>Open Forum Infectious Diseases</i> , 2015, 2, ofv024.	0.4	18
298	Hybridization masks speciation in the evolutionary history of the GalÃpagos marine iguana. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2015, 282, 20150425.	1.2	52
299	Evolution of the H9N2 influenza genotype that facilitated the genesis of the novel H7N9 virus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 548-553.	3.3	287
300	Extensive screen for bacterial endosymbionts reveals taxon-specific distribution patterns among bees (Hymenoptera, Anthophila). <i>FEMS Microbiology Ecology</i> , 2015, 91, .	1.3	27
301	Phylogenomic Analyses Indicate that Early Fungi Evolved Digesting Cell Walls of Algal Ancestors of Land Plants. <i>Genome Biology and Evolution</i> , 2015, 7, 1590-1601.	1.1	175
302	Employing Phylogenomics to Resolve the Relationships among Cnidarians, Ctenophores, Sponges, Placozoans, and Bilaterians. <i>Integrative and Comparative Biology</i> , 2015, 55, 1084-1095.	0.9	40
303	Origin, diversification and substrate specificity in the family of <sc>NCS</sc>1/<sc>FUR</sc> transporters. <i>Molecular Microbiology</i> , 2015, 96, 927-950.	1.2	56

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304	Public Health Investigation of Two Outbreaks of Shiga Toxin-Producing <i>Escherichia coli</i> O157 Associated with Consumption of Watercress. <i>Applied and Environmental Microbiology</i> , 2015, 81, 3946-3952.	1.4	68
305	Evolution of Feeding Structures in the Marine Nematode Order Enoplida. <i>Integrative and Comparative Biology</i> , 2015, 55, 228-240.	0.9	18
306	Bacterial versatility requires DEAD-box RNA helicases. <i>FEMS Microbiology Reviews</i> , 2015, 39, 392-412.	3.9	69
307	Impacts of Terraces on Phylogenetic Inference. <i>Systematic Biology</i> , 2015, 64, 709-726.	2.7	46
308	Interbreeding among deeply divergent mitochondrial lineages in the American cockroach (<i>Periplaneta</i>). <i>Evolution</i> , 2015, 69, 1023-1033.	1.8	23
309	Diagnostics for a troubled backbone: testing topological hypotheses of trapelioid lichenized fungi in a large-scale phylogeny of Ostropomycetidae (Lecanoromycetes). <i>Fungal Diversity</i> , 2015, 73, 239-258.	4.7	46
310	<i>Entamoeba</i> mitosomes play an important role in encystation by association with cholesteryl sulfate synthesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E2884-90.	3.3	62
311	Molecular Phylogenetic and Phylogenomic Approaches in Studies of Lichen Systematics and Evolution. <i>Journal of Systematics and Evolution</i> , 2015, 45-60.		7
312	Horsetails are the sister group to all other monilophytes and Marattiales are sister to leptosporangiate ferns. <i>Molecular Phylogenetics and Evolution</i> , 2015, 90, 140-149.	1.2	56
313	High molecular weight dissolved organic matter enrichment selects for methylotrophs in dilution to extinction cultures. <i>ISME Journal</i> , 2015, 9, 2725-2739.	4.4	58
314	Complete chloroplast genome sequence of pineapple (<i>Ananas comosus</i>). <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	0.6	24
315	Characterization of the pathogenome and phylogenomic classification of enteropathogenic <i>Escherichia coli</i> of the O157:non-H7 serotypes. <i>Pathogens and Disease</i> , 2015, 73, .	0.8	25
316	A genetic mechanism for female-limited Batesian mimicry in <i>Papilio</i> butterfly. <i>Nature Genetics</i> , 2015, 47, 405-409.	9.4	215
317	Evolution of an Epigenetic Gene Ensemble within the Genus <i>Anopheles</i> . <i>Genome Biology and Evolution</i> , 2015, 7, 901-915.	1.1	8
318	Molecular phylogeny and evolutionary dynamics of matrix gene of avian influenza viruses in China. <i>Infection, Genetics and Evolution</i> , 2015, 34, 344-351.	1.0	5
319	Re-evaluating the phylogeny of allopolyploid <i>Gossypium</i> L.. <i>Molecular Phylogenetics and Evolution</i> , 2015, 92, 45-52.	1.2	110
320	Fungal metabolic gene clusters "caravans" traveling across genomes and environments. <i>Frontiers in Microbiology</i> , 2015, 6, 161.	1.5	136
321	Bioinformatics and Biomedical Engineering. <i>Lecture Notes in Computer Science</i> , 2015, , .	1.0	3

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322	Phylogenomics of Phrynosomatid Lizards: Conflicting Signals from Sequence Capture versus Restriction Site Associated DNA Sequencing. <i>Genome Biology and Evolution</i> , 2015, 7, 706-719.	1.1	154
323	Genomic Data from Extinct North American <i>Camelops</i> Revise Camel Evolutionary History. <i>Molecular Biology and Evolution</i> , 2015, 32, 2433-2440.	3.5	72
324	Genetic diversity of free-living Symbiodinium in the Caribbean: the importance of habitats and seasons. <i>Coral Reefs</i> , 2015, 34, 927-939.	0.9	24
325	Strong biogeographic signal in the phylogenetic relationships of <i>Rocheftoria</i> Sw. (Ehretiaceae). <i>Tj ETQq1 1 0.784314.rgBT /Oyerlock 10</i>	0.3	11
326	Toward the genetic origins of a potentially non-native population of threespine stickleback (<i>Gasterosteus aculeatus</i>) in Alberta. <i>Conservation Genetics</i> , 2015, 16, 859-873.	0.8	3
327	Copper tolerance and distribution of epibiotic bacteria associated with giant kelp <i>Macrocystis pyrifera</i> in southern California. <i>Ecotoxicology</i> , 2015, 24, 1131-1140.	1.1	7
328	Coalescence vs. concatenation: Sophisticated analyses vs. first principles applied to rooting the angiosperms. <i>Molecular Phylogenetics and Evolution</i> , 2015, 91, 98-122.	1.2	77
329	Phylogenetic and phylogeographic mapping of the avian coronavirus spike protein-encoding gene in wild and synanthropic birds. <i>Virus Research</i> , 2015, 201, 101-112.	1.1	17
330	Laccase-like enzyme activities from chlorophycean green algae with potential for bioconversion of phenolic pollutants. <i>FEMS Microbiology Letters</i> , 2015, 362, .	0.7	35
331	How do divergent ecological strategies emerge among marine bacterioplankton lineages?. <i>Trends in Microbiology</i> , 2015, 23, 577-584.	3.5	65
332	Resolving relationships within the palm subfamily Arecoideae (Arecaceae) using plastid sequences derived from next-generation sequencing. <i>American Journal of Botany</i> , 2015, 102, 888-899.	0.8	31
333	The study of <i>Priapulus caudatus</i> reveals conserved molecular patterning underlying different gut morphogenesis in the Ecdysozoa. <i>BMC Biology</i> , 2015, 13, 29.	1.7	39
334	Functionally Divergent Alleles and Duplicated Loci Encoding an Acyltransferase Contribute to Acylsugar Metabolite Diversity in <i>Solanum</i> Trichomes. <i>Plant Cell</i> , 2015, 27, 1002-1017.	3.1	106
335	Inferring phylogenies of evolving sequences without multiple sequence alignment. <i>Scientific Reports</i> , 2014, 4, 6504.	1.6	62
336	A RESTful API for Access to Phylogenetic Tools via the CIPRES Science Gateway. <i>Evolutionary Bioinformatics</i> , 2015, 11, EBO.S21501.	0.6	390
337	Molecular Survey of <i>Codium</i> Species Diversity in Southern Madagascar. <i>Cryptogamie, Algologie</i> , 2015, 36, 171-187.	0.3	14
338	Towards a faster and accurate supertree inference. , 2015, , .		3
339	Comparative phylogeography and niche modeling for three species complexes of SE China (<i>Paradoxornis</i> spp., <i>Pycnonotus</i> spp., <i>Spizixos</i> spp.). <i>Environmental Epigenetics</i> , 2015, 61, 943-950.	0.9	1

#	ARTICLE	IF	CITATIONS
340	The global distribution of <i>Banana bunchy top virus</i> reveals little evidence for frequent recent, human-mediated long distance dispersal events. <i>Virus Evolution</i> , 2015, 1, vev009.	2.2	58
341	RDP4: Detection and analysis of recombination patterns in virus genomes. <i>Virus Evolution</i> , 2015, 1, vev003.	2.2	2,621
342	The Genome of the "Great Speciator" Provides Insights into Bird Diversification. <i>Genome Biology and Evolution</i> , 2015, 7, 2680-2691.	1.1	55
343	Novel insights into the historical biogeography of the streak-breasted scimitar babbler complex (Aves: Tj ETQq1 1 0.784314 rgBT /Ov	0.9	4
344	Comprehensive insights in the <i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i> genome using new WGS data of sheep strain JIII-386 from Germany. <i>Genome Biology and Evolution</i> , 2015, 7, evv154.	1.1	31
345	Molecular characterisation of hepatitis B virus in HIV-1 subtype C infected patients in Botswana. <i>BMC Infectious Diseases</i> , 2015, 15, 335.	1.3	16
346	Stelliosphaerols A and B, Sesquiterpene "Polyol Conjugates from an Ecuadorian Fungal Endophyte. <i>Journal of Natural Products</i> , 2015, 78, 3005-3010.	1.5	16
347	<i>Arenogigas armoricus</i> , a New Genus and Species of a Monostiliferous Hoplonemertean (Nemertea) from the North-West Coast of France. <i>Zoological Science</i> , 2015, 32, 605.	0.3	4
348	Cryptic infection of a broad taxonomic and geographic diversity of tadpoles by <i>Perkinsea</i> protists. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E4743-51.	3.3	68
349	Importance of Viral Sequence Length and Number of Variable and Informative Sites in Analysis of HIV Clustering. <i>AIDS Research and Human Retroviruses</i> , 2015, 31, 531-542.	0.5	17
350	ASTRAL-II: coalescent-based species tree estimation with many hundreds of taxa and thousands of genes. <i>Bioinformatics</i> , 2015, 31, i44-i52.	1.8	822
351	nextflu: real-time tracking of seasonal influenza virus evolution in humans. <i>Bioinformatics</i> , 2015, 31, 3546-3548.	1.8	153
352	The Rise and Fall of TRP-N, an Ancient Family of Mechanogated Ion Channels, in Metazoa. <i>Genome Biology and Evolution</i> , 2015, 7, 1713-1727.	1.1	36
353	Ancient Origin and Recent Innovations of RNA Polymerase IV and V. <i>Molecular Biology and Evolution</i> , 2015, 32, 1788-1799.	3.5	77
354	A common tRNA modification at an unusual location: the discovery of wyosine biosynthesis in mitochondria. <i>Nucleic Acids Research</i> , 2015, 43, 4262-4273.	6.5	22
355	The ancestor of modern Holozoa acquired the CCA-adding enzyme from Alphaproteobacteria by horizontal gene transfer. <i>Nucleic Acids Research</i> , 2015, 43, 6739-6746.	6.5	14
356	PoMo: An Allele Frequency-Based Approach for Species Tree Estimation. <i>Systematic Biology</i> , 2015, 64, 1018-1031.	2.7	66
357	Spectral shifts of mammalian ultraviolet-sensitive pigments (short wavelength-sensitive opsin 1) are associated with eye length and photic niche evolution. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2015, 282, 20151817.	1.2	56

#	ARTICLE	IF	CITATIONS
358	A feedback insensitive isopropylmalate synthase affects acylsugar composition in cultivated and wild tomato. <i>Plant Physiology</i> , 2015, 169, pp.00474.2015.	2.3	73
359	Prevalence, Genetic Characterization, and 18S Small Subunit Ribosomal RNA Diversity of <i>Trypanosoma rangeli</i> in Triatomine and Mammal Hosts in Endemic Areas for Chagas Disease in Ecuador. <i>Vector-Borne and Zoonotic Diseases</i> , 2015, 15, 732-742.	0.6	19
360	Trans-oligomerization of duplicated aminoacyl-tRNA synthetases maintains genetic code fidelity under stress. <i>Nucleic Acids Research</i> , 2015, 43, gkv1020.	6.5	17
361	Structural Insight into How Bacteria Prevent Interference between Multiple Divergent Type IV Secretion Systems. <i>MBio</i> , 2015, 6, e01867-15.	1.8	33
362	Linked selection and recombination rate variation drive the evolution of the genomic landscape of differentiation across the speciation continuum of <i>Ficedula</i> flycatchers. <i>Genome Research</i> , 2015, 25, 1656-1665.	2.4	385
363	Unexpectedly Streamlined Mitochondrial Genome of the Euglenozoan <i>Euglena gracilis</i> . <i>Genome Biology and Evolution</i> , 2015, 7, 3358-3367.	1.1	57
364	A Genome-Scale Investigation of Incongruence in Culicidae Mosquitoes. <i>Genome Biology and Evolution</i> , 2015, 7, 3463-3471.	1.1	8
365	Analysis of mtDNA and nuclear markers points to homoploid hybrid origin of the new species of Far Eastern redfins of the genus <i>Tribolodon</i> (Pisces, Cyprinidae). <i>Russian Journal of Genetics</i> , 2015, 51, 1075-1087.	0.2	6
366	Integrating dynamic occupancy modeling and genetics to infer the status of the imperiled flattened musk turtle. <i>Biological Conservation</i> , 2015, 192, 294-303.	1.9	5
367	Whole-Genome Sequencing Confirms that <i>Burkholderia pseudomallei</i> Multilocus Sequence Types Common to Both Cambodia and Australia Are Due to Homoplasy. <i>Journal of Clinical Microbiology</i> , 2015, 53, 323-326.	1.8	44
368	Intrahost Dynamics of Antiviral Resistance in Influenza A Virus Reflect Complex Patterns of Segment Linkage, Reassortment, and Natural Selection. <i>MBio</i> , 2015, 6, .	1.8	58
369	Evolution and development of the adelphophagic, intracapsular Schmidt's larva of the nemertean <i>Lineus ruber</i> . <i>EvoDevo</i> , 2015, 6, 28.	1.3	32
370	Scale insect host ranges are broader in the tropics. <i>Biology Letters</i> , 2015, 11, 20150924.	1.0	19
371	Genome-Wide Architecture of Disease Resistance Genes in Lettuce. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 2655-2669.	0.8	54
372	Insights from the genome of <i>Ophiocordyceps polyrhachis-furcata</i> to pathogenicity and host specificity in insect fungi. <i>BMC Genomics</i> , 2015, 16, 881.	1.2	34
373	Molecular phylogenetics, morphology and a revised classification of the complex genus <i>Saxifraga</i> (Saxifragaceae). <i>Taxon</i> , 2015, 64, 1159-1187.	0.4	54
374	Genetic data support independent glacial refugia and open ocean barriers to dispersal for the Southern Ocean sea spider <i>Austropallene cornigera</i> (Märbius, 1902). <i>Journal of Crustacean Biology</i> , 2015, 35, 480-490.	0.3	49
375	Phylogenetic relationships among <i>Dorema</i> , <i>Ferula</i> and <i>Leutea</i> (Apiaceae: Scandiceae: Ferulinae) inferred from nrDNA ITS and cpDNA noncoding sequences. <i>Taxon</i> , 2015, 64, 770-783.	0.4	29

#	ARTICLE	IF	CITATIONS
376	A Time-Calibrated Road Map of Brassicaceae Species Radiation and Evolutionary History. <i>Plant Cell</i> , 2015, 27, tpc.15.00482.	3.1	200
377	Population Genomics of <i>Mycobacterium tuberculosis</i> in Ethiopia Contradicts the Virgin Soil Hypothesis for Human Tuberculosis in Sub-Saharan Africa. <i>Current Biology</i> , 2015, 25, 3260-3266.	1.8	94
378	Multiple glacial refugia lead to genetic structuring and the potential for reproductive isolation in a herbaceous plant. <i>American Journal of Botany</i> , 2015, 102, 1842-1853.	0.8	48
379	Evolutionary relationships of <i>Heimioporus</i> and <i>Boletellus</i> (Boletales), with an emphasis on Australian taxa including new species and new combinations in <i>Aureoboletus</i> , <i>Hemileccinum</i> and <i>Xerocomus</i> . <i>Australian Systematic Botany</i> , 2015, 28, 1.	0.3	32
380	Complete genome sequences of bacteriophages P12002L and P12002S, two lytic phages that infect a marine <i>Polaribacter</i> strain. <i>Standards in Genomic Sciences</i> , 2015, 10, 82.	1.5	25
381	Evolutionary History of <i>Blepharis</i> (Acanthaceae) and the Origin of C_4 Photosynthesis in Section <i>Acanthodium</i> . <i>International Journal of Plant Sciences</i> , 2015, 176, 770-790.	0.6	36
382	A coastal sand dune in New Zealand reveals high arbuscular mycorrhizal fungal diversity. <i>Symbiosis</i> , 2015, 66, 111-121.	1.2	14
383	Multiple origins and chromosomal novelty in the allotetraploid <i>Tragopogon castellanus</i> (Asteraceae). <i>New Phytologist</i> , 2015, 206, 1172-1183.	3.5	27
384	Biogeography of the smooth snake (<i>Coronella austriaca</i>): origin and conservation of the northernmost population. <i>Biological Journal of the Linnean Society</i> , 2015, 114, 426-435.	0.7	6
385	The identification of <i>oppA</i> gene homologues as part of the oligopeptide transport system in mycoplasmas. <i>Gene</i> , 2015, 558, 31-40.	1.0	9
386	Genomic sequences of six botulinum neurotoxin-producing strains representing three clostridial species illustrate the mobility and diversity of botulinum neurotoxin genes. <i>Infection, Genetics and Evolution</i> , 2015, 30, 102-113.	1.0	70
387	New <i>Wolbachia</i> supergroups detected in quill mites (Acari: Syringophilidae). <i>Infection, Genetics and Evolution</i> , 2015, 30, 140-146.	1.0	120
388	Diet strongly influences the gut microbiota of surgeonfishes. <i>Molecular Ecology</i> , 2015, 24, 656-672.	2.0	194
389	Taxonomic study of a new eustigmatophycean alga, <i>Vacuoliviride crystalliferum</i> gen. et sp. nov.. <i>Journal of Plant Research</i> , 2015, 128, 249-257.	1.2	22
390	Higher-level phylogeny of the Hymenoptera inferred from mitochondrial genomes. <i>Molecular Phylogenetics and Evolution</i> , 2015, 84, 34-43.	1.2	69
391	Analysis of a Local HIV-1 Epidemic in Portugal Highlights Established Transmission of Non-B and Non-G Subtypes. <i>Journal of Clinical Microbiology</i> , 2015, 53, 1506-1514.	1.8	26
392	Generic concepts in <i>Nectriaceae</i> . <i>Studies in Mycology</i> , 2015, 80, 189-245.	4.5	337
393	Molecular phylogenetics and species delimitation of leaf-toed geckos (Phyllodactylidae:). <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 6</i> 2015, 84, 254-265.	1.2	25

#	ARTICLE	IF	CITATIONS
394	A Complex Interplay of Tandem- and Whole-Genome Duplication Drives Expansion of the L-Type Lectin Receptor Kinase Gene Family in the Brassicaceae. <i>Genome Biology and Evolution</i> , 2015, 7, 720-734.	1.1	46
395	Operational criteria for cryptic species delimitation when evidence is limited, as exemplified by North American <i>Entomobrya</i> (Collembola: Entomobryidae). <i>Zoological Journal of the Linnean Society</i> , 2015, 173, 818-840.	1.0	34
396	Divergent Mitochondrial Respiratory Chains in Phototrophic Relatives of Apicomplexan Parasites. <i>Molecular Biology and Evolution</i> , 2015, 32, 1115-1131.	3.5	79
397	First phylogenetic analysis of the tribe Phyllotini (Rodentia: Sigmodontinae) combining morphological and molecular data. <i>Cladistics</i> , 2015, 31, 593-620.	1.5	15
398	Whole-genome sequencing reveals absence of recent gene flow and separate demographic histories for <i>Anopheles punctulatus</i> mosquitoes in Papua New Guinea. <i>Molecular Ecology</i> , 2015, 24, 1263-1274.	2.0	13
399	Botulinum neurotoxin homologs in non- <i>Clostridium</i> species. <i>FEBS Letters</i> , 2015, 589, 342-348.	1.3	85
400	Phylogeny and polyploidy: Resolving the classification of cyprinine fishes (Teleostei: Cypriniformes). <i>Molecular Phylogenetics and Evolution</i> , 2015, 85, 97-116.	1.2	218
401	Evolution of FOXRED1, an FAD-dependent oxidoreductase necessary for NADH:ubiquinone oxidoreductase (Complex I) assembly. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2015, 1847, 451-457.	0.5	16
402	Biogeography of Heterotrophic Flagellate Populations Indicates the Presence of Generalist and Specialist Taxa in the Arctic Ocean. <i>Applied and Environmental Microbiology</i> , 2015, 81, 2137-2148.	1.4	38
403	No Genome-Wide Protein Sequence Convergence for Echolocation. <i>Molecular Biology and Evolution</i> , 2015, 32, 1237-1241.	3.5	94
404	Multi-Threaded Hierarchical Clustering by Parallel Nearest-Neighbor Chaining. <i>IEEE Transactions on Parallel and Distributed Systems</i> , 2015, 26, 2534-2548.	4.0	13
405	Functional Evolution of Phosphatidylethanolamine Binding Proteins in Soybean and Arabidopsis. <i>Plant Cell</i> , 2015, 27, 323-336.	3.1	113
406	Mitochondrial genome plasticity among species of the nematode genus <i>Meloidogyne</i> (Nematoda: Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	1.0	18
407	<i>dev</i> is an Evolutionarily Young Negative Regulator of <i>Myxococcus xanthus</i> Development. <i>Journal of Bacteriology</i> , 2015, 197, 1249-1262.	1.0	28
408	Origin and Proliferation of Multiple-Drug Resistance in Bacterial Pathogens. <i>Microbiology and Molecular Biology Reviews</i> , 2015, 79, 101-116.	2.9	183
409	Novel basal, fungal lineages from freshwater phytoplankton and lake samples. <i>Environmental Microbiology Reports</i> , 2015, 7, 435-441.	1.0	72
410	Brazilian potato virus Y isolates identified as members of a new clade facilitate the reconstruction of evolutionary traits within this species. <i>Plant Pathology</i> , 2015, 64, 799-807.	1.2	9
411	A generation-time effect on the rate of molecular evolution in bacteria. <i>Evolution; International Journal of Organic Evolution</i> , 2015, 69, 643-652.	1.1	70

#	ARTICLE	IF	CITATIONS
412	Lateral Gene Transfer and Gene Duplication Played a Key Role in the Evolution of <i>Mastigamoeba balamuthi</i> Hydrogenosomes. <i>Molecular Biology and Evolution</i> , 2015, 32, 1039-1055.	3.5	63
413	Using More Than the Oldest Fossils: Dating Osmundaceae with Three Bayesian Clock Approaches. <i>Systematic Biology</i> , 2015, 64, 396-405.	2.7	56
414	Hedgehog Expression During Development and Regeneration in the Hemichordate, <i>Ptychodera flava</i> . <i>Zoological Science</i> , 2015, 32, 33-37.	0.3	13
415	Evolution of sexual traits influencing vectorial capacity in anopheline mosquitoes. <i>Science</i> , 2015, 347, 985-988.	6.0	68
416	Genome-Enabled Phylogeographic Investigation of the Quarantine Pathogen <i>Ralstonia solanacearum</i> Race 3 Biovar 2 and Screening for Sources of Resistance Against Its Core Effectors. <i>Phytopathology</i> , 2015, 105, 597-607.	1.1	51
417	Resolving Relationships within Valerianaceae (Dipsacales): New Insights and Hypotheses from Low-Copy Nuclear Regions. <i>Systematic Botany</i> , 2015, 40, 327-335.	0.2	11
418	Hybrid origins and the earliest stages of diploidization in the highly successful recent polyploid <i>Capsella bursa-pastoris</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 2806-2811.	3.3	128
419	Phylogenetic Analysis of <i>Aphaenogaster</i> Supports the Resurrection of <i>Novomessor</i> (Hymenoptera: Tj ETQq1 1 0.784314 rgBT / Overlock 1.3 19	1.3	19
420	Anti-MRSA-acting carbamidocyclophanes H ₂ L from the Vietnamese cyanobacterium <i>Nostoc</i> sp. CAVN2. <i>Journal of Antibiotics</i> , 2015, 68, 165-177.	1.0	31
421	Hippos stem from the longest sequence of terrestrial cetartiodactyl evolution in Africa. <i>Nature Communications</i> , 2015, 6, 6264.	5.8	42
422	Host specificity, pathogenicity, and mixed infections of trypanoplasms from freshwater fishes. <i>Parasitology Research</i> , 2015, 114, 1071-1078.	0.6	11
423	MitoPhAST, a new automated mitogenomic phylogeny tool in the post-genomic era with a case study of 89 decapod mitogenomes including eight new freshwater crayfish mitogenomes. <i>Molecular Phylogenetics and Evolution</i> , 2015, 85, 180-188.	1.2	71
424	A lycopene β -cyclase/lycopene β -cyclase/light harvesting complex fusion protein from the green alga <i>Ostreococcus lucimarinus</i> can be modified to produce β -carotene and β -carotene at different ratios. <i>Plant Journal</i> , 2015, 82, 582-595.	2.8	29
425	Improving recombinant Rubisco biogenesis, plant photosynthesis and growth by coexpressing its ancillary RAF1 chaperone. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 3564-3569.	3.3	105
426	Enhancing our understanding of anatomical diversity in <i>Tomentella</i> ectomycorrhizas: characterization of six new morphotypes. <i>Mycorrhiza</i> , 2015, 25, 419-429.	1.3	11
427	Ancient dynamin segments capture early stages of host mitochondrial integration. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 2800-2805.	3.3	41
428	Disentangling the complex evolutionary history of the Western Palearctic blue tits (<i>Cyanistes</i>) isolation. <i>Molecular Ecology</i> , 2015, 24, 2477-2494. Tj ETQq0 0 0 rgBT / Overlock 10 Tf 2.0 39	2.0	39
429	Sequencing of the mitochondrial genome of the avocado lace bug <i>Pseudacysta perseae</i> (Heteroptera,) Tj ETQq1 1 0.784314 rgBT / Overlock 0.1 18	0.1	18

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430	New insights into DNA barcoding of seagrasses. <i>Systematics and Biodiversity</i> , 2015, 13, 496-508.	0.5	27
431	Contribution to the Revision of the Genus <i>Sargassum</i> (Fucales, Phaeophyceae) in Madagascar Using Morphological and Molecular Data. <i>Cryptogamie, Algologie</i> , 2015, 36, 143-169.	0.3	9
432	ExaML version 3: a tool for phylogenomic analyses on supercomputers. <i>Bioinformatics</i> , 2015, 31, 2577-2579.	1.8	209
433	Phylogenetics of HIV-1 subtype G env: Greater complexity and older origins than previously reported. <i>Infection, Genetics and Evolution</i> , 2015, 35, 9-18.	1.0	6
434	16S rDNA analysis of archaea indicates dominance of <i>Methanobacterium</i> and high abundance of <i>Methanomassiliococcaceae</i> in rumen of Nili-Ravi buffalo. <i>Anaerobe</i> , 2015, 35, 3-10.	1.0	20
435	On the design of shared memory approaches to parallelize a multiobjective bee-inspired proposal for phylogenetic reconstruction. <i>Information Sciences</i> , 2015, 324, 163-185.	4.0	8
436	Uncultivated thermophiles: current status and spotlight on <i>Aigarchaeota</i> . <i>Current Opinion in Microbiology</i> , 2015, 25, 136-145.	2.3	70
437	Seagrass (<i>Zostera marina</i>) Colonization Promotes the Accumulation of Diazotrophic Bacteria and Alters the Relative Abundances of Specific Bacterial Lineages Involved in Benthic Carbon and Sulfur Cycling. <i>Applied and Environmental Microbiology</i> , 2015, 81, 6901-6914.	1.4	87
438	Insights into thermoadaptation and the evolution of mesophily from the bacterial phylum <i>Thermotogae</i> . <i>Canadian Journal of Microbiology</i> , 2015, 61, 655-670.	0.8	47
439	Articulating <i>Archiannelids</i> : Phylogenomics and Annelid Relationships, with Emphasis on Meiofaunal Taxa. <i>Molecular Biology and Evolution</i> , 2015, 32, 2860-2875.	3.5	128
440	FGF signaling repertoire of the indirect developing hemichordate <i>Ptychodera flava</i> . <i>Marine Genomics</i> , 2015, 24, 167-175.	0.4	6
441	Tracking Nosocomial <i>Klebsiella pneumoniae</i> Infections and Outbreaks by Whole-Genome Analysis: Small-Scale Italian Scenario within a Single Hospital. <i>Journal of Clinical Microbiology</i> , 2015, 53, 2861-2868.	1.8	71
442	Genetic profiles of <i>Propionibacterium acnes</i> and identification of a unique transposon with novel insertion sequences in sarcoid and non-sarcoid isolates. <i>Scientific Reports</i> , 2015, 5, 9832.	1.6	12
443	Exploring Tree-Like and Non-Tree-Like Patterns Using Genome Sequences: An Example Using the Inbreeding Plant Species <i>Arabidopsis thaliana</i> (L.) Heynh. <i>Systematic Biology</i> , 2015, 64, 809-823.	2.7	57
444	Genes with minimal phylogenetic information are problematic for coalescent analyses when gene tree estimation is biased. <i>Molecular Phylogenetics and Evolution</i> , 2015, 92, 63-71.	1.2	104
445	Gene fusion, fission, lateral transfer, and loss: Not-so-rare events in the evolution of eukaryotic ATP citrate lyase. <i>Molecular Phylogenetics and Evolution</i> , 2015, 91, 12-16.	1.2	13
446	Multilocus Species Trees Show the Recent Adaptive Radiation of the Mimetic <i>Heliconius</i> Butterflies. <i>Systematic Biology</i> , 2015, 64, 505-524.	2.7	204
447	The draft genome of <i>Mycobacterium aurum</i> , a potential model organism for investigating drugs against <i>Mycobacterium tuberculosis</i> and <i>Mycobacterium leprae</i> . <i>International Journal of Mycobacteriology</i> , 2015, 4, 207-216.	0.3	19

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448	Recurrence due to Relapse or Reinfection With <i>Mycobacterium tuberculosis</i> : A Whole-Genome Sequencing Approach in a Large, Population-Based Cohort With a High HIV Infection Prevalence and Active Follow-up. <i>Journal of Infectious Diseases</i> , 2015, 211, 1154-1163.	1.9	149
449	Marine sediments microbes capable of electrode oxidation as a surrogate for lithotrophic insoluble substrate metabolism. <i>Frontiers in Microbiology</i> , 2014, 5, 784.	1.5	86
450	Selection Maintains Low Genomic GC Content in Marine SAR11 Lineages. <i>Molecular Biology and Evolution</i> , 2015, 32, 2738-2748.	3.5	47
451	Examination of the Enterotoxigenic <i>Escherichia coli</i> Population Structure during Human Infection. <i>MBio</i> , 2015, 6, e00501.	1.8	39
452	Cancer, Warts, or Asymptomatic Infections: Clinical Presentation Matches Codon Usage Preferences in Human Papillomaviruses. <i>Genome Biology and Evolution</i> , 2015, 7, 2117-2135.	1.1	16
453	A phylogenomic and molecular markers based analysis of the phylum Chlamydiae: proposal to divide the class Chlamydia into two orders, Chlamydiales and Parachlamydiales ord. nov., and emended description of the class Chlamydia. <i>Antonie Van Leeuwenhoek</i> , 2015, 108, 765-781.	0.7	38
454	Long-Range HIV Genotyping Using Viral RNA and Proviral DNA for Analysis of HIV Drug Resistance and HIV Clustering. <i>Journal of Clinical Microbiology</i> , 2015, 53, 2581-2592.	1.8	24
455	<i>Bacillus stamsii</i> sp. nov., a facultatively anaerobic sugar degrader that is numerically dominant in freshwater lake sediment. <i>Systematic and Applied Microbiology</i> , 2015, 38, 379-389.	1.2	17
456	Genetic and molecular characterization of a locus involved in avirulence of <i>Blumeria graminis</i> f. sp. <i>tritici</i> on wheat Pm3 resistance alleles. <i>Fungal Genetics and Biology</i> , 2015, 82, 181-192.	0.9	50
457	Identification of common horsetail (<i>Equisetum arvense</i> L.; Equisetaceae) using Thin Layer Chromatography versus DNA barcoding. <i>Scientific Reports</i> , 2015, 5, 11942.	1.6	36
458	Resolving Evolutionary Relationships in Closely Related Species with Whole-Genome Sequencing Data. <i>Systematic Biology</i> , 2015, 64, 1000-1017.	2.7	102
459	Complete mitochondrial genomes and nuclear ribosomal RNA operons of two species of <i>Diplostomum</i> (Platyhelminthes: Trematoda): a molecular resource for taxonomy and molecular epidemiology of important fish pathogens. <i>Parasites and Vectors</i> , 2015, 8, 336.	1.0	56
461	Unusual biology across a group comprising more than 15% of domain Bacteria. <i>Nature</i> , 2015, 523, 208-211.	13.7	1,050
462	Origin and evolution of lysyl oxidases. <i>Scientific Reports</i> , 2015, 5, 10568.	1.6	86
463	Evolutionary analysis of the female-specific avian W chromosome. <i>Nature Communications</i> , 2015, 6, 7330.	5.8	121
464	Exploring the Limits for Reduction of Plastid Genomes: A Case Study of the Mycoheterotrophic Orchids <i>Epipogium aphyllum</i> and <i>Epipogium roseum</i> . <i>Genome Biology and Evolution</i> , 2015, 7, 1179-1191.	1.1	116
465	Inferring Cell Differentiation Processes Based on Phylogenetic Analysis of Genome-Wide Epigenetic Information: Hematopoiesis as a Model Case. <i>Genome Biology and Evolution</i> , 2015, 7, 699-705.	1.1	8
466	Insights on the Emergence of <i>Mycobacterium tuberculosis</i> from the Analysis of <i>Mycobacterium kansasii</i> . <i>Genome Biology and Evolution</i> , 2015, 7, 856-870.	1.1	79

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467	HAMAP in 2015: updates to the protein family classification and annotation system. <i>Nucleic Acids Research</i> , 2015, 43, D1064-D1070.	6.5	135
468	Whole-genome sequencing for prediction of <i>Mycobacterium tuberculosis</i> drug susceptibility and resistance: a retrospective cohort study. <i>Lancet Infectious Diseases</i> , The, 2015, 15, 1193-1202.	4.6	553
469	The use of evolutionary approaches to understand single cell genomes. <i>Frontiers in Microbiology</i> , 2015, 6, 174.	1.5	7
470	Toward monophyletic generic concepts in Magnaporthales: species with <i>Harpophora</i> asexual states. <i>Mycologia</i> , 2015, 107, 641-646.	0.8	23
471	Evolution of Spermophagus seed beetles (Coleoptera, Bruchinae, Amblycerini) indicates both synchronous and delayed colonizations of host plants. <i>Molecular Phylogenetics and Evolution</i> , 2015, 89, 91-103.	1.2	14
472	Phylogeny of <i>Rosa</i> sections <i>Chinenses</i> and <i>Synstylae</i> (Rosaceae) based on chloroplast and nuclear markers. <i>Molecular Phylogenetics and Evolution</i> , 2015, 87, 50-64.	1.2	42
473	Comparative Genomics Reveals the Origins and Diversity of Arthropod Immune Systems. <i>Molecular Biology and Evolution</i> , 2015, 32, 2111-2129.	3.5	136
474	An ancestral bacterial division system is widespread in eukaryotic mitochondria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 10239-10246.	3.3	70
475	Positive and purifying selection in mitochondrial genomes of a bird with mitonuclear discordance. <i>Molecular Ecology</i> , 2015, 24, 2820-2837.	2.0	112
476	<i>Chlamydia psittaci</i> comparative genomics reveals intraspecies variations in the putative outer membrane and type III secretion system genes. <i>Microbiology (United Kingdom)</i> , 2015, 161, 1378-1391.	0.7	24
477	Apparent similarity, underlying homoplasy: Morphology and molecular phylogeny of the North American clade of <i>Manihot</i> . <i>American Journal of Botany</i> , 2015, 102, 520-532.	0.8	5
478	Reconstruction of Cyclooxygenase Evolution in Animals Suggests Variable, Lineage-Specific Duplications, and Homologs with Low Sequence Identity. <i>Journal of Molecular Evolution</i> , 2015, 80, 193-208.	0.8	7
479	Two tribes hidden in one genus: the case of <i>Agaedioxenis</i> Villeneuve (Diptera: Tachinidae: Exoristinae). <i>Organisms Diversity and Evolution</i> , 2015, 15, 489-512.	0.7	5
480	First record of a wilt disease of banana plants associated with phytoplasmas in Solomon Islands. <i>Australasian Plant Disease Notes</i> , 2015, 10, 1.	0.4	10
481	Genomic diversity of <i>Oenococcus oeni</i> populations from Castilla La Mancha and La Rioja Tempranillo red wines. <i>Food Microbiology</i> , 2015, 49, 82-94.	2.1	12
482	<i>Cortinarius nolaneiformis</i> , a vernal species new to Britain. <i>Field Mycology</i> , 2015, 16, 45-48.	0.0	0
483	Automatic selection of partitioning schemes for phylogenetic analyses using iterative k-means clustering of site rates. <i>BMC Evolutionary Biology</i> , 2015, 15, 13.	3.2	95
484	Evolutionary history and leaf succulence as explanations for medicinal use in aloes and the global popularity of <i>Aloe vera</i> . <i>BMC Evolutionary Biology</i> , 2015, 15, 29.	3.2	79

#	ARTICLE	IF	CITATIONS
485	Outbreak with clonally related isolates of <i>Corynebacterium ulcerans</i> in a group of water rats. <i>BMC Microbiology</i> , 2015, 15, 42.	1.3	17
486	An ontology approach to comparative phenomics in plants. <i>Plant Methods</i> , 2015, 11, 10.	1.9	53
487	Molecular phylogeny of Neotropical monogeneans (Platyhelminthes: Monogenea) from catfishes (Siluriformes). <i>Parasites and Vectors</i> , 2015, 8, 164.	1.0	70
488	Structural and evolutionary divergence of cyclic nucleotide binding domains in eukaryotic pathogens: Implications for drug design. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2015, 1854, 1575-1585.	1.1	15
489	A Transcriptomic-Phylogenomic Analysis of the Evolutionary Relationships of Flatworms. <i>Current Biology</i> , 2015, 25, 1347-1353.	1.8	160
490	Octocoral Mitochondrial Genomes Provide Insights into the Phylogenetic History of Gene Order Rearrangements, Order Reversals, and Cnidarian Phylogenetics. <i>Genome Biology and Evolution</i> , 2015, 7, 391-409.	1.1	60
491	Speciation dynamics during the global radiation of extant bats. <i>Evolution; International Journal of Organic Evolution</i> , 2015, 69, 1528-1545.	1.1	257
492	Inter- and intra-domain horizontal gene transfer, gain-loss asymmetry and positive selection mark the evolutionary history of the <i>CBM14</i> family. <i>FEBS Journal</i> , 2015, 282, 2014-2028.	2.2	13
493	Long non-coding RNA discovery across the genus <i>Anopheles</i> reveals conserved secondary structures within and beyond the Gambiae complex. <i>BMC Genomics</i> , 2015, 16, 337.	1.2	85
494	Relationship between protein thermodynamic constraints and variation of evolutionary rates among sites. <i>Physical Biology</i> , 2015, 12, 025002.	0.8	49
495	Minimally destructive sampling of type specimens of <i>Pyropia</i> (Bangiales, Rhodophyta) recovers complete plastid and mitochondrial genomes. <i>Scientific Reports</i> , 2014, 4, 5113.	1.6	53
496	<i>Acaulospora ignota</i> and <i>Claroideoglossum hanlinii</i> , two new species of arbuscular mycorrhizal fungi (Glomeromycota) from Brazil and Cuba. <i>Mycological Progress</i> , 2015, 14, 1.	0.5	16
497	Diversity of Viruses Infecting the Green Microalga <i>Ostreococcus lucimarinus</i> . <i>Journal of Virology</i> , 2015, 89, 5812-5821.	1.5	35
498	Amphibians crossing the Bering Land Bridge: Evidence from holarctic treefrogs (<i>Hyla</i> , Hylidae, Anura). <i>Molecular Phylogenetics and Evolution</i> , 2015, 87, 80-90.	1.2	49
499	Complex histories of repeated gene flow in Cameroon crater lake cichlids cast doubt on one of the clearest examples of sympatric speciation. <i>Evolution; International Journal of Organic Evolution</i> , 2015, 69, 1406-1422.	1.1	122
500	Phylogenetic Molecular Species Delimitations Unravel Potential New Species in the Pest Genus <i>Spodoptera</i> Guenée, 1852 (Lepidoptera, Noctuidae). <i>PLoS ONE</i> , 2015, 10, e0122407.	1.1	67
501	Rapid diversification associated with ecological specialization in Neotropical <i>Adelpha</i> butterflies. <i>Molecular Ecology</i> , 2015, 24, 2392-2405.	2.0	73
502	Endosymbiosis undone by stepwise elimination of the plastid in a parasitic dinoflagellate. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 5767-5772.	3.3	88

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503	DNA replication fidelity in <i>Mycobacterium tuberculosis</i> is mediated by an ancestral prokaryotic proofreader. <i>Nature Genetics</i> , 2015, 47, 677-681.	9.4	63
504	<i>Pellucidodinium psammophilum</i> gen. & sp. nov. and <i>Nusuttodinium desymbiontum</i> sp. nov. (Dinophyceae), two novel heterotrophs closely related to kleptochloroplastidic dinoflagellates. <i>Phycologia</i> , 2015, 54, 192-209.	0.6	13
505	Global Multilocus Sequence Type Analysis of <i>Chlamydia trachomatis</i> Strains from 16 Countries. <i>Journal of Clinical Microbiology</i> , 2015, 53, 2172-2179.	1.8	46
506	Adaptive mutation related to cellulose producibility in <i>Komagataeibacter medellinensis</i> (<i>Gluconacetobacter xylinus</i>) NBRC 3288. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 7229-7240.	1.7	54
507	Ecological Overlap and Horizontal Gene Transfer in <i>Staphylococcus aureus</i> and <i>Staphylococcus epidermidis</i> . <i>Genome Biology and Evolution</i> , 2015, 7, 1313-1328.	1.1	130
508	A co-evolutionary relationship exists between <i>Endoraecium</i> (& <i>Pucciniales</i>) and its <i>Acacia</i> hosts in Australia. <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2015, 35, 50-62.	1.6	31
509	Unique repeat and plasmid sequences in the mitochondrial genome of <i>Gracilaria chilensis</i> (<i>Gracilariales</i> , <i>Rhodophyta</i>). <i>Phycologia</i> , 2015, 54, 20-23.	0.6	13
510	The phylogenetic position of poroid <i>Hymenochaetaceae</i> (<i>Hymenochaetales</i> , <i>Basidiomycota</i>) from Patagonia, Argentina. <i>Mycologia</i> , 2015, 107, 754-767.	0.8	21
511	Complex archaea that bridge the gap between prokaryotes and eukaryotes. <i>Nature</i> , 2015, 521, 173-179.	13.7	995
512	Error, signal, and the placement of <i>Ctenophora</i> sister to all other animals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 5773-5778.	3.3	279
513	Genomic tests of the species-pump hypothesis: Recent island connectivity cycles drive population divergence but not speciation in Caribbean crickets across the Virgin Islands. <i>Evolution; International Journal of Organic Evolution</i> , 2015, 69, 1501-1517.	1.1	88
514	Ancient proteins resolve the evolutionary history of Darwin's South American ungulates. <i>Nature</i> , 2015, 522, 81-84.	13.7	273
515	Planktonic eukaryote molecular diversity: discrimination of minerotrophic and ombrotrophic peatland pools in Tierra del Fuego (Argentina). <i>Journal of Plankton Research</i> , 2015, 37, 645-655.	0.8	19
516	Evolutionary dynamics of a common sub-Antarctic octocoral family. <i>Molecular Phylogenetics and Evolution</i> , 2015, 84, 185-204.	1.2	23
517	Intercontinental long-distance dispersal of <i>Canellaceae</i> from the New to the Old World revealed by a nuclear single copy gene and chloroplast loci. <i>Molecular Phylogenetics and Evolution</i> , 2015, 84, 205-219.	1.2	29
518	An improved taxonomic sampling is a necessary but not sufficient condition for resolving inter-families relationships in Caridean decapods. <i>Genetica</i> , 2015, 143, 195-205.	0.5	45
519	The nervous system of <i>Xenacoelomorpha</i> : a genomic perspective. <i>Journal of Experimental Biology</i> , 2015, 218, 618-628.	0.8	36
520	Out of the Water: Origin and Diversification of the LBD Gene Family. <i>Molecular Biology and Evolution</i> , 2015, 32, 1996-2000.	3.5	33

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521	Origins and Evolutionary Dynamics of H3N2 Canine Influenza Virus. <i>Journal of Virology</i> , 2015, 89, 5406-5418.	1.5	65
522	16S rRNA gene high-throughput sequencing data mining of microbial diversity and interactions. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 4119-4129.	1.7	79
523	Trans-Pacific RAD-Seq population genomics confirms introgressive hybridization in Eastern Pacific Pocillopora corals. <i>Molecular Phylogenetics and Evolution</i> , 2015, 88, 154-162.	1.2	77
524	Multiplexed amplicon genotyping data resolve phylogeny within a very recently derived insular lineage. <i>American Journal of Botany</i> , 2015, 102, 634-641.	0.8	37
525	Skipper genome sheds light on unique phenotypic traits and phylogeny. <i>BMC Genomics</i> , 2015, 16, 639.	1.2	38
526	A Multilocus Molecular Phylogeny for <i>Chaetostoma</i> Clade Genera and Species with a Review of <i>Chaetostoma</i> (Siluriformes: Loricariidae) from the Central Andes. <i>Copeia</i> , 2015, 103, 664-701.	1.4	22
527	Characterization of multiple isolates from an <i>Alexandrium ostenfeldii</i> bloom in The Netherlands. <i>Harmful Algae</i> , 2015, 49, 94-104.	2.2	59
528	Functionally Structured Genomes in <i>Lactobacillus kunkeei</i> Colonizing the Honey Crop and Food Products of Honeybees and Stingless Bees. <i>Genome Biology and Evolution</i> , 2015, 7, 1455-1473.	1.1	50
529	Shared <i>Escovopsis</i> parasites between leaf-cutting and non-leaf-cutting ants in the higher attine fungus-growing ant symbiosis. <i>Royal Society Open Science</i> , 2015, 2, 150257.	1.1	23
530	POTION: an end-to-end pipeline for positive Darwinian selection detection in genome-scale data through phylogenetic comparison of protein-coding genes. <i>BMC Genomics</i> , 2015, 16, 567.	1.2	44
531	The <i>Lingula</i> genome provides insights into brachiopod evolution and the origin of phosphate biomineralization. <i>Nature Communications</i> , 2015, 6, 8301.	5.8	159
532	Positive Selection Underlies Faster-Z Evolution of Gene Expression in Birds. <i>Molecular Biology and Evolution</i> , 2015, 32, 2646-2656.	3.5	52
533	Whole Genome Sequencing of the Asian Arowana (<i>Scleropages formosus</i>) Provides Insights into the Evolution of Ray-Finned Fishes. <i>Genome Biology and Evolution</i> , 2015, 7, 2885-2895.	1.1	43
534	Resolving basal lamiid phylogeny and the circumscription of Icacinaceae with a plastome-scale data set. <i>American Journal of Botany</i> , 2015, 102, 1794-1813.	0.8	95
535	Evolution of the Sandpaper Clade (Miconieae, Melastomataceae). <i>International Journal of Plant Sciences</i> , 2015, 176, 607-626.	0.6	25
536	Comparison against 186 canid whole-genome sequences reveals survival strategies of an ancient clonally transmissible canine tumor. <i>Genome Research</i> , 2015, 25, 1646-1655.	2.4	63
537	<i>Uromykladium acaciae</i> , the cause of a sudden, severe disease epidemic on <i>Acacia mearnsii</i> in South Africa. <i>Australasian Plant Pathology</i> , 2015, 44, 637-645.	0.5	24
538	Analysis of phylogenomic datasets reveals conflict, concordance, and gene duplications with examples from animals and plants. <i>BMC Evolutionary Biology</i> , 2015, 15, 150.	3.2	350

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539	<i>Umbelopsis longicollis</i> comb. nov. and the synonymy of <i>U. roseonana</i> and <i>U. versiformis</i> with <i>U. nana</i>. Mycologia, 2015, 107, 1023-1032.	0.8	7
540	Two contemporaneous mitogenomes from terminal Pleistocene burials in eastern Beringia. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 13833-13838.	3.3	56
541	Utility of Whole-Genome Sequencing of Escherichia coli O157 for Outbreak Detection and Epidemiological Surveillance. Journal of Clinical Microbiology, 2015, 53, 3565-3573.	1.8	70
542	Early Divergent Strains of Yersinia pestis in Eurasia 5,000 Years Ago. Cell, 2015, 163, 571-582.	13.5	425
543	Methane metabolism in the archaeal phylum Bathyarchaeota revealed by genome-centric metagenomics. Science, 2015, 350, 434-438.	6.0	677
544	Origin and evolution of Petrocosmea (Gesneriaceae) inferred from both DNA sequence and novel findings in morphology with a test of morphology-based hypotheses. BMC Plant Biology, 2015, 15, 167.	1.6	18
545	Using the taxon-specific genes for the taxonomic classification of bacterial genomes. BMC Genomics, 2015, 16, 396.	1.2	15
546	Exploring the utility of cross-laboratory RAD-sequencing datasets for phylogenetic analysis. BMC Research Notes, 2015, 8, 299.	0.6	29
547	Generalised Implementation for Fixed-Length Approximate String Matching under Hamming Distance and Applications. , 2015, , .		4
548	High levels of interspecific gene flow in an endemic cichlid fish adaptive radiation from an extreme lake environment. Molecular Ecology, 2015, 24, 3421-3440.	2.0	53
549	<i>Philyrophyllum</i> (Asteraceae) transferred from Gnaphalieae to Athroismeae based on phylogenetic analysis of nuclear and plastid DNA sequence data. Taxon, 2015, 64, 975-986.	0.4	6
550	Phylogenetics of H1N1/2009 influenza reveals the transition from host adaptation to immune-driven selection. Nature Communications, 2015, 6, 7952.	5.8	107
551	Genomic Epidemiology of a Protracted Hospital Outbreak Caused by a Toxin A-Negative Clostridium difficile Sublineage PCR Ribotype 017 Strain in London, England. Journal of Clinical Microbiology, 2015, 53, 3141-3147.	1.8	46
552	Anaerobic biosynthesis of the lower ligand of vitamin B ₁₂. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 10792-10797.	3.3	91
553	Host abundance, durability, basidiome form and phylogenetic isolation determine fungivore species richness. Biological Journal of the Linnean Society, 2015, 114, 699-708.	0.7	20
554	A functionally critical single nucleotide polymorphism in the gene encoding the membrane-bound alcohol dehydrogenase found in ethanol oxidation-deficient Gluconobacter thailandicus. Gene, 2015, 567, 201-207.	1.0	2
555	Diversity of <i>Rhodopirellula</i> and related planctomycetes in a North Sea coastal sediment employing <i>carB</i> as molecular marker. FEMS Microbiology Letters, 2015, 362, fnv127.	0.7	7
556	Molecular Evidence for Convergence and Parallelism in Evolution of Complex Brains of Cephalopod Molluscs: Insights from Visual Systems. Integrative and Comparative Biology, 2015, 55, 1070-1083.	0.9	54

#	ARTICLE	IF	CITATIONS
557	The Status of <i>Heligmosomoides americanus</i> , Representative of an American Clade of Vole-Infecting Nematodes. <i>Journal of Parasitology</i> , 2015, 101, 382-385.	0.3	6
558	A Skull Might Lie: Modeling Ancestral Ranges and Diet from Genes and Shape of Tree Squirrels. <i>Systematic Biology</i> , 2015, 64, 1074-1088.	2.7	23
559	Sustained Software for Cyberinfrastructure. , 2015, , .		3
560	The Dynamics of Genetic Interactions between <i>Vibrio metoecus</i> and <i>Vibrio cholerae</i> , Two Close Relatives Co-Occurring in the Environment. <i>Genome Biology and Evolution</i> , 2015, 7, 2941-2954.	1.1	33
561	Intercontinental distributions of species of <i>Cortinarius</i> , subgenus <i>Phlegmacium</i> , associated with <i>Populus</i> in western North America. <i>Botany</i> , 2015, 93, 711-721.	0.5	7
562	Localization and Evolution of Putative Triose Phosphate Translocators in the Diatom <i>Phaeodactylum tricornutum</i> . <i>Genome Biology and Evolution</i> , 2015, 7, 2955-2969.	1.1	53
563	Multiple Avirulence Loci and Allele-Specific Effector Recognition Control the <i>Pm3</i> Race-Specific Resistance of Wheat to Powdery Mildew. <i>Plant Cell</i> , 2015, 27, tpc.15.00171.	3.1	135
564	Molecular phylogeny of Squaliformes and first occurrence of bioluminescence in sharks. <i>BMC Evolutionary Biology</i> , 2015, 15, 162.	3.2	48
565	Complete chloroplast genome sequence of MD-2 pineapple and its comparative analysis among nine other plants from the subclass Commelinidae. <i>BMC Plant Biology</i> , 2015, 15, 196.	1.6	65
566	Diversification of the ant odorant receptor gene family and positive selection on candidate cuticular hydrocarbon receptors. <i>BMC Research Notes</i> , 2015, 8, 380.	0.6	58
567	A comprehensive phylogeny of birds (Aves) using targeted next-generation DNA sequencing. <i>Nature</i> , 2015, 526, 569-573.	13.7	1,341
568	Expanding the biotechnology potential of lactobacilli through comparative genomics of 213 strains and associated genera. <i>Nature Communications</i> , 2015, 6, 8322.	5.8	488
569	Dating Tips for Divergence-Time Estimation. <i>Trends in Genetics</i> , 2015, 31, 637-650.	2.9	126
570	Comparative mitogenomic analysis of the superfamily Pentatomoidea (Insecta: Hemiptera: Heteroptera) and phylogenetic implications. <i>BMC Genomics</i> , 2015, 16, 460.	1.2	97
571	Phylogeny and speciation in <i>Saxifraga</i> sect. <i>Ciliatae</i> (Saxifragaceae): Evidence from <i>psbA</i> , <i>trnH</i> and ITS sequences. <i>Taxon</i> , 2015, 64, 703-713.	0.4	25
572	MatrixConverter: Facilitating construction of phenomic character matrices. <i>Applications in Plant Sciences</i> , 2015, 3, 1400088.	0.8	6
573	Species diversity in the <i>Antrodia crassa</i> group (Polyporales, Basidiomycota). <i>Fungal Biology</i> , 2015, 119, 1291-1310.	1.1	25
574	Taxonomic Clarification of the Unusual Dinophyte <i>Gymnodinium limneticum</i> W oÅ,osz . (<i>Gymnodiniaceae</i>) from the Tatra Mountains. <i>Protist</i> , 2015, 166, 621-637.	0.6	23

#	ARTICLE	IF	CITATIONS
575	A new cryptic species in a new cryptic genus in the <i>Caesalpinia</i> group (Leguminosae) from the seasonally dry inter-Andean valleys of South America. <i>Taxon</i> , 2015, 64, 468-490.	0.4	27
576	The genus <i>Hebeloma</i> in the alpine belt of the Carpathians including two new species. <i>Mycologia</i> , 2015, 107, 1285-1303.	0.8	14
577	Phylogeny and classification of the East Asian <i>Amitostigma</i> alliance (Orchidaceae: Orchideae) based on six DNA markers. <i>BMC Evolutionary Biology</i> , 2015, 15, 96.	3.2	24
578	Multilevel Task Parallelism Exploitation on Asymmetric Sets of Tasks and When Using Third-Party Tools. , 2015, , .		3
579	<i>Cortinarius koldingensis</i> a new species of <i>Cortinarius</i> , subgenus <i>Phlegmacium</i> related to <i>Cortinarius sulfurinus</i> . <i>Mycological Progress</i> , 2015, 14, 1.	0.5	5
580	Buying in to bioinformatics: an introduction to commercial sequence analysis software. <i>Briefings in Bioinformatics</i> , 2015, 16, 700-709.	3.2	36
581	Ebolavirus is evolving but not changing: No evidence for functional change in EBOV from 1976 to the 2014 outbreak. <i>Virology</i> , 2015, 482, 202-207.	1.1	31
582	A RAD-based phylogenetics for <i>Orestias</i> fishes from Lake Titicaca. <i>Molecular Phylogenetics and Evolution</i> , 2015, 93, 307-317.	1.2	23
583	Acetogenesis from H ₂ plus CO ₂ and nitrogen fixation by an endosymbiotic spirochete of a termite-gut cellulolytic protist. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 10224-10230.	3.3	108
584	Comparative Genomics of a Bacterivorous Green Alga Reveals Evolutionary Causalities and Consequences of Phago-Mixotrophic Mode of Nutrition. <i>Genome Biology and Evolution</i> , 2015, 7, 3047-3061.	1.1	36
585	Short Tree, Long Tree, Right Tree, Wrong Tree: New Acquisition Bias Corrections for Inferring SNP Phylogenies. <i>Systematic Biology</i> , 2015, 64, 1032-1047.	2.7	286
586	Chemoreceptor Evolution in Hymenoptera and Its Implications for the Evolution of Eusociality. <i>Genome Biology and Evolution</i> , 2015, 7, 2407-2416.	1.1	141
587	Phyldynamic Inference with Kernel ABC and Its Application to HIV Epidemiology. <i>Molecular Biology and Evolution</i> , 2015, 32, 2483-2495.	3.5	37
588	Rooting the tree of life: the phylogenetic jury is still out. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20140329.	1.8	77
589	Whole-Genome Sequencing Identifies Emergence of a Quinolone Resistance Mutation in a Case of <i>Stenotrophomonas maltophilia</i> Bacteremia. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 7117-7120.	1.4	24
590	Towards a comprehensive picture of alloacceptor tRNA remodeling in metazoan mitochondrial genomes. <i>Nucleic Acids Research</i> , 2015, 43, 8044-8056.	6.5	22
591	Stepwise evolution of corolla symmetry in <i>CYCLOIDEA2</i> -like and <i>RADIALIS</i> -like gene expression patterns in Lamiales. <i>American Journal of Botany</i> , 2015, 102, 1260-1267.	0.8	24
592	Independent Co-Option of a Tailed Bacteriophage into a Killing Complex in <i>Pseudomonas</i> . <i>MBio</i> , 2015, 6, e00452.	1.8	66

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593	Molecular Phylogenetics of <i>Ficus</i> Section <i>Pharmacosycea</i> and the Description of <i>Ficus</i> Subsection <i>Carautaea</i> (Moraceae). <i>Systematic Botany</i> , 2015, 40, 504-509.	0.2	11
594	Phylogenomics of Horned Lizards (Genus: <i>Phrynosoma</i>) Using Targeted Sequence Capture Data. <i>Copeia</i> , 2015, 103, 586-594.	1.4	22
595	Orchid phylogenomics and multiple drivers of their extraordinary diversification. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2015, 282, 20151553.	1.2	361
596	Five new <i>Pseudophialophora</i> species from grass roots in the oligotrophic pine barrens ecosystem. <i>Fungal Biology</i> , 2015, 119, 1205-1215.	1.1	19
597	No release for the wicked: enemy release is dynamic and not associated with invasiveness. <i>Ecology</i> , 2015, 96, 2446-2457.	1.5	63
598	An integrative approach to understanding the evolution and diversity of <i>Copiapoa</i> (Cactaceae), a threatened endemic Chilean genus from the Atacama Desert. <i>American Journal of Botany</i> , 2015, 102, 1506-1520.	0.8	29
599	Origin and Possible Genetic Recombination of the Middle East Respiratory Syndrome Coronavirus from the First Imported Case in China: Phylogenetics and Coalescence Analysis. <i>MBio</i> , 2015, 6, e01280-15.	1.8	86
600	Taxonomy and molecular phylogeny of two novel ciliates, with establishment of a new genus, <i>Pseudogastrostyla</i> n. g. (Ciliophora, Hypotrichia, Oxytrichidae). <i>European Journal of Protistology</i> , 2015, 51, 374-385.	0.5	21
601	A novel method of consensus pan-chromosome assembly and large-scale comparative analysis reveal the highly flexible pan-genome of <i>Acinetobacter baumannii</i> . <i>Genome Biology</i> , 2015, 16, 143.	13.9	122
602	The phylogenetic analysis of fungi associated with lichenized ascomycete genus <i>Bryoria</i> reveals new lineages in the Tremellales including a new species <i>Tremella huuskonenii</i> hyperparasitic on <i>Phacopsis huuskonenii</i> . <i>Fungal Biology</i> , 2015, 119, 844-856.	1.1	20
603	Phylogeny and photosynthesis of the grass tribe Paniceae. <i>American Journal of Botany</i> , 2015, 102, 1493-1505.	0.8	58
604	Gene expression during zombie ant biting behavior reflects the complexity underlying fungal parasitic behavioral manipulation. <i>BMC Genomics</i> , 2015, 16, 620.	1.2	107
605	Early genome duplications in conifers and other seed plants. <i>Science Advances</i> , 2015, 1, e1501084.	4.7	236
606	Genomic data do not support comb jellies as the sister group to all other animals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 15402-15407.	3.3	286
607	Macroevolutionary assembly of ant/plant symbioses: <i>Pseudomyrmex</i> ants and their ant-housing plants in the Neotropics. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2015, 282, 20152200.	1.2	51
608	Natural history and systematic position of <i>Rhetus belphegor</i> (n. comb.) (Lepidoptera: Riodinidae), an endangered butterfly with narrow distribution in Southeast Brazil. <i>Journal of Insect Conservation</i> , 2015, 19, 1141-1151.	0.8	12
609	The African buffalo parasite <i>Theileria</i> sp. (buffalo) can infect and immortalize cattle leukocytes and encodes divergent orthologues of <i>Theileria parva</i> antigen genes. <i>International Journal for Parasitology: Parasites and Wildlife</i> , 2015, 4, 333-342.	0.6	32
610	Primary structure of 28S rRNA gene confirms monophyly of free-living heterotrophic and phototrophic apicomplexans (Alveolata). <i>Biochemistry (Moscow)</i> , 2015, 80, 1492-1499.	0.7	1

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611	Three new arbuscular mycorrhizal <i>Diversispora</i> species in Glomeromycota. <i>Mycological Progress</i> , 2015, 14, 1.	0.5	12
612	Phylogeny of section <i>Leuce</i> (<i>Populus</i> , <i>Salicaceae</i>) inferred from 34 chloroplast DNA fragments. <i>Biochemical Systematics and Ecology</i> , 2015, 63, 212-217.	0.6	6
613	Molecular analysis of the fungal microbiome associated with the olive fruit fly <i>Bactrocera oleae</i> . <i>Fungal Ecology</i> , 2015, 18, 67-74.	0.7	20
614	Identification of a new order of root-colonising fungi in the Entorrhizomycota: <i>Talbotiomycetales</i> ord. nov. on eudicotyledons. <i>IMA Fungus</i> , 2015, 6, 129-133.	1.7	14
615	Molecular phylogeny of four homeobox genes from the purple sea star <i>Pisaster ochraceus</i> . <i>Development Genes and Evolution</i> , 2015, 225, 359-365.	0.4	1
616	Complete nitrification by <i>Nitrospira</i> bacteria. <i>Nature</i> , 2015, 528, 504-509.	13.7	1,878
617	Two new genera, <i>Dominikia</i> and <i>Kamienskia</i> , and <i>D. disticha</i> sp. nov. in Glomeromycota. <i>Nova Hedwigia</i> , 2015, 100, 225-238.	0.2	49
618	Invasion of the Orange Ping-Pong Bats: the rapidly changing distribution of <i>Favolaschia calocera</i> . <i>Field Mycology</i> , 2015, 16, 113-120.	0.0	4
619	Whole genome sequencing identifies circulating Beijing-lineage <i>Mycobacterium tuberculosis</i> strains in Guatemala and an associated urban outbreak. <i>Tuberculosis</i> , 2015, 95, 810-816.	0.8	16
620	Whole genome sequence analysis of <i>Mycobacterium suricattae</i> . <i>Tuberculosis</i> , 2015, 95, 682-688.	0.8	52
621	Evolutionary origin of a streamlined marine bacterioplankton lineage. <i>ISME Journal</i> , 2015, 9, 1423-1433.	4.4	32
622	A new and critically endangered species and genus of Onychophora (<i>Peripatidae</i>) from the Brazilian savannah – a vulnerable biodiversity hotspot. <i>Systematics and Biodiversity</i> , 2015, 13, 211-233.	0.5	12
623	High-stakes species delimitation in eyeless cave spiders (<i>Cicurina</i> , <i>Dictynidae</i> , <i>Araneae</i>) from central Texas. <i>Molecular Ecology</i> , 2015, 24, 346-361.	2.0	62
624	Three Novel Virophage Genomes Discovered from Yellowstone Lake Metagenomes. <i>Journal of Virology</i> , 2015, 89, 1278-1285.	1.5	76
625	Coalescent Methods Are Robust to the Simultaneous Effects of Long Branches and Incomplete Lineage Sorting. <i>Molecular Biology and Evolution</i> , 2015, 32, 791-805.	3.5	69
626	Spore-based study of arbuscular mycorrhizal fungi of semiarid sandy areas in Hungary, with <i>Diversispora jakucsiae</i> sp. nov.. <i>Mycological Progress</i> , 2015, 14, 1.	0.5	34
627	Extensive introgression in a malaria vector species complex revealed by phylogenomics. <i>Science</i> , 2015, 347, 1258-1264.	6.0	527
628	Mechanisms of Cl^- uptake in rainbow trout: Cloning and expression of <i>slc26a6</i> , a prospective $\text{Cl}^-/\text{HCO}_3^-$ exchanger. <i>Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology</i> , 2015, 180, 43-50.	0.8	34

#	ARTICLE	IF	CITATIONS
629	Glomus tetrastratosum, a new species of arbuscular mycorrhizal fungi (Glomeromycota). Mycoscience, 2015, 56, 280-286.	0.3	14
630	The evolution of eukaryotic cells from the perspective of peroxisomes. BioEssays, 2015, 37, 195-203.	1.2	47
631	Genomic Epidemiology of Klebsiella pneumoniae in Italy and Novel Insights into the Origin and Global Evolution of Its Resistance to Carbapenem Antibiotics. Antimicrobial Agents and Chemotherapy, 2015, 59, 389-396.	1.4	97
632	Highly evolvable malaria vectors: The genomes of 16 <i>Anopheles</i> mosquitoes. Science, 2015, 347, 1258-1262.	6.0	492
633	Initial Phylogenetic Relatedness of Saprotrophic Fungal Communities Affects Subsequent Litter Decomposition Rates. Microbial Ecology, 2015, 69, 748-757.	1.4	13
634	Assessing the global phylum level diversity within the bacterial domain: A review. Journal of Advanced Research, 2015, 6, 269-282.	4.4	57
635	Ecological Transition Predictably Associated with Gene Degeneration. Molecular Biology and Evolution, 2015, 32, 347-354.	3.5	53
636	The origins and radiation of Australian Coptotermes termites: From rainforest to desert dwellers. Molecular Phylogenetics and Evolution, 2015, 82, 234-244.	1.2	25
637	Insights into the metabolism, lifestyle and putative evolutionary history of the novel archaeal phylum "Diapherotrites"™. ISME Journal, 2015, 9, 447-460.	4.4	89
638	Seeing the wood for the trees: philosophical aspects of classical, Bayesian and likelihood approaches in statistical inference and some implications for phylogenetic analysis. Biology and Philosophy, 2015, 30, 505-525.	0.7	6
639	Polypore Genera <i>Antella</i> , <i>Austeria</i> , <i>Butyrea</i> , <i>Citripora</i> , <i>Metuloidea</i> and <i>Trulla</i> (Steccherinaceae, Tj ETQq0 0 0	0.1	7
640	Evidence for the validity of Protatlanta sculpta (Gastropoda: Pterotracheoidea). Contributions To Zoology, 2016, 85, 423-435.	0.2	6
641	Evidence of extensive positive selection acting on cherry (Prunus avium L.) resistance gene analogs (RGAs). Australian Journal of Crop Science, 2016, 10, 1324-1329.	0.1	7
642	First Record of <i>Poecilobdella nanjingensis</i> (Hirudinida: Arhynchobdellida). Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 187 Td (2016, 21, 127-134.	0.1	8
643	Systematic review of the Cinnamon-throated Woodcreep Dendrexetastes rufigula (Aves:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 187 Td (358-369.	0.2	4
644	Two Linked Enteroinvasive <i>Escherichia coli</i> Outbreaks, Nottingham, UK, June 2014. Emerging Infectious Diseases, 2016, 22, 1178-1184.	2.0	46
645	Lineage-Specific Reductions of Plastid Genomes in an Orchid Tribe with Partially and Fully Mycoheterotrophic Species. Genome Biology and Evolution, 2016, 8, 2164-2175.	1.1	81
646	Complete Chloroplast Genome Sequence of <i>Musa balbisiana</i> Corroborates Structural Heterogeneity of Inverted Repeats in Wild Progenitors of Cultivated Bananas and Plantains. Plant Genome, 2016, 9, plantgenome2015.09.0089.	1.6	34

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647	Diversity of Marine-Derived <i>Aspergillus</i> from Tidal Mudflats and Sea Sand in Korea. <i>Mycobiology</i> , 2016, 44, 237-247.	0.6	25
648	<i>Antrodia neotropica</i> sp. nov. (Polyporales, Basidiomycota): a new South American species of <i>Antrodia</i> s.s. from Brazil based on morphological, molecular and ecological data. <i>Nova Hedwigia</i> , 2016, 103, 125-143.	0.2	3
649	Phenotypic plasticity can explain evolution of sympatric polymorphism in the hairy snail <i>Trochulus hispidus</i> (Linnaeus, 1758). <i>Environmental Epigenetics</i> , 2017, 63, zow082.	0.9	10
650	Comparative Analysis of HaSNPV-AC53 and Derived Strains. <i>Viruses</i> , 2016, 8, 280.	1.5	5
651	Phylogenetic and comparative genomics of the family Leptotrichiaceae and introduction of a novel fingerprinting MLVA for <i>Streptobacillus moniliformis</i> . <i>BMC Genomics</i> , 2016, 17, 864.	1.2	29
652	Chloroplast Genome Evolution in Actinidiaceae: clpP Loss, Heterogenous Divergence and Phylogenomic Practice. <i>PLoS ONE</i> , 2016, 11, e0162324.	1.1	45
653	Phylogeny of Apiaceae subtribe Daucinae and the taxonomic delineation of its genera. <i>Taxon</i> , 2016, 65, 563-585.	0.4	48
654	A new generic system for the pantropical <i>Caesalpinia</i> group (Leguminosae). <i>PhytoKeys</i> , 2016, 71, 1-160.	0.4	96
655	Comparative Large-Scale Mitogenomics Evidences Clade-Specific Evolutionary Trends in Mitochondrial DNAs of Bivalvia. <i>Genome Biology and Evolution</i> , 2016, 8, 2544-2564.	1.1	51
656	The Complete Mitochondrial Genome of <i>Brachmia macroscopa</i> (Lepidoptera: Gelechiidae) and Its Related Phylogenetic Analysis. <i>Journal of Insect Science</i> , 2016, 16, 9.	0.6	8
657	Zebra Alpha herpesviruses (EHV-1 and EHV-9): Genetic Diversity, Latency and Co-Infections. <i>Viruses</i> , 2016, 8, 262.	1.5	19
658	State aggregation for fast likelihood computations in molecular evolution. <i>Bioinformatics</i> , 2017, 33, 354-362.	1.8	7
659	Identification of Source of <i>Brucella suis</i> Infection in Human by Using Whole-Genome Sequencing, United States and Tonga. <i>Emerging Infectious Diseases</i> , 2016, 22, 79-82.	2.0	12
660	Draft Genome of the Scarab Beetle <i>Oryctes borbonicus</i> on La Réunion Island. <i>Genome Biology and Evolution</i> , 2016, 8, 2093-2105.	1.1	35
661	Variations in Spike Glycoprotein Gene of MERS-CoV, South Korea, 2015. <i>Emerging Infectious Diseases</i> , 2016, 22, 100-104.	2.0	36
662	Phylogenetic analyses and morphological characteristics support the description of a second species of <i>Tridimeris</i> (Annonaceae). <i>PhytoKeys</i> , 2016, 74, 79-85.	0.4	9
663	<i>Mycosarcoma</i> (Ustilaginaceae), a resurrected generic name for corn smut (<i>Ustilago maydis</i>) and its close relatives with hypertrophied, tubular sori. <i>IMA Fungus</i> , 2016, 7, 309-315.	1.7	28
664	A Genome-Scale Investigation of How Sequence, Function, and Tree-Based Gene Properties Influence Phylogenetic Inference. <i>Genome Biology and Evolution</i> , 2016, 8, 2565-2580.	1.1	70

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665	Mitochondrion-to-Chloroplast DNA Transfers and Intragenomic Proliferation of Chloroplast Group II Introns in <i>Gloeotilopsis</i> Green Algae (Ulotrichales, Ulvophyceae). <i>Genome Biology and Evolution</i> , 2016, 8, 2789-2805.	1.1	34
666	Population Structure in the Model Grass <i>Brachypodium distachyon</i> Is Highly Correlated with Flowering Differences across Broad Geographic Areas. <i>Plant Genome</i> , 2016, 9, plantgenome2015.08.0074.	1.6	29
667	Spider phylogenomics: untangling the Spider Tree of Life. <i>PeerJ</i> , 2016, 4, e1719.	0.9	253
668	Specimens at the Center: An Informatics Workflow and Toolkit for Specimen-level Analysis of Public DNA Database Data. <i>Systematic Botany</i> , 2016, 41, 529-539.	0.2	8
669	SNP-sites: rapid efficient extraction of SNPs from multi-FASTA alignments. <i>Microbial Genomics</i> , 2016, 2, e000056.	1.0	888
670	Co-occurrence of ecologically equivalent cryptic species of spider wasps. <i>Royal Society Open Science</i> , 2016, 3, 160119.	1.1	10
671	Phylogenetic structure of European <i>Salmonella</i> Enteritidis outbreak correlates with national and international egg distribution network. <i>Microbial Genomics</i> , 2016, 2, e000070.	1.0	67
672	<i>Bacillus wiedmannii</i> sp. nov., a psychrotolerant and cytotoxic <i>Bacillus cereus</i> group species isolated from dairy foods and dairy environments. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 4744-4753.	0.8	157
673	Population genomics reveals the origin and asexual evolution of human infective trypanosomes. <i>ELife</i> , 2016, 5, e11473.	2.8	88
674	Geography and host species shape the evolutionary dynamics of U genogroup infectious hematopoietic necrosis virus. <i>Virus Evolution</i> , 2016, 2, vew034.	2.2	15
675	Genetic Characterization and Comparative Genome Analysis of <i>Brucella melitensis</i> Isolates from India. <i>International Journal of Genomics</i> , 2016, 2016, 1-13.	0.8	12
676	Reconstructing the Phylogeny of <i>Capsosiphon fulvescens</i> (Ulotrichales, Chlorophyta) from Korea Based on <i>rbcL</i> and 18S rDNA Sequences. <i>BioMed Research International</i> , 2016, 2016, 1-6.	0.9	7
677	The Mitochondrial Genomes of the Zoonotic Canine Filariid Parasites <i>Dirofilaria</i> (<i>Nochtiella</i>) <i>repens</i> and <i>Candidatus Dirofilaria</i> (<i>Nochtiella</i>) <i>Honkongensis</i> Provide Evidence for Presence of Cryptic Species. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0005028.	1.3	47
678	Diversity and phylogeny of south-east Queensland Bathynellacea. <i>Australian Journal of Zoology</i> , 2016, 64, 36.	0.6	7
679	The Rough-Toothed Dolphin, <i>Steno bredanensis</i> , in the Eastern Mediterranean Sea. <i>Advances in Marine Biology</i> , 2016, 75, 233-258.	0.7	10
680	Single and multi-gene phylogeny of <i>Hepatospora</i> (Microsporidia) – a generalist pathogen of farmed and wild crustacean hosts. <i>Parasitology</i> , 2016, 143, 971-982.	0.7	17
681	Global <i>Escherichia coli</i> Sequence Type 131 Clade with <i>bla</i> _{CTX-M-27} Gene. <i>Emerging Infectious Diseases</i> , 2016, 22, 1900-1907.	2.0	146
682	A Genome-Wide Identification and Analysis of the Basic Helix-Loop-Helix Transcription Factors in Brown Planthopper, <i>Nilaparvata lugens</i> . <i>Genes</i> , 2016, 7, 100.	1.0	8

#	ARTICLE	IF	CITATIONS
683	A complete toolset for the study of <i>Ustilago bromivora</i> and <i>Brachypodium</i> sp. as a fungal-temperate grass pathosystem. <i>ELife</i> , 2016, 5, .	2.8	49
684	Correlated Evolution of Short Wavelength Sensitive Photoreceptor Sensitivity and Color Pattern in Lake Malawi Cichlids. <i>Frontiers in Ecology and Evolution</i> , 2016, 4, .	1.1	4
685	Inactivation of Cone-Specific Phototransduction Genes in Rod Monochromatic Cetaceans. <i>Frontiers in Ecology and Evolution</i> , 2016, 4, .	1.1	27
686	The Complete Plastid Genome Sequence of the Wild Rice <i>Zizania latifolia</i> and Comparative Chloroplast Genomics of the Rice Tribe <i>Oryzeae</i> , <i>Poaceae</i> . <i>Frontiers in Ecology and Evolution</i> , 2016, 4, .	1.1	22
687	Diversity, Specificity, and Phylogenetic Relationships of Endohyphal Bacteria in Fungi That Inhabit Tropical Seeds and Leaves. <i>Frontiers in Ecology and Evolution</i> , 2016, 4, .	1.1	41
688	Draft Genomes Shed Light on the Dual Bacterial Symbiosis that Dominates the Microbiome of the Coral Reef Sponge <i>Amphimedon queenslandica</i> . <i>Frontiers in Marine Science</i> , 2016, 3, .	1.2	60
689	Ontogenetic Changes in the Bacterial Symbiont Community of the Tropical Demosponge <i>Amphimedon queenslandica</i> : Metamorphosis Is a New Beginning. <i>Frontiers in Marine Science</i> , 2016, 3, .	1.2	49
690	Metagenomic Analysis Indicates <i>Epsilonproteobacteria</i> as a Potential Cause of Microbial Corrosion in Pipelines Injected with Bisulfite. <i>Frontiers in Microbiology</i> , 2016, 7, 28.	1.5	27
691	Applications of Bayesian Phylodynamic Methods in a Recent U.S. Porcine Reproductive and Respiratory Syndrome Virus Outbreak. <i>Frontiers in Microbiology</i> , 2016, 7, 67.	1.5	61
692	Comparative Genomic Analysis Reveals a Diverse Repertoire of Genes Involved in Prokaryote-Eukaryote Interactions within the <i>Pseudovibrio</i> Genus. <i>Frontiers in Microbiology</i> , 2016, 7, 387.	1.5	36
693	Quantifying the Relative Importance of Phylogeny and Environmental Preferences As Drivers of Gene Content in Prokaryotic Microorganisms. <i>Frontiers in Microbiology</i> , 2016, 7, 433.	1.5	19
694	Transcriptome Analysis of <i>Scrippsiella trochoidea</i> CCMP 3099 Reveals Physiological Changes Related to Nitrate Depletion. <i>Frontiers in Microbiology</i> , 2016, 7, 639.	1.5	33
695	Phylogenetic Analysis of the <i>Bifidobacterium</i> Genus Using Glycolysis Enzyme Sequences. <i>Frontiers in Microbiology</i> , 2016, 7, 657.	1.5	21
696	Phylogenomic Study of <i>Burkholderia glathei</i> -like Organisms, Proposal of 13 Novel <i>Burkholderia</i> Species and Emended Descriptions of <i>Burkholderia sordidicola</i> , <i>Burkholderia zhejiangensis</i> , and <i>Burkholderia grimmiae</i> . <i>Frontiers in Microbiology</i> , 2016, 7, 877.	1.5	120
697	Phylogenomic Analyses and Comparative Studies on Genomes of the Bifidobacteriales: Identification of Molecular Signatures Specific for the Order Bifidobacteriales and Its Different Subclades. <i>Frontiers in Microbiology</i> , 2016, 7, 978.	1.5	23
698	The Crystal Structure of the C-Terminal Domain of the <i>Salmonella enterica</i> PduO Protein: An Old Fold with a New Heme-Binding Mode. <i>Frontiers in Microbiology</i> , 2016, 7, 1010.	1.5	8
699	A Phenotypic and Genotypic Analysis of the Antimicrobial Potential of Cultivable <i>Streptomyces</i> Isolated from Cave Moonmilk Deposits. <i>Frontiers in Microbiology</i> , 2016, 7, 1455.	1.5	64
700	Expanding the Knowledge on Lignocellulolytic and Redox Enzymes of Worker and Soldier Castes from the Lower Termite <i>Coptotermes gestroi</i> . <i>Frontiers in Microbiology</i> , 2016, 7, 1518.	1.5	26

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701	Genome Sequencing and Comparative Genomics Analysis Revealed Pathogenic Potential in <i>Penicillium capsulatum</i> as a Novel Fungal Pathogen Belonging to Eurotiales. <i>Frontiers in Microbiology</i> , 2016, 7, 1541.	1.5	11
702	Photosynthetic Versatility in the Genome of <i>Geitlerinema</i> sp. PCC 9228 (Formerly <i>Oscillatoria</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 1071 <i>Microbiology</i> , 2016, 7, 1546.	1.5	37
703	Classification of a Hypervirulent <i>Aeromonas hydrophila</i> Pathotype Responsible for Epidemic Outbreaks in Warm-Water Fishes. <i>Frontiers in Microbiology</i> , 2016, 7, 1615.	1.5	76
704	Molecular Keys to the <i>Janthinobacterium</i> and <i>Duganella</i> spp. Interaction with the Plant Pathogen <i>Fusarium graminearum</i> . <i>Frontiers in Microbiology</i> , 2016, 7, 1668.	1.5	66
705	Livestock-Associated Methicillin Resistant <i>Staphylococcus aureus</i> (LA-MRSA) Clonal Complex (CC) 398 Isolated from UK Animals belong to European Lineages. <i>Frontiers in Microbiology</i> , 2016, 7, 1741.	1.5	61
706	The Microbiome and Occurrence of Methanotrophy in Carnivorous Sponges. <i>Frontiers in Microbiology</i> , 2016, 7, 1781.	1.5	26
707	Rapid Fermentable Substance Modulates Interactions between Ruminal Commensals and Toll-Like Receptors in Promotion of Immune Tolerance of Goat Rumen. <i>Frontiers in Microbiology</i> , 2016, 7, 1812.	1.5	57
708	Evidence for Ecological Flexibility in the Cosmopolitan Genus <i>Curtobacterium</i> . <i>Frontiers in Microbiology</i> , 2016, 7, 1874.	1.5	66
709	Diazotroph Diversity in the Sea Ice, Melt Ponds, and Surface Waters of the Eurasian Basin of the Central Arctic Ocean. <i>Frontiers in Microbiology</i> , 2016, 7, 1884.	1.5	39
710	Genome-Based Taxonomic Classification of Bacteroidetes. <i>Frontiers in Microbiology</i> , 2016, 7, 2003.	1.5	493
711	<i>Fuerstia marisgermanicae</i> gen. nov., sp. nov., an Unusual Member of the Phylum Planctomycetes from the German Wadden Sea. <i>Frontiers in Microbiology</i> , 2016, 7, 2079.	1.5	49
712	Whole-genome Sequencing for Surveillance of Invasive Pneumococcal Diseases in Ontario, Canada: Rapid Prediction of Genotype, Antibiotic Resistance and Characterization of Emerging Serotype 22F. <i>Frontiers in Microbiology</i> , 2016, 7, 2099.	1.5	7
713	Comprehensive Transcriptome Analysis Provides Evidence of Local Thermal Adaptation in Three Loaches (Genus: <i>Misgurnus</i>). <i>International Journal of Molecular Sciences</i> , 2016, 17, 1943.	1.8	8
714	Regulation of Expression and Evolution of Genes in Plastids of Rhodophytic Branch. <i>Life</i> , 2016, 6, 7.	1.1	2
715	Distribution of Type I Restriction Modification Systems in <i>Streptococcus suis</i> : An Outlook. <i>Pathogens</i> , 2016, 5, 62.	1.2	23
716	Biodegradable Plastic-degrading Activity of Various Species of <i>Paraphoma</i> . <i>Journal of Oleo Science</i> , 2016, 65, 621-627.	0.6	8
717	Evaluation of properties over phylogenetic trees using stochastic logics. <i>BMC Bioinformatics</i> , 2016, 17, 235.	1.2	3
718	Pathogen metadata platform: software for accessing and analyzing pathogen strain information. <i>BMC Bioinformatics</i> , 2016, 17, 379.	1.2	3

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719	Whole genome sequencing reveals mycobacterial microevolution among concurrent isolates from sputum and blood in HIV infected TB patients. <i>BMC Infectious Diseases</i> , 2016, 16, 371.	1.3	11
720	Arginine deiminase pathway enzymes: evolutionary history in metamonads and other eukaryotes. <i>BMC Evolutionary Biology</i> , 2016, 16, 197.	3.2	40
721	Shedding light on the expansion and diversification of the Cdc48 protein family during the rise of the eukaryotic cell. <i>BMC Evolutionary Biology</i> , 2016, 16, 215.	3.2	15
722	Deep divergence and rapid evolutionary rates in gut-associated <i>Acetobacteraceae</i> of ants. <i>BMC Microbiology</i> , 2016, 16, 140.	1.3	38
723	Two cases of serotypeable and non-serotypeable variants of <i>Streptococcus pneumoniae</i> detected simultaneously during invasive disease. <i>BMC Microbiology</i> , 2016, 16, 126.	1.3	2
724	On the reversibility of parasitism: adaptation to a free-living lifestyle via gene acquisitions in the diplomonad <i>Trepomonas</i> sp. PC1. <i>BMC Biology</i> , 2016, 14, 62.	1.7	38
725	Redescription, molecular characterisation and taxonomic re-evaluation of a unique African monitor lizard haemogregarine <i>Karyolysus paradoxa</i> (Dias, 1954) n. comb. (<i>Karyolysidae</i>). <i>Parasites and Vectors</i> , 2016, 9, 347.	1.0	25
726	Identification of internalin-A-like virulent proteins in <i>Leishmania donovani</i> . <i>Parasites and Vectors</i> , 2016, 9, 557.	1.0	5
727	Depletion of Shine-Dalgarno Sequences Within Bacterial Coding Regions Is Expression Dependent. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 3467-3474.	0.8	18
728	Generic hyper-diversity in <i>Stachybotriaceae</i> . <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2016, 36, 156-246.	1.6	112
729	Dealing with propositions, not with the characters: the ability of three-taxon statement analysis to recognise groups based solely on "reversals", under the maximum-likelihood criteria. <i>Australian Systematic Botany</i> , 2016, 29, 119.	0.3	30
730	Limitations of Species Delimitation Based on Phylogenetic Analyses: A Case Study in the <i>Hypogymnia hypotrypa</i> Group (<i>Parmeliaceae</i> , <i>Ascomycota</i>). <i>PLoS ONE</i> , 2016, 11, e0163664.	1.1	13
731	Bryophyte-Feeders in a Basal Brachyceran Lineage (Diptera: Rhagionidae: Spaniinae): Adult Oviposition Behavior and Changes in the Larval Mouthpart Morphology Accompanied with the Diet Shifts. <i>PLoS ONE</i> , 2016, 11, e0165808.	1.1	7
732	Chromosomal-Level Assembly of the Asian Seabass Genome Using Long Sequence Reads and Multi-layered Scaffolding. <i>PLoS Genetics</i> , 2016, 12, e1005954.	1.5	105
733	Descriptive Epidemiology and Whole Genome Sequencing Analysis for an Outbreak of Bovine Tuberculosis in Beef Cattle and White-Tailed Deer in Northwestern Minnesota. <i>PLoS ONE</i> , 2016, 11, e0145735.	1.1	50
734	Actinobacteria Isolated from an Underground Lake and Moonmilk Speleothem from the Biggest Conglomeratic Karstic Cave in Siberia as Sources of Novel Biologically Active Compounds. <i>PLoS ONE</i> , 2016, 11, e0149216.	1.1	62
735	Complete Plastid Genome of the Recent Holoparasite <i>Lathraea squamaria</i> Reveals Earliest Stages of Plastome Reduction in <i>Orobanchaceae</i> . <i>PLoS ONE</i> , 2016, 11, e0150718.	1.1	56
736	Functional Sites Induce Long-Range Evolutionary Constraints in Enzymes. <i>PLoS Biology</i> , 2016, 14, e1002452.	2.6	94

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737	Practical Approaches for Detecting Selection in Microbial Genomes. <i>PLoS Computational Biology</i> , 2016, 12, e1004739.	1.5	21
738	Inferring Phylogenetic Networks with Maximum Pseudolikelihood under Incomplete Lineage Sorting. <i>PLoS Genetics</i> , 2016, 12, e1005896.	1.5	348
739	Comparative Genomics of the Sigatoka Disease Complex on Banana Suggests a Link between Parallel Evolutionary Changes in <i>Pseudocercospora fijiensis</i> and <i>Pseudocercospora eumusae</i> and Increased Virulence on the Banana Host. <i>PLoS Genetics</i> , 2016, 12, e1005904.	1.5	51
740	Transposable Elements versus the Fungal Genome: Impact on Whole-Genome Architecture and Transcriptional Profiles. <i>PLoS Genetics</i> , 2016, 12, e1006108.	1.5	177
741	Complex Ancestries of Lager-Brewing Hybrids Were Shaped by Standing Variation in the Wild Yeast <i>Saccharomyces eubayanus</i> . <i>PLoS Genetics</i> , 2016, 12, e1006155.	1.5	94
742	Multiple Independent Retroelement Insertions in the Promoter of a Stress Response Gene Have Variable Molecular and Functional Effects in <i>Drosophila</i> . <i>PLoS Genetics</i> , 2016, 12, e1006249.	1.5	46
743	Multiple Origins of the Pathogenic Yeast <i>Candida orthopsilosis</i> by Separate Hybridizations between Two Parental Species. <i>PLoS Genetics</i> , 2016, 12, e1006404.	1.5	125
744	Genome-Wide Comparative Analysis of Chemosensory Gene Families in Five Tsetse Fly Species. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004421.	1.3	28
745	Geological Changes of the Americas and their Influence on the Diversification of the Neotropical Kissing Bugs (Hemiptera: Reduviidae: Triatominae). <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004527.	1.3	72
746	Extended Evaluation of Virological, Immunological and Pharmacokinetic Endpoints of CELADEN: A Randomized, Placebo-Controlled Trial of Celgosivir in Dengue Fever Patients. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004851.	1.3	53
747	Polyphenol-Rich Diets Exacerbate AMPK-Mediated Autophagy, Decreasing Proliferation of Mosquito Midgut Microbiota, and Extending Vector Lifespan. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0005034.	1.3	15
748	Polyphyly of Asian Tree Toads, Genus <i>Pedostibes</i> Günther, 1876 (Anura: Bufonidae), and the Description of a New Genus from Southeast Asia. <i>PLoS ONE</i> , 2016, 11, e0145903.	1.1	11
749	On the Evolutionary History of <i>Uleiella chilensis</i> , a Smut Fungus Parasite of <i>Araucaria araucana</i> in South America: <i>Uleiellales</i> ord. nov. in <i>Ustilaginomycetes</i> . <i>PLoS ONE</i> , 2016, 11, e0147107.	1.1	17
750	A Phylogenomic Approach Based on PCR Target Enrichment and High Throughput Sequencing: Resolving the Diversity within the South American Species of <i>Bartsia</i> L. (Orobanchaceae). <i>PLoS ONE</i> , 2016, 11, e0148203.	1.1	70
751	A New Miocene-Divergent Lineage of Old World Racer Snake from India. <i>PLoS ONE</i> , 2016, 11, e0148380.	1.1	15
752	Identification and Characterization of <i>msf</i> , a Novel Virulence Factor in <i>Haemophilus influenzae</i> . <i>PLoS ONE</i> , 2016, 11, e0149891.	1.1	15
753	Multilocus Phylogeography and Species Delimitation in the Cumberland Plateau Salamander, <i>Plethodon kentucki</i> : Incongruence among Data Sets and Methods. <i>PLoS ONE</i> , 2016, 11, e0150022.	1.1	20
754	From GenBank to GBIF: Phylogeny-Based Predictive Niche Modeling Tests Accuracy of Taxonomic Identifications in Large Occurrence Data Repositories. <i>PLoS ONE</i> , 2016, 11, e0151232.	1.1	28

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755	HIV-1 Genetic Variation Resulting in the Development of New Quasispecies Continues to Be Encountered in the Peripheral Blood of Well-Suppressed Patients. PLoS ONE, 2016, 11, e0155382.	1.1	29
756	Intron Derived Size Polymorphism in the Mitochondrial Genomes of Closely Related Chrysoporthe Species. PLoS ONE, 2016, 11, e0156104.	1.1	68
757	Subspecific Differentiation Events of Montane Stag Beetles (Coleoptera, Lucanidae) Endemic to Formosa Island. PLoS ONE, 2016, 11, e0156600.	1.1	8
758	Multiple Events of Allopolyploidy in the Evolution of the Racemose Lineages in Prunus (Rosaceae) Based on Integrated Evidence from Nuclear and Plastid Data. PLoS ONE, 2016, 11, e0157123.	1.1	31
759	Chloroplast DNA Structural Variation, Phylogeny, and Age of Divergence among Diploid Cotton Species. PLoS ONE, 2016, 11, e0157183.	1.1	58
760	The End of the Cold Loneliness: 3D Comparison between <i>Doto antarctica</i> and a New Sympatric Species of <i>Doto</i> (Heterobranchia: Nudibranchia). PLoS ONE, 2016, 11, e0157941.	1.1	13
761	Factors Influencing Bacterial Diversity and Community Composition in Municipal Drinking Waters in the Ohio River Basin, USA. PLoS ONE, 2016, 11, e0157966.	1.1	70
762	Development of Molecular Markers for Determining Continental Origin of Wood from White Oaks (<i>Quercus L. sect. Quercus</i>). PLoS ONE, 2016, 11, e0158221.	1.1	34
763	Five Complete Chloroplast Genome Sequences from <i>Diospyros</i> : Genome Organization and Comparative Analysis. PLoS ONE, 2016, 11, e0159566.	1.1	48
764	Preservation Obscures Pelagic Deep-Sea Fish Diversity: Doubling the Number of Sole-Bearing Opisthoproctids and Resurrection of the Genus <i>Monacoa</i> (Opisthoproctidae, Argentiniformes). PLoS ONE, 2016, 11, e0159762.	1.1	11
765	Molecular and Morphological Inference of Three Cryptic Species within the <i>Merodon aureus</i> Species Group (Diptera: Syrphidae). PLoS ONE, 2016, 11, e0160001.	1.1	33
766	Genomic and Evolutionary Analysis of Two <i>Salmonella enterica</i> Serovar Kentucky Sequence Types Isolated from Bovine and Poultry Sources in North America. PLoS ONE, 2016, 11, e0161225.	1.1	39
767	Comparative Genomic and Phenotypic Characterization of Pathogenic and Non-Pathogenic Strains of <i>Xanthomonas arboricola</i> Reveals Insights into the Infection Process of Bacterial Spot Disease of Stone Fruits. PLoS ONE, 2016, 11, e0161977.	1.1	31
768	Computational Evaluation of the Strict Master and Random Template Models of Endogenous Retrovirus Evolution. PLoS ONE, 2016, 11, e0162454.	1.1	2
769	Early Gnathostome Phylogeny Revisited: Multiple Method Consensus. PLoS ONE, 2016, 11, e0163157.	1.1	54
770	The Chloroplast Genome of <i>Utricularia reniformis</i> Sheds Light on the Evolution of the <i>ndh</i> Gene Complex of Terrestrial Carnivorous Plants from the Lentibulariaceae Family. PLoS ONE, 2016, 11, e0165176.	1.1	57
771	Exploring Canadian Echinoderm Diversity through DNA Barcodes. PLoS ONE, 2016, 11, e0166118.	1.1	39
772	Patchiness of Ciliate Communities Sampled at Varying Spatial Scales along the New England Shelf. PLoS ONE, 2016, 11, e0167659.	1.1	17

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773	Revealing the Micro-scale Signature of Endemic Zoonotic Disease Transmission in an African Urban Setting. <i>PLoS Pathogens</i> , 2016, 12, e1005525.	2.1	65
774	Discovery of a Natural Microsporidian Pathogen with a Broad Tissue Tropism in <i>Caenorhabditis elegans</i> . <i>PLoS Pathogens</i> , 2016, 12, e1005724.	2.1	48
775	The Origin and Evolution of the Trace Amine-Associated Receptor Family in Vertebrates. , 2016, , 45-62.		2
776	Insights into the innate immunome of actinurians using a comparative genomic approach. <i>BMC Genomics</i> , 2016, 17, 850.	1.2	42
777	Molecular Characterization of Aquaporin 1 and Aquaporin 3 from the Gills of the African Lungfish, <i>Protopterus annectens</i> , and Changes in Their Branchial mRNA Expression Levels and Protein Abundance during Three Phases of Aestivation. <i>Frontiers in Physiology</i> , 2016, 7, 532.	1.3	14
778	The Phenotypic and Genetic Underpinnings of Flower Size in Polemoniaceae. <i>Frontiers in Plant Science</i> , 2015, 6, 1144.	1.7	21
779	Transcriptome and Biochemical Analysis of a Flower Color Polymorphism in <i>Silene littorea</i> (Caryophyllaceae). <i>Frontiers in Plant Science</i> , 2016, 7, 204.	1.7	30
780	Complete Chloroplast Genome Sequence of <i>Aquilaria sinensis</i> (Lour.) Gilg and Evolution Analysis within the Malvales Order. <i>Frontiers in Plant Science</i> , 2016, 7, 280.	1.7	62
781	Evolution of Electrogenic Ammonium Transporters (AMTs). <i>Frontiers in Plant Science</i> , 2016, 7, 352.	1.7	57
782	Genome-Wide Identification, Classification, and Expression Analysis of Amino Acid Transporter Gene Family in <i>Glycine Max</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 515.	1.7	47
783	Comparative Chloroplast Genome Analyses of Streptophyte Green Algae Uncover Major Structural Alterations in the Klebsormidiophyceae, Coleochaetophyceae and Zygnematophyceae. <i>Frontiers in Plant Science</i> , 2016, 7, 697.	1.7	62
784	Search for Nodulation and Nodule Development-Related Cystatin Genes in the Genome of Soybean (<i>Glycine max</i>). <i>Frontiers in Plant Science</i> , 2016, 7, 1595.	1.7	27
785	Species Delimitation and Interspecific Relationships of the Genus <i>Orychophragmus</i> (Brassicaceae) Inferred from Whole Chloroplast Genomes. <i>Frontiers in Plant Science</i> , 2016, 7, 1826.	1.7	53
786	Sporadic Gene Loss After Duplication Is Associated with Functional Divergence of Sirtuin Deacetylases Among <i>Candida</i> Yeast Species. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 3297-3305.	0.8	8
787	Robinson-Foulds Median Trees. , 2016, , .		0
788	A Genomic Landscape of Haplotype Diversity and Signatures of Phylogeographic Distribution in Zaire Ebola virus during the 2014 EVD epidemic. , 2016, , .		0
789	Population genomics of the symbiotic plasmids of sympatric nitrogen-fixing <i>Rhizobium</i> species associated with <i>Phaseolus vulgaris</i> . <i>Environmental Microbiology</i> , 2016, 18, 2660-2676.	1.8	72
790	An evaluation of transcriptome-based exon capture for frog phylogenomics across multiple scales of divergence (Class: Amphibia, Order: Anura). <i>Molecular Ecology Resources</i> , 2016, 16, 1069-1083.	2.2	92

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791	CoMuS: simulating coalescent histories and polymorphic data from multiple species. <i>Molecular Ecology Resources</i> , 2016, 16, 1435-1448.	2.2	9
792	The biogeographical history of Asian keelback snakes of the genus <i>Hebius</i> (Squamata: Colubridae). <i>Tj ETQq1 1 0.784314 rgBT /Ov</i> 187-199.	0.7	23
793	Long-distance dispersal and inter-island colonization across the western Malagasy Region explain diversification in brush-warblers (Passeriformes:Nesillas). <i>Biological Journal of the Linnean Society</i> , 2016, 119, 873-889.	0.7	8
794	Genetic surfing, not allopatric divergence, explains spatial sorting of mitochondrial haplotypes in venomous coralsnakes. <i>Evolution; International Journal of Organic Evolution</i> , 2016, 70, 1435-1449.	1.1	33
795	Complete genome sequence of bacteriophage P2559Y, a marine phage that infects <i>Croceibacter atlanticus</i> HTCC2559. <i>Marine Genomics</i> , 2016, 29, 35-38.	0.4	20
796	Genomic analysis of snub-nosed monkeys (<i>Rhinopithecus</i>) identifies genes and processes related to high-altitude adaptation. <i>Nature Genetics</i> , 2016, 48, 947-952.	9.4	109
797	Composition and Genetic Diversity of Mosquitoes (Diptera: Culicidae) on Islands and Mainland Shores of Kenya's Lakes Victoria and Baringo. <i>Journal of Medical Entomology</i> , 2016, 53, 1348-1363.	0.9	21
798	Endogenous Gibbon Ape Leukemia Virus Identified in a Rodent (<i>Melomys burtoni</i> subsp.) from Wallacea (Indonesia). <i>Journal of Virology</i> , 2016, 90, 8169-8180.	1.5	24
799	Histories of host shifts and cospeciation among free-living parasitoids of <i>Rhagoletis</i> flies. <i>Journal of Evolutionary Biology</i> , 2016, 29, 1766-1779.	0.8	24
800	Description and Phylogeny of <i>Urostyla grandis wiackowskii</i> subsp. nov. (Ciliophora). <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 T</i> 247-261.	0.8	18
801	Population genomics of sexual and asexual lineages in fissiparous ribbon worms (Lineus, Nemertea): hybridization, polyploidy and the Meselson effect. <i>Molecular Ecology</i> , 2016, 25, 3356-3369.	2.0	58
802	The Neotropical polymorphic earless praying mantises " Part I: molecular phylogeny and revised higher-level systematics (Insecta: Mantodea, Acanthopoidea). <i>Systematic Entomology</i> , 2016, 41, 607-649.	1.7	42
803	When troglomorphism dupes taxonomists: morphology and molecules reveal the first pyramidopid harvestman (Arachnida, Opiliones, Pyramidopidae) from the New World. <i>Zoological Journal of the Linnean Society</i> , 2016, 177, 602-620.	1.0	24
804	A reinvestigation of phylogeny and divergence times of the <i>Ablepharus kitaibelii</i> species complex (Sauria, Scincidae) based on mtDNA and nuDNA genes. <i>Molecular Phylogenetics and Evolution</i> , 2016, 103, 199-214.	1.2	34
805	Whole genome sequencing improved case ascertainment in an outbreak of Shiga toxin-producing <i>Escherichia coli</i> O157 associated with raw drinking milk. <i>Epidemiology and Infection</i> , 2016, 144, 2812-2823.	1.0	49
806	<i>Scrophularia arguta</i> , a widespread annual plant in the Canary Islands: a single recent colonization event or a more complex phylogeographic pattern?. <i>Ecology and Evolution</i> , 2016, 6, 4258-4273.	0.8	19
807	Phylogenetic test of speciation by host shift in leaf cone moths (<i>Caloptilia</i>) feeding on maples (<i>Acer</i>) <i>Tj ETQq0 0 0 rgBT /Overlock 10 T</i>	0.8	25
808	Assembled Plastid and Mitochondrial Genomes, as well as Nuclear Genes, Place the Parasite Family Cynomoriaceae in the Saxifragales. <i>Genome Biology and Evolution</i> , 2016, 8, 2214-2230.	1.1	62

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809	A Small Number of Phylogenetically Distinct Clonal Complexes Dominate a Coastal <i>Vibrio cholerae</i> Population. <i>Applied and Environmental Microbiology</i> , 2016, 82, 5576-5586.	1.4	24
810	Comparative Cell Biology and Evolution of Annexins in Diplomonads. <i>MSphere</i> , 2016, 1, .	1.3	9
811	Morphology, Ontogeny, and Molecular Phylogeny of Two Freshwater Species of <i>Deviata</i> (Ciliophora, Hypotrichia) from Southern China. <i>Journal of Eukaryotic Microbiology</i> , 2016, 63, 771-785.	0.8	16
812	A New Heterotrophic Cryptomonad: <i>Hemiarma marina</i> n. g., n. sp.. <i>Journal of Eukaryotic Microbiology</i> , 2016, 63, 804-812.	0.8	21
813	The abiotic and biotic drivers of rapid diversification in <i>Andean</i> bellflowers (Campanulaceae). <i>New Phytologist</i> , 2016, 210, 1430-1442.	3.5	325
814	How many species of <i>Hipposideros</i> have occurred on Madagascar since the Late Pleistocene?. <i>Zoological Journal of the Linnean Society</i> , 2016, 177, 428-449.	1.0	13
815	Naturally Occurring Isoleucyl-tRNA Synthetase without tRNA-dependent Pre-transfer Editing. <i>Journal of Biological Chemistry</i> , 2016, 291, 8618-8631.	1.6	14
816	High Diversity Revealed in Leaf-Associated Protists (Rhizaria: Cercozoa) of Brassicaceae. <i>Journal of Eukaryotic Microbiology</i> , 2016, 63, 635-641.	0.8	52
817	Rickettsial endosymbiont in the early-diverging streptophyte green alga <i>Mesostigma viride</i> . <i>Journal of Phycology</i> , 2016, 52, 219-229.	1.0	21
818	Genomic evidence for ecological divergence against a background of population homogeneity in the marine snail <i>Chlorostoma funebris</i> . <i>Molecular Ecology</i> , 2016, 25, 3557-3573.	2.0	39
819	An unprecedented new genus and family of Tetractinellida (Porifera, Demospongiae) from New Zealand's Colville Ridge, with a new type of mitochondrial group I intron. <i>Zoological Journal of the Linnean Society</i> , 2016, 177, 335-352.	1.0	15
820	Potential Mechanisms for Microbial Energy Acquisition in Oxidic Deep-Sea Sediments. <i>Applied and Environmental Microbiology</i> , 2016, 82, 4232-4243.	1.4	51
821	Two Unrelated 8-Vinyl Reductases Ensure Production of Mature Chlorophylls in <i>Acaryochloris marina</i> . <i>Journal of Bacteriology</i> , 2016, 198, 1393-1400.	1.0	11
822	Novel Highly Pathogenic Avian A(H5N2) and A(H5N8) Influenza Viruses of Clade 2.3.4.4 from North America Have Limited Capacity for Replication and Transmission in Mammals. <i>MSphere</i> , 2016, 1, .	1.3	56
823	Functional diversification of sea urchin ABCC1 (MRP1) by alternative splicing. <i>American Journal of Physiology - Cell Physiology</i> , 2016, 310, C911-C920.	2.1	7
824	Functional metagenomic selection of ribulose 1, 5-bisphosphate carboxylase/oxygenase from uncultivated bacteria. <i>Environmental Microbiology</i> , 2016, 18, 1187-1199.	1.8	26
825	Phylogeny, landmark analysis and the use of wing venation to study the evolution of social wasps (Hymenoptera: Vespidae: Vespinae). <i>Cladistics</i> , 2016, 32, 406-425.	1.5	28
826	TNT version 1.5, including a full implementation of phylogenetic morphometrics. <i>Cladistics</i> , 2016, 32, 221-238.	1.5	1,654

#	ARTICLE	IF	CITATIONS
827	Evolution of the YABBY gene family in seed plants. <i>Evolution & Development</i> , 2016, 18, 116-126.	1.1	87
828	The conserved genetic background for pluteus arm development in brittle stars and sea urchin. <i>Evolution & Development</i> , 2016, 18, 89-95.	1.1	9
829	Molecular Phylogenetic Analysis of <i>Infidum similis</i> , Including Morphological Data and Estimation of its Genome Size. <i>Journal of Parasitology</i> , 2016, 102, 468-475.	0.3	3
830	Identification of imine reductase-specific sequence motifs. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 600-610.	1.5	36
831	Inference of Episodic Changes in Natural Selection Acting on Protein Coding Sequences via CODEML. <i>Current Protocols in Bioinformatics</i> , 2016, 54, 6.15.1-6.15.32.	25.8	13
832	Ancient river systems and phylogeographical structure in the spring salamander, <i>Gyrinophilus porphyriticus</i> . <i>Journal of Biogeography</i> , 2016, 43, 639-652.	1.4	18
833	Multi-locus sequence data reveal a new species of coral reef goby (Teleostei: Gobiidae: <i>Eviota</i>), and evidence of Pliocene vicariance across the Coral Triangle. <i>Journal of Fish Biology</i> , 2016, 88, 1811-1834.	0.7	15
834	Characterization of equine cytochrome P450: role of <i>CYP3A</i> in the metabolism of diazepam. <i>Journal of Veterinary Pharmacology and Therapeutics</i> , 2016, 39, 478-487.	0.6	7
835	Evolutionary history and conservation significance of the Javan leopard <i>Panthera pardus melas</i> . <i>Journal of Zoology</i> , 2016, 299, 239-250.	0.8	20
836	The true identity of <i>Oobama</i> (Platyhelminthes: Geoplanidae) flatworm spreading across Europe. <i>Zoological Journal of the Linnean Society</i> , 2016, 177, 5-28.	1.0	36
837	<i>Wolbachia</i> endosymbionts distort DNA barcoding in the parasitoid wasp genus <i>Diplazon</i> (Hymenoptera: Ichneumonidae). <i>Zoological Journal of the Linnean Society</i> , 2016, 177, 541-557.	1.0	47
838	A multiple-gene phylogeny reveals polyphyly among eastern North American <i>Aphaenogaster</i> species (Hymenoptera: Formicidae). <i>Zoologica Scripta</i> , 2016, 45, 512-520.	0.7	28
839	Taxonomic revision and species delimitation of coccoid green algae currently assigned to the genus <i>Dictyochloropsis</i> (Trebouxiophyceae, Chlorophyta). <i>Journal of Phycology</i> , 2016, 52, 599-617.	1.0	58
840	Evolutionary history and species diversity of African pouched mice (<i>Rodentia</i> : <i>Tj ETQq1 1.0784314</i>). <i>Journal of Biogeography</i> , 2016, 43, 107-120.	0.7	20
841	Phylogeographic study revealed microrefugia for an endemic species on the Qinghai-Tibetan Plateau: <i>Rhodiola chrysanthemifolia</i> (Crassulaceae). <i>Plant Systematics and Evolution</i> , 2016, 302, 1179-1193.	0.3	31
842	All that glitters is not <i>Ramularia</i> . <i>Studies in Mycology</i> , 2016, 83, 49-163.	4.5	88
843	Capturing the diversity of the human gut microbiota through culture-enriched molecular profiling. <i>Genome Medicine</i> , 2016, 8, 72.	3.6	150
844	Interspecies Dissemination of a Mobilizable Plasmid Harboring <i>bla</i> and the Possibility of Horizontal Gene Transfer in a Single Patient. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 5412-5419.	1.4	17

#	ARTICLE	IF	CITATIONS
845	<l>Domeykoa andina<l> (Apiaceae; Azorelloideae), a New Species from Northern Chile. Systematic Botany, 2016, 41, 457-463.	0.2	1
846	Complete mitochondrial genome of the <i>Nemipterus virgatus</i> (Perciformes: Nemipteridae). Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2016, 27, 3485-3486.	0.7	4
847	Methodological congruence in phylogenomic analyses with morphological support for teiid lizards (Sauria: Teiidae). Molecular Phylogenetics and Evolution, 2016, 103, 75-84.	1.2	45
848	<i>Vermistella arctica</i> n. sp. Nominates the Genus <i>Vermistella</i> as a Candidate for Taxon with Bipolar Distribution. Journal of Eukaryotic Microbiology, 2016, 63, 210-219.	0.8	4
849	A new phylogeny and environmental DNA insight into paramyxids: an increasingly important but enigmatic clade of protistan parasites of marine invertebrates. International Journal for Parasitology, 2016, 46, 605-619.	1.3	39
850	Increasing genetic diversity of Zika virus in the Latin American outbreak. Emerging Microbes and Infections, 2016, 5, 1-3.	3.0	28
851	Additions to<i>Sporormiaceae</i>: Introducing Two Novel Genera,<i>Sparticola</i>and<i>Forliomyces</i>, from<i>Spartium</i>. Cryptogamie, Mycologie, 2016, 37, 75-97.	0.2	22
852	Analysis of the core genome and pangenome of <scp><i>P</i></scp><i>seudomonas putida</i>. Environmental Microbiology, 2016, 18, 3268-3283.	1.8	65
853	Comparative and transcriptional analysis of the predicted secretome in the lignocelluloseâ€degrading basidiomycete fungus <i>Pleurotus ostreatus</i>. Environmental Microbiology, 2016, 18, 4710-4726.	1.8	77
854	Changes in the dominant assembly mechanism drive species loss caused by declining resources. Ecology Letters, 2016, 19, 163-170.	3.0	60
855	Trans-species variation in<i>Dmrt1</i>is associated with sex determination in four European tree-frog species. Evolution; International Journal of Organic Evolution, 2016, 70, 840-847.	1.1	27
856	Phylogeny of the Highly Divergent Echinosteliales (Amoebozoa). Journal of Eukaryotic Microbiology, 2016, 63, 453-459.	0.8	19
857	Morphological Description and Molecular Phylogeny of Two Species of <i>Levicolaps</i> (Ciliophora,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf Korea. Journal of Eukaryotic Microbiology, 2016, 63, 471-480.	0.8	5
858	<i>Tetrahymena australis</i> (Protozoa, Ciliophora): A Wellâ€Known But â€Nonâ€Existingâ€Taxon â€“ Consideration of Its Identification, Definition and Systematic Position. Journal of Eukaryotic Microbiology, 2016, 63, 760-770.	0.8	17
859	Not going with the flow: a comprehensive timeâ€calibrated phylogeny of dragonflies (Anisoptera:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf Ecology, 2016, 25, 1340-1353.	2.0	59
860	At least some meiofaunal species are not everywhere. Indication of geographic, ecological and geological barriers affecting the dispersion of species of <i>Ototyphlonemertes</i> (Nemertea,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf	0.7	3
861	Genomic evidence for polyphyletic origins and interlineage gene flow within complex taxa: a case study of <i>Picea brachytyla</i> in the Qinghaiâ€Tibet Plateau. Molecular Ecology, 2016, 25, 2373-2386.	2.0	29
862	Identification of novel <scp><i>X</i></scp><i>anthomonas euvesicatoria</i> type <scp>III</scp> effector proteins by a machineâ€learning approach. Molecular Plant Pathology, 2016, 17, 398-411.	2.0	66

#	ARTICLE	IF	CITATIONS
863	The Mouse Universal Genotyping Array: From Substrains to Subspecies. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 263-279.	0.8	199
864	Host jumps shaped the diversity of extant rust fungi (Pucciniales). <i>New Phytologist</i> , 2016, 209, 1149-1158.	3.5	73
865	Evolution of Neuroadaptation in the Periphery and Purifying Selection in the Brain Contribute to Compartmentalization of Simian Immunodeficiency Virus (SIV) in the Brains of Rhesus Macaques with SIV-Associated Encephalitis. <i>Journal of Virology</i> , 2016, 90, 6112-6126.	1.5	14
866	Multiple introductions and onward transmission of non-pandemic HIV-1 subtype B strains in North America and Europe.. <i>Scientific Reports</i> , 2016, 6, 33971.	1.6	13
867	Threatened or Threatening? Evidence for Independent Introductions of <i>Macrothele calpeiana</i> (Araneae: Hexathelidae) and First Observation of Reproduction Outside its Natural Distribution Range. <i>Arachnology</i> , 2016, 17, 137-141.	0.4	4
868	Evolutionary relationships in Panicoid grasses based on plastome phylogenomics (Panicaceae; Poaceae). <i>Journal of Biotechnology</i> , 2016, 14, 107-114.	1.6	72
869	The mitochondrial genome of <i>Murina huttoni rubella</i> (Chiroptera: Vespertilionidae) from China. <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 438-440.	0.2	4
870	A new species and four new records of <i>Amanita</i> (Amanitaceae; Basidiomycota) from Northern Thailand. <i>Phytotaxa</i> , 2016, 286, 211.	0.1	18
871	Complete Genome Sequencing and Comparative Genomic Analysis of the Thermotolerant Acetic Acid Bacterium, <i>Acetobacter pasteurianus</i> SKU1108, Provide a New Insight into Thermotolerance. <i>Microbes and Environments</i> , 2016, 31, 395-400.	0.7	13
872	Inter- and intra-specific genetic divergence of Asian tiger frogs (genus <i>Hoplobatrachus</i>), with special reference to the population structure of <i>H. tigerinus</i> in Bangladesh. <i>Genes and Genetic Systems</i> , 2016, 91, 217-227.	0.2	3
873	The complete mitochondrial genome of <i>Entylia carinata</i> (Hemiptera: Membracidae). <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 662-663.	0.2	21
874	Complete plastid genome of <i>Astragalus membranaceus</i> (Fisch.) Bunge var. <i>membranaceus</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 517-519.	0.2	9
875	Methuselah/Methuselah-like G protein-coupled receptors constitute an ancient metazoan gene family. <i>Scientific Reports</i> , 2016, 6, 21801.	1.6	24
876	Genomic Analyses of Dominant U.S. Clonal Lineages of <i>Phytophthora infestans</i> Reveals a Shared Common Ancestry for Clonal Lineages US11 and US18 and a Lack of Recently Shared Ancestry Among All Other U.S. Lineages. <i>Phytopathology</i> , 2016, 106, 1393-1403.	1.1	16
877	Siderophore-based microbial adaptations to iron scarcity across the eastern Pacific Ocean. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 14237-14242.	3.3	179
878	The mitochondrial genome map of <i>Nelumbo nucifera</i> reveals ancient evolutionary features. <i>Scientific Reports</i> , 2016, 6, 30158.	1.6	40
879	Multigene phylogenetic analysis redefines dung beetles relationships and classification (Coleoptera: Scarabaeidae). <i>Journal of Biotechnology</i> , 2016, 14, 107-114.	3.2	78
880	Genesis, Evolution and Prevalence of H5N6 Avian Influenza Viruses in China. <i>Cell Host and Microbe</i> , 2016, 20, 810-821.	5.1	257

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881	Multigenomic Delineation of <i>Plasmodium</i> Species of the <i>Laverania</i> Subgenus Infecting Wild-Living Chimpanzees and Gorillas. <i>Genome Biology and Evolution</i> , 2016, 8, 1929-1939.	1.1	38
882	Chonocoleaceae (Lophocoleineae) is a synonym of Cephalozellaceae (Cephaloziiineae) and Rivulariella (Jungermanniineae) belongs to Scapaniaceae s.l. (Cephaloziiineae). <i>Phytotaxa</i> , 2016, 267, 91.	0.1	10
883	Papuaneon, a new genus of jumping spiders from Papua New Guinea (Araneae: Salticidae: Neonini). <i>Zootaxa</i> , 2016, 4200, zootaxa.4200.3.9.	0.2	11
884	Heme pathway evolution in kinetoplastid protists. <i>BMC Evolutionary Biology</i> , 2016, 16, 109.	3.2	19
885	Complete mitochondrial genome of <i>Copadichromis virginalis</i> (Cichlidae). <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 152-153.	0.2	0
886	Insights into Adaptations to a Near-Obligate Nematode Endoparasitic Lifestyle from the Finished Genome of <i>Drechmeria coniospora</i> . <i>Scientific Reports</i> , 2016, 6, 23122.	1.6	32
887	Lectotypification of <i>Adiantopsis alata</i> (Pteridaceae) and Descriptions of New Palmate Species in the Guiana Shield. <i>Systematic Botany</i> , 2016, 41, 906-918.	0.2	1
888	Recurrent evolution of gut symbiotic bacteria in pentatomid stinkbugs. <i>Zoological Letters</i> , 2016, 2, 24.	0.7	33
889	Complete mitochondrial genomes of the Laotian Rock Rat (<i>Laonastes aenigmamus</i>) confirm deep divergence within the species. <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 479-482.	0.2	0
890	The female and male mitochondrial genomes of <i>Unio delphinus</i> and the phylogeny of freshwater mussels (Bivalvia: Unionida). <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 954-957.	0.2	23
891	The Evolution of the FT/TFL1 Genes in Amaranthaceae and Their Expression Patterns in the Course of Vegetative Growth and Flowering in <i>Chenopodium rubrum</i> . <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 3065-3076.	0.8	15
892	Phylogenetic Relationships among Members of the Neotropical Clade of Miliuseae (Annonaceae): Generic Non-monophyly of <i>Desmopsis</i> and <i>Stenanona</i> . <i>Systematic Botany</i> , 2016, 41, 815-822.	0.2	17
893	Plate tectonics drive tropical reef biodiversity dynamics. <i>Nature Communications</i> , 2016, 7, 11461.	5.8	136
895	Phylogenomics-guided discovery of a novel conserved cassette of short linear motifs in BubR1 essential for the spindle checkpoint. <i>Open Biology</i> , 2016, 6, 160315.	1.5	33
896	A PRELIMINARY CHARACTERISATION OF <i>SYMBIODINIUM</i> DIVERSITY IN SOME COMMON CORALS FROM SINGAPORE. <i>Cosmos</i> , 2016, 12, 15-27.	0.4	19
897	Divergence time estimates and the evolution of major lineages in the florideophyte red algae. <i>Scientific Reports</i> , 2016, 6, 21361.	1.6	139
898	Habitat-driven variation in mycorrhizal communities in the terrestrial orchid genus <i>Dactylorhiza</i> . <i>Scientific Reports</i> , 2016, 6, 37182.	1.6	45
899	Phylogeny and relationships of the neotropical <i>Adiantum raddianum</i> group (Pteridaceae). <i>Taxon</i> , 2016, 65, 1225-1235.	0.4	9

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900	Effector Diversification Contributes to <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> Phenotypic Adaptation in a Semi-Isolated Environment. <i>Scientific Reports</i> , 2016, 6, 34137.	1.6	76
901	Molecular phylogenetics provides new insights into the systematics of <i>Pimelea</i> and <i>Thecanthes</i> (Thymelaeaceae). <i>Australian Systematic Botany</i> , 2016, 29, 185.	0.3	9
902	Coral snakes predict the evolution of mimicry across New World snakes. <i>Nature Communications</i> , 2016, 7, 11484.	5.8	126
903	Mitogenomes from type specimens, a genotyping tool for morphologically simple species: ten genomes of agar-producing red algae. <i>Scientific Reports</i> , 2016, 6, 35337.	1.6	41
904	Complete mitochondrial genomes of living and extinct pigeons revise the timing of the columbiform radiation. <i>BMC Evolutionary Biology</i> , 2016, 16, 230.	3.2	38
905	Genome sequence of OXA-23 producing <i>Acinetobacter baumannii</i> IHIT7853, a carbapenem-resistant strain from a cat belonging to international clone IC1. <i>Gut Pathogens</i> , 2016, 8, 37.	1.6	41
906	<i>Ormocarpopsis Anosyana</i> Thulin & Razafim. (Fabaceae), a New Species from Southern Madagascar and Its Phylogenetic Position. <i>Candollea</i> , 2016, 71, 281-286.	0.1	0
907	Towards a phylogenetic classification of <i>Leptothecata</i> (Cnidaria, Hydrozoa). <i>Scientific Reports</i> , 2016, 6, 18075.	1.6	64
908	Evolutionary Insights into Taste Perception of the Invasive Pest <i>Drosophila suzukii</i> . <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 4185-4196.	0.8	35
909	Genotyping-by-sequencing provides the discriminating power to investigate the subspecies of <i>Daucus carota</i> (Apiaceae). <i>BMC Evolutionary Biology</i> , 2016, 16, 234.	3.2	44
910	Complete genomes of Hairstreak butterflies, their speciation and nucleo-mitochondrial incongruence. <i>Scientific Reports</i> , 2016, 6, 24863.	1.6	44
911	The plastid genome of some eustigmatophyte algae harbours a bacteria-derived six-gene cluster for biosynthesis of a novel secondary metabolite. <i>Open Biology</i> , 2016, 6, 160249.	1.5	35
912	Evolution of chemosensory gene families in arthropods: Insight from the first inclusive comparative transcriptome analysis across spider appendages. <i>Genome Biology and Evolution</i> , 2017, 9, eww296.	1.1	43
913	Towards a monophyletic classification of <i>Lejeuneaceae</i> V: the systematic position of <i>Pictolejeunea</i> . <i>Phytotaxa</i> , 2016, 280, 259.	0.1	17
914	<i>Pterocладиella maribagoensis</i> (Gelidiales, Rhodophyta), a new marine alga from Cebu, Philippines. <i>Phytotaxa</i> , 2016, 288, 239.	0.1	5
915	<i>Pustula junggarensis</i> (Albuginales, Oomycota), a new species of white blister rust on <i>Takhtajiantha pusilla</i> from Junggar Basin in China. <i>Phytotaxa</i> , 2016, 289, 83.	0.1	5
916	Multi-locus phylogeny using topotype specimens sheds light on the systematics of <i>Niviventer</i> (Rodentia, Muridae) in China. <i>BMC Evolutionary Biology</i> , 2016, 16, 261.	3.2	11
917	Determinants of FIV and HIV Vif sensitivity of feline APOBEC3 restriction factors. <i>Retrovirology</i> , 2016, 13, 46.	0.9	21

#	ARTICLE	IF	CITATIONS
918	Greenwoodiella, a New Genus of Spiranthinae (Orchidaceae) from North and Central America and the Greater Antilles, with a New Species from the Chihuahuan Desert. Systematic Botany, 2016, 41, 823-838.	0.2	5
919	Putting <i>Parasemia</i> in its phylogenetic place: a molecular analysis of the subtribe Arctiina (Lepidoptera). Systematic Entomology, 2016, 41, 844-853.	1.7	55
920	Phylloporia spathulata sensu stricto and two new South American stipitate species of Phylloporia (Hymenochaetaceae). Phytotaxa, 2016, 257, 133.	0.1	14
921	Phellinotus, a new neotropical genus in the Hymenochaetaceae (Basidiomycota, Hymenochaetales). Phytotaxa, 2016, 261, 218.	0.1	25
922	No longer shipwrecked—Selkirkia (Boraginaceae) back on the mainland with generic rearrangements in South American <i>Omphalodes</i> -based on molecular data. Phytotaxa, 2016, 270, 231.	0.1	12
923	A new species of Youngia (Asteraceae, tribe Cichorieae) from Yunnan, China. Phytotaxa, 2016, 275, 140.	0.1	5
924	Begonia leipingensis (Begoniaceae), a new compound-leaved species with unique petiolule pattern from Guangxi of China. Phytotaxa, 2016, 244, 45.	0.1	12
925	A phylogenetic re-definition of the diatom genus Bacterosira (Thalassiosirales, Bacillariophyta), with the transfer of Thalassiosira constricta based on morphological and molecular characters. Phytotaxa, 2016, 245, 1.	0.1	9
926	Three new species of Russulaceae from India based on morphology and molecular phylogeny. Phytotaxa, 2016, 246, 61.	0.1	6
927	Genetic differentiating Aphis fabae and Aphis craccivora (Hemiptera: Sternorrhyncha: Aphididae) populations in Egypt using mitochondrial COI. Biologia (Poland), 2016, 71, 1266-1273.	0.8	2
928	Assessment of virulence potential of uncharacterized Enterococcus faecalis strains using pan genomic approach—Identification of pathogen-specific and habitat-specific genes. Scientific Reports, 2016, 6, 38648.	1.6	24
929	<i>Aspergillus</i> is monophyletic: Evidence from multiple gene phylogenies and extrolites profiles. Studies in Mycology, 2016, 85, 199-213.	4.5	61
930	Archelosaurian color vision, parietal eye loss and the crocodylian nocturnal bottleneck. Molecular Biology and Evolution, 2017, 34, msw265.	3.5	31
931	Identification of aphid (Hemiptera: Aphididae) species of economic importance in Kenya using DNA barcodes and PCR-RFLP-based approach. Bulletin of Entomological Research, 2016, 106, 63-72.	0.5	18
932	Phylogeny of Stenopodidea (Crustacea : Decapoda) shrimps inferred from nuclear and mitochondrial genes reveals non-monophyly of the families Spongicolidae and Stenopididae and most of their composite genera. Invertebrate Systematics, 2016, 30, 479.	0.5	22
933	Redescription of Pelagia benovici into a new jellyfish genus, Mawia, gen. nov., and its phylogenetic position within Pelagiidae (Cnidaria : Scyphozoa : Semaestomeae). Invertebrate Systematics, 2016, 30, 523.	0.5	16
934	Inocybe gregaria, a new species of the Inosperma clade from tropical India. Phytotaxa, 2016, 286, 107.	0.1	8
935	A tiny new species of Specklinia from Haiti—Parc National Naturel Macaya and new combinations in Acianthera (Pleurothallidinae, Epidendreae, Epidendroideae, Orchidaceae). Phytotaxa, 2016, 275, 263.	0.1	0

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936	Fossil record of stem groups employed in evaluating the chronogram of insects (Arthropoda: Tj ETQq0 0 0 rgBT /Oyrllock 10 Tf 50 742	1.6	36
937	Amauroderma calcitum sp. nov. and notes on taxonomy and distribution of Amauroderma species (Ganodermataceae). Phytotaxa, 2016, 244, 101.	0.1	14
938	T-BAS: Tree-Based Alignment Selector toolkit for phylogenetic-based placement, alignment downloads and metadata visualization: an example with the Pezizomycotina tree of life. Bioinformatics, 2017, 33, 1160-1168.	1.8	55
939	Evolution of DNA Methylation across Insects. Molecular Biology and Evolution, 2017, 34, msw264.	3.5	246
940	Genetic variation in Mycobacterium tuberculosis isolates from a London outbreak associated with isoniazid resistance. BMC Medicine, 2016, 14, 117.	2.3	16
941	Using nearly full-genome HIV sequence data improves phylogeny reconstruction in a simulated epidemic. Scientific Reports, 2016, 6, 39489.	1.6	23
942	Genomes of coral dinoflagellate symbionts highlight evolutionary adaptations conducive to a symbiotic lifestyle. Scientific Reports, 2016, 6, 39734.	1.6	303
943	The complete chloroplast genome sequence of <i>Schefflera octophylla</i> . Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2016, 27, 4685-4686.	0.7	6
944	Global map of oxytocin/vasopressin-like neuropeptide signalling in insects. Scientific Reports, 2016, 6, 39177.	1.6	35
945	A Phylogeny-Based Global Nomenclature System and Automated Annotation Tool for H1 Hemagglutinin Genes from Swine Influenza A Viruses. MSphere, 2016, 1, .	1.3	151
946	On the identity of <i>Sium frigidum</i> (Apiaceae). Phytotaxa, 2016, 288, 265.	0.1	1
947	Sequential Turnovers of Sex Chromosomes in African Clawed Frogs (<i>Xenopus</i>) Suggest Some Genomic Regions Are Good at Sex Determination. G3: Genes, Genomes, Genetics, 2016, 6, 3625-3633.	0.8	45
948	Origin of a major infectious disease in vertebrates: The timing of Cryptosporidium evolution and its hosts. Parasitology, 2016, 143, 1683-1690.	0.7	17
949	Three new species of Entoloma subgenus Nolanea from India based on morphology and molecular phylogeny. Phytotaxa, 2016, 286, 232.	0.1	3
950	Sarcodontia crocea (Basidiomycota, Polyporales) is unrelated to Spongipellis. Phytotaxa, 2016, 288, 197.	0.1	6
951	Genome Sequence and Analysis of a Stress-Tolerant, Wild-Derived Strain of Saccharomyces cerevisiae Used in Biofuels Research. G3: Genes, Genomes, Genetics, 2016, 6, 1757-1766.	0.8	61
952	An outbreak of Shiga toxin-producing <i>Escherichia coli</i> serogroup O157 linked to a lamb-feeding event. Epidemiology and Infection, 2016, 144, 2494-2500.	1.0	21
953	The genome of Rhizobiales bacteria in predatory ants reveals urease gene functions but no genes for nitrogen fixation. Scientific Reports, 2016, 6, 39197.	1.6	55

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954	Three new species of <i>Calocybella</i> from India based on morphology and molecular phylogeny. <i>Phytotaxa</i> , 2016, 255, 133.	0.1	8
955	Phylogenetic Position and Morphological Observation of the <i>Ctenocladus circinnatus</i> Borzi, a rare green alga from Changtang Plateau, China. <i>Phytotaxa</i> , 2016, 260, 75.	0.1	5
956	A new species of <i>Inocybe</i> representing the <i>Nothocybe</i> lineage. <i>Phytotaxa</i> , 2016, 267, 40.	0.1	9
957	<i>Gloeocantharellus aculeatus</i> (Gomphaceae), a new neotropical species in the gomphoid-phalloid clade. <i>Phytotaxa</i> , 2016, 268, 193.	0.1	7
958	<i>Tuber shii</i> sp. nov., a sister species of <i>T. jinshajiangense</i> from China in <i>Puberulum</i> group. <i>Phytotaxa</i> , 2016, 269, 279.	0.1	4
959	Marasmioid and gymnopoid fungi of the Republic of Korea. 8. <i>Gymnopus</i> section <i>Impudicae</i> . <i>Phytotaxa</i> , 2016, 286, 75.	0.1	9
960	The genome of the Gulf pipefish enables understanding of evolutionary innovations. <i>Genome Biology</i> , 2016, 17, 258.	3.8	76
961	The Timetree of Prokaryotes: New Insights into Their Evolution and Speciation. <i>Molecular Biology and Evolution</i> , 2017, 34, msw245.	3.5	69
962	Embryonic chirality and the evolution of spiralian left-right asymmetries. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2016, 371, 20150411.	1.8	24
963	The fungal genus <i>Tricholomopsis</i> (Agaricales) in New Zealand, including <i>Tricholomopsis scabra</i> sp. nov.. <i>Phytotaxa</i> , 2016, 288, 69.	0.1	6
964	Slowly dispersing neotenic beetles can speciate on a penny coin and generate space-limited diversity in the tropical mountains. <i>Scientific Reports</i> , 2016, 6, 33579.	1.6	29
965	The complete mitochondrial genome of the parthenogenetic Caucasian rock lizard <i>Darevskia unisexualis</i> (Squamata: Lacertidae) contains long tandem repeat formed by 59bp monomer. <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 875-877.	0.2	1
966	“Missing links” alive? Novel taxa represent morphological transitions between distinctive phenotypes among extant Graphidaceae (lichenized Ascomycota: Ostropales). <i>Phytotaxa</i> , 2016, 268, 110.	0.1	6
967	<i>Chondrophycus anabeliae</i> (Rhodomelaceae, Ceramiales), a new species in the <i>Laurencia</i> complex from the Mexican Caribbean. <i>Phytotaxa</i> , 2016, 283, 259.	0.1	5
968	Evolutionary study of <i>Yersinia</i> genomes deciphers emergence of human pathogenic species. <i>Scientific Reports</i> , 2016, 6, 36116.	1.6	14
969	Production of hemolysin BL by <i>Bacillus cereus</i> group isolates of dairy origin is associated with whole-genome phylogenetic clade. <i>BMC Genomics</i> , 2016, 17, 581.	1.2	77
970	Extreme genomic erosion after recurrent demographic bottlenecks in the highly endangered Iberian lynx. <i>Genome Biology</i> , 2016, 17, 251.	3.8	131
972	A new species of <i>Zygaspis</i> (Reptilia: Squamata: Amphisbaenidae) from north-eastern Mozambique. <i>African Journal of Herpetology</i> , 2016, 65, 115-122.	0.3	10

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973	Comprehensive Genome Analysis of Carbapenemase-Producing <i>Enterobacter</i> spp.: New Insights into Phylogeny, Population Structure, and Resistance Mechanisms. <i>MBio</i> , 2016, 7, .	1.8	154
974	Mitochondrial Phylogenomics yields Strongly Supported Hypotheses for Ascaridomorph Nematodes. <i>Scientific Reports</i> , 2016, 6, 39248.	1.6	26
975	Phylogenetic position and independent generic status of <i>Indocypraea</i> (Asteraceae-Heliantheae-Ecliptinae): evidence from chloroplast DNA sequences. <i>Phytotaxa</i> , 2016, 277, 146.	0.1	2
976	Deep divergence and evidence for translocations between Iranian and European populations of the alfalfa weevil (Coleoptera: Curculionidae) based on mitochondrial DNA. <i>Canadian Entomologist</i> , 2016, 148, 703-715.	0.4	2
977	New species in <i>Bryoria</i> (<i>Parmeliaceae</i> , Lecanoromycetes) from north-west North America. <i>Lichenologist</i> , 2016, 48, 355-365.	0.5	3
978	The nuclear genome of <i>Rhazya stricta</i> and the evolution of alkaloid diversity in a medically relevant clade of Apocynaceae. <i>Scientific Reports</i> , 2016, 6, 33782.	1.6	26
979	A Preliminary Molecular and Phylogenetic Analysis of the Genome of a Novel Endogenous Retrovirus in the Sea Slug <i>Elysia chlorotica</i> . <i>Biological Bulletin</i> , 2016, 231, 236-244.	0.7	5
980	The impact of fossil data on annelid phylogeny inferred from discrete morphological characters. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016, 283, 20161378.	1.2	41
981	Corrigendum to: Phylogeny of Stenopodidea (Crustacea: Decapoda) shrimps inferred from nuclear and mitochondrial genes reveals non-monophyly of the families Spongicolidae and Stenopididae and most of their composite genera. <i>Invertebrate Systematics</i> , 2016, 30, 650.	0.5	0
982	Complex Evolutionary Dynamics of Massively Expanded Chemosensory Receptor Families in an Extreme Generalist Chelicerate Herbivore. <i>Genome Biology and Evolution</i> , 2016, 8, 3323-3339.	1.1	42
983	The Asian arowana (<i>Scleropages formosus</i>) genome provides new insights into the evolution of an early lineage of teleosts. <i>Scientific Reports</i> , 2016, 6, 24501.	1.6	89
984	Chloroplast phylogenomic analyses reveal the deepest-branching lineage of the Chlorophyta, Palmophyllophyceae class. nov.. <i>Scientific Reports</i> , 2016, 6, 25367.	1.6	98
985	Shedding new light on old algae: Matching names and sequences in the brown algal genus <i>Lobophora</i> (Dictyotales, Phaeophyceae). <i>Taxon</i> , 2016, 65, 689-707.	0.4	36
986	Effective application of next-generation sequencing (NGS) approaches in systematics and population genetics: case studies in <i>Eucalyptus</i> and <i>Acacia</i> . <i>Australian Systematic Botany</i> , 2016, 29, 235.	0.3	3
987	Integrative analysis of the West African <i>Ceraceosorus africanus</i> sp. nov. provides insights into the diversity, biogeography, and evolution of the enigmatic Ceraceosorales (Fungi: Ustilaginomycotina). <i>Organisms Diversity and Evolution</i> , 2016, 16, 743-760.	0.7	13
988	The complete salmonid IGF-IR gene repertoire and its transcriptional response to disease. <i>Scientific Reports</i> , 2016, 6, 34806.	1.6	16
989	Complete mitochondrial genome of the parrotfish <i>Calotomus japonicus</i> (Osteichthyes: Scaridae) with implications based on the phylogenetic position. <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 643-645.	0.2	2
990	The Divisible Load Balance Problem with Shared Cost and Its Application to Phylogenetic Inference. , 2016, , .		5

#	ARTICLE	IF	CITATIONS
991	Discrete phenotypes are not underpinned by genome-wide genetic differentiation in the squat lobster <i>Munida gregaria</i> (Crustacea: Decapoda: Munididae): a multi-marker study covering the Patagonian shelf. <i>BMC Evolutionary Biology</i> , 2016, 16, 258.	3.2	8
992	Efficient Detection of Repeating Sites to Accelerate Phylogenetic Likelihood Calculations. <i>Systematic Biology</i> , 2017, 66, syw075.	2.7	22
993	Morphological, chemical and species delimitation analyses provide new taxonomic insights into two groups of <i>Rinodina</i> . <i>Lichenologist</i> , 2016, 48, 469-488.	0.5	22
994	Redefining the generic limits of <i>Winthemia</i> (Diptera : Tachinidae). <i>Invertebrate Systematics</i> , 2016, 30, 274.	0.5	3
995	Close ecological relationship among species facilitated horizontal transfer of retrotransposons. <i>BMC Evolutionary Biology</i> , 2016, 16, 201.	3.2	12
996	Transcriptome sequencing and marker development in winged bean (<i>Psophocarpus tetragonolobus</i> ;) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	1.6	67
997	Ebola Virus Persistence in Breast Milk After No Reported Illness: A Likely Source of Virus Transmission From Mother to Child. <i>Clinical Infectious Diseases</i> , 2016, 64, ciw793.	2.9	70
998	Large-Scale Comparative Analysis Reveals the Mechanisms Driving Plastomic Compaction, Reduction, and Inversions in Conifers II (Cupressophytes). <i>Genome Biology and Evolution</i> , 2016, 8, eww278.	1.1	41
999	Aquatic Snails <i>Ecrobia maritima</i> (Milaschewitsch, 1916) and <i>E. Ventrosa</i> (Montagu, 1803) (Caenogastropoda: Hydrobiidae) in the East Mediterranean and Black Sea. <i>Annales Zoologici</i> , 2016, 66, 477-486.	0.1	19
1000	Receptor tyrosine kinase genes respond transcriptionally to sublethal doses of five insecticides by a mode-of-action independent way in <i>Leptinotarsa decemlineata</i> (Say). <i>Journal of Asia-Pacific Entomology</i> , 2016, 19, 1103-1110.	0.4	3
1001	Multiple host switching events shape the evolution of symbiotic palaemonid shrimps (Crustacea:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.6	64
1002	Whole genome resequencing of the human parasite <i>Schistosoma mansoni</i> reveals population history and effects of selection. <i>Scientific Reports</i> , 2016, 6, 20954.	1.6	72
1003	The forgotten <i>Calonectria</i> collection: Pouring old wine into new bags. <i>Studies in Mycology</i> , 2016, 85, 159-198.	4.5	38
1004	Rapid dissemination of taxonomic discoveries based on DNA barcoding and morphology. <i>Scientific Reports</i> , 2016, 6, 37066.	1.6	36
1005	Dental scales could occur in all scaled subfamilies of Entomobryidae (Collembola): new definition of Entomobryinae with description of a new genus and three new species. <i>Invertebrate Systematics</i> , 2016, 30, 598.	0.5	9
1006	From sequence reads to evolutionary inferences. , 0, , 305-335.		0
1007	Comprehensive analysis of draft genomes of two closely related pseudomonas syringae phylogroup 2b strains infecting mono- and dicotyledon host plants. <i>BMC Genomics</i> , 2016, 17, 1010.	1.2	8
1008	Genetic Drift, Not Life History or RNAi, Determine Long-Term Evolution of Transposable Elements. <i>Genome Biology and Evolution</i> , 2016, 8, 2964-2978.	1.1	58

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1010	Genetic diversity of Bartonella genotypes found in the striped field mouse (<i>Apodemus agrarius</i>) in Central Europe. <i>Parasitology</i> , 2016, 143, 1437-1442.	0.7	23
1011	Molecular Evolutionary Consequences of Island Colonization. <i>Genome Biology and Evolution</i> , 2016, 8, 1876-1888.	1.1	33
1012	HPTree: Reconstructing phylogenetic trees for ultra-large unaligned DNA sequences via NJ model and Hadoop. , 2016, , .		8
1013	The Number, Organization, and Size of Polymorphic Membrane Protein Coding Sequencesas well as the Most Conserved Pmp Protein Differ within and across <i>Chlamydia</i> Species. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2016, 26, 333-344.	1.0	10
1014	Evidence from Multiple Species that Spider Silk Glue Component ASG2 is a Spidroin. <i>Scientific Reports</i> , 2016, 6, 21589.	1.6	54
1015	Seven at one blow: the origin of major lineages of the viviparous Lycian salamanders (<i>Lyciasalamandra</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 373-387.	0.1	16
1016	Evidence of positive selection associated with placental loss in tiger sharks. <i>BMC Evolutionary Biology</i> , 2016, 16, 126.	3.2	18
1017	libFLASM: a software library for fixed-length approximate string matching. <i>BMC Bioinformatics</i> , 2016, 17, 454.	1.2	6
1018	Development of a universal and simplified ddRAD library preparation approach for SNP discovery and genotyping in angiosperm plants. <i>Plant Methods</i> , 2016, 12, 39.	1.9	86
1019	Multilocus phylogenetic analyses reveal unexpected abundant diversity and significant disjunct distribution pattern of the Hedgehog Mushrooms (<i>Hydnum</i> L.). <i>Scientific Reports</i> , 2016, 6, 25586.	1.6	29
1020	Molecular classification based on apomorphic amino acids (Arthropoda, Hexapoda): Integrative taxonomy in the era of phylogenomics. <i>Scientific Reports</i> , 2016, 6, 28308.	1.6	4
1021	Expansion of the molecular and morphological diversity of Acanthamoebidae (Centramoebida,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 58	1.9	58
1022	A molecular phylogeny of the <i>Laelia</i> alliance (Orchidaceae) and a reassessment of <i>Laelia</i> and <i>Schomburgkia</i>. <i>Taxon</i> , 2016, 65, 1249-1262.	0.4	14
1024	Identification and characterization of toll-like receptors (TLRs) in the Chinese tree shrew (<i>Tupaia</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 22	1.0	22
1025	Phylogenetic relationship of Japanese isolates belonging to the <i>Grosmannia piceiperda</i> complex (Ophiostomatales). <i>Mycoscience</i> , 2016, 57, 123-135.	0.3	5
1026	Revisiting phylogenetic diversity and cryptic species of <i>Cenococcum geophilum</i> sensu lato. <i>Mycorrhiza</i> , 2016, 26, 529-540.	1.3	41
1027	Identification and characterization of <i>Ditylenchus</i> spp. populations from garlic in New York State, USA. <i>Tropical Plant Pathology</i> , 2016, 41, 193-197.	0.8	6
1028	Whole genome sequencing to complement tuberculosis drug resistance surveys in Uganda. <i>Infection, Genetics and Evolution</i> , 2016, 40, 8-16.	1.0	28

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1029	Emerging investigators series: microbial communities in full-scale drinking water distribution systems – a meta-analysis. <i>Environmental Science: Water Research and Technology</i> , 2016, 2, 631-644.	1.2	98
1030	<i>Enomicrobium proavitum</i> , the first isolate of <i>Enomicrobia</i> class. nov. (phylum <i>Enomicrobia</i>) – an ultramicrobacterium with an unusual cell cycle that fixes nitrogen with a <i>GS</i> nitrogenase. <i>Environmental Microbiology</i> , 2016, 18, 191-204.	1.8	125
1031	Global Genomic Diversity of Human Papillomavirus 11 Based on 433 Isolates and 78 Complete Genome Sequences. <i>Journal of Virology</i> , 2016, 90, 5503-5513.	1.5	20
1032	Two Outbreak Sources of Influenza A (H7N9) Viruses Have Been Established in China. <i>Journal of Virology</i> , 2016, 90, 5561-5573.	1.5	92
1033	Sorting out relationships among the grouse and ptarmigan using intron, mitochondrial, and ultra-conserved element sequences. <i>Molecular Phylogenetics and Evolution</i> , 2016, 98, 123-132.	1.2	32
1034	Decoupled genomic elements and the evolution of partner quality in nitrogen-fixing rhizobia. <i>Ecology and Evolution</i> , 2016, 6, 1317-1327.	0.8	14
1035	Complete mitochondrial DNA genome of bonnethead shark, <i>Sphyrna tiburo</i> , and phylogenetic relationships among main superorders of modern elasmobranchs. <i>Meta Gene</i> , 2016, 7, 48-55.	0.3	15
1036	Clade-specific positive selection on a developmental gene: BRANCHLESS TRICHOME and the evolution of stellate trichomes in <i>Physaria</i> (Brassicaceae). <i>Molecular Phylogenetics and Evolution</i> , 2016, 100, 31-40.	1.2	9
1037	Pseudocospiculation of the mycoparasite <i>Cosmospora</i> with their fungal hosts. <i>Ecology and Evolution</i> , 2016, 6, 1504-1514.	0.8	16
1038	Chromosome number reduction in the sister clade of <i>Carica papaya</i> with concomitant genome size doubling. <i>American Journal of Botany</i> , 2016, 103, 1082-1088.	0.8	26
1039	Data supporting the nuclear phylogenomics of the palm subfamily Arecoideae (Arecaceae). <i>Data in Brief</i> , 2016, 7, 532-536.	0.5	1
1040	The main nitrate transporter of the dinoflagellate <i>Lingulodinium polyedrum</i> is constitutively expressed and not responsible for daily variations in nitrate uptake rates. <i>Harmful Algae</i> , 2016, 55, 272-281.	2.2	9
1041	Resolving the higher-order phylogenetic relationships of the circumtropical Mabuya group (Squamata: Scincidae): An out-of-Asia diversification. <i>Molecular Phylogenetics and Evolution</i> , 2016, 102, 220-232.	1.2	44
1042	Phylogeographic and population genetic analyses reveal multiple species of <i>Boa</i> and independent origins of insular dwarfism. <i>Molecular Phylogenetics and Evolution</i> , 2016, 102, 104-116.	1.2	47
1043	Opsin Repertoire and Expression Patterns in Horseshoe Crabs: Evidence from the Genome of <i>Limulus polyphemus</i> (Arthropoda: Chelicerata). <i>Genome Biology and Evolution</i> , 2016, 8, 1571-1589.	1.1	50
1044	An evolutionary roadmap to the microtubule-associated protein MAP Tau. <i>BMC Genomics</i> , 2016, 17, 264.	1.2	48
1045	Evolution of the SOUL Heme-Binding Protein Superfamily Across Eukarya. <i>Journal of Molecular Evolution</i> , 2016, 82, 279-290.	0.8	15
1046	Mole ghrelin: cDNA cloning, gene expression, and diverse molecular forms in <i>Mogera imaizumii</i> . <i>General and Comparative Endocrinology</i> , 2016, 232, 199-210.	0.8	2

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1047	Multiple instances of paraphyletic species and cryptic taxa revealed by mitochondrial and nuclear RAD data for Calandrella larks (Aves: Alaudidae). <i>Molecular Phylogenetics and Evolution</i> , 2016, 102, 233-245.	1.2	17
1048	New species and new records in the genus <i>Usnea</i> (Parmeliaceae), lichenized Ascomycota) from tropical South America. <i>Lichenologist</i> , 2016, 48, 71-93.	0.5	12
1049	Species limits, interspecific hybridization and phylogeny in the cryptic land snail complex <i>Pyramidula</i> : The power of RADseq data. <i>Molecular Phylogenetics and Evolution</i> , 2016, 101, 267-278.	1.2	53
1050	Characterization of the Cadherin-Catenin Complex of the Sea Anemone <i>Nematostella vectensis</i> and Implications for the Evolution of Metazoan Cell Adhesion. <i>Molecular Biology and Evolution</i> , 2016, 33, 2016-2029.	3.5	22
1051	Nondegenerative Evolution in Ancient Heritable Bacterial Endosymbionts of Fungi. <i>Molecular Biology and Evolution</i> , 2016, 33, 2216-2231.	3.5	14
1052	Evaluation of Molecular Methods for Serotyping <i>Shigella flexneri</i> . <i>Journal of Clinical Microbiology</i> , 2016, 54, 1456-1461.	1.8	32
1053	Regulation of genetic flux between bacteria by restriction-modification systems. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 5658-5663.	3.3	161
1054	Fungal diversity notes 253-366: taxonomic and phylogenetic contributions to fungal taxa. <i>Fungal Diversity</i> , 2016, 78, 1-237.	4.7	239
1055	Molecular Phylogeny of Cypridoid Freshwater Ostracods (Crustacea: Ostracoda), Inferred from 18S and 28S rDNA Sequences. <i>Zoological Science</i> , 2016, 33, 179.	0.3	24
1056	Phylogenetic position of the Wallcreeper <i>Tichodroma muraria</i> . <i>Journal of Ornithology</i> , 2016, 157, 913-918.	0.5	5
1057	Evolutionary Changes on the Way to Clathrin-Mediated Endocytosis in Animals. <i>Genome Biology and Evolution</i> , 2016, 8, 588-606.	1.1	23
1058	Sexual differences in prevalence of a new species of trypanosome infecting tamar frogs. <i>International Journal for Parasitology: Parasites and Wildlife</i> , 2016, 5, 40-47.	0.6	39
1059	Population genomics of local adaptation versus speciation in coral reef fishes (<i>Hypoplectrus</i> spp.). <i>Evolution</i> , 2016, 70, 1000-1010.	0.8	30
1060	New molecular data shed light on the global phylogeny and species limits of the <i>Rhipicephalus sanguineus</i> complex. <i>Ticks and Tick-borne Diseases</i> , 2016, 7, 798-807.	1.1	32
1061	Molecular phylogenetics of the <i>Ronbergia</i> Alliance (Bromeliaceae, Bromelioideae) and insights into their morphological evolution. <i>Molecular Phylogenetics and Evolution</i> , 2016, 100, 1-20.	1.2	43
1062	Phylogenomic analysis of <i>Candidatus</i> <i>Thaumoglossum</i> species: free-living representatives from a <i>Tenericutes</i> clade found in methane seeps. <i>ISME Journal</i> , 2016, 10, 2679-2692.	4.4	88
1063	First report of the land planarian <i>Diversibipalium multilineatum</i> (Makino & Shirasawa, 1983) (Platyhelminthes, Tricladida, Continenticola) in Europe. <i>Zootaxa</i> , 2016, 4067, 577-80.	0.2	17
1064	Indels ascertain the phylogenetic position of <i>Coleodactylus elizae</i> Gon& Salves, Torquato, Skuk & Sena, 2012 (Gekkota: Sphaerodactylidae). <i>Zootaxa</i> , 2016, 4084, 147-50.	0.2	1

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1065	A New Orthology Assessment Method for Phylogenomic Data: Unrooted Phylogenetic Orthology. <i>Molecular Biology and Evolution</i> , 2016, 33, 2117-2134.	3.5	67
1066	Bivalve-specific gene expansion in the pearl oyster genome: implications of adaptation to a sessile lifestyle. <i>Zoological Letters</i> , 2016, 2, 3.	0.7	133
1067	Phylogenomic analyses reveal novel relationships among snake families. <i>Molecular Phylogenetics and Evolution</i> , 2016, 100, 160-169.	1.2	46
1068	Two asian jumbo phages, Φ RSL2 and Φ RSF1, infect <i>Ralstonia solanacearum</i> and show common features of Φ KZ-related phages. <i>Virology</i> , 2016, 494, 56-66.	1.1	56
1069	The resurrection of the genus <i>Bergia</i> (Anthozoa, Zoantharia, Parazoanthidae). <i>Systematics and Biodiversity</i> , 2016, 14, 63-73.	0.5	11
1070	Apolipoprotein L1 Variant Associated with Increased Susceptibility to Trypanosome Infection. <i>MBio</i> , 2016, 7, e02198-15.	1.8	18
1071	A new species of <i>Rattus</i> (Rodentia: Muridae) from Manus Island, Papua New Guinea. <i>Journal of Mammalogy</i> , 2016, 97, 861-878.	0.6	13
1072	Genomic and Phylogenetic Analysis of the Complete Plastid Genome of the California Endemic Seaweed <i>Wildemanella schizophylla</i> (Bangiaceae). <i>Madroño</i> , 2016, 63, 34-38.	0.3	5
1073	A fungal pathogen secretes plant alkalizing peptides to increase infection. <i>Nature Microbiology</i> , 2016, 1, 16043.	5.9	249
1074	Molecular phylogenetic relationships of the Andean genus <i>Aylosteria</i> Sp. (Cactaceae, Trichocereae), a new classification and a morphological identification key. <i>Plant Systematics and Evolution</i> , 2016, 302, 763-780.	0.3	5
1075	<i>Dionysia robusta</i> (Primulaceae), a new species from W Iran. <i>Willdenowia</i> , 2016, 46, 105.	0.5	2
1076	The Genome and Methyloome of a Subsocial Small Carpenter Bee, <i>Ceratina calcarata</i> . <i>Genome Biology and Evolution</i> , 2016, 8, 1401-1410.	1.1	71
1077	Detection of the plasmid-mediated <i>mcr-1</i> gene conferring colistin resistance in human and food isolates of <i>Salmonella enterica</i> and <i>Escherichia coli</i> in England and Wales. <i>Journal of Antimicrobial Chemotherapy</i> , 2016, 71, 2300-2305.	1.3	247
1078	Identification of glutathione S-transferase genes in <i>Leptinotarsa decemlineata</i> and their expression patterns under stress of three insecticides. <i>Pesticide Biochemistry and Physiology</i> , 2016, 133, 26-34.	1.6	68
1079	A robust phylogeny among major lineages of the East African cichlids. <i>Molecular Phylogenetics and Evolution</i> , 2016, 100, 234-242.	1.2	30
1080	Genome Sequencing of the Phytoseiid Predatory Mite <i>Metaseiulus occidentalis</i> Reveals Completely Atomized <i>Hox</i> Genes and Superdynamic Intron Evolution. <i>Genome Biology and Evolution</i> , 2016, 8, 1762-1775.	1.1	102
1081	Genomics of a phototrophic nitrite oxidizer: insights into the evolution of photosynthesis and nitrification. <i>ISME Journal</i> , 2016, 10, 2669-2678.	4.4	32
1082	Molecular inference, multivariate morphometrics and ecological assessment are applied in concert to delimit species in the <i>Russula clavipes</i> complex. <i>Mycologia</i> , 2016, 108, 716-730.	0.8	14

#	ARTICLE	IF	CITATIONS
1083	Phylogenetics, classification, and biogeography of the treefrogs (Amphibia: Anura: Arboranae). <i>Zootaxa</i> , 2016, 4104, 1-109.	0.2	294
1084	<i>Sarcodon</i> in the Neotropics II: four new species from Colombia and a key to the regional species. <i>Mycologia</i> , 2016, 108, 791-805.	0.8	9
1085	Phylogenetic analysis of canine distemper virus in South America clade 1 reveals unique molecular signatures of the local epidemic. <i>Infection, Genetics and Evolution</i> , 2016, 41, 135-141.	1.0	22
1086	Out of the Sichuan Basin: Rapid species diversification of the freshwater crabs in Sinopotamon (Decapoda: Brachyura: Potamidae) endemic to China. <i>Molecular Phylogenetics and Evolution</i> , 2016, 100, 80-94.	1.2	22
1087	Genetic characterization of Enterovirus 71 strains circulating in Vietnam in 2012. <i>Virology</i> , 2016, 495, 1-9.	1.1	25
1088	Genomic analysis and D-xylose fermentation of three novel <i>Spathaspora</i> species: <i>Spathaspora girioi</i> sp. nov., <i>Spathaspora hagerdaliae</i> f. a., sp. nov. and <i>Spathaspora gorwiae</i> f. a., sp. nov.. <i>FEMS Yeast Research</i> , 2016, 16, fow044.	1.1	47
1089	Combining genetic and distributional approaches to sourcing introduced species: a case study on the Nile monitor (<i>Varanus niloticus</i>) in Florida. <i>Royal Society Open Science</i> , 2016, 3, 150619.	1.1	4
1090	Morphology, phylogeny, and taxonomy of <i>Microthlaspi</i> (Brassicaceae: Coluteocarpeae) and related genera. <i>Taxon</i> , 2016, 65, 79-98.	0.4	30
1091	A phylogeny of Cephaloziaceae (Jungermanniopsida) based on nuclear and chloroplast DNA markers. <i>Organisms Diversity and Evolution</i> , 2016, 16, 727-742.	0.7	18
1092	Unexpected Interfarm Transmission Dynamics during a Highly Pathogenic Avian Influenza Epidemic. <i>Journal of Virology</i> , 2016, 90, 6401-6411.	1.5	14
1094	The world's smallest Campanulaceae: <i>Lysipomia mitsyae</i> sp. nov.. <i>Taxon</i> , 2016, 65, 305-314.	0.4	2
1095	An Outbreak of Human Listeriosis in England between 2010 and 2012 Associated with the Consumption of Pork Pies. <i>Journal of Food Protection</i> , 2016, 79, 732-740.	0.8	19
1096	The <i>Ophiostoma clavatum</i> species complex: a newly defined group in the Ophiostomatales including three novel taxa. <i>Antonie Van Leeuwenhoek</i> , 2016, 109, 987-1018.	0.7	22
1097	Genetics, Transcriptional Profiles, and Catalytic Properties of the UDP-Arabinose Mutase Family from Barley. <i>Biochemistry</i> , 2016, 55, 322-334.	1.2	13
1098	Inconsistency of Species Tree Methods under Gene Flow. <i>Systematic Biology</i> , 2016, 65, 843-851.	2.7	146
1099	Exploring Phylogenetic Relationships within Myriapoda and the Effects of Matrix Composition and Occupancy on Phylogenomic Reconstruction. <i>Systematic Biology</i> , 2016, 65, 871-889.	2.7	93
1100	Hiding in plain sight: <i>Koshicola spirodelophila</i> gen. et sp. nov. (Chaetopeltidales,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 107 Td (C) polyrhiza. <i>American Journal of Botany</i> , 2016, 103, 865-875.	0.8	27
1101	The logic of DNA replication in double-stranded DNA viruses: insights from global analysis of viral genomes. <i>Nucleic Acids Research</i> , 2016, 44, 4551-4564.	6.5	80

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1102	Terrace Aware Data Structure for Phylogenomic Inference from Supermatrices. <i>Systematic Biology</i> , 2016, 65, 997-1008.	2.7	1,453
1103	Population-Scale Sequencing Data Enable Precise Estimates of Y-STR Mutation Rates. <i>American Journal of Human Genetics</i> , 2016, 98, 919-933.	2.6	65
1104	Cultural and cytological characterization of <i>Dacryopinax primogenitus</i> , a new species in the <i>Dacrymycetes</i> with a fully sequenced genome. <i>Mycologia</i> , 2016, 108, 457-468.	0.8	4
1105	Reducing long-branch effects in multi-protein data uncovers a close relationship between Alveolata and Rhizaria. <i>Molecular Phylogenetics and Evolution</i> , 2016, 101, 1-7.	1.2	25
1106	Two DNA barcodes and morphology for multi-method species delimitation in <i>Bonnetina</i> tarantulas (Araneae: Theraphosidae). <i>Molecular Phylogenetics and Evolution</i> , 2016, 101, 176-193.	1.2	51
1107	Metagenomic Evidence for the Presence of <i>Comammox Nitrospira</i> -Like Bacteria in a Drinking Water System. <i>MSphere</i> , 2016, 1, .	1.3	229
1108	Redescription <i>Cyrtodactylus lateralis</i> (Werner) (Squamata: Gekkonidae) and Phylogeny of the Prehensile-tailed <i>Cyrtodactylus</i> . <i>Zootaxa</i> , 2016, 4107, 517-40.	0.2	19
1109	Revisiting the phylogeny of <i>Bombacoideae</i> (Malvaceae): Novel relationships, morphologically cohesive clades, and a new tribal classification based on multilocus phylogenetic analyses. <i>Molecular Phylogenetics and Evolution</i> , 2016, 101, 56-74.	1.2	50
1110	The species pair <i>Pseudocyphellaria pilosella-piloselloides</i> (lichenized Ascomycota: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50,422 Td (0.5	10
1111	RubisCO of a nucleoside pathway known from Archaea is found in diverse uncultivated phyla in bacteria. <i>ISME Journal</i> , 2016, 10, 2702-2714.	4.4	98
1112	Consensus properties and their large-scale applications for the gene duplication problem. <i>Journal of Bioinformatics and Computational Biology</i> , 2016, 14, 1642005.	0.3	5
1113	Phylogenetics and biogeography of the endemic Madagascan millipede assassin bugs (Hemiptera: Tj ETQq1 1 0.784314 rgBT /Overlock 12	1.2	12
1114	<i>Phylo.io</i> : Interactive Viewing and Comparison of Large Phylogenetic Trees on the Web. <i>Molecular Biology and Evolution</i> , 2016, 33, 2163-2166.	3.5	170
1115	A barrier to homologous recombination between sympatric strains of the cooperative soil bacterium <i>Myxococcus xanthus</i> . <i>ISME Journal</i> , 2016, 10, 2468-2477.	4.4	52
1116	Punctuated bursts in human male demography inferred from 1,244 worldwide Y-chromosome sequences. <i>Nature Genetics</i> , 2016, 48, 593-599.	9.4	273
1117	Unraveling the origin of the Appalachian gametophyte, <i>Vittaria appalachiana</i> . <i>American Journal of Botany</i> , 2016, 103, 668-676.	0.8	12
1118	Sequencing of whole plastid genomes and nuclear ribosomal DNA of <i>Diospyros</i> species (Ebenaceae) endemic to New Caledonia: many species, little divergence. <i>Annals of Botany</i> , 2016, 117, 1175-1185.	1.4	34
1119	A Rapid and Scalable Method for Multilocus Species Delimitation Using Bayesian Model Comparison and Rooted Triplets. <i>Systematic Biology</i> , 2016, 65, 759-771.	2.7	56

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1120	Identification of fimbrial subunits in the genome of <i>Trueperella pyogenes</i> and association between serum antibodies against fimbrial proteins and uterine conditions in dairy cows. <i>Journal of Dairy Science</i> , 2016, 99, 3765-3776.	1.4	10
1121	A re-evaluation of the taxonomy of phytopathogenic genera <i>Dickeya</i> and <i>Pectobacterium</i> using whole-genome sequencing data. <i>Systematic and Applied Microbiology</i> , 2016, 39, 252-259.	1.2	97
1122	Contrasting evolutionary patterns of 28S and ITS rRNA genes reveal high intragenomic variation in <i>Cephalenchus</i> (Nematoda): Implications for species delimitation. <i>Molecular Phylogenetics and Evolution</i> , 2016, 98, 244-260.	1.2	24
1123	Genomic variation among populations of threatened coral: <i>Acropora cervicornis</i> . <i>BMC Genomics</i> , 2016, 17, 286.	1.2	57
1124	Phylogeny-aware identification and correction of taxonomically mislabeled sequences. <i>Nucleic Acids Research</i> , 2016, 44, 5022-5033.	6.5	97
1125	On simulated annealing phase transitions in phylogeny reconstruction. <i>Molecular Phylogenetics and Evolution</i> , 2016, 101, 46-55.	1.2	11
1126	Multiplexed shotgun sequencing reveals congruent three-genome phylogenetic signals for four botanical sections of the flax genus <i>Linum</i> . <i>Molecular Phylogenetics and Evolution</i> , 2016, 101, 122-132.	1.2	15
1127	Whole-Genome Sequencing for Routine Pathogen Surveillance in Public Health: a Population Snapshot of Invasive <i>Staphylococcus aureus</i> in Europe. <i>MBio</i> , 2016, 7, .	1.8	192
1128	Use of Whole Genome Sequencing and Patient Interviews To Link a Case of Sporadic Listeriosis to Consumption of Prepackaged Lettuce. <i>Journal of Food Protection</i> , 2016, 79, 806-809.	0.8	20
1129	Extensive characterization of the new genus <i>Rickiopora</i> (Polyporales). <i>Fungal Biology</i> , 2016, 120, 1002-1009.	1.1	9
1130	A Novel Lineage of "Naked Filose Amoebae"; <i>Kraken carinae</i> gen. nov. sp. nov. (Cercozoa) with a Remarkable Locomotion by Disassembly of its Cell Body. <i>Protist</i> , 2016, 167, 268-278.	0.6	19
1131	Fast Coalescent-Based Computation of Local Branch Support from Quartet Frequencies. <i>Molecular Biology and Evolution</i> , 2016, 33, 1654-1668.	3.5	650
1132	The complete mitochondrial genome of <i>Anomaloglossus baobatrachus</i> (Amphibia: Anura). <i>Genome Biology and Evolution</i> , 2016, 8, 1-10.	0.2	3
1133	The genome of the largest bony fish, ocean sunfish (<i>Mola mola</i>), provides insights into its fast growth rate. <i>GigaScience</i> , 2016, 5, 36.	3.3	32
1134	<i>Pseudomonas aeruginosa</i> ATCC 9027 is a non-virulent strain suitable for mono-rhamnolipids production. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 9995-10004.	1.7	47
1135	Syllidae mitochondrial gene order is unusually variable for Annelida. <i>Gene</i> , 2016, 594, 89-96.	1.0	17
1136	Microbial Genomics of Ancient Plagues and Outbreaks. <i>Trends in Microbiology</i> , 2016, 24, 978-990.	3.5	50
1137	Microbiome changes through ontogeny of a tick pathogen vector. <i>Molecular Ecology</i> , 2016, 25, 4963-4977.	2.0	140

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1138	A hypervariable genomic island identified in clinical and environmental <i>Mycobacterium avium</i> subsp. <i>hominissuis</i> isolates from Germany. <i>International Journal of Medical Microbiology</i> , 2016, 306, 495-503.	1.5	12
1139	Multi-locus phylogenetic inference among New World Vultures (Aves: Cathartidae). <i>Molecular Phylogenetics and Evolution</i> , 2016, 105, 193-199.	1.2	33
1140	The draft genome of MD-2 pineapple using hybrid error correction of long reads. <i>DNA Research</i> , 2016, 23, 427-439.	1.5	35
1141	Oligotrophic lagoons of the South Pacific Ocean are home to a surprising number of novel eukaryotic microorganisms. <i>Environmental Microbiology</i> , 2016, 18, 4549-4563.	1.8	23
1142	Species of <i>Padina</i> (Dictyotales, Phaeophyceae) in tropical Mexican waters based on molecular-assisted taxonomy. <i>Phycologia</i> , 2016, 55, 673-687.	0.6	11
1143	<i>Seifertia shangrilaensis</i> sp. nov. (Melanommataceae), a new species from Southwest China. <i>Phytotaxa</i> , 2016, 273, 34.	0.1	9
1144	Population Genetics of <i>Hirsutella rhossiliensis</i> , a Dominant Parasite of Cyst Nematode Juveniles on a Continental Scale. <i>Applied and Environmental Microbiology</i> , 2016, 82, 6317-6325.	1.4	9
1145	Transcriptome sequencing reveals genome-wide variation in molecular evolutionary rate among ferns. <i>BMC Genomics</i> , 2016, 17, 692.	1.2	16
1146	Phylogeny and generic delimitation in Molluginaceae, new pigment data in Caryophyllales, and the new family Corbichoniaceae. <i>Taxon</i> , 2016, 65, 775-793.	0.4	38
1147	Organohalide-Respiring Deltaproteobacteria. , 2016, , 235-258.		8
1148	bcgTree: automatized phylogenetic tree building from bacterial core genomes. <i>Genome</i> , 2016, 59, 783-791.	0.9	151
1149	Multi-locus Analyses Reveal Four Giraffe Species Instead of One. <i>Current Biology</i> , 2016, 26, 2543-2549.	1.8	175
1150	Evolution and Ecology of <i>Actinobacteria</i> and Their Bioenergy Applications. <i>Annual Review of Microbiology</i> , 2016, 70, 235-254.	2.9	249
1151	Domestication and Divergence of <i>Saccharomyces cerevisiae</i> Beer Yeasts. <i>Cell</i> , 2016, 166, 1397-1410.e16.	13.5	580
1152	Mitogenomics of <i>Hesperelaea</i> , an extinct genus of Oleaceae. <i>Gene</i> , 2016, 594, 197-202.	1.0	34
1153	<i>Theobroma cacao</i> L. pathogenesis-related gene tandem array members show diverse expression dynamics in response to pathogen colonization. <i>BMC Genomics</i> , 2016, 17, 363.	1.2	45
1154	A Genomic Analysis of Factors Driving lincRNA Diversification: Lessons from Plants. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 2881-2891.	0.8	28
1155	Morphological and phylogenetic studies of two new neotropical species of <i>Loweomyces</i> (Polyporales). <i>Tj ETQq1 1 0,784314 ggBT / Overl</i>	0,5	

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1156	DNA sequencing confirms PCR-RFLP identification of wild caught Larrousius sand flies from Crete and Cyprus. <i>Acta Tropica</i> , 2016, 164, 314-320.	0.9	8
1157	Resurgence of Ebola Virus Disease in Guinea Linked to a Survivor With Virus Persistence in Seminal Fluid for More Than 500 Days. <i>Clinical Infectious Diseases</i> , 2016, 63, 1353-1356.	2.9	201
1158	Evolution of prokaryotic respiratory molybdoenzymes and the frequency of their genomic co-occurrence. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw187.	1.3	13
1159	Interspecific metabolic diversity of root-colonizing endophytic fungi revealed by enzyme activity tests. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw190.	1.3	48
1160	Toward a Self-Updating Platform for Estimating Rates of Speciation and Migration, Ages, and Relationships of Taxa. <i>Systematic Biology</i> , 2017, 66, syw066.	2.7	42
1161	Function and Phylogeny of Bacterial Butyryl Coenzyme A:Acetate Transferases and Their Diversity in the Proximal Colon of Swine. <i>Applied and Environmental Microbiology</i> , 2016, 82, 6788-6798.	1.4	24
1162	<i>Arthonia parietinaria</i> – A common but frequently misunderstood lichenicolous fungus on species of the <i>Xanthoria parietina</i> -group. <i>Fungal Biology</i> , 2016, 120, 1341-1353.	1.1	16
1163	Reversible polymorphism-aware phylogenetic models and their application to tree inference. <i>Journal of Theoretical Biology</i> , 2016, 407, 362-370.	0.8	70
1164	Evidence of canine parvovirus transmission to a civet cat (<i>Paradoxurus musangus</i>) in Singapore. <i>One Health</i> , 2016, 2, 122-125.	1.5	11
1165	Molecular phylogeny reveals the non-monophyly of tribe Yinshanieae (Brassicaceae) and description of a new tribe, Hillielleae. <i>Plant Diversity</i> , 2016, 38, 171-182.	1.8	12
1166	An integrative revision of <i>Mesocrista</i> Pilato, 1987 (Tardigrada: Eutardigrada: Hypsibiidae). <i>Journal of Natural History</i> , 2016, 50, 2803-2828.	0.2	41
1167	Recent independent emergence of multiple multidrug-resistant <i>Serratia marcescens</i> clones within the United Kingdom and Ireland. <i>Genome Research</i> , 2016, 26, 1101-1109.	2.4	74
1168	A molecular analysis of the phylogenetic position of the suborder Cavernicola within the Tricladida (Platyhelminthes), with the description of a new species of stygobiont flatworm from Benin. <i>Zoological Journal of the Linnean Society</i> , 2016, 178, 482-491.	1.0	9
1169	Emergence of wheat blast in Bangladesh was caused by a South American lineage of <i>Magnaporthe oryzae</i> . <i>BMC Biology</i> , 2016, 14, 84.	1.7	355
1170	A complex of <i>Cardicola</i> Short, 1953 (Digenea: Apocotylidae) species infecting the milkfish <i>Chanos chanos</i> Forsskål (Gonorynchiformes), with descriptions of two new species. <i>Systematic Parasitology</i> , 2016, 93, 831-846.	0.5	17
1171	Versatile glycoside hydrolase family 18 chitinases for fungi ingestion and reproduction in the pinewood nematode <i>Bursaphelenchus xylophilus</i> . <i>International Journal for Parasitology</i> , 2016, 46, 819-828.	1.3	13
1172	HCV1b genome evolution under selective pressure of the cyclophilin inhibitor alisporivir during the DEB-025-HCV-203 phase II clinical trial. <i>Infection, Genetics and Evolution</i> , 2016, 44, 169-181.	1.0	3
1173	A sister of PIN1 gene in tomato (<i>Solanum lycopersicum</i>) defines leaf and flower organ initiation patterns by maintaining epidermal auxin flux. <i>Developmental Biology</i> , 2016, 419, 85-98.	0.9	41

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1174	Two distinct RNase activities of CRISPR-C2c2 enable guide-RNA processing and RNA detection. <i>Nature</i> , 2016, 538, 270-273.	13.7	854
1175	FastRFS: fast and accurate Robinson-Foulds Supertrees using constrained exact optimization. <i>Bioinformatics</i> , 2017, 33, 631-639.	1.8	29
1176	Genomic divergence and lack of introgressive hybridization between two 13-year periodical cicadas support life cycle switching in the face of climate change. <i>Molecular Ecology</i> , 2016, 25, 5543-5556.	2.0	10
1177	The whole genome sequence of the Mediterranean fruit fly, <i>Ceratitis capitata</i> (Wiedemann), reveals insights into the biology and adaptive evolution of a highly invasive pest species. <i>Genome Biology</i> , 2016, 17, 192.	3.8	130
1178	Characterization of new transposable element sub-families from white clover (<i>Trifolium repens</i>) using PCR amplification. <i>Genetica</i> , 2016, 144, 577-589.	0.5	1
1179	A <i>Ralstonia solanacearum</i> phage Φ RP15 is closely related to Viunlikeviruses and encodes 19 tRNA-related sequences. <i>Virology Reports</i> , 2016, 6, 61-73.	0.4	6
1180	Eight new mitogenomes for exploring the phylogeny and classification of Vetigastropoda. <i>Journal of Molluscan Studies</i> , 2016, 82, 534-541.	0.4	26
1181	Floral similarity and vegetative divergence in a new species of <i>Bletia</i> (Orchidaceae) from Mexico. <i>Phytotaxa</i> , 2016, 275, 112.	0.1	5
1182	Fungal diversity notes 367-490: taxonomic and phylogenetic contributions to fungal taxa. <i>Fungal Diversity</i> , 2016, 80, 1-270.	4.7	314
1183	Cytosuclear incompatibility contributes to the early stages of speciation. <i>Evolution; International Journal of Organic Evolution</i> , 2016, 70, 2752-2766.	1.1	44
1184	Genome divergence and diversification within a geographic mosaic of coevolution. <i>Molecular Ecology</i> , 2016, 25, 5705-5718.	2.0	43
1185	De-novo transcriptome assembly for gene identification, analysis, annotation, and molecular marker discovery in <i>Onobrychis vicifolia</i> . <i>BMC Genomics</i> , 2016, 17, 756.	1.2	32
1186	New records and observations of macroalgae and associated pathogens from the Falkland Islands, Patagonia and Tierra del Fuego. <i>Botanica Marina</i> , 2016, 59, 105-121.	0.6	13
1187	Molecular phylogenetics of <i>Sarcolaenaceae</i> (Malvales), Madagascar's largest endemic plant family. <i>Botanical Journal of the Linnean Society</i> , 2016, 182, 729-743.	0.8	9
1188	Regeneration in bipinnaria larvae of the bat star <i>Patiria miniata</i> induces rapid and broad new gene expression. <i>Mechanisms of Development</i> , 2016, 142, 10-21.	1.7	16
1189	Mitochondrial and plastid genome analysis of the marine red alga <i>Coeloseira compressa</i> (Champiaceae, Trentepohliaceae). <i>Journal of Applied Phycology</i> , 2016, 30, 107-114.	0.2	3
1190	Genome skimming reveals the complete chloroplast genome of <i>Ampelocalamus naibunensis</i> (Poaceae: Bambusoideae: Arundinarieae) with phylogenomic implication. <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 635-637.	0.2	10
1191	Mitochondrial and plastid genome analysis of the heteromorphic red alga <i>Mastocarpus papillatus</i> (C. Agardh) Kötzing (Phyllophoraceae, Rhodophyta) reveals two characteristic florideophyte organellar genomes. <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 676-677.	0.2	8

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1192	Persistence of a dominant bovine lineage of group <i>B</i> reveals genomic signatures of host adaptation. <i>Environmental Microbiology</i> , 2016, 18, 4216-4229.	1.8	38
1193	Genomic Comparisons of <i>Lactobacillus crispatus</i> and <i>Lactobacillus iners</i> Reveal Potential Ecological Drivers of Community Composition in the Vagina. <i>Applied and Environmental Microbiology</i> , 2016, 82, 7063-7073.	1.4	114
1194	<i>Microthlaspi erraticum</i> (Jord.) T. Ali et Thines has a wide distribution, ranging from the Alps to the Tien Shan. <i>Flora: Morphology, Distribution, Functional Ecology of Plants</i> , 2016, 225, 76-81.	0.6	17
1195	Family-Joining: A Fast Distance-Based Method for Constructing Generally Labeled Trees. <i>Molecular Biology and Evolution</i> , 2016, 33, 2720-2734.	3.5	4
1196	Functional and Evolutionary Characterization of a Gene Transfer Agent's Multilocus "Genome". <i>Molecular Biology and Evolution</i> , 2016, 33, 2530-2543.	3.5	58
1197	Fruit rot of sweet cherries and raspberries caused by <i>Penicillium crustosum</i> and <i>Mucor piriformis</i> in South Patagonia, Argentina. <i>Canadian Journal of Plant Pathology</i> , 2016, 38, 511-516.	0.8	9
1198	The Evolution of Silicon Transport in Eukaryotes. <i>Molecular Biology and Evolution</i> , 2016, 33, 3226-3248.	3.5	107
1199	Fine-Tuning Motile Cilia and Flagella: Evolution of the Dynein Motor Proteins from Plants to Humans at High Resolution. <i>Molecular Biology and Evolution</i> , 2016, 33, 3249-3267.	3.5	54
1200	Identification of rust fungi (Pucciniales) on species of <i>Allium</i> in Australia. <i>Australasian Plant Pathology</i> , 2016, 45, 581-592.	0.5	22
1201	Genetic basis of priority effects: insights from nectar yeast. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016, 283, 20161455.	1.2	44
1202	Atopic Dermatitis Susceptibility Variants in <i>Filaggrin</i> Hitchhike <i>Hornerin</i> Selective Sweep. <i>Genome Biology and Evolution</i> , 2016, 8, 3240-3255.	1.1	35
1203	Accounting for Uncertainty in Gene Tree Estimation: Summary-Coalescent Species Tree Inference in a Challenging Radiation of Australian Lizards. <i>Systematic Biology</i> , 2017, 66, syw089.	2.7	56
1204	Phylogenomic Reconstruction of Sportive Lemurs (genus <i>Lepilemur</i>) Recovered from Mitogenomes with Inferences for Madagascar Biogeography. <i>Journal of Heredity</i> , 2016, 108, esw072.	1.0	8
1205	Genome-wide sequence data suggest the possibility of pollinator sharing by host shift in dioecious figs (Moraceae, <i>Ficus</i>). <i>Molecular Ecology</i> , 2016, 25, 5732-5746.	2.0	23
1206	A new genus <i>Phyllophorella</i> gen. nov. (Phyllophoraceae, Rhodophyta) from central Peru, including <i>Phyllophorella peruviana</i> comb. nov., <i>Phyllophorella humboldtiana</i> sp. nov., and <i>Phyllophorella limaensis</i> sp. nov.. <i>Botanica Marina</i> , 2016, 59, 339-352.	0.6	7
1207	Gene transfers from diverse bacteria compensate for reductive genome evolution in the chromatophore of <i>Paulinella chromatophora</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 12214-12219.	3.3	127
1208	Temporal patterns of local adaptation in soil pseudomonads. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016, 283, 20161652.	1.2	5
1209	Convergent local adaptation to climate in distantly related conifers. <i>Science</i> , 2016, 353, 1431-1433.	6.0	303

#	ARTICLE	IF	CITATIONS
1210	Hybothoracaphis, a new genus of Nipponaphidini (Hemiptera, Aphididae, Hormaphidinae) from China and its phylogenetic placement based on multiple genes. <i>Zootaxa</i> , 2016, 4170, 375.	0.2	0
1211	Genome-wide survey and phylogeny of S-Ribosylhomocysteinase (LuxS) enzyme in bacterial genomes. <i>BMC Genomics</i> , 2016, 17, 742.	1.2	12
1212	Phylogenomics of Lophotrochozoa with Consideration of Systematic Error. <i>Systematic Biology</i> , 2017, 66, syw079.	2.7	164
1213	Just off the beach: intrageneric distinctiveness of the bandtail goatfish <i>Upeneus taeniopterus</i> (Mullidae) based on a comprehensive alpha-taxonomy and barcoding approach. <i>Marine Biology Research</i> , 2016, 12, 675-694.	0.3	10
1214	Arctic <i>Pholoe</i> (Polychaeta: Pholoidae): when integrative taxonomy helps to sort out barcodes. <i>Zoological Journal of the Linnean Society</i> , 2016, , .	1.0	6
1215	Carbon Flux and Carbohydrate Gene Families in Pineapple. <i>Tropical Plant Biology</i> , 2016, 9, 200-213.	1.0	8
1216	Identification of distinctive molecular traits that are characteristic of the phylum <i>Deinococcus-Thermus</i> and distinguish its main constituent groups. <i>Systematic and Applied Microbiology</i> , 2016, 39, 453-463.	1.2	23
1217	Body mass corrected molecular rate for bird mitochondrial DNA. <i>Molecular Ecology</i> , 2016, 25, 4438-4449.	2.0	70
1218	Contrasting Levels of Molecular Evolution on the Mouse X Chromosome. <i>Genetics</i> , 2016, 203, 1841-1857.	1.2	32
1219	Out of Tibet: the spatio-temporal evolution of <i>Gentiana</i> (Gentianaceae). <i>Journal of Biogeography</i> , 2016, 43, 1967-1978.	1.4	143
1220	Parsing polyphyletic <i>Pueraria</i> : Delimiting distinct evolutionary lineages through phylogeny. <i>Molecular Phylogenetics and Evolution</i> , 2016, 104, 44-59.	1.2	49
1221	High-level phylogeny of the Coleoptera inferred with mitochondrial genome sequences. <i>Molecular Phylogenetics and Evolution</i> , 2016, 104, 99-111.	1.2	85
1222	Getting a grip at the edge: recolonization and introgression in eastern Pacific <i>Porites</i> corals. <i>Journal of Biogeography</i> , 2016, 43, 2147-2159.	1.4	21
1223	The role of forest expansion and contraction in species diversification among <i>Galagos</i> (Primates): Tj ETQq1 1 0.784314 rgBJ/Overl	1.4	59
1224	Phylogenetic Revision of the Genus <i>Bartsia</i> (Orobanchaceae): Disjunct Distributions Correlate to Independent Lineages. <i>Systematic Botany</i> , 2016, 41, 672-684.	0.2	13
1225	The geographic distribution and complex evolutionary history of the NX-2 trichothecene chemotype from <i>Fusarium graminearum</i> . <i>Fungal Genetics and Biology</i> , 2016, 95, 39-48.	0.9	55
1226	Relaxed selective constraints drove functional modifications in peripheral photoreception of the cavefish <i>P. andruzzii</i> and provide insight into the time of cave colonization. <i>Heredity</i> , 2016, 117, 383-392.	1.2	35
1227	Complete mitochondrial genomes are not necessarily more informative than individual mitochondrial genes to recover a well-established annelid phylogeny. <i>Gene Reports</i> , 2016, 5, 10-17.	0.4	14

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1228	Sequence capture using RAD probes clarifies phylogenetic relationships and species boundaries in <i>Primula</i> sect. <i>Auricula</i> . <i>Molecular Phylogenetics and Evolution</i> , 2016, 104, 60-72.	1.2	25
1229	Transfer of selected <i>Ahnfeltiopsis</i> (Phylloporaceae, Rhodophyta) species to the genus <i>Besa</i> and description of <i>Schottera koreana</i> sp. nov.. <i>European Journal of Phycology</i> , 2016, 51, 431-443.	0.9	9
1230	Organ boundary NAC domain transcription factors are implicated in the evolution of petal fusion. <i>Plant Biology</i> , 2016, 18, 893-902.	1.8	22
1231	A Phylogenomic Framework to Study the Diversity and Evolution of Stramenopiles (=Heterokonts). <i>Molecular Biology and Evolution</i> , 2016, 33, 2890-2898.	3.5	125
1232	Ancient DNA reveals differences in behaviour and sociality between brown bears and extinct cave bears. <i>Molecular Ecology</i> , 2016, 25, 4907-4918.	2.0	58
1233	A new species of the genus <i>Leptobrachium</i> (Anura: Megophryidae) from the Gaoligongshan Mountain Range, China. <i>Zootaxa</i> , 2016, 4150, 133-48.	0.2	10
1234	Identification and evidence of positive selection upon resistance gene analogs in cotton (<i>Gossypium</i>) Tj ETQq0 0 0 14 / Overlock 10 Tf	1.4	3
1235	Phylogenomics Using Transcriptome Data. <i>Methods in Molecular Biology</i> , 2016, 1452, 65-80.	0.4	2
1236	True Truffle (<i>Tuber</i> spp.) in the World. <i>Soil Biology</i> , 2016, , .	0.6	42
1237	A Brief Overview of the Systematics, Taxonomy, and Ecology of the <i>Tuber rufum</i> Clade. <i>Soil Biology</i> , 2016, , 125-136.	0.6	6
1238	Typification of Friesian names in <i>Cortinarius</i> sections <i>Anomali</i> , <i>Spilomei</i> , and <i>Bolares</i> , and description of two new species from northern Europe. <i>Mycological Progress</i> , 2016, 15, 903-919.	0.5	15
1239	<i>Petrosaltator</i> gen. nov., a new genus replacement for the North African sengi <i>Elephantulus rozeti</i> (Macroscelidea; Macroscelididae). <i>Zootaxa</i> , 2016, 4136, 567-79.	0.2	11
1240	Tales from the crypt: genome mining from fungarium specimens improves resolution of the mushroom tree of life. <i>Biological Journal of the Linnean Society</i> , 2016, 117, 11-32.	0.7	77
1241	Tropical Asian species show that the Old World clade of <i>Solanum</i> subgenus <i>Leptostemonum</i> pro parte (<i>Solanaceae</i>) is not monophyletic. <i>Botanical Journal of the Linnean Society</i> , 2016, 181, 199-223.	0.8	45
1242	<i>Dasya adela</i> sp. nov. (Rhodophyta, Charales), an enigmatic new <i>Dasya</i> from a landlocked fjord in southwest Norway. <i>Phycological Research</i> , 2016, 64, 79-94.	0.8	7
1243	Computational Intelligence Methods for Bioinformatics and Biostatistics. <i>Lecture Notes in Computer Science</i> , 2016, , .	1.0	1
1244	Irrational exuberance for resolved species trees. <i>Evolution; International Journal of Organic Evolution</i> , 2016, 70, 7-17.	1.1	177
1245	Morpho morphometrics: Shared ancestry and selection drive the evolution of wing size and shape in <i>Morpho</i> butterflies. <i>Evolution; International Journal of Organic Evolution</i> , 2016, 70, 181-194.	1.1	69

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1246	Molecular phylogeny of the horse flies: a framework for renewing tabanid taxonomy. <i>Systematic Entomology</i> , 2016, 41, 56-72.	1.7	34
1247	A taxonomic framework for cable bacteria and proposal of the candidate genera <i>Electrothrix</i> and <i>Electronema</i> . <i>Systematic and Applied Microbiology</i> , 2016, 39, 297-306.	1.2	151
1248	Cryptic host-specific diversity among western hemisphere broomrapes (<i>Orobancha</i> s.l.)	1.4	29
1249	Ultrastructural and molecular characterization of diversity among small araphid diatoms all lacking rimoportulae. I. Five new genera, eight new species. <i>Journal of Phycology</i> , 2016, 52, 1018-1036.	1.0	15
1250	Repeated replacement of an intrabacterial symbiont in the tripartite nested mealybug symbiosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E5416-24.	3.3	222
1251	Evolutionary systematics and biogeography of the arid habitat-adapted rodent genus <i>Gerbillus</i> (Rodentia, Muridae): a mostly Plio-Pleistocene African history. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2016, 54, 299-317.	0.6	22
1252	The Diversification of eIF4E Family Members in Plants and Their Role in the Plant-Virus Interaction. , 2016, , 187-205.		7
1253	High diversity of picornaviruses in rats from different continents revealed by deep sequencing. <i>Emerging Microbes and Infections</i> , 2016, 5, 1-8.	3.0	14
1254	Down-regulation of the glucan synthase-like 6 gene (<i>HvGsl6</i>) in barley leads to decreased callose accumulation and increased cell wall penetration by <i>Blumeria graminis</i> f. sp. <i>hordei</i> . <i>New Phytologist</i> , 2016, 212, 434-443.	3.5	41
1255	The Molecular Determinants of Antibody Recognition and Antigenic Drift in the H3 Hemagglutinin of Swine Influenza A Virus. <i>Journal of Virology</i> , 2016, 90, 8266-8280.	1.5	54
1256	<i>Neosergipea</i> , a new name for the lichen fungus <i>Sergipea</i> , with an updated phylogeny and notes on the genus <i>Dichosporidium</i> (lichenized Ascomycota: Arthoniales)		7
1257	Hidden histories of gene flow in highland birds revealed with genomic markers. <i>Molecular Ecology</i> , 2016, 25, 5144-5157.	2.0	64
1258	<i>Transversotrema</i> Witenberg, 1944 (Trematoda: Transversotrematidae) from inshore fishes of Australia: description of a new species and significant range extensions for three congeners. <i>Systematic Parasitology</i> , 2016, 93, 639-652.	0.5	29
1259	Phylogenetic evidence places the coralloid jelly fungus <i>Tremellodendropsis tuberosa</i> (Tremellodendropsidales) among early diverging Agaricomycetes. <i>Mycological Progress</i> , 2016, 15, 939-946.	0.5	4
1260	Ancient origins of metazoan gonadotropin-releasing hormone and their receptors revealed by phylogenomic analyses. <i>General and Comparative Endocrinology</i> , 2016, 234, 10-19.	0.8	46
1261	<i>Cortinarius</i> subgenus <i>Callistei</i> in North America and Europe—type studies, diversity, and distribution of species. <i>Mycologia</i> , 2016, 108, 1018-1027.	0.8	8
1262	Evolution of the immune system influences speciation rates in teleost fishes. <i>Nature Genetics</i> , 2016, 48, 1204-1210.	9.4	226
1263	Structural basis for the CsrA-dependent modulation of translation initiation by an ancient regulatory protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 10168-10173.	3.3	41

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1264	A contribution to the study of the cortinarioid mycoflora of New Zealand, VII. New Zealand Journal of Botany, 2016, 54, 344-365.	0.8	13
1265	Guyanagarika, a new ectomycorrhizal genus of Agaricales from the Neotropics. Fungal Biology, 2016, 120, 1540-1553.	1.1	28
1266	Evolutionary history of chloridoid grasses estimated from 122 nuclear loci. Molecular Phylogenetics and Evolution, 2016, 105, 1-14.	1.2	21
1267	Phylogenetics and biogeography of the dung beetle genus <i>Onthophagus</i> inferred from mitochondrial genomes. Molecular Phylogenetics and Evolution, 2016, 105, 86-95.	1.2	58
1268	Squamate Phylogenetics, Molecular Branch Lengths, and Molecular Apomorphies: A Response to McMahan et al.. Copeia, 2016, 104, 702-707.	1.4	8
1269	Genetic reconstruction of a bullfrog invasion to elucidate vectors of introduction and secondary spread. Ecology and Evolution, 2016, 6, 5221-5233.	0.8	12
1270	Elucidating modes of activation and herbicide resistance by sequence assembly and molecular modelling of the Acetolactate synthase complex in sugarcane. Journal of Theoretical Biology, 2016, 407, 184-197.	0.8	9
1272	The Trichoptera barcode initiative: a strategy for generating a species-level Tree of Life. Philosophical Transactions of the Royal Society B: Biological Sciences, 2016, 371, 20160025.	1.8	62
1273	The complete chloroplast genome sequence of <i>Lilium fargesii</i> (Lilium, Liliaceae). Conservation Genetics Resources, 2016, 8, 419-422.	0.4	8
1274	Characterization of the whole chloroplast genome of <i>Caragana microphylla</i> Lam (Fabaceae). Conservation Genetics Resources, 2016, 8, 371-373.	0.4	5
1275	Genetic structure of a morphological species within the amoeba genus <i>Korotnevella</i> (Amoebozoa: Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	0.5	20
1276	Visual Pigments, Ocular Filters and the Evolution of Snake Vision. Molecular Biology and Evolution, 2016, 33, 2483-2495.	3.5	65
1277	Complete mitochondrial genomes of three crickets (Orthoptera: Gryllidae) and comparative analyses within Ensifera mitogenomes. Zootaxa, 2016, 4092, 529-47.	0.2	13
1278	What are the evolutionary mechanisms explaining the similar species richness patterns in tropical mosses? Insights from the phylogeny of the pantropical genus <i>Pelekium</i> . Molecular Phylogenetics and Evolution, 2016, 105, 139-145.	1.2	11
1279	Phylogenetic distribution of regeneration and asexual reproduction in Annelida: regeneration is ancestral and fission evolves in regenerative clades. Invertebrate Biology, 2016, 135, 400-414.	0.3	72
1280	<i>Lactifluus foetens</i> and <i>Lf. albomembranaceus</i> sp. nov. (Russulaceae): look-alike milkcaps from gallery forests in tropical Africa. Phytotaxa, 2016, 277, 159.	0.1	6
1281	Genome sequence and comparative analysis of clavicipitaceous insect-pathogenic fungus <i>Aschersonia badia</i> with <i>Metarhizium</i> spp.. BMC Genomics, 2016, 17, 367.	1.2	12
1282	The making of a pest: Insights from the evolution of chemosensory receptor families in a pestiferous and invasive fly, <i>Drosophila suzukii</i> . BMC Genomics, 2016, 17, 648.	1.2	50

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1283	Novel avian influenza A (H5N6) viruses isolated in migratory waterfowl before the first human case reported in China, 2014. <i>Scientific Reports</i> , 2016, 6, 29888.	1.6	57
1284	Blueberry fruit drop-associated virus: A New Member of the Family Caulimoviridae Isolated From Blueberry Exhibiting Fruit-Drop Symptoms. <i>Plant Disease</i> , 2016, 100, 2211-2214.	0.7	9
1285	Detection of spring viraemia of carp virus in imported amphibians reveals an unanticipated foreign animal disease threat. <i>Emerging Microbes and Infections</i> , 2016, 5, 1-7.	3.0	15
1286	A genomic island in <i>Vibrio cholerae</i> with VPI-1 site-specific recombination characteristics contains CRISPR-Cas and type VI secretion modules. <i>Scientific Reports</i> , 2016, 6, 36891.	1.6	40
1287	Species delineation in the <i>Capitella</i> species complex (Annelida: Capitellidae): geographic and genetic variation in the northern Gulf of Mexico. <i>Invertebrate Biology</i> , 2016, 135, 415-422.	0.3	9
1288	Preliminary phylogeny of <i>Fordiophyton</i> (Melastomataceae), with the description of two new species. <i>Phytotaxa</i> , 2016, 247, 45.	0.1	38
1289	Prevalence and epidemiology of meningococcal carriage in Southern Ethiopia prior to implementation of MenAfriVac, a conjugate vaccine. <i>BMC Infectious Diseases</i> , 2016, 16, 639.	1.3	20
1290	Genetic diversity of two <i>Daphnia</i> -infecting microsporidian parasites, based on sequence variation in the internal transcribed spacer region. <i>Parasites and Vectors</i> , 2016, 9, 293.	1.0	8
1291	ATP phosphoribosyltransferase from symbiont <i>Entomomyces delphacidicola</i> involved in histidine biosynthesis of <i>Nilaparvata lugens</i> (Stål). <i>Amino Acids</i> , 2016, 48, 2605-2617.	1.2	6
1292	Reciprocal genomic evolution in the ant-fungus agricultural symbiosis. <i>Nature Communications</i> , 2016, 7, 12233.	5.8	106
1293	Transcriptomics and neuroanatomy of the clonal raider ant implicate an expanded clade of odorant receptors in chemical communication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 14091-14096.	3.3	107
1294	<i>Saprolegnia milanezii</i> sp. nov., a new species of Saprolegniales (Oomycota, Straminipila) from Brazil. <i>Phytotaxa</i> , 2016, 270, 286.	0.1	4
1295	<i>Tubaria keralensis</i> , a new species of <i>T. furfuracea</i> complex from tropical India. <i>Phytotaxa</i> , 2016, 278, 287.	0.1	1
1296	A New Species of Pipistrelle Bat (Chiroptera: Vespertilionidae) from Southern Arabia. <i>Acta Chiropterologica</i> , 2016, 18, 301-323.	0.2	9
1297	Support Measures, Phylogenetic Tree. , 2016, , 256-260.		0
1298	Energy efficiency trade-offs drive nucleotide usage in transcribed regions. <i>Nature Communications</i> , 2016, 7, 11334.	5.8	104
1299	<i>Cladophialophora inabaensis</i> sp. nov., a New Species among the Dark Septate Endophytes from a Secondary Forest in Tottori, Japan. <i>Microbes and Environments</i> , 2016, 31, 357-360.	0.7	14
1300	The Evolutionary Fates of a Large Segmental Duplication in Mouse. <i>Genetics</i> , 2016, 204, 267-285.	1.2	21

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1301	Evolutionary Consequences of DNA Methylation in a Basal Metazoan. <i>Molecular Biology and Evolution</i> , 2016, 33, 2285-2293.	3.5	57
1302	Evolutionary History of the Nesophontidae, the Last Unplaced Recent Mammal Family. <i>Molecular Biology and Evolution</i> , 2016, 33, 3095-3103.	3.5	38
1303	User behavior and usage patterns for a highly accessed science gateway. , 2016, , .		0
1304	- Next-Generation Sequencing and Metagenomics. , 2016, , 344-364.		0
1305	Safety assessment of dicamba mono-oxygenases that confer dicamba tolerance to various crops. <i>Regulatory Toxicology and Pharmacology</i> , 2016, 81, 171-182.	1.3	19
1306	Lost crops of the Incas: Origins of domestication of the Andean pulse crop tarwi, <i>Lupinus mutabilis</i> . <i>American Journal of Botany</i> , 2016, 103, 1592-1606.	0.8	47
1307	Who Let the CAT Out of the Bag? Accurately Dealing with Substitutional Heterogeneity in Phylogenomic Analyses. <i>Systematic Biology</i> , 2017, 66, syw084.	2.7	57
1308	Picking holes in traditional species delimitations: an integrative taxonomic reassessment of the <i>Parmotrema perforatum</i> group (Parmeliaceae, Ascomycota). <i>Botanical Journal of the Linnean Society</i> , 2016, 182, 868-884.	0.8	18
1309	<i>Cladorhiza corallophila</i> sp. nov., a new carnivorous sponge (Cladorhizidae, Demospongiae) living in close association with <i>Lophelia pertusa</i> and <i>Madrepora oculata</i> (Scleractinia). <i>Zootaxa</i> , 2016, 4168, 512-524.	0.2	4
1310	X-rays and virtual taphonomy resolve the first <i>Cissus</i> (Vitaceae) macrofossils from Africa as early-diverging members of the genus. <i>American Journal of Botany</i> , 2016, 103, 1657-1677.	0.8	15
1311	Support vector machine applied to predict the zoonotic potential of <i>E. coli</i> O157 cattle isolates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 11312-11317.	3.3	55
1312	Evaluating the Impact of Genomic Data and Priors on Bayesian Estimates of the Angiosperm Evolutionary Timescale. <i>Systematic Biology</i> , 2017, 66, syw086.	2.7	117
1313	Comparative phylogeography of the endemic Japanese weasel (<i>Mustela itatsi</i>) and the continental Siberian weasel (<i>Mustela sibirica</i>) revealed by complete mitochondrial genome sequences. <i>Biological Journal of the Linnean Society</i> , 2016, , .	0.7	4
1314	First report on nematode parasite infection in the yellowbar angelfish <i>Pomacanthus maculosus</i> (Perciformes: Pomacanthidae) from the Iraqi coral reef, with description of a new species of <i>Cucullanus</i> (Nematoda: Ascaridida) using the integrated approaches. <i>Parasitology International</i> , 2016, 65, 677-684.	0.6	13
1315	The molecular phylogeny of the sea star <i>Echinaster</i> (Asteroidea: Echinasteridae) provides insights for genus taxonomy. <i>Invertebrate Biology</i> , 2016, 135, 235-244.	0.3	9
1316	<i>Etmopterus alphus</i> n. sp.: a new lanternshark (Squaliformes: Etmopteridae) from the south-western Indian Ocean. <i>African Journal of Marine Science</i> , 2016, 38, 329-340.	0.4	8
1317	From Sequence Data Including Orthologs, Paralogs, and Xenologs to Gene and Species Trees. , 2016, , 373-392.		16
1318	Mutations in Human Accelerated Regions Disrupt Cognition and Social Behavior. <i>Cell</i> , 2016, 167, 341-354.e12.	13.5	280

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1319	Evidence for the Introduction, Reassortment, and Persistence of Diverse Influenza A Viruses in Antarctica. <i>Journal of Virology</i> , 2016, 90, 9674-9682.	1.5	61
1320	Sustained live poultry market surveillance contributes to early warnings for human infection with avian influenza viruses. <i>Emerging Microbes and Infections</i> , 2016, 5, 1-8.	3.0	12
1321	Phylogenetic Tree Estimation With and Without Alignment: New Distance Methods and Benchmarking. <i>Systematic Biology</i> , 2016, 66, syw074.	2.7	17
1322	Evolutionary Dynamics of Abundant Stop Codon Readthrough. <i>Molecular Biology and Evolution</i> , 2016, 33, 3108-3132.	3.5	53
1323	Complete genome characterisation and phylogenetic position of Tigray hantavirus from the Ethiopian white-footed mouse, <i>Stenocephalemys albipes</i> . <i>Infection, Genetics and Evolution</i> , 2016, 45, 242-245.	1.0	7
1324	A revised generic classification of vittarioid ferns (Pteridaceae) based on molecular, micromorphological, and geographic data. <i>Taxon</i> , 2016, 65, 708-722.	0.4	27
1325	Molecular Phylogeny, Revised Higher Classification, and Implications for Conservation of Endangered Hawaiian Leaf-Mining Moths (Lepidoptera: Gracillariidae: <i>Philodoria</i>)1. <i>Pacific Science</i> , 2016, 70, 361.	0.2	5
1326	Phylogenetic Placement of the Monotypic Genus <i>Schwackaea</i> (Melastomeae: Melastomataceae) and the Evolution of Its Unique Fruit. <i>International Journal of Plant Sciences</i> , 2016, 177, 440-448.	0.6	10
1327	The Evolution of Olfactory Gene Families in <i>Drosophila</i> and the Genomic Basis of chemical-Ecological Adaptation in <i>Drosophila suzukii</i> . <i>Genome Biology and Evolution</i> , 2016, 8, 2297-2311.	1.1	76
1328	The complete mitochondrial genome of the land snail <i>Cerion incanum</i> (Gastropoda: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 Molluscan Studies, 2016, 82, 525-533.	0.4	8
1329	Genomics of speciation and introgression in Princess cichlid fishes from Lake Tanganyika. <i>Molecular Ecology</i> , 2016, 25, 6143-6161.	2.0	68
1330	Transcriptome-wide identification and characterization of CAD isoforms specific for podophyllotoxin biosynthesis from <i>Podophyllum hexandrum</i> . <i>Plant Molecular Biology</i> , 2016, 92, 1-23.	2.0	18
1331	Local transmission and global dissemination of New Delhi Metallo-Beta-Lactamase (NDM): a whole genome analysis. <i>BMC Genomics</i> , 2016, 17, 452.	1.2	26
1332	HybPiper: Extracting coding sequence and introns for phylogenetics from high-throughput sequencing reads using target enrichment. <i>Applications in Plant Sciences</i> , 2016, 4, 1600016.	0.8	506
1333	Effector profiles distinguish <i>formae speciales</i> of <i>Fusarium oxysporum</i> . <i>Environmental Microbiology</i> , 2016, 18, 4087-4102.	1.8	179
1334	The complete chloroplast genome of <i>Lilium cernuum</i> : genome structure and evolution. <i>Conservation Genetics Resources</i> , 2016, 8, 375-378.	0.4	11
1335	Unexpected biodiversity of ciliates in marine samples from below the photic zone. <i>Molecular Ecology</i> , 2016, 25, 3987-4000.	2.0	48
1336	Basidiomycete yeasts in the cortex of ascomycete macrolichens. <i>Science</i> , 2016, 353, 488-492.	6.0	409

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1337	Phylogeny of the <i>Rosidae</i> : A dense taxon sampling analysis. <i>Journal of Systematics and Evolution</i> , 2016, 54, 363-391.	1.6	118
1338	Tree of life for the genera of Chinese vascular plants. <i>Journal of Systematics and Evolution</i> , 2016, 54, 277-306.	1.6	88
1339	Phylogenetic diversity and its conservation in the presence of phylogenetic uncertainty: a case study of cladoceran communities in urban waterbodies. <i>Biodiversity and Conservation</i> , 2016, 25, 2113-2136.	1.2	7
1340	Sequencing of the genus <i>Arabidopsis</i> identifies a complex history of nonbifurcating speciation and abundant trans-specific polymorphism. <i>Nature Genetics</i> , 2016, 48, 1077-1082.	9.4	198
1341	A new species of the <i>Craugastor</i> <i>podiciferus</i> species group (Anura): <i>Tj ETQq0 0 0 rgBT /Overlock 10 3</i> 2016, 4132, 347.	0.2	3
1342	Characterization of a venom gland-associated rhabdovirus in the parasitoid wasp <i>Diachasmimorpha longicaudata</i> . <i>Journal of Insect Physiology</i> , 2016, 91-92, 48-55.	0.9	15
1343	Molecular phylogenetics and diversification of trap-jaw ants in the genera <i>Anochetus</i> and <i>Odontomachus</i> (Hymenoptera: Formicidae). <i>Molecular Phylogenetics and Evolution</i> , 2016, 103, 143-154.	1.2	30
1344	The complete mitochondrial genome of the Chilean endemic frog <i>Telmatobius chusmisensis</i> Formas, Cuevas & Nuñez, 2006 (Anura, Telmatobiidae). <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 136-137.	0.2	0
1345	Comprehensive phylogeny, biogeography and new classification of the diverse bee tribe Megachilini: Can we use DNA barcodes in phylogenies of large genera?. <i>Molecular Phylogenetics and Evolution</i> , 2016, 103, 245-259.	1.2	50
1346	Willet be one species or two? A genomic view of the evolutionary history of <i>Tringa semipalmata</i> . <i>Auk</i> , 2016, 133, 593-614.	0.7	36
1347	Contribution to the study of <i>Acanthodactylus</i> (Sauria: Lacertidae) mtDNA diversity focusing on the <i>A. boskianus</i> species group. <i>Mitochondrion</i> , 2016, 30, 78-94.	1.6	4
1348	Here We Are, But Where Do We Go? A Systematic Review of Crustacean Transcriptomic Studies from 2014–2015. <i>Integrative and Comparative Biology</i> , 2016, 56, 1055-1066.	0.9	21
1349	Characterization of the complete chloroplast genome of <i>Populus ilicifolia</i> . <i>Conservation Genetics Resources</i> , 2016, 8, 391-393.	0.4	9
1350	Phylogenetic incongruence and the evolutionary origins of cardenolide-resistant forms of <i>Na⁺K⁺-ATPase</i> in <i>Danaus</i> butterflies. <i>Evolution; International Journal of Organic Evolution</i> , 2016, 70, 1913-1921.	1.1	16
1351	Highly pathogenic avian influenza H5N1 Clade 2.3.2.1c virus in migratory birds, 2014–2015. <i>Virologica Sinica</i> , 2016, 31, 300-305.	1.2	39
1352	The mitogenome of the bed bug <i>Cimex lectularius</i> (Hemiptera: Cimicidae). <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 425-427.	0.2	5
1353	Organellar genome analysis of the marine red alga <i>Dasya binghamiae</i> (Dasyaceae, Rhodophyta) reveals an uncharacteristic florideophyte mitogenome structure. <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 510-511.	0.2	3
1354	The Identification of the Closest Living Relative(s) of Tetrapods: Phylogenomic Lessons for Resolving Short Ancient Internodes. <i>Systematic Biology</i> , 2016, 65, 1057-1075.	2.7	45

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1355	Rapid outbreak sequencing of Ebola virus in Sierra Leone identifies transmission chains linked to sporadic cases. <i>Virus Evolution</i> , 2016, 2, vew016.	2.2	105
1356	Composition of long chain alkenones and alkenoates as a function of growth temperature in marine haptophyte <i>Tisochrysis lutea</i> . <i>Organic Geochemistry</i> , 2016, 99, 78-89.	0.9	19
1357	The genomic content and context of auxiliary metabolic genes in marine cyanomyoviruses. <i>Virology</i> , 2016, 499, 219-229.	1.1	99
1358	A new species of microphallid (Trematoda: Digenea) infecting a novel host family, the Muraenidae, on the northern Great Barrier Reef, Australia. <i>Systematic Parasitology</i> , 2016, 93, 863-876.	0.5	16
1359	Barcoding Heliozoa: Perspectives of 18S rDNA for Distinguishing Between <i>Acanthocystis</i> Species. <i>Protist</i> , 2016, 167, 555-567.	0.6	10
1360	The physiology and habitat of the last universal common ancestor. <i>Nature Microbiology</i> , 2016, 1, 16116.	5.9	739
1361	The dissemination of multidrug-resistant <i>Enterobacter cloacae</i> throughout the UK and Ireland. <i>Nature Microbiology</i> , 2016, 1, 16173.	5.9	24
1362	Identifying lineage effects when controlling for population structure improves power in bacterial association studies. <i>Nature Microbiology</i> , 2016, 1, 16041.	5.9	247
1363	Reconstructing metabolic pathways of hydrocarbon-degrading bacteria from the Deepwater Horizon oil spill. <i>Nature Microbiology</i> , 2016, 1, 16057.	5.9	173
1364	Geogenetic patterns in mouse lemurs (genus <i>Microcebus</i>) reveal the ghosts of Madagascar's forests past. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 8049-8056.	3.3	81
1365	Taxonomic classification of the reef coral family Lobophylliidae (Cnidaria: Anthozoa: Scleractinia). <i>Zoological Journal of the Linnean Society</i> , 2016, 178, 436-481.	1.0	33
1366	The pangenome of an agronomically important crop plant <i>Brassica oleracea</i> . <i>Nature Communications</i> , 2016, 7, 13390.	5.8	375
1367	Searching Tree Space, <i>Methods for</i> , 2016, , 499-504.		0
1368	Conserved differences in protein sequence determine the human pathogenicity of Ebolaviruses. <i>Scientific Reports</i> , 2016, 6, 23743.	1.6	40
1369	The 2014 Ebola virus outbreak in West Africa highlights no evidence of rapid evolution or adaptation to humans. <i>Scientific Reports</i> , 2016, 6, 35822.	1.6	6
1370	The <i>Enantiaethys</i> Complex: Insights from COI Confirm the Species Complex and Reveal a New Potential Cryptic Species. <i>Southwestern Entomologist</i> , 2016, 41, 1005-1020.	0.1	5
1371	A perspective on 16S rRNA operational taxonomic unit clustering using sequence similarity. <i>Npj Biofilms and Microbiomes</i> , 2016, 2, 16004.	2.9	208
1372	The evolution of genes encoding for green fluorescent proteins: insights from cephalochordates (amphioxus). <i>Scientific Reports</i> , 2016, 6, 28350.	1.6	6

#	ARTICLE	IF	CITATIONS
1373	Comprehensive analysis of SET domain gene family in foxtail millet identifies the putative role of SiSET14 in abiotic stress tolerance. <i>Scientific Reports</i> , 2016, 6, 32621.	1.6	50
1374	Tissue, developmental, and caste-specific expression of odorant binding proteins in a eusocial insect, the red imported fire ant, <i>Solenopsis invicta</i> . <i>Scientific Reports</i> , 2016, 6, 35452.	1.6	24
1375	The Case of the Missing Ancient Fungal Polyploids. <i>American Naturalist</i> , 2016, 188, 602-614.	1.0	38
1376	Micro- and Macroevolutionary Trade-Offs in Plant-Feeding Insects. <i>American Naturalist</i> , 2016, 188, 640-650.	1.0	16
1377	A genomic view of food-related and probiotic <i>Enterococcus</i> strains. <i>DNA Research</i> , 2017, 24, dsw043.	1.5	38
1378	Sequence capture and next-generation sequencing of ultraconserved elements in a large genome salamander. <i>Molecular Ecology</i> , 2016, 25, 6162-6174.	2.0	28
1379	A revised classification of the Gelidiellaceae (Rhodophyta) with descriptions of three new genera: <i>Huismaniella</i> , <i>Millerella</i> and <i>Perronella</i> . <i>Taxon</i> , 2016, 65, 965-979.	0.4	21
1380	Glucosinolate diversity within a phylogenetic framework of the tribe Cardamineae (Brassicaceae) unraveled with HPLC-MS/MS and NMR-based analytical distinction of 70 desulfoglucosinolates. <i>Phytochemistry</i> , 2016, 132, 33-56.	1.4	68
1381	The <i>Gonium pectorale</i> genome demonstrates co-option of cell cycle regulation during the evolution of multicellularity. <i>Nature Communications</i> , 2016, 7, 11370.	5.8	125
1382	Progressive and Biased Divergent Evolution Underpins the Origin and Diversification of Peridinin Dinoflagellate Plastids. <i>Molecular Biology and Evolution</i> , 2016, 34, msw235.	3.5	13
1383	Genome sequence and analysis of the Japanese morning glory <i>Ipomoea nil</i> . <i>Nature Communications</i> , 2016, 7, 13295.	5.8	138
1384	Resolving evolutionary relationships in lichen-forming fungi using diverse phylogenomic datasets and analytical approaches. <i>Scientific Reports</i> , 2016, 6, 22262.	1.6	42
1385	Metabolism of Toxic Sugars by Strains of the Bee Gut Symbiont <i>Gilliamella apicola</i> . <i>MBio</i> , 2016, 7, .	1.8	216
1386	Two new Cambodian semi-aquatic earthworms in the genus <i>Glyphidrilus</i> Horst, 1889 (Oligochaeta). <i>Tj ETQq1 1 0.784314 rgBT /Overl</i>	0.2	4
1387	Dispersal in the sub-Antarctic: king penguins show remarkably little population genetic differentiation across their range. <i>BMC Evolutionary Biology</i> , 2016, 16, 211.	3.2	30
1388	Comparative genome analysis between Southeast Asian and South American Zika viruses. <i>Asian Pacific Journal of Tropical Medicine</i> , 2016, 9, 1048-1054.	0.4	13
1389	<i>Dominikia lithuanica</i> and <i>Kamienskia divaricata</i> : new species in the Glomeromycota. <i>Botany</i> , 2016, 94, 1075-1085.	0.5	9
1390	Estimation of Gene Insertion/Deletion Rates with Missing Data. <i>Genetics</i> , 2016, 204, 513-529.	1.2	3

#	ARTICLE	IF	CITATIONS
1391	Two species of Southeast Asian cats in the genus <i>Catopuma</i> with diverging histories: an island endemic forest specialist and a widespread habitat generalist. Royal Society Open Science, 2016, 3, 160350.	1.1	17
1392	Bats, Primates, and the Evolutionary Origins and Diversification of Mammalian Gammaherpesviruses. MBio, 2016, 7, .	1.8	31
1393	Pseudoscorpion diversity and distribution in the West Indies: sequence data confirm single island endemism for some clades, but not others. Journal of Arachnology, 2016, 44, 257-271.	0.3	24
1394	Rapid postglacial diversification and long-term stasis within the songbird genus <i>Junco</i> : phylogeographic and phylogenomic evidence. Molecular Ecology, 2016, 25, 6175-6195.	2.0	47
1395	Phylogeography of the heavily poached African common pangolin (<i>Pholidota</i> , <i>Manis</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf . Molecular Ecology, 2016, 25, 5975-5993.	2.0	39
1396	Diversification in wild populations of the model organism <i>Anolis carolinensis</i> : A genome-wide phylogeographic investigation. Ecology and Evolution, 2016, 6, 8115-8125.	0.8	17
1397	Characterization of the complete chloroplast genome of the endangered species <i>Carya sinensis</i> (Juglandaceae). Conservation Genetics Resources, 2016, 8, 467-470.	0.4	4
1398	Thousands of microbial genomes shed light on interconnected biogeochemical processes in an aquifer system. Nature Communications, 2016, 7, 13219.	5.8	994
1399	Investigation of the cause of geographic disparities in IDEXX ELISA sensitivity in serum samples from <i>Mycobacterium bovis</i> -infected cattle. Scientific Reports, 2016, 6, 22763.	1.6	20
1400	A pre-metazoan origin of the CRK gene family and co-opted signaling network. Scientific Reports, 2016, 6, 34349.	1.6	7
1401	1970s and "Patient 0"™ HIV-1 genomes illuminate early HIV/AIDS history in North America. Nature, 2016, 539, 98-101.	13.7	177
1402	Reconstructing the complex evolutionary history of mobile plasmids in red algal genomes. Scientific Reports, 2016, 6, 23744.	1.6	42
1403	Mitogenomic perspectives on the origin of Tibetan loaches and their adaptation to high altitude. Scientific Reports, 2016, 6, 29690.	1.6	90
1404	Molecular phylogeny, morphology and taxonomy of Moroccan <i>Triops granarius</i> (Lucas, 1864) (Crustacea: Notostraca), with the description of two new species. Zootaxa, 2016, 4178, 328-346.	0.2	17
1405	Past climate changes, population dynamics and the origin of Bison in Europe. BMC Biology, 2016, 14, 93.	1.7	48
1406	A <i>Francisella</i> -like endosymbiont in the Gulf Coast tick evolved from a mammalian pathogen. Scientific Reports, 2016, 6, 33670.	1.6	78
1407	Whole genome analysis of halotolerant and alkalotolerant plant growth-promoting rhizobacterium <i>Klebsiella</i> sp. D5A. Scientific Reports, 2016, 6, 26710.	1.6	90
1408	<i>Pseudomonas</i> spp. diversity is negatively associated with suppression of the wheat take-all pathogen. Scientific Reports, 2016, 6, 29905.	1.6	46

#	ARTICLE	IF	CITATIONS
1409	One African baobab species or two? Synonymy of <i>Adansonia kilima</i> and <i>A. digitata</i> . <i>Taxon</i> , 2016, 65, 1037-1049.	0.4	21
1410	Identity and Distribution of Introduced Slugs (Veronicellidae) in the Hawaiian and Samoan Islands. <i>Pacific Science</i> , 2016, 70, 477-493.	0.2	10
1411	Characterization of <i>Aspergillus fumigatus</i> Isolates from Air and Surfaces of the International Space Station. <i>MSphere</i> , 2016, 1, .	1.3	108
1412	Widespread adaptive evolution during repeated evolutionary radiations in New World lupins. <i>Nature Communications</i> , 2016, 7, 12384.	5.8	80
1413	Intraspecific and heteroplasmic variations, gene losses and inversions in the chloroplast genome of <i>Astragalus membranaceus</i> . <i>Scientific Reports</i> , 2016, 6, 21669.	1.6	116
1414	Inferring phylogeny and speciation of <i>Gymnosporangium</i> species and their coevolution with host plants. <i>Scientific Reports</i> , 2016, 6, 29339.	1.6	23
1415	Speciation with Gene Flow in North American <i>Myotis</i> Bats. <i>Systematic Biology</i> , 2017, 66, syw100.	2.7	50
1416	Do Macrophylogenies Yield Stable Macroevolutionary Inferences? An Example from Squamate Reptiles. <i>Systematic Biology</i> , 2017, 66, syw102.	2.7	19
1417	Mapping the genomic diversity of HCV subtypes 1a and 1b: Implications of structural and immunological constraints for vaccine and drug development. <i>Virus Evolution</i> , 2016, 2, vew024.	2.2	17
1418	Reconstructing contact network parameters from viral phylogenies. <i>Virus Evolution</i> , 2016, 2, vew029.	2.2	10
1419	A global map of genetic diversity in <i>Babesia microti</i> reveals strong population structure and identifies variants associated with clinical relapse. <i>Nature Microbiology</i> , 2016, 1, 16079.	5.9	82
1420	Genome of <i>Leptomonas pyrhorcoris</i> : a high-quality reference for monoxenous trypanosomatids and new insights into evolution of <i>Leishmania</i> . <i>Scientific Reports</i> , 2016, 6, 23704.	1.6	74
1421	Misconceptions on Missing Data in RAD-seq Phylogenetics with a Deep-scale Example from Flowering Plants. <i>Systematic Biology</i> , 2017, 66, syw092.	2.7	167
1422	Phylogenomic analyses of bat subordinal relationships based on transcriptome data. <i>Scientific Reports</i> , 2016, 6, 27726.	1.6	69
1423	Evolutionary inactivation of a sialidase in group B <i>Streptococcus</i> . <i>Scientific Reports</i> , 2016, 6, 28852.	1.6	31
1424	A single gene of a commensal microbe affects host susceptibility to enteric infection. <i>Nature Communications</i> , 2016, 7, 11606.	5.8	31
1425	Tectonic collision and uplift of Wallacea triggered the global songbird radiation. <i>Nature Communications</i> , 2016, 7, 12709.	5.8	183
1426	Biogeography and environmental genomics of the <i>Roseobacter</i> -affiliated pelagic CHAB-I-5 lineage. <i>Nature Microbiology</i> , 2016, 1, 16063.	5.9	36

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1427	Genomic survey of a hyperparasitic microsporidian <i>Amphiblyss</i> sp. (Metchnikovellidae). <i>Genome Biology and Evolution</i> , 2016, 9, evw235.	1.1	41
1428	Evolutionary trajectories of snake genes and genomes revealed by comparative analyses of five-pacer viper. <i>Nature Communications</i> , 2016, 7, 13107.	5.8	88
1429	Molecular archeological evidence in support of the repeated loss of a papillomavirus gene. <i>Scientific Reports</i> , 2016, 6, 33028.	1.6	36
1430	Understanding the evolution of holoparasitic plants: the complete plastid genome of the holoparasite <i>Cytinus hypocistis</i> (Cytinaceae). <i>Annals of Botany</i> , 2016, 118, 885-896.	1.4	55
1431	Rumen metagenome and metatranscriptome analyses of low methane yield sheep reveals a <i>Sharpea</i> -enriched microbiome characterised by lactic acid formation and utilisation. <i>Microbiome</i> , 2016, 4, 56.	4.9	268
1432	<i>Viola woosanensis</i> , a recurrent spontaneous hybrid between <i>V. ulleungdoensis</i> and <i>V. chaerophylloides</i> (Violaceae) endemic to Ulleung Island, Korea. <i>Journal of Plant Research</i> , 2016, 129, 807-822.	1.2	11
1433	Comparative analysis of plastid genomes of non-photosynthetic Ericaceae and their photosynthetic relatives. <i>Scientific Reports</i> , 2016, 6, 30042.	1.6	47
1434	Expression of segment polarity genes in brachiopods supports a non-segmental ancestral role of engrailed for bilaterians. <i>Scientific Reports</i> , 2016, 6, 32387.	1.6	35
1435	Construction of a Species-Level Tree of Life for the Insects and Utility in Taxonomic Profiling. <i>Systematic Biology</i> , 2016, 66, syw099.	2.7	29
1436	Genomic analysis reveals hidden biodiversity within colugos, the sister group to primates. <i>Science Advances</i> , 2016, 2, e1600633.	4.7	64
1437	The draft genome of the C3 panicoid grass species <i>Dichantherium oligosanthes</i> . <i>Genome Biology</i> , 2016, 17, 223.	3.8	48
1438	Resolving phylogenetic relationships and species delimitations in closely related gymnosperms using high-throughput NGS, Sanger sequencing and morphology. <i>Plant Systematics and Evolution</i> , 2016, 302, 1345-1365.	0.3	26
1439	Adaptive radiation by waves of gene transfer leads to fine-scale resource partitioning in marine microbes. <i>Nature Communications</i> , 2016, 7, 12860.	5.8	140
1440	A Comparative Analysis of Sonic Defences in Bombycoidea Caterpillars. <i>Scientific Reports</i> , 2016, 6, 31469.	1.6	16
1441	Pangenome and Phylogenomic Analysis of the Pathogenic Actinobacterium <i>Rhodococcus equi</i> . <i>Genome Biology and Evolution</i> , 2016, 8, 3140-3148.	1.1	58
1442	The Effects of Signal Erosion and Core Genome Reduction on the Identification of Diagnostic Markers. <i>MBio</i> , 2016, 7, .	1.8	49
1443	Taxonomy and molecular phylogeny of the Platystictidae of Sri Lanka (Insecta: Odonata). <i>Zootaxa</i> , 2016, 4182, 1.	0.2	6
1444	A beautiful new yellow salamander, genus <i>Bolitoglossa</i> (Caudata: Plethodontidae), from the northeastern slopes of the Cordillera de Talamanca, Costa Rica. <i>Zootaxa</i> , 2016, 4184, 329-346.	0.2	5

#	ARTICLE	IF	CITATIONS
1445	Systematics of <i>Diplazium laffanianum</i> (Athuriaceae), a Fern Species Endemic to Bermuda. <i>American Fern Journal</i> , 2016, 106, 206-222.	0.2	3
1446	A method for identification of highly conserved elements and evolutionary analysis of superphylum Alveolata. <i>BMC Bioinformatics</i> , 2016, 17, 385.	1.2	9
1447	Chloroplast genomes as a tool to resolve red algal phylogenies: a case study in the Nemaliales. <i>BMC Evolutionary Biology</i> , 2016, 16, 205.	3.2	36
1448	Occurrence of the <i>Paracalanus parvus</i> species complex in offshore waters south of Japan and their genetic and morphological identification to species. <i>Plankton and Benthos Research</i> , 2016, 11, 131-143.	0.2	12
1449	Host records of <i>Grammia ursina</i> Schmidt, 2009 (Lepidoptera: Noctuidae: Arctiinae) on San Clemente Island and its potential effect on rare plant restoration. <i>Pan-Pacific Entomologist</i> , 2016, 92, 151-156.	0.1	0
1450	Reconstructing the Backbone of the Saccharomycotina Yeast Phylogeny Using Genome-Scale Data. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 3927-3939.	0.8	187
1451	The Simple Chordate <i>Ciona intestinalis</i> Has a Reduced Complement of Genes Associated with Fanconi Anemia. <i>Evolutionary Bioinformatics</i> , 2016, 12, EBO.S37920.	0.6	6
1452	Phylogenomic approaches to determine the zoonotic potential of Shiga toxin-producing <i>Escherichia coli</i> (STEC) isolated from Zambian dairy cattle. <i>Scientific Reports</i> , 2016, 6, 26589.	1.6	15
1453	Evolution of the EGFR pathway in Metazoa and its diversification in the planarian <i>Schmidtea mediterranea</i> . <i>Scientific Reports</i> , 2016, 6, 28071.	1.6	32
1454	Evolution of short inverted repeat in cupressophytes, transfer of <i>accD</i> to nucleus in <i>Sciadopitys verticillata</i> and phylogenetic position of <i>Sciadopityaceae</i> . <i>Scientific Reports</i> , 2016, 6, 20934.	1.6	25
1455	The Establishment and Diversification of Epidemic-Associated Serogroup W Meningococcus in the African Meningitis Belt, 1994 to 2012. <i>MSphere</i> , 2016, 1, .	1.3	29
1456	Comparative Genomics of a Parthenogenesis-Inducing <i>Wolbachia</i> Symbiont. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 2113-2123.	0.8	56
1457	Allostery Wiring Map for Kinesin Energy Transduction and Its Evolution. <i>Journal of Biological Chemistry</i> , 2016, 291, 20932-20945.	1.6	11
1458	Hidden diversity of Acoelomorpha revealed through metabarcoding. <i>Biology Letters</i> , 2016, 12, 20160674.	1.0	17
1459	Resurrecting ancestral structural dynamics of an antiviral immune receptor: adaptive binding pocket reorganization repeatedly shifts RNA preference. <i>BMC Evolutionary Biology</i> , 2016, 16, 241.	3.2	6
1460	Structural differences and differential expression among rhabdomeric opsins reveal functional change after gene duplication in the bay scallop, <i>Argopecten irradians</i> (Pectinidae). <i>BMC Evolutionary Biology</i> , 2016, 16, 250.	3.2	10
1461	A core phylogeny of <i>Dictyostelia</i> inferred from genomes representative of the eight major and minor taxonomic divisions of the group. <i>BMC Evolutionary Biology</i> , 2016, 16, 251.	3.2	19
1462	Histological characterization of orphan transporter MCT14 (SLC16A14) shows abundant expression in mouse CNS and kidney. <i>BMC Neuroscience</i> , 2016, 17, 43.	0.8	10

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1463	The multiple evolutionary origins of the eukaryotic N-glycosylation pathway. <i>Biology Direct</i> , 2016, 11, 36.	1.9	46
1464	Complex Admixture Preceded and Followed the Extinction of Wisent in the Wild. <i>Molecular Biology and Evolution</i> , 2017, 34, msw254.	3.5	30
1465	<i>Sporidesmioides thailandica</i> gen. et sp. nov. (Dothideomycetes) from northern Thailand. <i>Mycological Progress</i> , 2016, 15, 1169-1178.	0.5	13
1466	Monoplacophoran mitochondrial genomes: convergent gene arrangements and little phylogenetic signal. <i>BMC Evolutionary Biology</i> , 2016, 16, 274.	3.2	10
1467	The psoriasis-associated deletion of late cornified envelope genes LCE3B and LCE3C has been maintained under balancing selection since Human Denisovan divergence. <i>BMC Evolutionary Biology</i> , 2016, 16, 265.	3.2	35
1468	Anchoring quartet-based phylogenetic distances and applications to species tree reconstruction. <i>BMC Genomics</i> , 2016, 17, 783.	1.2	24
1469	Exploring phylogenetic hypotheses via Gibbs sampling on evolutionary networks. <i>BMC Genomics</i> , 2016, 17, 784.	1.2	2
1470	Genomic epidemiology of Lineage 4 <i>Mycobacterium tuberculosis</i> subpopulations in New York City and New Jersey, 1999–2009. <i>BMC Genomics</i> , 2016, 17, 947.	1.2	13
1471	Non-canonical Helitrons in <i>Fusarium oxysporum</i> . <i>Mobile DNA</i> , 2016, 7, 27.	1.3	13
1472	Madagascar's grasses and grasslands: anthropogenic or natural?. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016, 283, 20152262.	1.2	83
1473	Evidence of functional divergence in MSP7 paralogous proteins: a molecular-evolutionary and phylogenetic analysis. <i>BMC Evolutionary Biology</i> , 2016, 16, 256.	3.2	17
1474	Draft genome sequence of the marine Rhodobacteraceae strain O3.65, cultivated from oil-polluted seawater of the Deepwater Horizon oil spill. <i>Standards in Genomic Sciences</i> , 2016, 11, 81.	1.5	11
1475	Limited Antigenic Diversity in Contemporary H7 Avian-Origin Influenza A Viruses from North America. <i>Scientific Reports</i> , 2016, 6, 20688.	1.6	22
1476	gEVE: a genome-based endogenous viral element database provides comprehensive viral protein-coding sequences in mammalian genomes. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, baw087.	1.4	56
1477	Mitochondrial genome analysis of <i>Mylochromis lateristriga</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 43-44.	0.2	0
1478	The complete mitogenome of <i>Mycosphaerella pinodes</i> (Ascomycota, Mycosphaerellaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 48-49.	0.2	4
1479	Complete mitochondrial genome of the Greek nine-spined stickleback <i>Pungitius hellenicus</i> (Gasterosteiformes, Gasterosteidae). <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 66-67.	0.2	2
1480	Complete mitochondrial genome of the Ukrainian nine-spined stickleback <i>Pungitius platygaster</i> (Gasterosteiformes, Gasterosteidae). <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 68-69.	0.2	1

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1481	Complete mitochondrial genomes of the smooth tail nine-spined sticklebacks <i>Pungitius laevis</i> (Gasterosteiformes, Gasterosteidae). <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 70-71.	0.2	2
1482	Complete mitochondrial genome of the nine-spined stickleback <i>Pungitius pungitius</i> (Gasterosteiformes, Gasterosteidae). <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 72-73.	0.2	5
1483	Complete mitochondrial genome of the Sakhalin nine-spined stickleback <i>Pungitius tymensis</i> (Gasterosteiformes, Gasterosteidae). <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 74-75.	0.2	1
1484	Mitogenome of <i>Mytilus trossulus</i> (Mytilidae, Bivalvia) isolated from a 1920 herbarium specimen. <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 452-453.	0.2	1
1485	The complete mitochondrial genome of the semiterrestrial crab, <i>Chiromantes neglectum</i> (Eubrachyura: Grapsoidea: Sesarmidae). <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 461-463.	0.2	16
1486	The complete plastome sequence of <i>Pentactina rupicola</i> Nakai (Rosaceae), a genus endemic to Korea. <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 698-700.	0.2	2
1487	First Detection of Bat White-Nose Syndrome in Western North America. <i>MSphere</i> , 2016, 1, .	1.3	78
1488	Diversity and Divergence of Dinoflagellate Histone Proteins. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 397-422.	0.8	38
1489	Heterotrophic <i>Proteobacteria</i> in the vicinity of diffuse hydrothermal venting. <i>Environmental Microbiology</i> , 2016, 18, 4348-4368.	1.8	63
1490	Genetic structure and host-parasite co-divergence: evidence for trait-specific local adaptation. <i>Biological Journal of the Linnean Society</i> , 2016, 118, 344-358.	0.7	27
1491	Phylogenetics, delimitation and historical biogeography of the pantropical tree genus <i>Thespesia</i> (Malvaceae, Gossypieae). <i>Botanical Journal of the Linnean Society</i> , 2016, 181, 171-198.	0.8	15
1492	Phylogenetic divergences of the true bugs (Insecta: Hemiptera: Heteroptera), with emphasis on the aquatic lineages: the last piece of the aquatic insect jigsaw originated in the Late Permian/Early Triassic. <i>Cladistics</i> , 2016, 32, 390-405.	1.5	65
1493	Phylogenomics and historical biogeography of the monocot order Liliales: out of Australia and through Antarctica. <i>Cladistics</i> , 2016, 32, 581-605.	1.5	61
1494	The phylogenetic position of the world's smallest passerine, the Pygmy Bushtit <i>Psaltria exilis</i> . <i>Ibis</i> , 2016, 158, 519-529.	1.0	1
1495	The importance of long-distance dispersal and establishment events in small insects: historical biogeography of metalmark moths (Lepidoptera, Choreutidae). <i>Journal of Biogeography</i> , 2016, 43, 1254-1265.	1.4	36
1496	<i>Entamoeba marina</i> n. sp.; a New Species of <i>Entamoeba</i> Isolated from Tidal Flat Sediment of Iriomote Island, Okinawa, Japan. <i>Journal of Eukaryotic Microbiology</i> , 2016, 63, 280-286.	0.8	10
1497	Multigene analyses resolve early diverging lineages in the Rhodymeniophycidae (Florideophyceae, Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	1.0	9
1498	Reticulate evolutionary history and extensive introgression in mosquito species revealed by phylogenetic network analysis. <i>Molecular Ecology</i> , 2016, 25, 2361-2372.	2.0	98

#	ARTICLE	IF	CITATIONS
1499	Massive intracellular gene transfer during plastid genome reduction in nongreen Orobanchaceae. <i>New Phytologist</i> , 2016, 210, 680-693.	3.5	86
1500	Large-scale molecular phylogeny of Cryptorhynchinae (Coleoptera, Curculionidae) from multiple genes suggests American origin and later Australian radiation. <i>Systematic Entomology</i> , 2016, 41, 492-503.	1.7	14
1501	Functional Divergence of the Nuclear Receptor <i>NR2C1</i> as a Modulator of Pluripotentiality During Hominid Evolution. <i>Genetics</i> , 2016, 203, 905-922.	1.2	33
1502	Transmission Clusters of Methicillin-Resistant <i>Staphylococcus Aureus</i> in Long-Term Care Facilities Based on Whole-Genome Sequencing. <i>Infection Control and Hospital Epidemiology</i> , 2016, 37, 685-691.	1.0	11
1503	Relationships of the sub-Saharan African genus <i>Zygotritonia</i> Mildbr. (Iridaceae: Crocoideae) inferred from molecular analysis. <i>South African Journal of Botany</i> , 2016, 106, 5-7.	1.2	1
1504	RAD-seq derived genome-wide nuclear markers resolve the phylogeny of tunas. <i>Molecular Phylogenetics and Evolution</i> , 2016, 102, 202-207.	1.2	75
1505	Hybrid origin of European Vipers (<i>Vipera magnifica</i> and <i>Vipera orlovi</i>) from the Caucasus determined using genomic scale DNA markers. <i>BMC Evolutionary Biology</i> , 2016, 16, 76.	3.2	29
1506	A maximum-likelihood approach for building cell-type trees by lifting. <i>BMC Genomics</i> , 2016, 17, 14.	1.2	6
1507	Structuprint: a scalable and extensible tool for two-dimensional representation of protein surfaces. <i>BMC Structural Biology</i> , 2016, 16, 4.	2.3	12
1508	A paneukaryotic genomic analysis of the small GTPase RABL2 underscores the significance of recurrent gene loss in eukaryote evolution. <i>Biology Direct</i> , 2016, 11, 5.	1.9	22
1509	Insights into the transcriptional and translational mechanisms of linear organellar chromosomes in the box jellyfish <i>Alatina alata</i> (Cnidaria: Medusozoa: Cubozoa). <i>RNA Biology</i> , 2016, 13, 799-809.	1.5	4
1510	Selection on different genes with equivalent functions: the convergence story told by Hox genes along the evolution of aquatic mammalian lineages. <i>BMC Evolutionary Biology</i> , 2016, 16, 113.	3.2	12
1511	Transfer of the leafy liverwort <i>Xenochila</i> from Plagiochilaceae (Lophocoleineae) to Jungermanniaceae (Jungermanniaceae). <i>Plant Systematics and Evolution</i> , 2016, 302, 891-899.	0.3	4
1512	Conservation genomics reveals multiple evolutionary units within Bell's Vireo (<i>Vireo bellii</i>). <i>Conservation Genetics</i> , 2016, 17, 455-471.	0.8	15
1513	Phylogeny of deepwater snappers (Genus <i>Etelis</i>) reveals a cryptic species pair in the Indo-Pacific and Pleistocene invasion of the Atlantic. <i>Molecular Phylogenetics and Evolution</i> , 2016, 100, 361-371.	1.2	26
1514	Multiple lines of evidence support the species status of the poorly known <i>Diasporus tigrillo</i> and the recently described <i>Diasporus citrinobapheus</i> (Anura: Eleutherodactylidae). <i>Neotropical Biodiversity</i> , 2016, 2, 59-68.	0.2	3
1515	Contrasting evolutionary histories of the legless lizards slow worms (<i>Anguis</i>) shaped by the topography of the Balkan Peninsula. <i>BMC Evolutionary Biology</i> , 2016, 16, 99.	3.2	46
1516	Comparative genomic analyses reveal broad diversity in botulinum-toxin-producing <i>Clostridia</i> . <i>BMC Genomics</i> , 2016, 17, 180.	1.2	71

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1517	Association between clinical antibiotic resistance and susceptibility of <i>Pseudomonas</i> in the cystic fibrosis lung. <i>Evolution, Medicine and Public Health</i> , 2016, 2016, 182-194.	1.1	34
1518	Genus-Wide Comparative Genome Analyses of <i>Colletotrichum</i> Species Reveal Specific Gene Family Losses and Gains during Adaptation to Specific Infection Lifestyles. <i>Genome Biology and Evolution</i> , 2016, 8, 1467-1481.	1.1	69
1519	Are There Rab GTPases in Archaea?. <i>Molecular Biology and Evolution</i> , 2016, 33, 1833-1842.	3.5	26
1520	W-IQ-TREE: a fast online phylogenetic tool for maximum likelihood analysis. <i>Nucleic Acids Research</i> , 2016, 44, W232-W235.	6.5	3,039
1521	Diel regulation of hydrogen peroxide defenses by open ocean microbial communities. <i>Journal of Plankton Research</i> , 2016, 38, 1103-1114.	0.8	35
1522	Isolation and preliminary characterization of a new pathogenic iridovirus from redclaw crayfish <i>Cherax quadricarinatus</i> . <i>Diseases of Aquatic Organisms</i> , 2016, 120, 17-26.	0.5	69
1523	Recruitment of Rod Photoreceptors from Short-Wavelength-Sensitive Cones during the Evolution of Nocturnal Vision in Mammals. <i>Developmental Cell</i> , 2016, 37, 520-532.	3.1	103
1524	The <i>Rickettsia</i> type IV secretion system: unrealized complexity mired by gene family expansion. <i>Pathogens and Disease</i> , 2016, 74, ftw058.	0.8	45
1525	Male Reproductive Morphology Across Latitudinal Clines and Under Long-Term Female Sex-Ratio Bias. <i>Integrative and Comparative Biology</i> , 2016, 56, 715-727.	0.9	7
1526	Most Compositae (Asteraceae) are descendants of a paleohexaploid and all share a paleotetraploid ancestor with the Calyceraceae. <i>American Journal of Botany</i> , 2016, 103, 1203-1211.	0.8	98
1527	Evolution of Sulfur Binding by Hemoglobin in Siboglinidae (Annelida) with Special Reference to Bone-Eating Worms, <i>Osedax</i> . <i>Journal of Molecular Evolution</i> , 2016, 82, 219-229.	0.8	5
1528	Genome-wide selective sweeps and gene-specific sweeps in natural bacterial populations. <i>ISME Journal</i> , 2016, 10, 1589-1601.	4.4	226
1529	Population genomics studies identify signatures of global dispersal and drug resistance in <i>Plasmodium vivax</i> . <i>Nature Genetics</i> , 2016, 48, 953-958.	9.4	194
1530	Transcriptome sequences spanning key developmental states as a resource for the study of the cestode <i>Schistocephalus solidus</i> , a threespine stickleback parasite. <i>GigaScience</i> , 2016, 5, 24.	3.3	49
1531	Widespread interspecies homologous recombination reveals reticulate evolution within the genus <i>Streptomyces</i> . <i>Molecular Phylogenetics and Evolution</i> , 2016, 102, 246-254.	1.2	29
1532	Unraveling the biogeographical history of Chrysobalanaceae from plastid genomes. <i>American Journal of Botany</i> , 2016, 103, 1089-1102.	0.8	20
1533	<i>Cynanchum</i> (Apocynaceae: Asclepiadoideae): A pantropical Asclepiadoid genus revisited. <i>Taxon</i> , 2016, 65, 467-486.	0.4	20
1534	Resolving the Phylogenetic Position of <i>Coelacanth</i> : The Closest Relative Is Not Always the Most Appropriate Outgroup. <i>Genome Biology and Evolution</i> , 2016, 8, 1208-1221.	1.1	29

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1535	Origin of Chrysanthemum cultivars – Evidence from nuclear low-copy LFY gene sequences. <i>Biochemical Systematics and Ecology</i> , 2016, 65, 129-136.	0.6	19
1536	Tidal Freshwater Marshes Harbor Phylogenetically Unique Clades of Sulfate Reducers That Are Resistant to Climate-Change-Induced Salinity Intrusion. <i>Estuaries and Coasts</i> , 2016, 39, 981-991.	1.0	4
1537	Rust (<i>Puccinia psidii</i>) recorded in Indonesia poses a threat to forests and forestry in South-East Asia. <i>Australasian Plant Pathology</i> , 2016, 45, 83-89.	0.5	36
1538	Pinworm diversity in free-ranging howler monkeys (<i>Alouatta</i> spp.) in Mexico: Morphological and molecular evidence for two new <i>Trypanoxyuris</i> species (Nematoda: Oxyuridae). <i>Parasitology International</i> , 2016, 65, 401-411.	0.6	16
1539	Environmental Breviatea harbour mutualistic <i>Arcobacter</i> epibionts. <i>Nature</i> , 2016, 534, 254-258.	13.7	68
1540	A novel orellanine containing mushroom <i>Cortinarius armillatus</i> . <i>Toxicon</i> , 2016, 114, 65-74.	0.8	15
1541	The Evolutionary History of the African Fruit Bats (Chiroptera: Pteropodidae). <i>Acta Chiropterologica</i> , 2016, 18, 73-90.	0.2	27
1542	The mitochondrial genome sequence of a deep-sea, hydrothermal vent limpet, <i>Lepetodrilus nux</i> , presents a novel vetigastropod gene arrangement. <i>Marine Genomics</i> , 2016, 28, 121-126.	0.4	16
1543	A novel phylogeny of the Gelidiales (Rhodophyta) based on five genes including the nuclear <i>CesA</i> , with descriptions of <i>Orthogonacladia</i> gen. nov. and <i>Orthogonacladiaceae</i> fam. nov.. <i>Molecular Phylogenetics and Evolution</i> , 2016, 101, 359-372.	1.2	45
1544	Reconstruction of ancestral chromosome architecture and gene repertoire reveals principles of genome evolution in a model yeast genus. <i>Genome Research</i> , 2016, 26, 918-932.	2.4	95
1545	Characterization of the complete chloroplast genome of <i>Idesia polycarpa</i> . <i>Conservation Genetics Resources</i> , 2016, 8, 271-273.	0.4	4
1546	Phylogenetically Structured Differences in rRNA Gene Sequence Variation among Species of Arbuscular Mycorrhizal Fungi and Their Implications for Sequence Clustering. <i>Applied and Environmental Microbiology</i> , 2016, 82, 4921-4930.	1.4	31
1547	Does the choice of nucleotide substitution models matter topologically?. <i>BMC Bioinformatics</i> , 2016, 17, 143.	1.2	32
1548	Multilocus phylogeny and ecological differentiation of the “ <i>Eupelmus urozonus</i> species group” (Hymenoptera, Eupelmidae) in the West-Palaeartic. <i>BMC Evolutionary Biology</i> , 2016, 16, 13.	3.2	15
1549	Genome-wide data reveal cryptic diversity and genetic introgression in an Oriental cynopterine fruit bat radiation. <i>BMC Evolutionary Biology</i> , 2016, 16, 41.	3.2	32
1550	Phylogenomics of a rapid radiation: is chromosomal evolution linked to increased diversification in north american spiny lizards (Genus <i>Sceloporus</i>)?. <i>BMC Evolutionary Biology</i> , 2016, 16, 63.	3.2	76
1551	Evolutionary history of endemic Sulawesi squirrels constructed from UCEs and mitogenomes sequenced from museum specimens. <i>BMC Evolutionary Biology</i> , 2016, 16, 80.	3.2	39
1552	Increasing genomic diversity and evidence of constrained lifestyle evolution due to insertion sequences in <i>Aeromonas salmonicida</i> . <i>BMC Genomics</i> , 2016, 17, 44.	1.2	46

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1553	Comparative genomics and prediction of conditionally dispensable sequences in legume-infecting <i>Fusarium oxysporum</i> formae speciales facilitates identification of candidate effectors. <i>BMC Genomics</i> , 2016, 17, 191.	1.2	109
1554	Genome-wide analysis of ionotropic receptors provides insight into their evolution in <i>Heliconius</i> butterflies. <i>BMC Genomics</i> , 2016, 17, 254.	1.2	38
1555	Elaboration of bilateral symmetry across <i>Knautia macedonica</i> capitula related to changes in ventral petal expression of CYCLOIDEA-like genes. <i>EvoDevo</i> , 2016, 7, 8.	1.3	22
1556	Temporally and spatially dynamic germ cell niches in <i>Botryllus schlosseri</i> revealed by expression of a TGF-beta family ligand and vasa. <i>EvoDevo</i> , 2016, 7, 9.	1.3	12
1557	Large genomic differences between <i>Moraxella bovoculi</i> isolates acquired from the eyes of cattle with infectious bovine keratoconjunctivitis versus the deep nasopharynx of asymptomatic cattle. <i>Veterinary Research</i> , 2016, 47, 31.	1.1	38
1558	Mycorrhizal detection of native and non-native truffles in a historic arboretum and the discovery of a new North American species, <i>Tuber arnoldianum</i> sp. nov.. <i>Mycorrhiza</i> , 2016, 26, 781-792.	1.3	17
1559	Cryptic Diversity of <i>Malassezia pachydermatis</i> from Healthy and Diseased Domestic Animals. <i>Mycopathologia</i> , 2016, 181, 681-688.	1.3	12
1560	Evidence for common horizontal transmission of <i>Wolbachia</i> among butterflies and moths. <i>BMC Evolutionary Biology</i> , 2016, 16, 118.	3.2	103
1561	A phylogenetic study of the tribe Antirrhineae: Genome duplications and long-distance dispersals from the Old World to the New World. <i>American Journal of Botany</i> , 2016, 103, 1071-1081.	0.8	15
1562	Epi-tyfication of <i>Fusisporium</i> (<i>Fusarium</i>) <i>solani</i> and its assignment to a common phylogenetic species in the <i>Fusarium solani</i> species complex. <i>Mycologia</i> , 2016, 108, 806-819.	0.8	81
1563	Maintenance of Species Boundaries Despite Ongoing Gene Flow in Ragworts. <i>Genome Biology and Evolution</i> , 2016, 8, 1038-1047.	1.1	18
1564	Novel Hydrogenosomes in the Microaerophilic Jakobid <i>Stygiella incarcerata</i> . <i>Molecular Biology and Evolution</i> , 2016, 33, 2318-2336.	3.5	52
1565	Highly diversified Zika viruses imported to China, 2016. <i>Protein and Cell</i> , 2016, 7, 461-464.	4.8	48
1566	Pangenome Evolution in the Marine Bacterium <i>Alteromonas</i> . <i>Genome Biology and Evolution</i> , 2016, 8, 1556-1570.	1.1	73
1567	Species-Level Para- and Polyphyly in DNA Barcode Gene Trees: Strong Operational Bias in European Lepidoptera. <i>Systematic Biology</i> , 2016, 65, 1024-1040.	2.7	160
1568	The genome of the yellow potato cyst nematode, <i>Globodera rostochiensis</i> , reveals insights into the basis of parasitism and virulence. <i>Genome Biology</i> , 2016, 17, 124.	3.8	156
1569	Isolation of Madre de Dios Virus (Orthobunyavirus; Bunyaviridae), an Oropouche Virus Species Reassortant, from a Monkey in Venezuela. <i>American Journal of Tropical Medicine and Hygiene</i> , 2016, 95, 328-338.	0.6	38
1570	Descriptions of two new species of Rhizorhina Hansen, 1892 (Copepoda: Siphonostomatoida): <i>Tj ETQq1</i> 1 0.784314 rgBT /Overlock <i>Systematic Parasitology</i> , 2016, 93, 57-68.	0.5	9

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1571	Independent evolution of pouched flowers in the Amazon is supported by the discovery of a new species of <i>Lesia</i> (Gesneriaceae) from Serra do Aracã; tepui in Brazil. <i>Plant Systematics and Evolution</i> , 2016, 302, 1109-1119.	0.3	7
1572	Morphological and niche divergence of pinyon pines. <i>Ecology and Evolution</i> , 2016, 6, 2886-2896.	0.8	12
1573	Intermediate divergence levels maximize the strength of structure–sequence correlations in enzymes and viral proteins. <i>Protein Science</i> , 2016, 25, 1341-1353.	3.1	7
1574	<i>Nocturama</i> gen. nov., <i>Nothocladus</i> s. lat. and other taxonomic novelties resulting from the further resolution of paraphyly in Australasian members of <i>Batrachospermum</i> (Batrachospermales, Rhodophyta). <i>Journal of Phycology</i> , 2016, 52, 384-396.	1.0	17
1575	Species diversity of the genus <i>Osmundea</i> (Ceramiales, Rhodophyta) in the Macaronesian region. <i>Journal of Phycology</i> , 2016, 52, 664-681.	1.0	15
1576	Additional insights into phylogenetic relationships of the Class Ophiuroidea (Echinodermata) from <i>scp</i> rRNA gene sequences. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2016, 54, 269-275.	0.6	3
1577	Ancient <i>scp</i> DNA from the extinct South American giant glyptodont <i>Doedicurus</i> sp. (Xenarthra: Glyptodontidae) reveals that glyptodonts evolved from Eocene armadillos. <i>Molecular Ecology</i> , 2016, 25, 3499-3508.	2.0	43
1578	Reconstruction of phylogenetic relationships in dermatomycete genus <i>Trichophyton</i> Malmsten 1848 based on ribosomal internal transcribed spacer region, partial 28S rRNA and beta-tubulin genes sequences. <i>Mycoses</i> , 2016, 59, 566-575.	1.8	26
1579	Analyses of transcriptome sequences reveal multiple ancient large-scale duplication events in the ancestor of Sphagnopsida (Bryophyta). <i>New Phytologist</i> , 2016, 211, 300-318.	3.5	56
1580	Sebacinales – one thousand and one interactions with land plants. <i>New Phytologist</i> , 2016, 211, 20-40.	3.5	274
1581	Taxonomy and phylogeny of three heterotrich ciliates (Protozoa, Ciliophora), with description of a new <i>Blepharisma</i> species. <i>Zoological Journal of the Linnean Society</i> , 2016, 177, 320-334.	1.0	31
1582	Snake evolution in Melanesia: origin of the Hydrophiinae (Serpentes, Elapidae), and the evolutionary history of the enigmatic New Guinean elapid <i>Toxicocalamus</i> . <i>Zoological Journal of the Linnean Society</i> , 2016, 178, 663-678.	1.0	23
1583	Cryptic species in Pacific sipunculans (Sipuncula: Phascolosomatidae): east–west divergence between non-sister taxa. <i>Zoologica Scripta</i> , 2016, 45, 455-463.	0.7	7
1584	Genome Structural Diversity among 31 <i>Bordetella pertussis</i> Isolates from Two Recent U.S. Whooping Cough Statewide Epidemics. <i>MSphere</i> , 2016, 1, .	1.3	51
1585	Deacetylation of Fungal Exopolysaccharide Mediates Adhesion and Biofilm Formation. <i>MBio</i> , 2016, 7, e00252-16.	1.8	91
1586	Target enrichment of thousands of ultraconserved elements sheds new light on early relationships within New World sparrows (Aves: Passerellidae). <i>Auk</i> , 2016, 133, 451-458.	0.7	17
1587	Contagious Ecthyma, Rangeliferine Brucellosis, and Lungworm Infection in a Muskox (<i>Ovibos</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 100	0.3	26
1588	Rapid and recent diversification of curassows, guans, and chachalacas (Galliformes: Cracidae) out of Mesoamerica: Phylogeny inferred from mitochondrial, intron, and ultraconserved element sequences. <i>Molecular Phylogenetics and Evolution</i> , 2016, 102, 320-330.	1.2	33

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1589	Genome-Wide Survey of Gut Fungi (Harpellales) Reveals the First Horizontally Transferred Ubiquitin Gene from a Mosquito Host. <i>Molecular Biology and Evolution</i> , 2016, 33, 2544-2554.	3.5	28
1590	Host specialization of the blast fungus <i>Magnaporthe oryzae</i> is associated with dynamic gain and loss of genes linked to transposable elements. <i>BMC Genomics</i> , 2016, 17, 370.	1.2	157
1591	Whole genome sequencing reveals extensive community-level transmission of group A <i>Streptococcus</i> in remote communities. <i>Epidemiology and Infection</i> , 2016, 144, 1991-1998.	1.0	19
1592	The borage family (Boraginaceae s.str.): A revised infrafamilial classification based on new phylogenetic evidence, with emphasis on the placement of some enigmatic genera. <i>Taxon</i> , 2016, 65, 523-546.	0.4	83
1593	The Genome of <i>Intoshia linei</i> Affirms Orthonectids as Highly Simplified Spiralian. <i>Current Biology</i> , 2016, 26, 1768-1774.	1.8	50
1594	Complete chloroplast genomes of <i>Saccharum spontaneum</i> , <i>Saccharum officinarum</i> and <i>Miscanthus floridulus</i> (Panicoideae: Andropogoneae) reveal the plastid view on sugarcane origins. <i>Systematics and Biodiversity</i> , 2016, 14, 548-571.	0.5	34
1595	Phylogeny of the titi monkeys of the <i>Callicebus moloch</i> group (Pitheciidae, Primates). <i>American Journal of Primatology</i> , 2016, 78, 904-913.	0.8	15
1596	Chlamydial seasonal dynamics and isolation of <i>Chlamydia trachomatis</i> and <i>Chlamydia pneumoniae</i> from a T ₁ tyrrhenian coastal lake. <i>Environmental Microbiology</i> , 2016, 18, 2405-2417.	1.8	21
1597	New biosynthetic pathway for pink pigments from uncultured oceanic viruses. <i>Environmental Microbiology</i> , 2016, 18, 4337-4347.	1.8	23
1598	Temporal and spatial mosaics: deep host association and shallow geographic drivers shape genetic structure in a widespread pinworm, <i>Rauschtineria eutamii</i> (Nematoda: Oxyuridae). <i>Biological Journal of the Linnean Society</i> , 2016, 119, 397-413.	0.7	10
1599	An introduction to plant phylogenomics with a focus on palms. <i>Botanical Journal of the Linnean Society</i> , 2016, 182, 234-255.	0.8	42
1600	Phylogenetic hypothesis of Sphaerodoridae Malmgren, 1867 (Annelida) and its position within Phyllococida. <i>Cladistics</i> , 2016, 32, 335-350.	1.5	6
1601	Phenotypic shifts in urban areas in the tropical lizard <i>Anolis cristatellus</i> . <i>Evolution; International Journal of Organic Evolution</i> , 2016, 70, 1009-1022.	1.1	162
1602	The complete mitochondrial genome of the gilthead seabream <i>Sparus aurata</i> L. (Sparidae). <i>Mitochondrial DNA</i> , 2016, 27, 781-782.	0.6	9
1603	<i>Symplectella rowi</i> (Porifera: Hexactinellida: Lyssacinosida) is a rossellid, not a euplectellid. <i>Journal of the Marine Biological Association of the United Kingdom</i> , 2016, 96, 291-295.	0.4	3
1604	Phylogenomic reconstruction supports supercontinent origins for <i>Leishmania</i> . <i>Infection, Genetics and Evolution</i> , 2016, 38, 101-109.	1.0	49
1605	Diversity-dependent cladogenesis throughout western Mexico: Evolutionary biogeography of rattlesnakes (Viperidae: Crotalinae: <i>Crotalus</i> and <i>Sistrurus</i>). <i>Molecular Phylogenetics and Evolution</i> , 2016, 97, 145-154.	1.2	34
1606	A phylotranscriptomic analysis of gene family expansion and evolution in the largest order of pleurocarpous mosses (Hypnales, Bryophyta). <i>Molecular Phylogenetics and Evolution</i> , 2016, 98, 29-40.	1.2	29

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1607	Niche partitioning and biogeography of high light adapted <i>Prochlorococcus</i> across taxonomic ranks in the North Pacific. <i>ISME Journal</i> , 2016, 10, 1555-1567.	4.4	63
1608	The Diversity and Molecular Evolution of B-Cell Receptors during Infection. <i>Molecular Biology and Evolution</i> , 2016, 33, 1147-1157.	3.5	72
1609	Comparison of Target-Capture and Restriction-Site Associated DNA Sequencing for Phylogenomics: A Test in Cardinalid Tanagers (Aves, Genus: <i>Piranga</i>). <i>Systematic Biology</i> , 2016, 65, 640-650.	2.7	92
1610	Multiple rod-cone and cone-rod photoreceptor transmutations in snakes: evidence from visual opsin gene expression. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016, 283, 20152624.	1.2	42
1611	The complete mitochondrial genome of <i>Koerneria sudhausi</i> (Diplogasteromorpha: Nematoda) supports monophyly of Diplogasteromorpha within Rhabditomorpha. <i>Current Genetics</i> , 2016, 62, 391-403.	0.8	8
1612	<i>Gnomoniopsis smithogilvyi</i> causes chestnut canker symptoms in <i>Castanea sativa</i> shoots in Switzerland. <i>Fungal Genetics and Biology</i> , 2016, 87, 9-21.	0.9	33
1613	Genomic reconstruction of a novel, deeply branched sediment archaeal phylum with pathways for acetogenesis and sulfur reduction. <i>ISME Journal</i> , 2016, 10, 1696-1705.	4.4	161
1614	Hybridization of powdery mildew strains gives rise to pathogens on novel agricultural crop species. <i>Nature Genetics</i> , 2016, 48, 201-205.	9.4	192
1615	Dissecting Japan's Dengue Outbreak in 2014. <i>American Journal of Tropical Medicine and Hygiene</i> , 2016, 94, 409-412.	0.6	53
1616	Identification and in silico characterisation of defective molecules associated with isolates of banana bunchy top virus. <i>Archives of Virology</i> , 2016, 161, 1019-1026.	0.9	3
1617	Performance evaluation of dominance-based and indicator-based multiobjective approaches for phylogenetic inference. <i>Information Sciences</i> , 2016, 330, 293-314.	4.0	18
1618	Do diversity patterns of the spring-inhabiting snail <i>Bythinella</i> (Gastropoda, Bythinellidae) on the Aegean Islands reflect geological history?. <i>Hydrobiologia</i> , 2016, 765, 225-243.	1.0	21
1619	Molecular biodiversity of Red Sea demosponges. <i>Marine Pollution Bulletin</i> , 2016, 105, 507-514.	2.3	41
1620	Towards a monophyletic classification of Lejeuneaceae IV: reinstatement of <i>Allorgella</i> , transfer of <i>Microlejeunea aphanella</i> to <i>Vitalianthus</i> and refinements of the subtribal classification. <i>Plant Systematics and Evolution</i> , 2016, 302, 187-201.	0.3	32
1621	Population-Level Immune-Mediated Adaptation in HIV-1 Polymerase during the North American Epidemic. <i>Journal of Virology</i> , 2016, 90, 1244-1258.	1.5	13
1622	The complete chloroplast genome sequence of <i>Tetrastigma hemsleyanum</i> Diels at Gilg. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 3729-3730.	0.7	4
1623	Episodic Diversifying Selection Shaped the Genomes of Gibbon Ape Leukemia Virus and Related Gammaretroviruses. <i>Journal of Virology</i> , 2016, 90, 1757-1772.	1.5	8
1624	High Degree of HIV-1 Group M (HIV-1M) Genetic Diversity within Circulating Recombinant Forms: Insight into the Early Events of HIV-1M Evolution. <i>Journal of Virology</i> , 2016, 90, 2221-2229.	1.5	25

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1625	Genomic Features of Environmental and Clinical <i>Vibrio parahaemolyticus</i> Isolates Lacking Recognized Virulence Factors Are Dissimilar. <i>Applied and Environmental Microbiology</i> , 2016, 82, 1102-1113.	1.4	38
1626	Plastid Phylogenomic Analyses Resolve Tofieldiaceae as the Root of the Early Diverging Monocot Order Alismatales. <i>Genome Biology and Evolution</i> , 2016, 8, 932-945.	1.1	34
1627	Examining the sensitivity of molecular species delimitations to the choice of mitochondrial marker. <i>Organisms Diversity and Evolution</i> , 2016, 16, 467-480.	0.7	12
1628	Olfactory receptors and behavioural isolation: a study on <i>Microtus voles</i> . <i>Mammal Research</i> , 2016, 61, 399-407.	0.6	1
1629	The phylogenetic position and diversity of the enigmatic mongrel frog <i>Nothophryne Poynton</i> , 1963 (Amphibia, Anura). <i>Molecular Phylogenetics and Evolution</i> , 2016, 99, 89-102.	1.2	22
1630	Discovery of a new <i>Wolbachia</i> supergroup in cave spider species and the lateral transfer of phage WO among distant hosts. <i>Infection, Genetics and Evolution</i> , 2016, 41, 1-7.	1.0	39
1631	RAD sequencing enables unprecedented phylogenetic resolution and objective species delimitation in recalcitrant divergent taxa. <i>Molecular Phylogenetics and Evolution</i> , 2016, 100, 70-79.	1.2	125
1632	Molecular characterization and expression analysis of the first Porifera tumor necrosis factor superfamily member and of its putative receptor in the marine sponge <i>Chondrosia reniformis</i> . <i>Developmental and Comparative Immunology</i> , 2016, 57, 88-98.	1.0	17
1633	Strain-level microbial epidemiology and population genomics from shotgun metagenomics. <i>Nature Methods</i> , 2016, 13, 435-438.	9.0	328
1634	Protein networks identify novel symbiogenetic genes resulting from plastid endosymbiosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 3579-3584.	3.3	47
1635	The Epidemic Dynamics of Four Major Lineages of HIV-1 CRF01_AE Strains After Their Introduction into China. <i>AIDS Research and Human Retroviruses</i> , 2016, 32, 420-426.	0.5	16
1636	Comparative Genomic Analyses of the <i>Moraxella catarrhalis</i> Serosensitive and Seroresistant Lineages Demonstrate Their Independent Evolution. <i>Genome Biology and Evolution</i> , 2016, 8, 955-974.	1.1	20
1637	Novel Trypanosomatid-Bacterium Association: Evolution of Endosymbiosis in Action. <i>MBio</i> , 2016, 7, e01985.	1.8	64
1638	Resolving the phylogenetic position of <i>Ombrocharis</i> (Lamiaceae), with reference to the molecular phylogeny of tribe Elsholtzieae. <i>Taxon</i> , 2016, 65, 123-136.	0.4	32
1639	Population genomics of divergence among extreme and intermediate color forms in a polymorphic insect. <i>Ecology and Evolution</i> , 2016, 6, 1075-1091.	0.8	31
1640	Parallel tagged amplicon sequencing of relatively long <i>PCR</i> products using the Illumina HiSeq platform and transcriptome assembly. <i>Molecular Ecology Resources</i> , 2016, 16, 91-102.	2.2	25
1641	Phylogenetic Overdispersion in Lepidoptera Communities of Amazonian White-Sand Forests. <i>Biotropica</i> , 2016, 48, 101-109.	0.8	9
1642	Computing the Internode Certainty and Related Measures from Partial Gene Trees. <i>Molecular Biology and Evolution</i> , 2016, 33, 1606-1617.	3.5	73

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1643	Variation in sperm morphology among Afrotropical sunbirds. <i>Ibis</i> , 2016, 158, 155-166.	1.0	6
1644	Effects of sequence diversity and recombination on the accuracy of phylogenetic trees estimated by $\langle \text{scp} \rangle \text{kSNP} \langle / \text{scp} \rangle$. <i>Cladistics</i> , 2016, 32, 90-99.	1.5	5
1645	An Exon-Capture System for the Entire Class Ophiuroidea. <i>Molecular Biology and Evolution</i> , 2016, 33, 281-294.	3.5	90
1646	The Eurasian invasion: phylogenomic data reveal multiple Southeast Asian origins for Indian Dragon Lizards. <i>BMC Evolutionary Biology</i> , 2016, 16, 43.	3.2	45
1647	Up high and down low: Molecular systematics and insight into the diversification of the ground beetle genus <i>Rhadine</i> LeConte. <i>Molecular Phylogenetics and Evolution</i> , 2016, 98, 161-175.	1.2	12
1648	Resurrection of the Comoran fish scale gecko <i>Geckolepis humbloti</i> Vaillant, 1887 reveals a disjunct distribution caused by natural overseas dispersal. <i>Organisms Diversity and Evolution</i> , 2016, 16, 289-298.	0.7	7
1649	Ecological Genomics of the Uncultivated Marine Roseobacter Lineage CHAB-I-5. <i>Applied and Environmental Microbiology</i> , 2016, 82, 2100-2111.	1.4	50
1650	The mitochondrial genome and ribosomal operon of <i>Brachycladium goliath</i> (Digenea: Brachycladiidae) recovered from a stranded minke whale. <i>Parasitology International</i> , 2016, 65, 271-275.	0.6	45
1651	The role of pollinators in the evolution of corolla shape variation, disparity and integration in a highly diversified plant family with a conserved floral bauplan. <i>Annals of Botany</i> , 2016, 117, 889-904.	1.4	54
1652	Replicated divergence in cichlid radiations mirrors a major vertebrate innovation. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016, 283, 20151413.	1.2	50
1653	Host switching of human lice to new world monkeys in South America. <i>Infection, Genetics and Evolution</i> , 2016, 39, 225-231.	1.0	13
1654	Phylogenetic analysis reveals an evolutionary transition from internal to external brooding in <i>Epiactis Verrill</i> (Cnidaria: Anthozoa: Actiniaria) and rejects the validity of the genus <i>Cnidopus</i> Carlgren. <i>Molecular Phylogenetics and Evolution</i> , 2016, 94, 548-558.	1.2	16
1655	High genetic diversity and frequent genetic reassortment of avian influenza A(H9N2) viruses along the East Asian–Australian migratory flyway. <i>Infection, Genetics and Evolution</i> , 2016, 39, 325-329.	1.0	18
1656	Chloroplast phylogenomic data from the green algal order Sphaeropleales (Chlorophyceae, Tj ETQq1 1 0.784314 rgBT /Overlock 10 TFS Evolution, 2016, 98, 176-183.	1.2	46
1657	Tracing the Archaeal Origins of Eukaryotic Membrane-Trafficking System Building Blocks. <i>Molecular Biology and Evolution</i> , 2016, 33, 1528-1541.	3.5	77
1658	Temperature calibration and phylogenetically distinct distributions for freshwater alkenones: Evidence from northern Alaskan lakes. <i>Geochimica Et Cosmochimica Acta</i> , 2016, 180, 177-196.	1.6	76
1659	Untangling <i>Pseudocrossidium crinitum</i> s. l. (Pottiaceae, Bryophyta) through molecular and morphometric analysis. <i>Nova Hedwigia</i> , 2016, 102, 89-106.	0.2	6
1660	Early-diverging wood-decaying fungi detected using three complementary sampling methods. <i>Molecular Phylogenetics and Evolution</i> , 2016, 98, 11-20.	1.2	16

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1661	A new species of <i>Exophiala</i> associated with roots. <i>Mycological Progress</i> , 2016, 15, 1.	0.5	22
1662	Major bacterial lineages are essentially devoid of CRISPR-Cas viral defence systems. <i>Nature Communications</i> , 2016, 7, 10613.	5.8	224
1663	Utilizing RADseq data for phylogenetic analysis of challenging taxonomic groups: A case study in <i>Carex</i> sect. <i>Racemosae</i> . <i>American Journal of Botany</i> , 2016, 103, 337-347.	0.8	55
1664	The arbuscular mycorrhizal fungi colonising roots and root nodules of New Zealand kauri <i>Agathis australis</i> . <i>Fungal Biology</i> , 2016, 120, 807-817.	1.1	23
1665	<i>Rhodophana squamulosa</i> a new species of Entolomataceae from India. <i>Mycoscience</i> , 2016, 57, 90-95.	0.3	8
1666	Analysis of a Rapid Evolutionary Radiation Using Ultraconserved Elements: Evidence for a Bias in Some Multispecies Coalescent Methods. <i>Systematic Biology</i> , 2016, 65, 612-627.	2.7	137
1667	A phylogenomic reappraisal of family-level divisions within the class Halobacteria: proposal to divide the order Halobacteriales into the families Halobacteriaceae, Haloarculaceae fam. nov., and Halococcaceae fam. nov., and the order Haloferacales into the families, Haloferacaceae and Halorubraceae fam nov.. <i>Antonie Van Leeuwenhoek</i> , 2016, 109, 565-587.	0.7	127
1668	Integration of complete chloroplast genome sequences with small amplicon datasets improves phylogenetic resolution in <i>Acacia</i> . <i>Molecular Phylogenetics and Evolution</i> , 2016, 96, 1-8.	1.2	78
1669	Xenacoelomorpha is the sister group to Nephrozoa. <i>Nature</i> , 2016, 530, 89-93.	13.7	301
1670	New deep-sea species of <i>Xenoturbella</i> and the position of Xenacoelomorpha. <i>Nature</i> , 2016, 530, 94-97.	13.7	124
1671	Late acquisition of mitochondria by a host with chimaeric prokaryotic ancestry. <i>Nature</i> , 2016, 531, 101-104.	13.7	204
1672	Genome assembly and geospatial phylogenomics of the bed bug <i>Cimex lectularius</i> . <i>Nature Communications</i> , 2016, 7, 10164.	5.8	79
1673	Real-time, portable genome sequencing for Ebola surveillance. <i>Nature</i> , 2016, 530, 228-232.	13.7	1,179
1674	PHYLUCE is a software package for the analysis of conserved genomic loci. <i>Bioinformatics</i> , 2016, 32, 786-788.	1.8	609
1675	Blood transcriptomes reveal novel parasitic zoonoses circulating in Madagascar's lemurs. <i>Biology Letters</i> , 2016, 12, 20150829.	1.0	28
1676	Nuclear introns outperform mitochondrial DNA in inter-specific phylogenetic reconstruction: Lessons from horseshoe bats (<i>Rhinolophidae</i> : Chiroptera). <i>Molecular Phylogenetics and Evolution</i> , 2016, 97, 196-212.	1.2	77
1677	Phylogenetic analyses of gazelles reveal repeated transitions of key ecological traits and provide novel insights into the origin of the genus <i>Gazella</i> . <i>Molecular Phylogenetics and Evolution</i> , 2016, 98, 1-10.	1.2	13
1678	The genomic basis of parasitism in the <i>Strongyloides</i> clade of nematodes. <i>Nature Genetics</i> , 2016, 48, 299-307.	9.4	226

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1679	The complete plastid genome of the middle Asian endemic of <i>Stipa lipskyi</i> (Poaceae). Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2016, 27, 4661-4662.	0.7	5
1680	Global biogeography of <i>Prochlorococcus</i> genome diversity in the surface ocean. ISME Journal, 2016, 10, 1856-1865.	4.4	76
1681	The royal irises (<i>Iris</i> subg. <i>Iris</i> sect. <i>Oncocyclus</i>): Plastid and low-copy nuclear data contribute to an understanding of their phylogenetic relationships. Taxon, 2016, 65, 35-46.	0.4	32
1682	A global perspective on Campanulaceae: Biogeographic, genomic, and floral evolution. American Journal of Botany, 2016, 103, 233-245.	0.8	37
1683	A polyphasic taxonomic approach in isolated strains of Cyanobacteria from thermal springs of Greece. Molecular Phylogenetics and Evolution, 2016, 98, 147-160.	1.2	42
1684	Whole-Genome Sequencing Reveals the Origin and Rapid Evolution of an Emerging Outbreak Strain of <i>Streptococcus pneumoniae</i> 12F. Clinical Infectious Diseases, 2016, 62, 1126-1132.	2.9	38
1685	Deep Roots for Aboriginal Australian Y Chromosomes. Current Biology, 2016, 26, 809-813.	1.8	54
1686	Evidence of horizontal gene transfer between obligate leaf nodule symbionts. ISME Journal, 2016, 10, 2092-2105.	4.4	63
1687	Analyzing Reticulate Relationships using CpDNA and Pyrosequenced ITS1 as Exemplified by <i>Veronica</i> Subgen. <i>Pseudolysimachium</i> (Plantaginaceae). Systematic Botany, 2016, 41, 105-119.	0.2	6
1688	Horizontal Gene Transfer from Bacteria Has Enabled the Plant-Parasitic Nematode <i>Globodera pallida</i> to Feed on Host-Derived Sucrose. Molecular Biology and Evolution, 2016, 33, 1571-1579.	3.5	52
1689	Computational Performance and Statistical Accuracy of *BEAST and Comparisons with Other Methods. Systematic Biology, 2016, 65, 381-396.	2.7	107
1690	Gene Tree Discordance Causes Apparent Substitution Rate Variation. Systematic Biology, 2016, 65, 711-721.	2.7	153
1691	Morphology and small subunit rRNA gene sequence of <i>Uronemita parabinucleata</i> n. sp. (Ciliophora). Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.5	11
1692	Two new living Entactinaria (Radiolaria) species from the Arctic province: <i>Joergensenium arcticum</i> n. sp. and <i>Joergensenium clevei</i> n. sp.. Marine Micropaleontology, 2016, 124, 75-94.	0.5	8
1693	Shape analysis of moss (Bryophyta) sporophytes: Insights into land plant evolution. American Journal of Botany, 2016, 103, 652-662.	0.8	27
1694	Fungal root endophytes of tomato from Kenya and their nematode biocontrol potential. Mycological Progress, 2016, 15, 1.	0.5	43
1695	Two new <i>Cordyceps</i> species from a community forest in Thailand. Mycological Progress, 2016, 15, 1.	0.5	12
1696	The spotted gar genome illuminates vertebrate evolution and facilitates human-teleost comparisons. Nature Genetics, 2016, 48, 427-437.	9.4	545

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1697	Evolutionary history of the chitin synthases of eukaryotes. <i>Glycobiology</i> , 2016, 26, 635-639.	1.3	28
1698	Clustering Genes of Common Evolutionary History. <i>Molecular Biology and Evolution</i> , 2016, 33, 1590-1605.	3.5	51
1699	Gene Duplicability of Core Genes Is Highly Consistent across All Angiosperms. <i>Plant Cell</i> , 2016, 28, 326-344.	3.1	202
1700	Allopatric speciation in the flightless <i>Phoberus capensis</i> (Coleoptera: Trogidae) group, with description of two new species. <i>Insect Systematics and Evolution</i> , 2016, 47, 149-179.	0.2	6
1701	Phylogenetic relationships of the New World titi monkeys (<i>Callicebus</i>): first appraisal of taxonomy based on molecular evidence. <i>Frontiers in Zoology</i> , 2016, 13, 10.	0.9	140
1702	Comparative transcriptomics reveals the conserved building blocks involved in parallel evolution of diverse phenotypic traits in ants. <i>Genome Biology</i> , 2016, 17, 43.	3.8	70
1703	Phylogenetic placement of the enigmatic fern genus <i>Trichoneuron</i> informs on the infra-familial relationship of Dryopteridaceae. <i>Plant Systematics and Evolution</i> , 2016, 302, 319-332.	0.3	25
1704	Data on phylogenetic analyses of gazelles (genus <i>Gazella</i>) based on mitochondrial and nuclear intron markers. <i>Data in Brief</i> , 2016, 7, 551-557.	0.5	3
1705	Ecological genomics of mutualism decline in nitrogen-fixing bacteria. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016, 283, 20152563.	1.2	45
1706	Disentangling generic limits in <i>Chionoloma</i> , <i>Oxystegus</i> , <i>Pachyneuroopsis</i> and <i>Pseudosymbplepharis</i> (Bryophyta: Pottiaceae): An inquiry into their phylogenetic relationships. <i>Taxon</i> , 2016, 65, 3-18.	0.4	21
1707	New species of <i>Polysphondylium</i> from Madagascar. <i>Mycologia</i> , 2016, 108, 80-109.	0.8	11
1708	Desmophlebiaceae and <i>Desmophlebium</i> : A new family and genus of Eupolypod II ferns. <i>Taxon</i> , 2016, 65, 19-34.	0.4	25
1709	Phylogenetic relationships within the cosmopolitan buckthorn family (Rhamnaceae) support the resurrection of <i>Sarcomphalus</i> and the description of <i>Pseudoziziphus</i> gen. nov.. <i>Taxon</i> , 2016, 65, 47-64.	0.4	54
1710	Analysis of the cosmopolitan buckthorn genera <i>Frangula</i> and <i>Rhamnus</i> s.l. supports the description of a new genus, <i>Ventia</i> . <i>Taxon</i> , 2016, 65, 65-78.	0.4	21
1711	Speciation in Cloudless Sulphurs Gleaned from Complete Genomes. <i>Genome Biology and Evolution</i> , 2016, 8, 915-931.	1.1	40
1712	Three nuclear and two membrane estrogen receptors in basal teleosts, <i>Anguilla</i> sp.: Identification, evolutionary history and differential expression regulation. <i>General and Comparative Endocrinology</i> , 2016, 235, 177-191.	0.8	32
1713	Cylindrofridins ¹⁴ C, Linear Cylindrocyclophane-Related Alkylresorcinols from the Cyanobacterium <i>Cylindrospermum stagnale</i> . <i>Journal of Natural Products</i> , 2016, 79, 106-115.	1.5	27
1714	Complete mitochondrial genomes render the Night Heron genus <i>Gorsachius</i> non-monophyletic. <i>Journal of Ornithology</i> , 2016, 157, 505-513.	0.5	6

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1715	Unexpected species diversity and contrasting evolutionary hypotheses in <i>Hebeloma</i> (Agaricales) sections <i>Sinapizantia</i> and <i>Velutipes</i> in Europe. <i>Mycological Progress</i> , 2016, 15, 1.	0.5	21
1716	Sex and the <i>Catasetinae</i> (Darwin's favourite orchids). <i>Molecular Phylogenetics and Evolution</i> , 2016, 97, 1-10.	1.2	19
1717	Evolution of geographical place and niche space: Patterns of diversification in the North American sedge (<i>Cyperaceae</i>) flora. <i>Molecular Phylogenetics and Evolution</i> , 2016, 95, 183-195.	1.2	40
1718	Birds, nutrients, and climate change: mtDNA haplotype diversity of Arctic <i>Daphnia</i> on Svalbard revisited. <i>Polar Biology</i> , 2016, 39, 1425-1437.	0.5	8
1719	Influence of geology and human activity on the genetic structure and demography of the Oriental fire-bellied toad (<i>Bombina orientalis</i>). <i>Molecular Phylogenetics and Evolution</i> , 2016, 97, 69-75.	1.2	20
1720	Towards a comprehensive, integrative analysis of the diversity of European microplanid land flatworms (<i>Platyhelminthes</i> , <i>Tricladida</i> , <i>Microplaninae</i>), with the description of two peculiar new species. <i>Systematics and Biodiversity</i> , 2016, 14, 9-31.	0.5	7
1721	Genomic analysis of 38 <i>Legionella</i> species identifies large and diverse effector repertoires. <i>Nature Genetics</i> , 2016, 48, 167-175.	9.4	235
1722	Clonal spread and interspecies transmission of clinically relevant ESBL-producing <i>Escherichia coli</i> of ST410—another successful pandemic clone?. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiv155.	1.3	120
1723	Radiation of <i>Grossuana</i> Radoman, 1973 (Caenogastropoda: Truncatelloidea) in the Balkans. <i>Journal of Molluscan Studies</i> , 2016, 82, 305-313.	0.4	13
1724	There and Back Again: Parallel Evolution of Cell Coverings in Centrohelid Heliozoans. <i>Protist</i> , 2016, 167, 51-66.	0.6	22
1725	An Integrated Perspective on Phylogenetic Workflows. <i>Trends in Ecology and Evolution</i> , 2016, 31, 116-126.	4.2	16
1726	Nuclear phylogenomics of the palm subfamily <i>Arecoideae</i> (<i>Arecaceae</i>). <i>Molecular Phylogenetics and Evolution</i> , 2016, 97, 32-42.	1.2	32
1727	<i>Paulinella longichromatophora</i> sp. nov., a New Marine Photosynthetic Testate Amoeba Containing a Chromatophore. <i>Protist</i> , 2016, 167, 1-12.	0.6	23
1728	Complete mitochondrial genome of the <i>Sepiella maindroni</i> (Sepioidea: Sepiidae). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 3766-3767.	0.7	4
1729	Complete chloroplast genome of <i>Ficus racemosa</i> (<i>Moraceae</i>). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 4655-4656.	0.7	4
1730	Avoiding Missing Data Biases in Phylogenomic Inference: An Empirical Study in the Landfowl (Aves: <i>Turdus</i>) Tj ETQq1 1 0.784314 rgBT / Overl	3.5	208
1731	Phylogenetic relationships of <i>Chacodelphys</i> (<i>Marsupialia</i> : <i>Didelphidae</i> : <i>Didelphinae</i>) based on ancient DNA sequences. <i>Journal of Mammalogy</i> , 2016, 97, 394-404.	0.6	12
1732	BRITTLE SHEATH1 encoding OsCYP96B4 is involved in secondary cell wall formation in rice. <i>Plant Cell Reports</i> , 2016, 35, 745-755.	2.8	25

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1733	Molecular analysis of Chinese truffles resembling <i>Tuber californicum</i> in morphology reveals a rich pattern of species diversity with emphasis on four new species. <i>Mycologia</i> , 2016, 108, 344-353.	0.8	13
1734	Colorful patterns indicate common ancestry in diverged tiger beetle taxa: Molecular phylogeny, biogeography, and evolution of elytral coloration of the genus <i>Cicindela</i> subgenus <i>Sophiodela</i> and its allies. <i>Molecular Phylogenetics and Evolution</i> , 2016, 95, 1-10.	1.2	13
1735	A Preliminary Molecular Phylogeny of the <i>Abarema</i> Alliance (Leguminosae) and Implications for Taxonomic Rearrangement. <i>International Journal of Plant Sciences</i> , 2016, 177, 34-43.	0.6	17
1736	A Molecular Phylogeny and New Infrageneric Classification of <i>Mucuna</i> Adans. (Leguminosae-Papilionoideae) including Insights from Morphology and Hypotheses about Biogeography. <i>International Journal of Plant Sciences</i> , 2016, 177, 76-89.	0.6	20
1737	The complete mitochondrial genome of the <i>Terapon jarbua</i> (Perciformes: Terapontidae). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 3430-3431.	0.7	4
1738	The Impact of Missing Data on Species Tree Estimation. <i>Molecular Biology and Evolution</i> , 2016, 33, 838-860.	3.5	134
1739	Mycobiont-photobiont interactions of the lichen <i>Cetraria aculeata</i> in high alpine regions of East Africa and South America. <i>Symbiosis</i> , 2016, 68, 25-37.	1.2	16
1740	A supergene determines highly divergent male reproductive morphs in the ruff. <i>Nature Genetics</i> , 2016, 48, 79-83.	9.4	411
1741	Characterization of the <i>Vibrio fischeri</i> Fatty Acid Chemoreceptors, VfcB and VfcB2. <i>Applied and Environmental Microbiology</i> , 2016, 82, 696-704.	1.4	14
1742	Complete mitochondrial genome of a red calcified alga <i>Calliarthron tuberculosum</i> (Corallinales). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 2554-2556.	0.7	7
1743	Effects of missing data on topological inference using a Total Evidence approach. <i>Molecular Phylogenetics and Evolution</i> , 2016, 94, 146-158.	1.2	72
1744	The systematics of carnivorous sponges. <i>Molecular Phylogenetics and Evolution</i> , 2016, 94, 327-345.	1.2	40
1745	Generic reclassification and species boundaries in the rediscovered freshwater mussel <i>Quadrula mitchelli</i> (Simpson in Dall, 1896). <i>Conservation Genetics</i> , 2016, 17, 279-292.	0.8	37
1746	An augmented supermatrix phylogeny of the avian family Picidae reveals uncertainty deep in the family tree. <i>Molecular Phylogenetics and Evolution</i> , 2016, 94, 313-326.	1.2	29
1747	Clarifying phylogenetic relationships and the evolutionary history of the bivalve order Arcida (Mollusca: Bivalvia: Pteriomorpha). <i>Molecular Phylogenetics and Evolution</i> , 2016, 94, 298-312.	1.2	21
1748	Species composition and abundance of copepods in the morphologically cryptic genus <i>Pseudocalanus</i> in the Bering Sea. <i>Deep-Sea Research Part II: Topical Studies in Oceanography</i> , 2016, 134, 173-180.	0.6	9
1749	Multiple Origins of Eukaryotic <i>cox15</i> Suggest Horizontal Gene Transfer from Bacteria to Jakobid Mitochondrial DNA. <i>Molecular Biology and Evolution</i> , 2016, 33, 122-133.	3.5	21
1750	Complete sequence and analysis of plastid genomes of <i>Pseudo-nitzschia multiseries</i> (Bacillariophyta). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 2897-2898.	0.7	21

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1751	Complete mitochondrial genome of <i>Fistulifera solaris</i> (Bacillariophycidae). Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2016, 27, 4405-4406.	0.7	9
1752	Characterisation of seven <i>Inocybe</i> ectomycorrhizal morphotypes from a semiarid woody steppe. Mycorrhiza, 2016, 26, 215-225.	1.3	9
1753	The complete mitochondrial genome of <i>Pseudo-nitzschia multiseriata</i> (Bacillariophyta). Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2016, 27, 2777-2778.	0.7	11
1754	Complete mitochondrial genome of the <i>Pseudopleuronectes yokohamae</i> (Pleuronectiformes: Tj ETQq1 1 0.784314 rgBT ₂ Overload	0.7	0.7
1755	Molecular and morphological evidence for an intercontinental range of the liverwort <i>Lejeunea pulchriflora</i> (Marchantiophyta: Lejeuneaceae). Organisms Diversity and Evolution, 2016, 16, 13-21.	0.7	10
1756	Phylogenomic analyses of a Mediterranean earthworm family (Annelida: Hormogastridae). Molecular Phylogenetics and Evolution, 2016, 94, 473-478.	1.2	19
1757	Metabarcoding as a tool for investigating arthropod diversity in <i>Nepenthes</i> pitcher plants. Austral Ecology, 2016, 41, 120-132.	0.7	24
1758	Implementing and testing the multispecies coalescent model: A valuable paradigm for phylogenomics. Molecular Phylogenetics and Evolution, 2016, 94, 447-462.	1.2	321
1759	Complete mitochondrial genome of the <i>Scorpaenopsis cirrhosa</i> (Scorpaeniformes: Scorpaenidae). Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2016, 27, 3449-3450.	0.7	1
1760	Diversity and distribution within the sea spider genus <i>Pallenopsis</i> (Chelicerata: Pycnogonida) in the Western Antarctic as revealed by mitochondrial DNA. Polar Biology, 2016, 39, 677-688.	0.5	20
1761	The taxonomy of the European species of <i>Hebeloma</i> section <i>Denudata</i> subsections <i>Hiemalia</i> , <i>Echinospira</i> subsect. nov. and <i>Clepsydroida</i> subsect. nov. and five new species. Fungal Biology, 2016, 120, 72-103.	1.1	20
1762	Molecular data from contemporary and historical collections reveal a complex story of cryptic diversification in the <i>Varanus</i> (<i>Polydaedalus</i>) <i>niloticus</i> Species Group. Molecular Phylogenetics and Evolution, 2016, 94, 591-604.	1.2	21
1763	Combining phylogenomic and supermatrix approaches, and a time-calibrated phylogeny for squamate reptiles (lizards and snakes) based on 52 genes and 4162 species. Molecular Phylogenetics and Evolution, 2016, 94, 537-547.	1.2	488
1764	Phylogeny of the island archipelago frog genus <i>Sanguirana</i> : Another endemic Philippine radiation that diversified "Out-of-Palawan". Molecular Phylogenetics and Evolution, 2016, 94, 531-536.	1.2	32
1765	Five new species of <i>Inocybe</i> (Agaricales) from tropical India. Mycologia, 2016, 108, 110-122.	0.8	14
1766	The complete mitochondrial genomes of the Galápagos iguanas, <i>Amblyrhynchus cristatus</i> and <i>Conolophus subcristatus</i> . Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2016, 27, 3699-3700.	0.7	7
1767	New animal phylogeny: future challenges for animal phylogeny in the age of phylogenomics. Organisms Diversity and Evolution, 2016, 16, 419-426.	0.7	47
1768	Structural and functional evolution of 2',3'-cyclic nucleotide 3'-phosphodiesterase. Brain Research, 2016, 1641, 64-78.	1.1	27

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1769	Phylogenetic analysis of the winter geometrid genus <i>Inurois</i> reveals repeated reproductive season shifts. <i>Molecular Phylogenetics and Evolution</i> , 2016, 94, 47-54.	1.2	9
1770	How Should Genes and Taxa be Sampled for Phylogenomic Analyses with Missing Data? An Empirical Study in Iguanian Lizards. <i>Systematic Biology</i> , 2016, 65, 128-145.	2.7	155
1771	Characterization of the complete mitochondrial genomes from Polycladida (Platyhelminthes) using next-generation sequencing. <i>Gene</i> , 2016, 575, 199-205.	1.0	19
1772	Rumbling Orchids: How To Assess Divergent Evolution Between Chloroplast Endosymbionts and the Nuclear Host. <i>Systematic Biology</i> , 2016, 65, 51-65.	2.7	65
1773	Processes Driving the Adaptive Radiation of a Tropical Tree (<i>Diospyros</i> , Ebenaceae) in New Caledonia, a Biodiversity Hotspot. <i>Systematic Biology</i> , 2016, 65, 212-227.	2.7	98
1774	Molecular phylogenetics and the morphology of the Lycopodiaceae subfamily Huperzioidae supports three genera: <i>Huperzia</i> , <i>Phlegmariurus</i> and <i>Phylloglossum</i> . <i>Molecular Phylogenetics and Evolution</i> , 2016, 94, 635-657.	1.2	52
1775	<i>Phakopsora myrtacearum</i> sp. nov., a newly described rust (Pucciniales) on eucalypts in eastern and southern Africa. <i>Plant Pathology</i> , 2016, 65, 189-195.	1.2	20
1776	Genetic and structural analyses of cytochrome P450 hydroxylases in sex hormone biosynthesis: Sequential origin and subsequent coevolution. <i>Molecular Phylogenetics and Evolution</i> , 2016, 94, 676-687.	1.2	35
1777	Mitochondrial genomes of four katydids (Orthoptera: Phaneropteridae): New gene rearrangements and their phylogenetic implications. <i>Gene</i> , 2016, 575, 702-711.	1.0	33
1778	Identification of a new marine algal species <i>Pyropia nitida</i> sp. nov. (Bangiales: Rhodophyta) from Monterey, California. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 3058-3062.	0.7	8
1779	The complete chloroplast genome of <i>Torreya fargesii</i> (Taxaceae). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 3512-3513.	0.7	12
1780	The complete mitochondrial genome of the <i>Ehippus orbis</i> (Perciformes: Ehippidae). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 3444-3445.	0.7	0
1781	The complete chloroplast genome sequence of <i>Amentotaxus argotaenia</i> (Taxaceae). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 2919-2920.	0.7	24
1782	Evolution of mitochondrial gene order in Annelida. <i>Molecular Phylogenetics and Evolution</i> , 2016, 94, 196-206.	1.2	77
1783	Complete mitochondrial genome of a hydrocarbon-producing green alga <i>Botryococcus braunii</i> strain Showa. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 2619-2620.	0.7	4
1784	Phylogenetic Inferences and the Evolution of Plastid DNA in Campynemataceae and the Mycoheterotrophic <i>Corsia dispar</i> D.L Jones & B. Gray (Corsiaceae). <i>Plant Molecular Biology Reporter</i> , 2016, 34, 192-210.	1.0	7
1785	PCR-free shotgun sequencing of the stone loach mitochondrial genome (<i>Barbatula barbatula</i>). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 4211-4212.	0.7	6
1786	Mitogenomic sequence and phylogenetic placement of the Hortle's whipray <i>Himantura hortlei</i> (Elasmobranchii: Dasyatidae). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 2437-2439.	0.7	1

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1787	Mitochondrial genome of <i>Esox flaviae</i> (Southern pike): announcement and comparison with other Esocidae. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 3037-3038.	0.7	3
1788	Complete mitochondrial genome of <i>Pseudoperonospora cubensis</i> . <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 3487-3488.	0.7	5
1789	Chaetomium-like fungi causing opportunistic infections in humans: a possible role for extremotolerance. <i>Fungal Diversity</i> , 2016, 76, 11-26.	4.7	24
1790	The complete mitochondrial genome of the <i>Hexagrammos otakii</i> (Scorpaeniformes: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 182	0.7	1
1791	Museomics illuminate the history of an extinct, paleoendemic plant lineage (<i>Hesperelaea</i>), Linnean Society, 2016, 117, 44-57.	0.7	87
1792	The complete mitochondrial genome of the devil firefish <i>Pterois miles</i> (Bennett, 1828) (Scorpaenidae). <i>Mitochondrial DNA</i> , 2016, 27, 783-784.	0.6	6
1793	Phylogenetic relationships among four new complete mitogenome sequences of <i>Pelophylax</i> (Amphibia: Anura) from the Balkans and Cyprus. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 3434-3437.	0.7	8
1794	The complete mitochondrial genome of the <i>Synanceia verrucosa</i> (Scorpaeniformes: Synanceiidae). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 4234-4235.	0.7	7
1795	The complete chloroplast genome sequence of <i>Clematis terniflora</i> DC. (Ranunculaceae). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 2470-2472.	0.7	11
1796	The complete mitochondrial genome of <i>Lacerta bilineata</i> and comparison with its closely related congener <i>L. Viridis</i> . <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2017, 28, 116-118.	0.7	5
1797	The chloroplast genome of <i>Ephedra foeminea</i> (Ephedraceae, Gnetales), an entomophilous gymnosperm endemic to the Mediterranean area. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2017, 28, 330-331.	0.7	3
1798	Complete mitochondrial genome of <i>Rhynchophorus ferrugineus</i> . <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2017, 28, 208-209.	0.7	3
1799	Complete mitochondrial genome of <i>Aulonocara stuartgranti</i> (Flavescent peacock cichlid). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2017, 28, 279-280.	0.7	2
1800	Phylogenetic relationships within <i>Lactuca</i> L. (Asteraceae), including African species, based on chloroplast DNA sequence comparisons. <i>Genetic Resources and Crop Evolution</i> , 2017, 64, 55-71.	0.8	25
1801	Complete mitochondrial genome of the sea anemone, <i>Anthopleura midori</i> (Actiniaria: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 182	0.7	6
1802	Characterization of mitochondrial genome of <i>Haemagogus janthinomys</i> (Diptera: Culicidae). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2017, 28, 50-51.	0.7	8
1803	Molecular phylogenetic reconstruction and taxonomic investigation of eelpouts (Cottoidei: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 107 T Mapping, Sequencing, and Analysis, 2017, 28, 547-557.	0.7	8
1804	On the paraphyly of Cytaeidae and placement of Cytaeis within the suborder Filifera (Hydrozoa: Tj ETQq1 1 0.784314 rgBT /Overlock 0,3	0.3	4

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1805	EPIC: A framework to exploit parallelism in irregular codes. <i>Concurrency Computation Practice and Experience</i> , 2017, 29, e3842.	1.4	1
1806	Diversity and biogeography of larval and juvenile notothenioid fishes in McMurdo Sound, Antarctica. <i>Polar Biology</i> , 2017, 40, 161-176.	0.5	9
1807	Parallel SuperFineâ€”A tool for fast and accurate supertree estimation: Features and limitations. <i>Future Generation Computer Systems</i> , 2017, 67, 441-454.	4.9	3
1808	Transcriptome of larvae representing the <i>Rhipicephalus sanguineus</i> complex. <i>Molecular and Cellular Probes</i> , 2017, 31, 85-90.	0.9	10
1809	Mitogenomic sequences support a northâ€”south subspecies subdivision within <i>Solenodon paradoxus</i> . <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2017, 28, 662-670.	0.7	9
1810	Genetic diversity and phylogeny of limpets of the genus <i>Nipponacmea</i> (Patellogastropoda: Lottiidae) based on mitochondrial DNA sequences. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2017, 28, 703-710.	0.7	2
1811	The complete mitochondrial genome of the cryptic species C of <i>Aneura pinguis</i> . <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2017, 28, 112-113.	0.7	6
1812	Carnivorous sponges (Porifera, Cladorhizidae) from the Southwest Indian Ocean Ridge seamounts. <i>Deep-Sea Research Part II: Topical Studies in Oceanography</i> , 2017, 137, 166-189.	0.6	12
1813	Fifteen species in one: deciphering the <i>Brachionus plicatilis</i> species complex (Rotifera, Monogononta) through DNA taxonomy. <i>Hydrobiologia</i> , 2017, 796, 39-58.	1.0	185
1814	Complete mitochondrial genome of <i>Tlacuatzin canescens</i> (Grayish Mouse Opossum). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2017, 28, 283-284.	0.7	0
1815	A historical biogeography of megadiverse <i>Sericini</i> â€”another story â€œout of Africaâ€?. <i>Cladistics</i> , 2017, 33, 183-197.	1.5	35
1816	Reference Tree and Environmental Sequence Diversity of <i>Labyrinthulomycetes</i> . <i>Journal of Eukaryotic Microbiology</i> , 2017, 64, 88-96.	0.8	40
1817	Adaptive evolution and functional innovation of <i>Populus</i> -specific recently evolved micro<scp>RNA</scp>s. <i>New Phytologist</i> , 2017, 213, 206-219.	3.5	36
1818	A molecular phylogeny of marine amphipods in the herbivorous family Ampithoidae. <i>Zoologica Scripta</i> , 2017, 46, 85-95.	0.7	14
1819	Morphological and Molecular Identification of the New Species, <i>Trichodina pseudoheterodontata</i> sp. n. (Ciliophora, Mobilida, Trichodinidae) from the Channel Catfish, <i>Ictalurus punctatus</i> , in Chongqing China. <i>Journal of Eukaryotic Microbiology</i> , 2017, 64, 45-55.	0.8	21
1820	Deep trees: Woodfall biodiversity dynamics in present and past oceans. <i>Deep-Sea Research Part II: Topical Studies in Oceanography</i> , 2017, 137, 282-287.	0.6	7
1821	Rounding up the usual suspects: a standard targetâ€”gene approach for resolving the interfamilial phylogenetic relationships of ecribellate orbâ€”weaving spiders with a new familyâ€”rank classification (Araneae, Araneoidea). <i>Cladistics</i> , 2017, 33, 221-250.	1.5	108
1822	Characterization and pathogenicity of <i>Cladobotryum mycophilum</i> in Spanish <i>Pleurotus eryngii</i> mushroom crops and its sensitivity to fungicides. <i>European Journal of Plant Pathology</i> , 2017, 147, 129-139.	0.8	19

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1823	Endozoicomonas genomes reveal functional adaptation and plasticity in bacterial strains symbiotically associated with diverse marine hosts. <i>Scientific Reports</i> , 2017, 7, 40579.	1.6	207
1824	Ultraconserved elements resolve the phylogeny of potoos (Aves: Nyctibiidae). <i>Journal of Avian Biology</i> , 2017, 48, 872-880.	0.6	14
1825	The NBS-LRR architectures of plant R-proteins and metazoan NLRs evolved in independent events. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 1063-1068.	3.3	113
1826	Evolutionary History of the Asian Horned Frogs (Megophryinae): Integrative Approaches to Timetree Dating in the Absence of a Fossil Record. <i>Molecular Biology and Evolution</i> , 2017, 34, msw267.	3.5	46
1827	Constructing Predictive Microbial Signatures at Multiple Taxonomic Levels. <i>Journal of the American Statistical Association</i> , 2017, 112, 1022-1031.	1.8	25
1828	Evolution of the diatoms: IX. Two datasets resolving monophyletic Classes of diatoms are used to explore the validity of adding short clone library sequences to the analysis. <i>European Journal of Phycology</i> , 2017, 52, 90-103.	0.9	5
1829	Genetic mechanisms of bone digestion and nutrient absorption in the bone-eating worm <i>Osedax japonicus</i> inferred from transcriptome and gene expression analyses. <i>BMC Evolutionary Biology</i> , 2017, 17, 17.	3.2	22
1830	Bacterial whole genome-based phylogeny: construction of a new benchmarking dataset and assessment of some existing methods. <i>BMC Genomics</i> , 2017, 18, 19.	1.2	40
1831	<i>Frankia discariae</i> sp. nov.: an infective and effective microsymbiont isolated from the root nodule of <i>Discaria trinervis</i> . <i>Archives of Microbiology</i> , 2017, 199, 641-647.	1.0	33
1832	A new giant egg-laying onychophoran (Peripatopsidae) reveals evolutionary and biogeographical aspects of Australian velvet worms. <i>Organisms Diversity and Evolution</i> , 2017, 17, 375-391.	0.7	9
1833	Biogeographic scenarios for the diversification of a widespread Neotropical species, <i>Glossophaga soricina</i> (Chiroptera: Phyllostomidae). <i>Systematics and Biodiversity</i> , 2017, 15, 440-450.	0.5	13
1834	<i>Wilsonosiphonia</i> gen. nov. (Rhodomelaceae, Rhodophyta) based on molecular and morpho-anatomical characters. <i>Journal of Phycology</i> , 2017, 53, 368-380.	1.0	15
1835	Anchored phylogenomics improves the resolution of evolutionary relationships in the rapid radiation of <i>Protea</i> L. <i>American Journal of Botany</i> , 2017, 104, 102-115.	0.8	108
1836	Arbuscular mycorrhizal fungal community composition associated with <i>Juniperus brevifolia</i> in native Azorean forest. <i>Acta Oecologica</i> , 2017, 79, 48-61.	0.5	19
1837	Post-Eocene climate change across continental Australia and the diversification of Australasian spiny trapdoor spiders (Idiopidae: Arbanitinae). <i>Molecular Phylogenetics and Evolution</i> , 2017, 109, 302-320.	1.2	51
1838	Development and validation of a real-time PCR assay for the glassy-winged sharpshooter <i>Homalodisca vitripennis</i> (Hemiptera: Cicadellidae). <i>Bulletin of Entomological Research</i> , 2017, 107, 332-339.	0.5	0
1839	The first imported case of Rift Valley fever in China reveals a genetic reassortment of different viral lineages. <i>Emerging Microbes and Infections</i> , 2017, 6, 1-7.	3.0	40
1840	Global and regional dissemination and evolution of <i>Burkholderia pseudomallei</i> . <i>Nature Microbiology</i> , 2017, 2, 16263.	5.9	124

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1841	Zika virus disrupts molecular fingerprinting of human neurospheres. <i>Scientific Reports</i> , 2017, 7, 40780.	1.6	120
1842	<i>Parahepatospora carcini</i> n. gen., n. sp., a parasite of invasive <i>Carcinus maenas</i> with intermediate features of sporogony between the Enterocytozoon clade and other microsporidia. <i>Journal of Invertebrate Pathology</i> , 2017, 143, 124-134.	1.5	26
1843	HTLV-1aA introduction into Brazil and its association with the trans-Atlantic slave trade. <i>Infection, Genetics and Evolution</i> , 2017, 48, 95-101.	1.0	9
1844	Eocene lantern fruits from Gondwanan Patagonia and the early origins of Solanaceae. <i>Science</i> , 2017, 355, 71-75.	6.0	80
1845	Horizontal gene transfer drives the evolution of Rh50 permeases in prokaryotes. <i>BMC Evolutionary Biology</i> , 2017, 17, 2.	3.2	18
1846	Confirmation of <i>Peronospora agrimoniae</i> as a distinct species. <i>European Journal of Plant Pathology</i> , 2017, 147, 887-896.	0.8	7
1847	Novel sub-lineages, recombinants and reassortants of severe fever with thrombocytopenia syndrome virus. <i>Ticks and Tick-borne Diseases</i> , 2017, 8, 385-390.	1.1	18
1848	Myrteae phylogeny, calibration, biogeography and diversification patterns: Increased understanding in the most species rich tribe of Myrtaceae. <i>Molecular Phylogenetics and Evolution</i> , 2017, 109, 113-137.	1.2	110
1849	ITS non-concerted evolution and rampant hybridization in the legume genus <i>Lespedeza</i> (Fabaceae). <i>Scientific Reports</i> , 2017, 7, 40057.	1.6	43
1850	Co-option and <i>de novo</i> gene evolution underlie molluscan shell diversity. <i>Molecular Biology and Evolution</i> , 2017, 34, msw294.	3.5	67
1851	Island floras as model systems for studies of plant speciation: Prospects and challenges. <i>Journal of Systematics and Evolution</i> , 2017, 55, 1-15.	1.6	28
1852	Against all odds: reconstructing the evolutionary history of <i>Scrophularia</i> (Scrophulariaceae) despite high levels of incongruence and reticulate evolution. <i>Organisms Diversity and Evolution</i> , 2017, 17, 323-349.	0.7	21
1853	Supra-operonic clusters of functionally related genes (SOCs) are a source of horizontal gene co-transfers. <i>Scientific Reports</i> , 2017, 7, 40294.	1.6	11
1854	Eggshell palaeogenomics: Palaeognath evolutionary history revealed through ancient nuclear and mitochondrial DNA from Madagascan elephant bird (<i>Aepyornis</i> sp.) eggshell. <i>Molecular Phylogenetics and Evolution</i> , 2017, 109, 151-163.	1.2	65
1855	Identification of microsporidia host-exposed proteins reveals a repertoire of rapidly evolving proteins. <i>Nature Communications</i> , 2017, 8, 14023.	5.8	88
1856	Resistance to type 1 interferons is a major determinant of HIV-1 transmission fitness. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E590-E599.	3.3	137
1857	Molecular phylogeny of <i>Sericostomatoidea</i> (Trichoptera) with the establishment of three new families. <i>Systematic Entomology</i> , 2017, 42, 240-266.	1.7	17
1858	Historical relationships of three enigmatic phasianid genera (Aves: Galliformes) inferred using phylogenomic and mitogenomic data. <i>Molecular Phylogenetics and Evolution</i> , 2017, 109, 217-225.	1.2	38

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1859	Complex modular architecture around a simple toolkit of wing pattern genes. <i>Nature Ecology and Evolution</i> , 2017, 1, 52.	3.4	179
1860	MtDNA metagenomics reveals large-scale invasion of belowground arthropod communities by introduced species. <i>Molecular Ecology</i> , 2017, 26, 3104-3115.	2.0	47
1861	Ecotype diversification of an abundant <i>Roseobacter</i> lineage. <i>Environmental Microbiology</i> , 2017, 19, 1625-1638.	1.8	17
1862	Genomic evidence of gene flow during reinforcement in Texas <i>Phlox</i> . <i>Molecular Ecology</i> , 2017, 26, 2317-2330.	2.0	25
1863	The genera <i>Melanothamnus</i> Bornet & Falkenberg and <i>Vertebrata</i> S.F. Gray constitute well-defined clades of the red algal tribe <i>Polysiphonieae</i> (<i>Rhodomelaceae</i> , <i>Ceramiales</i>). <i>European Journal of Phycology</i> , 2017, 52, 1-30.	0.9	51
1864	The phylogeny of the world's bulbuls (<i>Pycnonotidae</i>) inferred using a supermatrix approach. <i>Ibis</i> , 2017, 159, 498-509.	1.0	38
1865	Studying Vertical Microbiome Transmission from Mothers to Infants by Strain-Level Metagenomic Profiling. <i>MSystems</i> , 2017, 2, .	1.7	329
1866	Development of a human vasopressin V1a-receptor antagonist from an evolutionary-related insect neuropeptide. <i>Scientific Reports</i> , 2017, 7, 41002.	1.6	33
1867	A phosphorus threshold for mycoheterotrophic plants in tropical forests. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20162093.	1.2	22
1868	Evidence for concerted movement of nuclear and mitochondrial clines in a lizard hybrid zone. <i>Molecular Ecology</i> , 2017, 26, 2306-2316.	2.0	23
1869	Taxonomic divergence of the green naked-stipe members of the genus <i>Microglossum</i> (<i>Helotiales</i>). <i>Mycologia</i> , 2017, 109, 46-54.	0.8	3
1870	Dynamic diversification history with rate upshifts in Holarctic bellflowers (<i>Campanula</i> and) <i>Tj ETQq1 1 0.784314 rgBT/Overl</i>	1.5	27
1871	Phylogeography of the sergeants <i>Abudefduf sexfasciatus</i> and <i>A. vaigiensis</i> reveals complex introgression patterns between two widespread and sympatric Indo-West Pacific reef fishes. <i>Molecular Ecology</i> , 2017, 26, 2527-2542.	2.0	17
1872	Asgard archaea illuminate the origin of eukaryotic cellular complexity. <i>Nature</i> , 2017, 541, 353-358.	13.7	882
1873	Uncertain-tree: discriminating among competing approaches to the phylogenetic analysis of phenotype data. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20162290.	1.2	114
1874	Characterization of HSP90 isoforms in transformed bovine leukocytes infected with <i>Theileria annulata</i> . <i>Cellular Microbiology</i> , 2017, 19, e12669.	1.1	9
1875	A molecular phylogeny reveals the Cuban enigmatic genus <i>Behaimia</i> as a new piece in the <i>Brongniartieae</i> puzzle of papilionoid legumes. <i>Molecular Phylogenetics and Evolution</i> , 2017, 109, 191-202.	1.2	13
1876	Comparative genomics of <i>Mortierella elongata</i> and its bacterial endosymbiont <i>Mycoavidus cysteinexigens</i> . <i>Environmental Microbiology</i> , 2017, 19, 2964-2983.	1.8	154

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1877	EspL is a bacterial cysteine protease effector that cleaves RHIM proteins to block necroptosis and inflammation. <i>Nature Microbiology</i> , 2017, 2, 16258.	5.9	141
1878	A Novel, Enigmatic Basal Leafhopper Moth Lineage Pollinating a Derived Leafhopper Host Illustrates the Dynamics of Host Shifts, Partner Replacement, and Apparent Coadaptation in Intimate Mutualisms. <i>American Naturalist</i> , 2017, 189, 422-435.	1.0	15
1879	Phylogenomics provides new insight into evolutionary relationships and genealogical discordance in the reef-building coral genus <i>Acropora</i> . <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20162182.	1.2	30
1880	A fern <i>AINTEGUMENTA</i> gene mirrors <i>BABY BOOM</i> in promoting apogamy in <i>Ceratopteris richardii</i> . <i>Plant Journal</i> , 2017, 90, 122-132.	2.8	46
1881	The birth of aposematism: High phenotypic divergence and low genetic diversity in a young clade of poison frogs. <i>Molecular Phylogenetics and Evolution</i> , 2017, 109, 283-295.	1.2	32
1882	Relative benefits of amino acid, codon, degeneracy, DNA, and purine-pyrimidine character coding for phylogenetic analyses of exons. <i>Journal of Systematics and Evolution</i> , 2017, 55, 85-109.	1.6	24
1883	Extensive recent secondary contacts between four European white oak species. <i>New Phytologist</i> , 2017, 214, 865-878.	3.5	113
1884	The measure of success: geographic isolation promotes diversification in <i>Pachydactylus</i> geckos. <i>BMC Evolutionary Biology</i> , 2017, 17, 9.	3.2	25
1885	A molecular and morphological re-examination of the generic limits of truffles in the tarzetta-geopyxis lineage "Densocarpa, Hydnocystis, and Paurocotylis. <i>Fungal Biology</i> , 2017, 121, 264-284.	1.1	8
1886	Inferring phylogenetic patterns of land snails of the genus <i>Albinaria</i> on the island of Dia (Crete, Greece). <i>Tj ETQq1 1 0.784314 rgBT / Overlock 10 0,5 3</i>		
1887	Rapid expansion of immune-related gene families in the house fly, <i>Musca domestica</i> . <i>Molecular Biology and Evolution</i> , 2017, 34, msw285.	3.5	35
1888	The rice paradox: Multiple origins but single domestication in Asian rice. <i>Molecular Biology and Evolution</i> , 2017, 34, msx049.	3.5	178
1889	New roles in hemicellulosic sugar fermentation for the uncultivated Bacteroidetes family BS11. <i>ISME Journal</i> , 2017, 11, 691-703.	4.4	115
1890	Antibody 10-1074 suppresses viremia in HIV-1-infected individuals. <i>Nature Medicine</i> , 2017, 23, 185-191.	15.2	399
1891	Phylogenomics using formalin-fixed and 100+ year-old intractable natural history specimens. <i>Molecular Ecology Resources</i> , 2017, 17, 1003-1008.	2.2	132
1892	Integrative taxonomy reveals the first record and a new species for the previously monotypic genus <i>Tethytimea</i> (Tethyida: Tethyidae) in the Gulf of Mexico. <i>Zootaxa</i> , 2017, 4226, 113.	0.2	8
1893	Whole genome sequencing data and de novo draft assemblies for 66 teleost species. <i>Scientific Data</i> , 2017, 4, 160132.	2.4	67
1894	Characterization of Phytochrome Interacting Factors from the Moss <i>Physcomitrella patens</i> Illustrates Conservation of Phytochrome Signaling Modules in Land Plants. <i>Plant Cell</i> , 2017, 29, 310-330.	3.1	61

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1895	High Prevalence of Tula Hantavirus in Common Voles in The Netherlands. <i>Vector-Borne and Zoonotic Diseases</i> , 2017, 17, 200-205.	0.6	15
1896	Enriching the ant tree of life: enhanced UCE bait set for genome-scale phylogenetics of ants and other Hymenoptera. <i>Methods in Ecology and Evolution</i> , 2017, 8, 768-776.	2.2	190
1897	Parasite infection of public databases: a data mining approach to identify apicomplexan contaminations in animal genome and transcriptome assemblies. <i>BMC Genomics</i> , 2017, 18, 100.	1.2	35
1898	A Lin28 homologue reprograms differentiated cells to stem cells in the moss <i>Physcomitrella patens</i> . <i>Nature Communications</i> , 2017, 8, 14242.	5.8	37
1899	Low CD21 expression defines a population of recent germinal center graduates primed for plasma cell differentiation. <i>Science Immunology</i> , 2017, 2, .	5.6	203
1900	Comparative morphology and genetics of two populations of spiny lizards (genus <i>Sceloporus</i>) from Central Mexico. <i>Zoologischer Anzeiger</i> , 2017, 267, 21-30.	0.4	8
1901	Resolving relationships at the animal-fungal divergence: A molecular phylogenetic study of the protist trichomycetes (Ichthyosporia, Eccrinida). <i>Molecular Phylogenetics and Evolution</i> , 2017, 109, 447-464.	1.2	9
1902	Syllids inhabiting holdfasts of <i>Lessonia spicata</i> in Central Chile: diversity, systematics, and description of three new species. <i>Systematics and Biodiversity</i> , 2017, 15, 520-531.	0.5	6
1903	Selective Whole-Genome Amplification Is a Robust Method That Enables Scalable Whole-Genome Sequencing of <i>Plasmodium vivax</i> from Unprocessed Clinical Samples. <i>MBio</i> , 2017, 8, .	1.8	59
1904	The pangenome of (Antarctic) <i>Pseudoalteromonas</i> bacteria: evolutionary and functional insights. <i>BMC Genomics</i> , 2017, 18, 93.	1.2	46
1905	Wood decay rates of 13 temperate tree species in relation to wood properties, enzyme activities and organismic diversities. <i>Forest Ecology and Management</i> , 2017, 391, 86-95.	1.4	151
1906	Identifying conserved genomic elements and designing universal bait sets to enrich them. <i>Methods in Ecology and Evolution</i> , 2017, 8, 1103-1112.	2.2	133
1907	Genetic Characterization of <i>Vibrio cholerae</i> O1 isolates from outbreaks between 2011 and 2015 in Tanzania. <i>BMC Infectious Diseases</i> , 2017, 17, 157.	1.3	29
1908	A new subfamily classification of the Leguminosae based on a taxonomically comprehensive phylogeny: The Legume Phylogeny Working Group (LPWG). <i>Taxon</i> , 2017, 66, 44-77.	0.4	803
1909	Mixed transmission modes and dynamic genome evolution in an obligate animal-bacterial symbiosis. <i>ISME Journal</i> , 2017, 11, 1359-1371.	4.4	35
1910	Phylogeny, biogeography, systematics and taxonomy of Salicornioideae (Amaranthaceae/Chenopodiaceae) – A cosmopolitan, highly specialized halophyte lineage dating back to the Oligocene. <i>Taxon</i> , 2017, 66, 109-132.	0.4	67
1911	Entire plastid phylogeny of the carrot genus (<i>Daucus</i> , Apiaceae): Concordance with nuclear data and mitochondrial and nuclear DNA insertions to the plastid. <i>American Journal of Botany</i> , 2017, 104, 296-312.	0.8	46
1912	Genome sequence, prevalence and quantification of the first iflavivirus identified in a phytoplasma insect vector. <i>Archives of Virology</i> , 2017, 162, 799-809.	0.9	14

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1913	Clavicipitaceous entomopathogens: new species in <i>Metarhizium</i> and a new genus <i>Nigelia</i> . <i>Mycological Progress</i> , 2017, 16, 369-391.	0.5	28
1914	Genotype-Specific Evolution of Hepatitis E Virus. <i>Journal of Virology</i> , 2017, 91, .	1.5	27
1915	A Murine Herpesvirus Closely Related to Ubiquitous Human Herpesviruses Causes T-Cell Depletion. <i>Journal of Virology</i> , 2017, 91, .	1.5	29
1916	The nucleotide composition of microbial genomes indicates differential patterns of selection on core and accessory genomes. <i>BMC Genomics</i> , 2017, 18, 151.	1.2	55
1917	<i>Macruropyxis fulva</i> sp. nov., a new rust (Pucciniales) infecting sugarcane in southern Africa. <i>Australasian Plant Pathology</i> , 2017, 46, 63-74.	0.5	11
1918	<i>Plasmodium falciparum</i> CRK4 directs continuous rounds of DNA replication during schizogony. <i>Nature Microbiology</i> , 2017, 2, 17017.	5.9	79
1919	Low-Pathogenic Influenza A Viruses in North American Diving Ducks Contribute to the Emergence of a Novel Highly Pathogenic Influenza A(H7N8) Virus. <i>Journal of Virology</i> , 2017, 91, .	1.5	27
1920	The genetic architecture of low-temperature adaptation in the wine yeast <i>Saccharomyces cerevisiae</i> . <i>BMC Genomics</i> , 2017, 18, 159.	1.2	58
1921	Comparative genomics reveals high biological diversity and specific adaptations in the industrially and medically important fungal genus <i>Aspergillus</i> . <i>Genome Biology</i> , 2017, 18, 28.	3.8	417
1922	Molecular systematics of the critically-endangered North American spiny mussels (Unionidae: Elliptio) <i>Tj ETQq1 1 0.784314 rgBT /Over</i>	0.8	15
1923	Characterization of the complete chloroplast genome of <i>Elaeagnus mollis</i> , a rare and endangered oil plant. <i>Conservation Genetics Resources</i> , 2017, 9, 439-442.	0.4	8
1924	Syntrophic linkage between predatory <i>Carpodomonas</i> and specific prokaryotic populations. <i>ISME Journal</i> , 2017, 11, 1205-1217.	4.4	21
1925	Transitions between phases of genomic differentiation during stick-insect speciation. <i>Nature Ecology and Evolution</i> , 2017, 1, 82.	3.4	144
1926	Genome Analysis of a Zygomycete Fungus <i>Choanephora cucurbitarum</i> Elucidates Necrotrophic Features Including Bacterial Genes Related to Plant Colonization. <i>Scientific Reports</i> , 2017, 7, 40432.	1.6	9
1927	Genetic analyses unravel the crucial role of a horizontally acquired alginate lyase for brown algal biomass degradation by <i>Zobellia galactanivorans</i> . <i>Environmental Microbiology</i> , 2017, 19, 2164-2181.	1.8	84
1928	<i>Helicascus mangrovei</i> sp. nov., a new intertidal mangrove fungus from Thailand. <i>Mycoscience</i> , 2017, 58, 174-180.	0.3	8
1929	High-resolution sequencing reveals unexplored archaeal diversity in freshwater wetland soils. <i>Environmental Microbiology</i> , 2017, 19, 2192-2209.	1.8	56
1930	Genome-resolved metagenomics of a bioremediation system for degradation of thiocyanate in mine water containing suspended solid tailings. <i>MicrobiologyOpen</i> , 2017, 6, e00446.	1.2	22

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1931	The Phylogeny of Placental Evolution Through Dynamic Integrations of Retrotransposons. <i>Progress in Molecular Biology and Translational Science</i> , 2017, 145, 89-109.	0.9	32
1932	Stomatal development in time: the past and the future. <i>Current Opinion in Genetics and Development</i> , 2017, 45, 1-9.	1.5	38
1933	Phylogeography of human Y-chromosome haplogroup Q3-L275 from an academic/citizen science collaboration. <i>BMC Evolutionary Biology</i> , 2017, 17, 18.	3.2	16
1934	Intertwining phylogenetic trees and networks. <i>Methods in Ecology and Evolution</i> , 2017, 8, 1212-1220.	2.2	211
1935	Phylogenomic species delimitation and host-symbiont coevolution in the fungus-farming ant genus <i>Sericomyrmex</i> (Mymaridae: Hymenoptera: Formicidae): ultraconserved elements (UCEs) resolve a recent radiation. <i>Systematic Entomology</i> , 2017, 42, 523-542.	1.7	67
1936	Generic Relationships and Classification of Tribe Paullinieae (Sapindaceae) with a New Concept of Supertribe Paullinioidae. <i>Systematic Botany</i> , 2017, 42, 96-114.	0.2	43
1937	Knockdown of a putative argininosuccinate lyase gene reduces arginine content and impairs nymphal development in <i>Nilaparvata lugens</i> . <i>Archives of Insect Biochemistry and Physiology</i> , 2017, 95, e21385.	0.6	2
1938	<i>Actinomadura alkaliterrae</i> sp. nov., isolated from an alkaline soil. <i>Antonie Van Leeuwenhoek</i> , 2017, 110, 787-794.	0.7	12
1939	Ecomorphological adaptation in three mudskippers (Teleostei: Gobioidi: Gobiidae) from the Persian Gulf and the Gulf of Oman. <i>Hydrobiologia</i> , 2017, 795, 91-111.	1.0	23
1940	Mitogenome evolution in Cephini (Hymenoptera: Cephidae): Evidence for parallel adaptive evolution. <i>Biochemical Systematics and Ecology</i> , 2017, 71, 137-146.	0.6	14
1941	Unique phylogenetic position of the African truffle-like fungus, <i>Octaviania ivoryana</i> (Boletaceae, Boletales), and the proposal of a new genus, <i>Afrocastellanoa</i> . <i>Mycologia</i> , 2017, 109, 323-332.	0.8	18
1942	Molecular and karyological data confirm that the enigmatic genus <i>Platypholis</i> from Bonin-Islands (SE Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 501) is a new genus. <i>Journal of Molecular Evolution</i> , 2017, 85, 130, 273-280.	1.2	18
1943	Identification, expression pattern, and feature analysis of cuticular protein genes in the pine moth <i>Dendrolimus punctatus</i> (Lepidoptera: Lasiocampidae). <i>Insect Biochemistry and Molecular Biology</i> , 2017, 83, 94-106.	1.2	46
1944	Impact of asynchronous emergence of two lethal pathogens on amphibian assemblages. <i>Scientific Reports</i> , 2017, 7, 43260.	1.6	46
1945	A Reverse Genetics Platform That Spans the Zika Virus Family Tree. <i>MBio</i> , 2017, 8, .	1.8	59
1946	Phylogenetic analysis of the Neotropical <i>Pristimantis leptolophus</i> species group (Anura: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 501). <i>Systematic Zoology</i> , 2017, 66, 4242, 313.	0.2	10
1947	A New Genus and Two New Species of Arboreal Toads from the Highlands of Sumatra with a Phylogeny of Sundaland Toad Genera. <i>Herpetologica</i> , 2017, 73, 63-75.	0.2	11
1948	Characterization of the complete chloroplast genome of Chinese fringetree (<i>Chionanthus retusus</i>). <i>Conservation Genetics Resources</i> , 2017, 9, 431-434.	0.4	3

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1949	Niche specialization of bacteria in permanently ice-covered lakes of the McMurdo Dry Valleys, Antarctica. <i>Environmental Microbiology</i> , 2017, 19, 2258-2271.	1.8	49
1950	Three rings for the evolution of plastid shape: a tale of land plant FtsZ. <i>Protoplasma</i> , 2017, 254, 1879-1885.	1.0	28
1951	Evolutionary and domestication history of <i>Cucurbita</i> (pumpkin and squash) species inferred from 44 nuclear loci. <i>Molecular Phylogenetics and Evolution</i> , 2017, 111, 98-109.	1.2	67
1952	<i>Candelariella blastidiata</i> sp. nov. (Ascomycota, Candelariaceae) from Eurasia and North America, and a key for grey thalli <i>Candelariella</i> . <i>Lichenologist</i> , 2017, 49, 117-126.	0.5	14
1953	Genomic changes associated with the evolutionary transition of an insect gut symbiont into a blood-borne pathogen. <i>ISME Journal</i> , 2017, 11, 1232-1244.	4.4	84
1954	Plastome phylogeny and early diversification of Brassicaceae. <i>BMC Genomics</i> , 2017, 18, 176.	1.2	137
1955	Revisiting the phylogeny of <i>Wolbachia</i> in Collembola. <i>Ecology and Evolution</i> , 2017, 7, 2009-2017.	0.8	21
1956	Phylogeny and biogeography of the imperial pigeons (Aves: Columbidae) in the Pacific Ocean. <i>Molecular Phylogenetics and Evolution</i> , 2017, 110, 19-26.	1.2	13
1957	The complete mitochondrial genome of the White-Nose Syndrome pathogen, <i>Pseudogymnoascus destructans</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 48-49.	0.2	1
1958	Biogeographical evidence for common vicariance and rare dispersal in a southern Appalachian harvestman (Sabaconidae, <i>Sabacon cavicolens</i>). <i>Journal of Biogeography</i> , 2017, 44, 1665-1678.	1.4	23
1959	The complex case of <i>Ceratitis cosyra</i> (Diptera: Tephritidae) and relatives. A DNA barcoding perspective. <i>Journal of Applied Entomology</i> , 2017, 141, 788-797.	0.8	4
1960	Morphology, songs and genetics identify two new cicada species from Morocco: <i>Tettigetta afroamissa</i> sp. nov. and <i>Berberigetta dimelodica</i> gen. nov. & sp. nov. (Hemiptera: Cicadettini). <i>Zootaxa</i> , 2017, 4237, 517.	0.2	4
1961	Molecular clocks indicate turnover and diversification of modern coleoid cephalopods during the Mesozoic Marine Revolution. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20162818.	1.2	86
1962	<i>Apertochrysa</i> (Neuroptera: Chrysopidae): A heterogeneric phantom? <i>Zootaxa</i> , 2017, 4238, zootaxa.4238.1.4.	0.2	7
1963	<i>Salvia</i> united: The greatest good for the greatest number. <i>Taxon</i> , 2017, 66, 133-145.	0.4	155
1964	The evolutionary history and taxonomic reevaluation of the Japanese coral snake, <i>Sinomicrurus japonicus</i> (Serpentes, Elapidae), endemic to the Ryukyu Archipelago, Japan, by use of molecular and morphological analyses. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2017, 55, 156-166.	0.6	6
1965	Resolving fine-grained dynamics of retrotransposons: comparative analysis of inferential methods and genomic resources. <i>Plant Journal</i> , 2017, 90, 979-993.	2.8	10
1966	Multiple measures could alleviate long-branch attraction in phylogenomic reconstruction of Cupressoideae (Cupressaceae). <i>Scientific Reports</i> , 2017, 7, 41005.	1.6	45

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1967	Cryptic diversity and discordance in single-locus species delimitation methods within horned lizards (Phrynosomatidae: <i>Phrynosoma</i>). <i>Molecular Ecology Resources</i> , 2017, 17, 1168-1182.	2.2	109
1968	Gut metagenomes of type 2 diabetic patients have characteristic single-nucleotide polymorphism distribution in <i>Bacteroides coprocola</i> . <i>Microbiome</i> , 2017, 5, 15.	4.9	41
1969	Floral scent and pollinators of <i>Ceropegia</i> trap flowers. <i>Flora: Morphology, Distribution, Functional Ecology of Plants</i> , 2017, 232, 169-182.	0.6	24
1970	Genome of the pitcher plant <i>Cephalotus</i> reveals genetic changes associated with carnivory. <i>Nature Ecology and Evolution</i> , 2017, 1, 59.	3.4	99
1971	High-throughput sequencing of multiple amplicons for barcoding and integrative taxonomy. <i>Scientific Reports</i> , 2017, 7, 41948.	1.6	101
1972	Evaluating multilocus Bayesian species delimitation for discovery of cryptic mycorrhizal diversity. <i>Fungal Ecology</i> , 2017, 26, 74-84.	0.7	17
1973	Microbial strain-level population structure and genetic diversity from metagenomes. <i>Genome Research</i> , 2017, 27, 626-638.	2.4	540
1974	Global Molecular Epidemiology of IMP-Producing Enterobacteriaceae. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	61
1975	Genomic Epidemiology of Penicillin-Nonsusceptible Pneumococci with Nonvaccine Serotypes Causing Invasive Disease in the United States. <i>Journal of Clinical Microbiology</i> , 2017, 55, 1104-1115.	1.8	44
1976	Ancient coexistence of norepinephrine, tyramine, and octopamine signaling in bilaterians. <i>BMC Biology</i> , 2017, 15, 6.	1.7	71
1977	Towards a higher-level Ensifera phylogeny inferred from mitogenome sequences. <i>Molecular Phylogenetics and Evolution</i> , 2017, 108, 22-33.	1.2	45
1978	Comparative <i>scp</i> DNA sequence analyses of <i>Pyramimonas parkeae</i> (Prasinophyceae) chloroplast genomes. <i>Journal of Phycology</i> , 2017, 53, 415-424.	1.0	9
1979	A pilot study applying the plant Anchored Hybrid Enrichment method to New World sages (<i>Salvia</i>) Tj ETQq0 0 0 rgBT, /Overlock 10 Tf 50	1.2	70
1980	A Mobile Element in <i>mutS</i> Drives Hypermutation in a Marine <i>Vibrio</i> . <i>MBio</i> , 2017, 8, .	1.8	26
1981	Maintaining stability of the rumen ecosystem is associated with changes of microbial composition and epithelial TLR signaling. <i>MicrobiologyOpen</i> , 2017, 6, e00436.	1.2	14
1982	Mitochondrial introgression suggests extensive ancestral hybridization events among <i>Saccharomyces</i> species. <i>Molecular Phylogenetics and Evolution</i> , 2017, 108, 49-60.	1.2	40
1983	Molecular phylogeny of extant Holothuroidea (Echinodermata). <i>Molecular Phylogenetics and Evolution</i> , 2017, 111, 110-131.	1.2	133
1984	Dated phylogenetic studies of the southernmost American buthids (Scorpiones; Buthidae). <i>Molecular Phylogenetics and Evolution</i> , 2017, 110, 39-49.	1.2	26

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1985	Plastomes of Mimosoideae: structural and size variation, sequence divergence, and phylogenetic implication. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	56
1986	Deciphering the distance to antibiotic resistance for the pneumococcus using genome sequencing data. <i>Scientific Reports</i> , 2017, 7, 42808.	1.6	25
1987	Chemosensory adaptations of the mountain fly <i>Drosophila nigrosarsa</i> (Insecta: Diptera) through genomics and structural biology's lenses. <i>Scientific Reports</i> , 2017, 7, 43770.	1.6	21
1988	Genome-wide survey of nuclear protein-coding markers for beetle phylogenetics and their application in resolving both deep and shallow-level divergences. <i>Molecular Ecology Resources</i> , 2017, 17, 1342-1358.	2.2	31
1989	Correlated patterns of genetic diversity and differentiation across an avian family. <i>Molecular Ecology</i> , 2017, 26, 3982-3997.	2.0	81
1990	Phylogenomic resolution of the bacterial genus <i>Pantoea</i> and its relationship with <i>Erwinia</i> and <i>Tatumella</i> . <i>Antonie Van Leeuwenhoek</i> , 2017, 110, 1287-1309.	0.7	48
1991	Mitochondrial genomic comparison of <i>Clonorchis sinensis</i> from South Korea with other isolates of this species. <i>Infection, Genetics and Evolution</i> , 2017, 51, 160-166.	1.0	13
1992	Mitochondrial genome diversity in dagger and needle nematodes (Nematoda: Longidoridae). <i>Scientific Reports</i> , 2017, 7, 41813.	1.6	20
1993	Geographic structure in two highly diverse lineages of <i>Tillandsia</i> (Bromeliaceae). <i>Botany</i> , 2017, 95, 641-651.	0.5	17
1994	Madagascar sheds new light on the molecular systematics and biogeography of grammitid ferns: New unexpected lineages and numerous long-distance dispersal events. <i>Molecular Phylogenetics and Evolution</i> , 2017, 111, 1-17.	1.2	37
1995	The biogeographic and evolutionary history of an endemic clade of Middle American sparrows: <i>Melospiza</i> and <i>Aimophila</i> (Aves: Passerellidae). <i>Molecular Phylogenetics and Evolution</i> , 2017, 110, 50-59.	1.2	8
1996	<i>Scapania paraphyllia</i> , a new synonym of <i>Scapania koponenii</i> (Marchantiophyta). <i>Bryology</i> , 2017, 39, 277-284.	0.4	2
1997	Heterologous Complementation Reveals a Specialized Activity for BacA in the <i>Medicago</i> - <i>Sinorhizobium meliloti</i> Symbiosis. <i>Molecular Plant-Microbe Interactions</i> , 2017, 30, 312-324.	1.4	24
1998	Susceptibility to type 2 diabetes may be modulated by haplotypes in G6PC2, a target of positive selection. <i>BMC Evolutionary Biology</i> , 2017, 17, 43.	3.2	14
1999	Chloroplast and ITS phylogenies to understand the evolutionary history of southern South American <i>Azorella</i> , <i>Laretia</i> and <i>Mulinum</i> (Azorelloideae, Apiaceae). <i>Molecular Phylogenetics and Evolution</i> , 2017, 108, 1-21.	1.2	10
2000	New natural products identified by combined genomics-metabolomics profiling of marine <i>Streptomyces</i> sp. MP131-18. <i>Scientific Reports</i> , 2017, 7, 42382.	1.6	86
2001	Re-analysis of unassigned hepatitis C virus (HCV) strain CYHCV025: Evidence of a highly divergent lineage within genotype 1. <i>Molecular Phylogenetics and Evolution</i> , 2017, 109, 362-366.	1.2	2
2002	Evolution of <i>Strigamia</i> centipedes (Chilopoda): a first molecular assessment of phylogeny and divergence times. <i>Zoologica Scripta</i> , 2017, 46, 486-495.	0.7	2

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2003	Molecular characterization of myostatin from the skeletal muscle of the African lungfish, <i>Protopterus annectens</i> , and changes in its mRNA and protein expression levels during three phases of aestivation. <i>Journal of Comparative Physiology B: Biochemical, Systemic, and Environmental Physiology</i> , 2017, 187, 575-589.	0.7	10
2004	The complete chloroplast genome of a vulnerable species <i>Champereia manillana</i> (Opiliaceae). <i>Conservation Genetics Resources</i> , 2017, 9, 415-418.	0.4	11
2005	The first complete genome sequences of the <i>acl</i> lineage, the most abundant freshwater Actinobacteria, obtained by whole-genome-amplification of dilution-to-extinction cultures. <i>Scientific Reports</i> , 2017, 7, 42252.	1.6	42
2006	Complete mitochondrial genomes of prasinophyte algae <i>Pyramimonas parkeae</i> and <i>Cymbomonas tetramitiformis</i> . <i>Journal of Phycology</i> , 2017, 53, 601-615.	1.0	10
2007	Genomic signatures of adaptation to wine biological ageing conditions in biofilm-forming flor yeasts. <i>Molecular Ecology</i> , 2017, 26, 2150-2166.	2.0	68
2008	Sensitive Next-Generation Sequencing Method Reveals Deep Genetic Diversity of HIV-1 in the Democratic Republic of the Congo. <i>Journal of Virology</i> , 2017, 91, .	1.5	39
2009	Complete mitochondrial genome of the endophytic fungus <i>Pestalotiopsis fici</i> : features and evolution. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 1593-1604.	1.7	51
2010	Infection-derived lipids elicit an immune deficiency circuit in arthropods. <i>Nature Communications</i> , 2017, 8, 14401.	5.8	103
2011	Origin of microbial biomineralization and magnetotaxis during the Archean. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 2171-2176.	3.3	98
2012	Phylogenetic analysis of the fish pathogen <i>Aeromonas salmonicida</i> underlines the dichotomy between European and Canadian strains for the <i>salmonicida</i> subspecies. <i>Journal of Fish Diseases</i> , 2017, 40, 1241-1247.	0.9	6
2013	Evolution of UhpC-type hexose-phosphate transporters in dinoflagellates. <i>Phycological Research</i> , 2017, 65, 166-170.	0.8	1
2014	Rapid transcriptional plasticity of duplicated gene clusters enables a clonally reproducing aphid to colonise diverse plant species. <i>Genome Biology</i> , 2017, 18, 27.	3.8	624
2015	Molecular Characterization and Phylogenetic Analysis of <i>Pseudomonas aeruginosa</i> Isolates Recovered from Greek Aquatic Habitats Implementing the Double-Locus Sequence Typing Scheme. <i>Microbial Ecology</i> , 2017, 74, 78-88.	1.4	7
2016	Phytochelatin 2 accumulates in roots of the seagrass <i>Enhalus acoroides</i> collected from sediment highly contaminated with lead. <i>BioMetals</i> , 2017, 30, 249-260.	1.8	11
2017	Expression map of a complete set of gustatory receptor genes in chemosensory organs of <i>Bombyx mori</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2017, 82, 74-82.	1.2	61
2018	Use of whole-genome sequencing to distinguish relapse from reinfection in a completed tuberculosis clinical trial. <i>BMC Medicine</i> , 2017, 15, 71.	2.3	57
2019	Molecular phylogeny and biogeography of the land snail family Hygromiidae (Gastropoda: Helicoidea). <i>Molecular Phylogenetics and Evolution</i> , 2017, 111, 169-184.	1.2	42
2020	Recurrent breakdowns of mutualisms with ants in the neotropical ant-plant genus <i>Cecropia</i> (Urticaceae). <i>Molecular Phylogenetics and Evolution</i> , 2017, 111, 196-205.	1.2	18

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2021	Genome-to-genome analysis highlights the effect of the human innate and adaptive immune systems on the hepatitis C virus. <i>Nature Genetics</i> , 2017, 49, 666-673.	9.4	129
2022	Genomic analyses of primitive, wild and cultivated citrus provide insights into asexual reproduction. <i>Nature Genetics</i> , 2017, 49, 765-772.	9.4	316
2023	Contentious relationships in phylogenomic studies can be driven by a handful of genes. <i>Nature Ecology and Evolution</i> , 2017, 1, 126.	3.4	365
2024	How Do Cold-Adapted Plants Respond to Climatic Cycles? Interglacial Expansion Explains Current Distribution and Genomic Diversity in <i>Primula farinosa</i> L.. <i>Systematic Biology</i> , 2017, 66, 715-736.	2.7	26
2025	Phylogenetic position of the coral symbiont <i>Ostreobium</i> (Ulvophyceae) inferred from chloroplast genome data. <i>Journal of Phycology</i> , 2017, 53, 790-803.	1.0	28
2026	Anoxybacillus sp. Strain UARK-01, a New Thermophilic Soil Bacterium with Hyperthermostable Alkaline Laccase Activity. <i>Current Microbiology</i> , 2017, 74, 762-771.	1.0	24
2027	Ecological determinants of butterfly vulnerability across the European continent. <i>Journal of Insect Conservation</i> , 2017, 21, 439-450.	0.8	32
2028	Dry habitats were crucibles of domestication in the evolution of agriculture in ants. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20170095.	1.2	130
2029	Consequences of divergence and introgression for speciation in Andean cloud forest birds. <i>Evolution; International Journal of Organic Evolution</i> , 2017, 71, 1815-1831.	1.1	33
2030	A unique, highly variable mitochondrial gene with coding capacity of <i>Heterosigma akashiwo</i> , class Raphidophyceae. <i>Journal of Applied Phycology</i> , 2017, 29, 2961-2969.	1.5	12
2031	A Global Coexpression Network Approach for Connecting Genes to Specialized Metabolic Pathways in Plants. <i>Plant Cell</i> , 2017, 29, 944-959.	3.1	225
2032	The structured diversity of specialized gut symbionts of the New World army ants. <i>Molecular Ecology</i> , 2017, 26, 3808-3825.	2.0	62
2033	Genetic Stability and Evolution of the <i>sigB</i> Allele, Used for <i>Listeria Sensu Stricto</i> Subtyping and Phylogenetic Inference. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	36
2034	Functional and evolutionary characterization of Ohr proteins in eukaryotes reveals many active homologs among pathogenic fungi. <i>Redox Biology</i> , 2017, 12, 600-609.	3.9	15
2035	Molecular phylogeny of obligate fish parasites of the family Cymothoidae (Isopoda, Crustacea): evolution of the attachment mode to host fish and the habitat shift from saline water to freshwater. <i>Marine Biology</i> , 2017, 164, 1.	0.7	59
2036	Two new species in the <i>Suillus spraguei</i> complex from China. <i>Mycologia</i> , 2017, 109, 296-307.	0.8	9
2037	Cryptic diversity in Amazonian frogs: Integrative taxonomy of the genus <i>Anomaloglossus</i> (Amphibia: Tj ETQq0 0 0 rgBT /Overlock 10 Tf Phylogenetics and Evolution, 2017, 112, 158-173.	1.2	55
2038	Noumeavirus replication relies on a transient remote control of the host nucleus. <i>Nature Communications</i> , 2017, 8, 15087.	5.8	91

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2039	Homology-aware Phylogenomics at Gigabase Scales. <i>Systematic Biology</i> , 2017, 66, syw104.	2.7	34
2040	StarBEAST2 Brings Faster Species Tree Inference and Accurate Estimates of Substitution Rates. <i>Molecular Biology and Evolution</i> , 2017, 34, 2101-2114.	3.5	371
2041	Multiple strong postmating and intrinsic postzygotic reproductive barriers isolate florally diverse species of <i>Jaltomata</i> (Solanaceae). <i>Evolution; International Journal of Organic Evolution</i> , 2017, 71, 1556-1571.	1.1	26
2042	The PerR-Regulated P _{1B-4} -Type ATPase (PmtA) Acts as a Ferrous Iron Efflux Pump in <i>Streptococcus pyogenes</i> . <i>Infection and Immunity</i> , 2017, 85, .	1.0	24
2043	On the Ability to Reconstruct Ancestral Genomes from Mycobacterium Genus. <i>Lecture Notes in Computer Science</i> , 2017, , 642-658.	1.0	1
2044	Y-chromosomal sequences of diverse Indian populations and the ancestry of the Andamanese. <i>Human Genetics</i> , 2017, 136, 499-510.	1.8	18
2045	Descriptions and phylogenetic relationships of four new species and a new name of <i>Habenaria</i> (Orchidaceae) from the cerrado and campos rupestres of Brazil. <i>Plant Systematics and Evolution</i> , 2017, 303, 873-899.	0.3	10
2046	Diversity, phylogeny and pathogenicity of Botryosphaeriaceae on non-native <i>Eucalyptus</i> grown in an urban environment: A case study. <i>Urban Forestry and Urban Greening</i> , 2017, 26, 139-148.	2.3	17
2047	<i>Planothidium lanceolatum</i> and <i>Planothidium frequentissimum</i> reinvestigated with molecular methods and morphology: four new species and the taxonomic importance of the sinus and cavum. <i>Diatom Research</i> , 2017, 32, 75-107.	0.5	40
2048	The complete mitochondrial genomes of the higher termites <i>Labiotermes labralis</i> and <i>Embiratermes neotenicus</i> (Termitidae: Syntermitinae). <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 109-110.	0.2	5
2049	The Emergence, Evolution, and Diversification of the miR390-TAS3-ARF Pathway in Land Plants. <i>Plant Cell</i> , 2017, 29, 1232-1247.	3.1	149
2050	Genetic basis for soma is present in undifferentiated volvocine green algae. <i>Journal of Evolutionary Biology</i> , 2017, 30, 1205-1218.	0.8	26
2051	A phylogeographic investigation of the kelp genus <i>Laminaria</i> (Laminariales, Phaeophyceae), with emphasis on the South Atlantic Ocean. <i>Journal of Phycology</i> , 2017, 53, 778-789.	1.0	30
2052	<i>Lecanicillium araneogenum</i> sp. nov., a new araneogenous fungus. <i>Phytotaxa</i> , 2017, 305, 29.	0.1	13
2053	Population Genomics of <i>Paramecium</i> Species. <i>Molecular Biology and Evolution</i> , 2017, 34, 1194-1216.	3.5	35
2054	A hypervariable mitochondrial protein coding sequence associated with geographical origin in a cosmopolitan bloom-forming alga, <i>Heterosigma akashiwo</i> . <i>Biology Letters</i> , 2017, 13, 20160976.	1.0	5
2055	Contribution of different bacterial dispersal sources to lakes: Population and community effects in different seasons. <i>Environmental Microbiology</i> , 2017, 19, 2391-2404.	1.8	50
2056	Draft genomes of the corallimorpharians <i>Amplexidiscus fenestrafer</i> and <i>Discosoma</i> sp.. <i>Molecular Ecology Resources</i> , 2017, 17, e187-e195.	2.2	22

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2057	Increased phylogenetic resolution within the ecologically important <i>Rhizopogon</i> subgenus <i>Amylopogon</i> using 10 anonymous nuclear loci. <i>Mycologia</i> , 2017, 109, 35-45.	0.8	6
2058	A day-flashing <i>Photinus</i> firefly (Coleoptera: Lampyridae) from central Panama: an emergent shift to predator-free space?. <i>Insect Systematics and Evolution</i> , 2017, 48, 512-531.	0.2	7
2059	LOCUST: a custom sequence locus typer for classifying microbial isolates. <i>Bioinformatics</i> , 2017, 33, 1725-1726.	1.8	16
2060	A New Species of <i>Orobdella</i> (Hirudinida: Arhynchobdellida: Orobdellidae) from Japan Reveals the Function of the <i>Orobdella</i> Gastroporal Duct. <i>Zoological Science</i> , 2017, 34, 161-172.	0.3	7
2061	Characterization of the complete chloroplast genome of seabuckthorn (<i>Hippophae rhamnoides</i> L.). <i>Conservation Genetics Resources</i> , 2017, 9, 623-626.	0.4	10
2062	Progenitor strain introduction of <i>Mycobacterium bovis</i> at the wildlife-livestock interface can lead to clonal expansion of the disease in a single ecosystem. <i>Infection, Genetics and Evolution</i> , 2017, 51, 235-238.	1.0	35
2063	Molecular phylogenetics and dating of the problematic New Guinea microhylid frogs (Amphibia): <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 5</i> <i>Phylogenetics and Evolution</i> , 2017, 112, 1-11.	1.2	24
2064	Contrasting evolutionary genome dynamics between domesticated and wild yeasts. <i>Nature Genetics</i> , 2017, 49, 913-924.	9.4	340
2065	Reconstructed ancestral enzymes suggest long-term cooling of Earth's photic zone since the Archean. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 4619-4624.	3.3	53
2066	DeCoSTAR: Reconstructing the Ancestral Organization of Genes or Genomes Using Reconciled Phylogenies. <i>Genome Biology and Evolution</i> , 2017, 9, 1312-1319.	1.1	32
2067	Interspecific Plastome Recombination Reflects Ancient Reticulate Evolution in <i>Picea</i> (Pinaceae). <i>Molecular Biology and Evolution</i> , 2017, 34, 1689-1701.	3.5	69
2068	Increased taxon sampling reveals thousands of hidden orthologs in flatworms. <i>Genome Research</i> , 2017, 27, 1263-1272.	2.4	39
2069	Sparse panicle1 is required for inflorescence development in <i>Setaria viridis</i> and maize. <i>Nature Plants</i> , 2017, 3, 17054.	4.7	63
2070	Molecular phylogeny of the marine <i>Prasiola</i> and <i>Rosenvingiella</i> species (Chlorophyta: Prasiolales) from southeastern Kamchatka. <i>Russian Journal of Marine Biology</i> , 2017, 43, 34-41.	0.2	3
2071	The choreography of the chemical defensive response to insecticide stress: insights into the <i>Anopheles stephensi</i> transcriptome using RNA-Seq. <i>Scientific Reports</i> , 2017, 7, 41312.	1.6	39
2072	The evolutionary history of bears is characterized by gene flow across species. <i>Scientific Reports</i> , 2017, 7, 46487.	1.6	176
2073	Primates, Lice and Bacteria: Speciation and Genome Evolution in the Symbionts of Hominid Lice. <i>Molecular Biology and Evolution</i> , 2017, 34, 1743-1757.	3.5	51
2074	Strong spatial genetic congruence between a wood-feeding cockroach and its bacterial endosymbiont, across a topographically complex landscape. <i>Journal of Biogeography</i> , 2017, 44, 1500-1511.	1.4	17

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2075	Mimaporina, a new genus of Epicopeiidae (Lepidoptera), with description of a new species from Vietnam. <i>Zootaxa</i> , 2017, 4254, 537.	0.2	10
2076	North American matsutake: names clarified and a new species described. <i>Mycologia</i> , 2017, 109, 379-390.	0.8	29
2077	Phylogenetic relationships within Adiaphanida (phylum Platyhelminthes) and the status of the crustacean parasitic genus <i>Genostoma</i> . <i>Invertebrate Biology</i> , 2017, 136, 184-198.	0.3	8
2078	Evolution and Antiviral Specificities of Interferon-Induced Mx Proteins of Bats against Ebola, Influenza, and Other RNA Viruses. <i>Journal of Virology</i> , 2017, 91, .	1.5	53
2079	Phylogenetic relationships and generic re-arrangements in "South Andean Loasas" (Loasaceae). <i>Taxon</i> , 2017, 66, 365-378.	0.4	9
2080	Cryptic speciation and gene flow in a migratory songbird Species Complex: Insights from the Red-Eyed Vireo (<i>Vireo olivaceus</i>). <i>Molecular Phylogenetics and Evolution</i> , 2017, 113, 67-75.	1.2	22
2081	Patterns of Genome-Wide Diversity and Population Structure in the <i>Drosophila athabasca</i> Species Complex. <i>Molecular Biology and Evolution</i> , 2017, 34, 1912-1923.	3.5	17
2082	Phylogenomics from Whole Genome Sequences Using aTRAM. <i>Systematic Biology</i> , 2017, 66, syw105.	2.7	47
2083	Geographically structured genetic variation in the <i>Medicago lupulina</i> – <i>Ensifer</i> mutualism. <i>Evolution; International Journal of Organic Evolution</i> , 2017, 71, 1787-1801.	1.1	25
2084	Detection and molecular status of <i>Isospora</i> sp. from the domestic pigeon (<i>Columba livia domestica</i>). <i>Parasitology International</i> , 2017, 66, 588-592.	0.6	10
2085	Species richness in the genus <i>Microplana</i> (Platyhelminthes, Tricladida, Microplaninae) in Europe: as yet no asymptote in sight. <i>Invertebrate Systematics</i> , 2017, 31, 269.	0.5	7
2086	The complete chloroplast genome sequence of <i>Hydrocotyle sibthorpioides</i> (Apiales: araliaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 29-30.	0.2	7
2087	Crop wild relative conservation: Wild yams are not that wild. <i>Biological Conservation</i> , 2017, 210, 325-333.	1.9	17
2088	Effective estimation of the minimum number of amino acid residues required for functional divergence between duplicate genes. <i>Molecular Phylogenetics and Evolution</i> , 2017, 113, 126-138.	1.2	7
2089	Discovery of herpesviruses in Canadian wildlife. <i>Archives of Virology</i> , 2017, 162, 449-456.	0.9	5
2090	Emergence of multidrug resistance in locally-acquired human infections with <i>Salmonella</i> Typhimurium in Australia owing to a new clade harbouring bla CTX-M-9. <i>International Journal of Antimicrobial Agents</i> , 2017, 50, 101-105.	1.1	20
2091	Exploring resistance pathways for first-generation NS3/4A protease inhibitors boceprevir and telaprevir using Bayesian network learning. <i>Infection, Genetics and Evolution</i> , 2017, 53, 15-23.	1.0	14
2092	Distribution of <i>Holttumochloa</i> (Poaceae: Bambusoideae) in China with description of a new species revealed by morphological and molecular evidence. <i>Plant Diversity</i> , 2017, 39, 135-139.	1.8	2

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2093	A new species of <i>Trachylepis</i> (Squamata: Scincidae) from Central Africa and a key to the <i>Trachylepis</i> of West and Central Africa. <i>Zootaxa</i> , 2017, 4268, 255-269.	0.2	8
2094	A taxonomic revision of cleistocarpous species of <i>Weissia</i> (Pottiaceae, Bryophyta) in Japan. <i>Phytotaxa</i> , 2017, 306, 1.	0.1	5
2095	Phylogenomic analysis of a rapid radiation of misfit fishes (Syngnathiformes) using ultraconserved elements. <i>Molecular Phylogenetics and Evolution</i> , 2017, 113, 33-48.	1.2	49
2096	eadem figura manet: Measuring morphological convergence in diplocentrid scorpions (Arachnida:) Tj ETQq1 1 0.784314 rgBT /Overlock 2017, 31, 233.	0.5	16
2097	The New Zealand endemic <i>Plagiochila caducifolia</i> is a disjunct population of <i>Plagiochila spinulosa</i> (Plagiochilaceae: Jungermanniopsida). <i>New Zealand Journal of Botany</i> , 2017, 55, 276-292.	0.8	1
2098	In silico screening for candidate chassis strains of free fatty acid-producing cyanobacteria. <i>BMC Genomics</i> , 2017, 18, 33.	1.2	11
2099	<i>Ambrosiella</i> in Taiwan including one new species. <i>Mycoscience</i> , 2017, 58, 242-252.	0.3	10
2100	<i>Filibryum</i> (Hypnaceae), a new moss genus with a new species from East Asia. <i>Journal of Bryology</i> , 2017, 39, 152-160.	0.4	4
2101	Unique Phylogenetic Distributions of the Ska and Dam1 Complexes Support Functional Analogy and Suggest Multiple Parallel Displacements of Ska by Dam1. <i>Genome Biology and Evolution</i> , 2017, 9, 1295-1303.	1.1	50
2102	Assembling a Taxonomic Monograph of Tribe Wirthiotremateae (Lichenized Ascomycota: Ostropales:) Tj ETQq1 1 0.784314 rgBT /Overlock 1.0	1.0	13
2103	ST3268: a geographically widespread primate MRSA clone. <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, 2401-2403.	1.3	12
2104	Widespread adenine N6-methylation of active genes in fungi. <i>Nature Genetics</i> , 2017, 49, 964-968.	9.4	292
2105	Mitochondrial genome divergence between beluga whales in Baffin Bay and the Sea of Okhotsk. <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 257-258.	0.2	1
2106	Rediscovery and description of <i>Paramormyrops sphekodes</i> (Sauvage, 1879) and a new cryptic <i>Paramormyrops</i> (Mormyridae: Osteoglossiformes) from the OgoouÃ© River of Gabon using morphometrics, DNA sequencing and electrophysiology. <i>Zoological Journal of the Linnean Society</i> , 2017, 180, 613-646.	1.0	9
2107	Closing gaps for performing a risk assessment on <i>Listeria monocytogenes</i> in ready-to-eat (RTE) foods: activity 3, the comparison of isolates from different compartments along the food chain, and from humans using whole genome sequencing (WGS) analysis. <i>EFSA Supporting Publications</i> , 2017, 14, 1151E.	0.3	72
2108	Rotiferan Hox genes give new insights into the evolution of metazoan bodyplans. <i>Nature Communications</i> , 2017, 8, 9.	5.8	149
2109	Large Cluster of <i>Neisseria meningitidis</i> Urethritis in Columbus, Ohio, 2015. <i>Clinical Infectious Diseases</i> , 2017, 65, 92-99.	2.9	52
2110	Genomic and Epidemiological Evidence for Community Origins of Hospital-Onset Methicillin-Resistant <i>Staphylococcus aureus</i> Bloodstream Infections. <i>Journal of Infectious Diseases</i> , 2017, 215, 1640-1647.	1.9	30

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2111	Shedding light on the Imps of Darkness: an integrative taxonomic revision of the Galápagos marine iguanas (genus <i>Amblyrhynchus</i>). <i>Zoological Journal of the Linnean Society</i> , 2017, 181, 678-710.	1.0	25
2112	Comparative Analysis of Extended-Spectrum- β -Lactamase CTX-M-65-Producing <i>Salmonella enterica</i> Serovar Infantis Isolates from Humans, Food Animals, and Retail Chickens in the United States. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	132
2113	Conservation genomics of the silktail (Aves: <i>Lamprolia victoriae</i>) suggests the need for increased protection of native forest on the Natewa Peninsula, Fiji. <i>Conservation Genetics</i> , 2017, 18, 1277-1285.	0.8	7
2114	The effects of Pleistocene climate change on biotic differentiation in a montane songbird clade from Wallacea. <i>Molecular Phylogenetics and Evolution</i> , 2017, 114, 353-366.	1.2	18
2115	Systematics and Molecular Phylogeny of the Ciliate Genus <i>Pseudokeronopsis</i> (Ciliophora, Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 5	0.8	16
2116	<i>Lactarius splendens</i> , a second species with white latex in <i>Lactarius</i> section <i>Deliciosi</i> . <i>Botany</i> , 2017, 95, 859-863.	0.5	5
2117	The Tea Tree Genome Provides Insights into Tea Flavor and Independent Evolution of Caffeine Biosynthesis. <i>Molecular Plant</i> , 2017, 10, 866-877.	3.9	563
2118	Single-Copy Genes as Molecular Markers for Phylogenomic Studies in Seed Plants. <i>Genome Biology and Evolution</i> , 2017, 9, 1130-1147.	1.1	75
2119	A time and a place for everything: phylogenetic history and geography as joint predictors of oak plastome phylogeny. <i>Genome</i> , 2017, 60, 720-732.	0.9	64
2120	The Taxonomic Status of <i>Oligoryzomys mattogrossae</i> (Allen 1916) (Rodentia: Cricetidae: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 5	0.2	20
2121	Phylogenetic analysis and evolution of morphological characters in <i>Metrodorea</i> and related species in Rutoideae (Rutaceae). <i>Plant Systematics and Evolution</i> , 2017, 303, 927-943.	0.3	6
2122	The Gondwanan connection of Southern temperate <i>Amanita</i> lineages and the description of the first sequestrate species from the Americas. <i>Fungal Biology</i> , 2017, 121, 638-651.	1.1	23
2123	Diversity and phylogeography of Northeast Asian brown frogs allied to <i>Rana dybowskii</i> (Anura, Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 26	1.2	21
2124	Genome sequence and physiological analysis of <i>Yamadazyma laniorum</i> f.a. sp. nov. and a reevaluation of the apocryphal xylose fermentation of its sister species, <i>Candida tenuis</i> . <i>FEMS Yeast Research</i> , 2017, 17, .	1.1	18
2125	Genomic landscape of extended-spectrum β -lactamase resistance in <i>Escherichia coli</i> from an urban African setting. <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, 1602-1609.	1.3	46
2126	How do seemingly non-vagile clades accomplish trans-marine dispersal? Trait and dispersal evolution in the landfowl (Aves: Galliformes). <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20170210.	1.2	45
2127	Fungal diversity notes 491-602: taxonomic and phylogenetic contributions to fungal taxa. <i>Fungal Diversity</i> , 2017, 83, 1-261.	4.7	180
2128	Evolution, structure and membrane association of NDUF6, an assembly factor for NADH:ubiquinone oxidoreductase (Complex I). <i>Mitochondrion</i> , 2017, 35, 13-22.	1.6	12

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2129	RNA Targeting by Functionally Orthogonal Type VI-A CRISPR-Cas Enzymes. <i>Molecular Cell</i> , 2017, 66, 373-383.e3.	4.5	229
2130	Sixty-Five Million Years of Change in Temperature and Topography Explain Evolutionary History in Eastern North American Plethodontid Salamanders. <i>American Naturalist</i> , 2017, 190, E1-E12.	1.0	7
2131	Species evolution and quality evaluation of four <i>Coptis</i> herbal medicinal materials in Southwest China. <i>3 Biotech</i> , 2017, 7, 62.	1.1	21
2132	Unique parallel radiations of high-mountainous species of the genus <i>Sedum</i> (Crassulaceae) on the continental island of Taiwan. <i>Molecular Phylogenetics and Evolution</i> , 2017, 113, 9-22.	1.2	21
2133	The enigmatic groundwater amphipod <i>Awacaris kawasawai</i> revisited: synonymisation of the genus <i>Sternomoera</i> , with molecular phylogenetic analyses of <i>Awacaris</i> and <i>Sternomoera</i> species (Crustacea). <i>Tj ETQq0 0 OrgBT /Overlock 10 T</i>		
2134	Convergently Evolved Toxic Secondary Metabolites in Plants Drive the Parallel Molecular Evolution of Insect Resistance. <i>American Naturalist</i> , 2017, 190, S29-S43.	1.0	42
2135	Interacting effects of land use and climate on rodent-borne pathogens in central Kenya. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017, 372, 20160116.	1.8	39
2136	The biogeographical history of the interaction between mycoheterotrophic <i>Thismia</i> (Thismiaceae) plants and mycorrhizal <i>Rhizophagus</i> (Glomeraceae) fungi. <i>Journal of Biogeography</i> , 2017, 44, 1869-1879.	1.4	25
2137	Contrasting dispersal histories of broad- and fine-leaved temperate Loliinae grasses: range expansion, founder events, and the roles of distance and barriers. <i>Journal of Biogeography</i> , 2017, 44, 1980-1993.	1.4	32
2138	Systematic position of <i>Oreosolen</i> (tribe Scrophularieae, Scrophulariaceae) based on nuclear and plastid sequences. <i>Journal of Systematics and Evolution</i> , 2017, 55, 446-452.	1.6	3
2139	<i>Tabula rasa</i> in the Patagonian Channels? The phylogeography of <i>Oreobolus obtusangulus</i> (Cyperaceae). <i>Molecular Ecology</i> , 2017, 26, 4027-4044.	2.0	9
2140	Integrated molecular and morphological studies of <i>Daucus</i> . <i>Acta Horticulturae</i> , 2017, , 265-272.	0.1	0
2141	Anthopleura and the phylogeny of Actinioidea (Cnidaria: Anthozoa: Actiniaria). <i>Organisms Diversity and Evolution</i> , 2017, 17, 545-564.	0.7	26
2142	Next-generation sequencing data used to determine the mitochondrial genomes and a preliminary phylogeny of Verophasmatodea insects. <i>Journal of Asia-Pacific Entomology</i> , 2017, 20, 713-719.	0.4	25
2143	Multi-locus phylogenetic analysis of the genus <i>Limnodrilus</i> (Annelida: Clitellata: Naididae). <i>Molecular Phylogenetics and Evolution</i> , 2017, 112, 244-257.	1.2	11
2144	Convergent evolution of a modified, acetate-driven TCA cycle in bacteria. <i>Nature Microbiology</i> , 2017, 2, 17067.	5.9	60
2145	Conservation and divergence of C-terminal domain structure in the retinoblastoma protein family. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 4942-4947.	3.3	33
2146	Evolutionary History of Chemosensory-Related Gene Families across the Arthropoda. <i>Molecular Biology and Evolution</i> , 2017, 34, 1838-1862.	3.5	157

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2147	Inferring Trees. <i>Methods in Molecular Biology</i> , 2017, 1525, 349-377.	0.4	5
2148	Scaling Up the Phylogenetic Detection of Lateral Gene Transfer Events. <i>Methods in Molecular Biology</i> , 2017, 1525, 421-432.	0.4	2
2149	Molecular diversity patterns among various phytoplankton size-fractions in West Greenland in late summer. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2017, 121, 54-69.	0.6	30
2150	Unparalleled replacement of native mitochondrial genes by foreign homologs in a holoparasitic plant. <i>New Phytologist</i> , 2017, 214, 376-387.	3.5	73
2151	Development of new methods for the quantitative detection and typing of <i>Lactobacillus parabuchneri</i> in dairy products. <i>International Dairy Journal</i> , 2017, 70, 65-71.	1.5	29
2152	Ribosomal RNA Internal Transcribed Regions Identify Possible Misidentification or Mislabeling among <i>Trifolium</i> (Clover) Specimens from Germplasm Collections. <i>Crop Science</i> , 2017, 57, 322-326.	0.8	2
2153	The developmental basis for the recurrent evolution of deuterostomy and protostomy. <i>Nature Ecology and Evolution</i> , 2017, 1, 5.	3.4	80
2154	<i>Tintelnotia</i> , a new genus in <i>Phaeosphaeriaceae</i> harbouring agents of cornea and nail infections in humans. <i>Mycoses</i> , 2017, 60, 244-253.	1.8	31
2155	Modulation of the heat shock response is associated with acclimation to novel temperatures but not adaptation to climatic variation in the ants <i>Aphaenogaster picea</i> and <i>A. rudis</i> . <i>Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology</i> , 2017, 204, 113-120.	0.8	20
2156	Vaginal <i>Candida</i> spp. genomes from women with vulvovaginal candidiasis. <i>Pathogens and Disease</i> , 2017, 75, .	0.8	14
2157	Genomic epidemiology of global VIM-producing <i>Enterobacteriaceae</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, 2249-2258.	1.3	47
2158	Conserved Nonexonic Elements: A Novel Class of Marker for Phylogenomics. <i>Systematic Biology</i> , 2017, 66, 1028-1044.	2.7	46
2159	Population genomics and the evolution of virulence in the fungal pathogen <i>Cryptococcus neoformans</i> . <i>Genome Research</i> , 2017, 27, 1207-1219.	2.4	134
2160	The genomic mosaicism of hybrid speciation. <i>Science Advances</i> , 2017, 3, e1602996.	4.7	138
2161	A new species of <i>Amaurobius</i> C.L. Koch, 1837 (Araneae: Amaurobiidae) from Apennine Mountains (Italy) with the description of the male of <i>A. pavesii</i> Pesarini, 1991. <i>Zootaxa</i> , 2017, 4276, .	0.2	3
2162	A comprehensive and integrative re-description of <i>Synchaeta tremula</i> (Müller, 1786) and the newly rediscovered <i>Synchaeta tremuloida</i> Pourriot, 1965 (Rotifera: Synchaetidae). <i>Zootaxa</i> , 2017, 4276, 503.	0.2	4
2163	A revised family-level classification of the Polyporales (Basidiomycota). <i>Fungal Biology</i> , 2017, 121, 798-824.	1.1	190
2164	A niche for cyanobacteria producing chlorophyll <i>f</i> within a microbial mat. <i>ISME Journal</i> , 2017, 11, 2368-2378.	4.4	62

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2165	High quality draft genome of <i>Nakamurella lactea</i> type strain, a rock actinobacterium, and emended description of <i>Nakamurella lactea</i> . <i>Standards in Genomic Sciences</i> , 2017, 12, 4.	1.5	14
2166	<i>Mycoplasma hominis</i> Infections Transmitted Through Amniotic Tissue Product. <i>Clinical Infectious Diseases</i> , 2017, 65, 1152-1158.	2.9	7
2167	The chloroplast genome sequence from <i>Eugenia uniflora</i> , a Myrtaceae from Neotropics. <i>Plant Systematics and Evolution</i> , 2017, 303, 1199-1212.	0.3	37
2168	Evolutionary and polymorphism analyses reveal the central role of <i>BTN3A2</i> in the concerted evolution of the <i>BTN3</i> gene family. <i>Immunogenetics</i> , 2017, 69, 379-390.	1.2	21
2169	Total evidence phylogeny of the North American harvestman family Stygnopsidae (Opiliones :). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 582</i>	0.5	16
2170	A genetic legacy of introgression confounds phylogeny and biogeography in oaks. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20170300.	1.2	105
2171	X-Cells Are Globally Distributed, Genetically Divergent Fish Parasites Related to Perkinsids and Dinoflagellates. <i>Current Biology</i> , 2017, 27, 1645-1651.e3.	1.8	29
2172	The New Red Algal Subphylum Proteorhodophytina Comprises the Largest and Most Divergent Plastid Genomes Known. <i>Current Biology</i> , 2017, 27, 1677-1684.e4.	1.8	89
2173	Evolution and structural diversification of <i>Nictaba</i> -like lectin genes in food crops with a focus on soybean (<i>Glycine max</i>). <i>Annals of Botany</i> , 2017, 119, mcw259.	1.4	9
2174	Millions of Boreal Shield Lakes can be used to Probe Archaean Ocean Biogeochemistry. <i>Scientific Reports</i> , 2017, 7, 46708.	1.6	33
2175	To be or not to be a valid genus: the systematic position of <i>Ophyra</i> R.â€D. revised (Diptera:). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50</i>	1.7	15
2176	Allopatric divergence and secondary contact without genetic admixture for <i>A<sc>richanna perimelaina</sc></i> (<i>L<sc>epidoptera: G<sc>eometridae</sc></i>), an alpine moth endemic to the <i>H<sc>engduan M<sc>ountains</sc></i> . <i>Systematic Entomology</i> , 2017, 42, 703-713.	1.7	4
2177	Multi-â€gene phylogeny of the <i>H<sc>emileuca maia</sc></i> complex (<i>S<sc>aturniidae</sc></i>) across <i>N<sc>orth A<sc>merica</sc></i> suggests complex phylogeography and rapid ecological diversification. <i>Systematic Entomology</i> , 2017, 42, 621-634.	1.7	11
2178	Iron-Dependent Enzyme Catalyzes the Initial Step in Biodegradation of <i>N</i>-Nitroglycine by <i>Variovorax</i> sp. Strain JS1663. <i>Applied and Environmental Microbiology</i>, 2017, 83, .</i>	1.4	11
2179	A new species and a new combination of <i>Rhodophana</i> (Entolomataceae, Agaricales) from Africa. <i>Phytotaxa</i> , 2017, 306, 223.	0.1	3
2180	Molecular phylogenetics and biogeography of the mint tribe Elsholtzieae (Nepetoideae, Lamiaceae), with an emphasis on its diversification in East Asia. <i>Scientific Reports</i> , 2017, 7, 2057.	1.6	30
2181	The origin and evolution of human glutaminases and their atypical C-terminal ankyrin repeats. <i>Journal of Biological Chemistry</i> , 2017, 292, 11572-11585.	1.6	19
2182	Toll-like receptor pathway evolution in deuterostomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 7055-7060.	3.3	49

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2183	A null model for microbial diversification. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E5414-E5423.	3.3	9
2184	Repeated and diverse losses of corolla bilateral symmetry in the Lamiaceae. Annals of Botany, 2017, 119, 1211-1223.	1.4	23
2185	Phylogenomics using Target-restricted Assembly Resolves Intra-generic Relationships of Parasitic Lice (Phthiraptera: <i>Columbicola</i>). Systematic Biology, 2017, 66, syx027.	2.7	22
2186	Intraspecific haplotype diversity in <i>Cherleria sedoides</i> L. (Caryophyllaceae) is best explained by chloroplast capture from an extinct species. Alpine Botany, 2017, 127, 171-183.	1.1	2
2187	Genomic comparison of virulent and non-virulent serotype V ST1 <i>Streptococcus agalactiae</i> in fish. Veterinary Microbiology, 2017, 207, 164-169.	0.8	11
2188	Rapid divergence of histones in Hydrozoa (Cnidaria) and evolution of a novel histone involved in DNA damage response in hydra. Zoology, 2017, 123, 53-63.	0.6	16
2189	Identification, genealogical structure and population genetics of S-alleles in <i>Malus sieversii</i> , the wild ancestor of domesticated apple. Heredity, 2017, 119, 185-196.	1.2	6
2190	Human Chitotriosidase: Catalytic Domain or Carbohydrate Binding Module, Who's Leading HCHT's Biological Function. Scientific Reports, 2017, 7, 2768.	1.6	14
2191	Insights into enterotoxigenic <i>Escherichia coli</i> diversity in Bangladesh utilizing genomic epidemiology. Scientific Reports, 2017, 7, 3402.	1.6	33
2192	Polyphyly of Arundinoideae (Poaceae) and evolution of the twisted geniculate lemma awn. Annals of Botany, 2017, 120, 725-738.	1.4	29
2193	SANDPUMA: ensemble predictions of nonribosomal peptide chemistry reveal biosynthetic diversity across <i>Actinobacteria</i> . Bioinformatics, 2017, 33, 3202-3210.	1.8	89
2194	Phylogeographic relationships among multi-island populations of the tree snail <i>Partula gibba</i> (Partulidae) in the Mariana Islands. Biological Journal of the Linnean Society, 2017, 121, 731-740.	0.7	5
2195	Genomic phylogeography of the endemic Mountain Black-eye of Borneo (<i>Chlorocharis emiliae</i>): montane and lowland populations differ in patterns of Pleistocene diversification. Journal of Biogeography, 2017, 44, 2272-2283.	1.4	16
2196	Genome mining reveals high incidence of putative lipopeptide biosynthesis <i>NRPS</i> / <i>PKS</i> clusters containing fatty acyl-AMP ligase genes in biofilm-forming cyanobacteria. Journal of Phycology, 2017, 53, 985-998.	1.0	21
2197	Do changes in gene expression contribute to sexual isolation and reinforcement in the house mouse?. Molecular Ecology, 2017, 26, 5189-5202.	2.0	18
2198	Recent origin and rapid speciation of Neotropical orchids in the world's richest plant biodiversity hotspot. New Phytologist, 2017, 215, 891-905.	3.5	170
2199	Novel Predators Reshape Holozoan Phylogeny and Reveal the Presence of a Two-Component Signaling System in the Ancestor of Animals. Current Biology, 2017, 27, 2043-2050.e6.	1.8	87
2200	The first Margaritiferidae male (M-type) mitogenome: mitochondrial gene order as a potential character for determining higher-order phylogeny within Unionida (Bivalvia). Journal of Molluscan Studies, 2017, 83, 249-252.	0.4	26

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2201	Reconciling morphological and molecular systematics in tarantulas (Araneae: Theraphosidae): revision of the Mexican endemic genus <i>Bonnetina</i> . <i>Zoological Journal of the Linnean Society</i> , 2017, 180, 819-886.	1.0	19
2202	Identification of <i>Pelomyxa palustris</i> Endosymbionts. <i>Protist</i> , 2017, 168, 408-424.	0.6	15
2203	Assessing the potential of RAD-sequencing to resolve phylogenetic relationships within species radiations: The fly genus <i>Chiastocheta</i> (Diptera: Anthomyiidae) as a case study. <i>Molecular Phylogenetics and Evolution</i> , 2017, 114, 189-198.	1.2	18
2204	Unexpected genomic features in widespread intracellular bacteria: evidence for motility of marine chlamydiae. <i>ISME Journal</i> , 2017, 11, 2334-2344.	4.4	34
2205	Morphology and molecular phylogeny of Trentepohliales (Chlorophyta) from China. <i>European Journal of Phycology</i> , 2017, 52, 330-341.	0.9	19
2206	Genome-wide analyses of <i>Listeria monocytogenes</i> from food-processing plants reveal clonal diversity and date the emergence of persisting sequence types. <i>Environmental Microbiology Reports</i> , 2017, 9, 428-440.	1.0	54
2207	A contaminant DNA barcode sequence reveals a new red algal order, Corynodactylales (Nemaliophycidae, Florideophyceae). <i>Botany</i> , 2017, 95, 561-566.	0.5	4
2208	Declines in plant palatability from polar to tropical latitudes depend on herbivore and plant identity. <i>Ecology</i> , 2017, 98, 2312-2321.	1.5	14
2209	A Phylogenomic Solution to the Origin of Insects by Resolving Crustacean-Hexapod Relationships. <i>Current Biology</i> , 2017, 27, 1818-1824.e5.	1.8	156
2210	High metabolic versatility of different toxigenic and non-toxigenic <i>Clostridioides difficile</i> isolates. <i>International Journal of Medical Microbiology</i> , 2017, 307, 311-320.	1.5	67
2211	Spatiotemporal dynamics of influenza A(H1N1)pdm09 in Brazil during the pandemic and post-pandemic periods. <i>Virus Research</i> , 2017, 238, 69-74.	1.1	2
2212	<i>Crenothrix</i> are major methane consumers in stratified lakes. <i>ISME Journal</i> , 2017, 11, 2124-2140.	4.4	146
2213	Functional and phylogenetic evidence of a bacterial origin for the first enzyme in sphingolipid biosynthesis in a phylum of eukaryotic protozoan parasites. <i>Journal of Biological Chemistry</i> , 2017, 292, 12208-12219.	1.6	20
2214	The complete chloroplast genome sequence of <i>Melastoma candidum</i> (Melastomataceae). <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 242-243.	0.2	24
2215	High-throughput sequencing of microbial eukaryotes in Lake Baikal reveals ecologically differentiated communities and novel evolutionary radiations. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	1.3	35
2216	Phylogenomic Synteny Network Analysis of MADS-Box Transcription Factor Genes Reveals Lineage-Specific Transpositions, Ancient Tandem Duplications, and Deep Positional Conservation. <i>Plant Cell</i> , 2017, 29, 1278-1292.	3.1	106
2217	Quantitative biogeography of picoprasinophytes establishes ecotype distributions and significant contributions to marine phytoplankton. <i>Environmental Microbiology</i> , 2017, 19, 3219-3234.	1.8	38
2218	Analysis of chloroplast genomes and a supermatrix inform reclassification of the Rhodomelaceae (Rhodophyta). <i>Journal of Phycology</i> , 2017, 53, 920-937.	1.0	58

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2219	The protein subunit of telomerase displays patterns of dynamic evolution and conservation across different metazoan taxa. <i>BMC Evolutionary Biology</i> , 2017, 17, 107.	3.2	22
2220	Reducing the information gap on Loricarioidei (Siluriformes) mitochondrial genomics. <i>BMC Genomics</i> , 2017, 18, 345.	1.2	12
2221	Parallel Evolution of Metazoan Mitochondrial Proteins. <i>Genome Biology and Evolution</i> , 2017, 9, 1341-1350.	1.1	23
2222	Spatio-temporal evolution of <i>Allium</i> L. in the Qinghai-Tibet-Plateau region: Immigration and in situ radiation. <i>Plant Diversity</i> , 2017, 39, 167-179.	1.8	34
2223	Purifying selection and concerted evolution of RNA-sensing toll-like receptors in migratory waders. <i>Infection, Genetics and Evolution</i> , 2017, 53, 135-145.	1.0	15
2224	Evolutionary and ecological forces influencing population diversification in Bornean montane passerines. <i>Molecular Phylogenetics and Evolution</i> , 2017, 113, 139-149.	1.2	9
2225	Another look at the phylogenetic relationships and intercontinental biogeography of eastern Asian and North American <i>Rhus</i> gall aphids (Hemiptera: Aphididae: Eriosomatinae): Evidence from mitogenome sequences via genome skimming. <i>Molecular Phylogenetics and Evolution</i> , 2017, 117, 102-110.	1.2	32
2226	Comparative genomic analysis of innate immunity reveals novel and conserved components in crustacean food crop species. <i>BMC Genomics</i> , 2017, 18, 389.	1.2	37
2227	Examination of species delimitation of ambiguous DNA-based <i>Ulva</i> (Ulvophyceae, Chlorophyta) clades by culturing and hybridisation. <i>Phycologia</i> , 2017, 56, 517-532.	0.6	22
2228	Tropical specialist vs. climate generalist: Diversification and demographic history of sister species of <i>Carlia</i> skinks from northwestern Australia. <i>Molecular Ecology</i> , 2017, 26, 4045-4058.	2.0	25
2229	A combined morphological and molecular approach to <i>Nitzschia varelae</i> sp. nov., with discussion of symmetry in Bacillariaceae. <i>European Journal of Phycology</i> , 2017, 52, 342-359.	0.9	18
2230	Herbicide targets and detoxification proteins in sugarcane: from gene assembly to structure modelling. <i>Genome</i> , 2017, 60, 601-617.	0.9	3
2231	HIV-1 Full-Genome Phylogenetics of Generalized Epidemics in Sub-Saharan Africa: Impact of Missing Nucleotide Characters in Next-Generation Sequences. <i>AIDS Research and Human Retroviruses</i> , 2017, 33, 1083-1098.	0.5	18
2232	Plastid and Seed Morphology Data Support a Revised Infrageneric Classification and an African Origin of the Pantropical Genus <i>Xylopia</i> (Annonaceae). <i>Systematic Botany</i> , 2017, 42, 211-225.	0.2	16
2233	Ten new species of <i>Macalpinomyces</i> in northern Australia. <i>Mycologia</i> , 2017, 109, 408-421.	0.8	5
2234	Flexible ammonia handling strategies using both cutaneous and branchial epithelia in the highly ammonia-tolerant Pacific hagfish. <i>American Journal of Physiology - Regulatory Integrative and Comparative Physiology</i> , 2017, 313, R78-R90.	0.9	14
2235	Diversity and ecology of and biomineralization by magnetotactic bacteria. <i>Environmental Microbiology Reports</i> , 2017, 9, 345-356.	1.0	83
2236	The phylogeny and biogeography of <i>Hakea</i> (Proteaceae) reveals the role of biome shifts in a continental plant radiation. <i>Evolution; International Journal of Organic Evolution</i> , 2017, 71, 1928-1943.	1.1	60

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2237	The giant cryptic amphipod species of the subterranean genus <i>Niphargus</i> (Crustacea), Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 742	0.7	32
2238	A comprehensive phylogenetic analysis of copper transporting P _{1B} ATPases from bacteria of the <i>Rhizobiales</i> order uncovers multiplicity, diversity and novel taxonomic subtypes. <i>MicrobiologyOpen</i> , 2017, 6, e00452.	1.2	10
2239	Genome-Wide SNP Analysis Reveals Distinct Origins of <i>Trypanosoma evansi</i> and <i>Trypanosoma equiperdum</i> . <i>Genome Biology and Evolution</i> , 2017, 9, 1990-1997.	1.1	33
2240	Phylogenomics. , 2017, , .		47
2241	Phylogenetic Analyses. , 2017, , 143-172.		1
2242	Phylogeny and biogeography of the genus <i>Stevia</i> (Asteraceae: Eupatorieae): an example of diversification in the Asteraceae in the new world. <i>Journal of Plant Research</i> , 2017, 130, 953-972.	1.2	12
2243	Correlated evolutionary rates across genomic compartments in Annonaceae. <i>Molecular Phylogenetics and Evolution</i> , 2017, 114, 63-72.	1.2	13
2244	Phylogenomic analysis of Lake Malawi cichlid fishes: Further evidence that the three-stage model of diversification does not fit. <i>Molecular Phylogenetics and Evolution</i> , 2017, 114, 40-48.	1.2	14
2245	Isothermal Amplification and Lateral-Flow Assay for Detecting Crown-Gall-Causing <i>Agrobacterium</i> spp.. <i>Phytopathology</i> , 2017, 107, 1062-1068.	1.1	24
2246	<i>Laurencia majuscula</i> var. <i>elegans</i> (Rhodophyta, Rhodomelaceae) is reinstated to specific rank as <i>L. elegans</i> . <i>Phycological Research</i> , 2017, 65, 127-135.	0.8	2
2247	Nearly complete mitogenome of hairy sawfly, <i>Corynis lateralis</i> (Brullé, 1832) (Hymenoptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 34	0.5	12
2248	Morphological and molecular characterisation of a new genus and new species of Parabathynellidae (Crustacea : Syncarida) in Queensland, Australia. <i>Invertebrate Systematics</i> , 2017, 31, 208.	0.5	6
2249	A phylogenetic framework for the kingdom Fungi based on 18S rRNA gene sequences. <i>Marine Genomics</i> , 2017, 36, 33-39.	0.4	47
2250	Ubiquity and quantitative significance of bacterioplankton lineages inhabiting the oxygenated hypolimnion of deep freshwater lakes. <i>ISME Journal</i> , 2017, 11, 2279-2293.	4.4	75
2251	High quality permanent draft genome sequence of <i>Chryseobacterium bovis</i> DSM 19482T, isolated from raw cow milk. <i>Standards in Genomic Sciences</i> , 2017, 12, 31.	1.5	2
2252	Plant Argonaute Proteins. <i>Methods in Molecular Biology</i> , 2017, , .	0.4	1
2253	Spatial mixing of mitochondrial lineages and greater genetic diversity in some invasive populations of the American mink (<i>Neovison vison</i>) compared to native populations. <i>Biological Invasions</i> , 2017, 19, 2663-2673.	1.2	10
2254	Excess of non-conservative amino acid changes in marine bacterioplankton lineages with reduced genomes. <i>Nature Microbiology</i> , 2017, 2, 17091.	5.9	41

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2255	<i>Bryoerythrophyllum duellii</i> Blockeel (Bryophyta: Pottiaceae), a new moss species from Greece and Cyprus, and its molecular affinities. <i>Journal of Bryology</i> , 2017, 39, 247-254.	0.4	9
2256	Extreme Mitogenomic Variation in Natural Populations of Chaetognaths. <i>Genome Biology and Evolution</i> , 2017, 9, 1374-1384.	1.1	21
2257	Ultraconserved elements show utility in phylogenetic inference of <i>Adephaga</i> (<i>Coleoptera</i>) and suggest paraphyly of "Hydradephaga" TM . <i>Systematic Entomology</i> , 2017, 42, 786-795.	1.7	77
2258	Species boundaries in the human pathogen <i>Paracoccidioides</i> . <i>Fungal Genetics and Biology</i> , 2017, 106, 9-25.	0.9	228
2259	Species boundaries in the <i>Astragalus cusickii</i> complex delimited using molecular phylogenetic techniques. <i>Molecular Phylogenetics and Evolution</i> , 2017, 114, 93-110.	1.2	5
2260	STELLS2: fast and accurate coalescent-based maximum likelihood inference of species trees from gene tree topologies. <i>Bioinformatics</i> , 2017, 33, 1789-1797.	1.8	14
2261	Genetic Structure and Phylogeography of the Leopard Cat (<i>Prionailurus bengalensis</i>) Inferred from Mitochondrial Genomes. <i>Journal of Heredity</i> , 2017, 108, 349-360.	1.0	31
2262	Purifying and Positive Selection Influence Patterns of Gene Loss and Gene Expression in the Evolution of a Plant Sex Chromosome System. <i>Molecular Biology and Evolution</i> , 2017, 34, 1140-1154.	3.5	50
2263	Identification and Evolutionary Characterization of ARGONAUTE-Binding Platforms. <i>Methods in Molecular Biology</i> , 2017, 1640, 257-266.	0.4	1
2264	The Near East as a cradle of biodiversity: A phylogeography of banded newts (genus <i>Ommatotriton</i>) reveals extensive inter- and intraspecific genetic differentiation. <i>Molecular Phylogenetics and Evolution</i> , 2017, 114, 73-81.	1.2	37
2265	Selective depletion of uropathogenic <i>E. coli</i> from the gut by a FimH antagonist. <i>Nature</i> , 2017, 546, 528-532.	13.7	231
2266	Parallel implementation of D ₂ Phylo algorithm for maximum likelihood clusters. <i>IET Nanobiotechnology</i> , 2017, 11, 134-142.	1.9	1
2267	Antagonistic interactions of soil pseudomonads are structured in time. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	1.3	11
2268	Feeding characteristics and molecular phylogeny of the thecate mixotrophic dinoflagellate <i>Fragilidium mexicanum</i> . <i>Harmful Algae</i> , 2017, 63, 154-163.	2.2	4
2269	Clock-dated phylogeny for 48% of the 700 species of <i>Crotalaria</i> (Fabaceae "Papilionoideae) resolves sections worldwide and implies conserved flower and leaf traits throughout its pantropical range. <i>BMC Evolutionary Biology</i> , 2017, 17, 61.	3.2	8
2270	Diversity and evolution of plastomes in Saharan mimosoids: potential use for phylogenetic and population genetic studies. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	10
2271	Novel antigenic shift in HA sequences of H1N1 viruses detected by big data analysis. <i>Infection, Genetics and Evolution</i> , 2017, 51, 138-142.	1.0	5
2272	Organelles that illuminate the origins of <i>Trichomonas</i> hydrogenosomes and <i>Giardia</i> mitosomes. <i>Nature Ecology and Evolution</i> , 2017, 1, 0092.	3.4	90

#	ARTICLE	IF	CITATIONS
2273	Genomic inferences of domestication events are corroborated by written records in <i>Brassica rapa</i> . <i>Molecular Ecology</i> , 2017, 26, 3373-3388.	2.0	66
2274	Molecular systematics of threadfin breams and relatives (Teleostei, Nemipteridae). <i>Zoologica Scripta</i> , 2017, 46, 536-551.	0.7	15
2275	<i>Frankia inefficax</i> sp. nov., an actinobacterial endophyte inducing ineffective, non nitrogen-fixing, root nodules on its actinorhizal host plants. <i>Antonie Van Leeuwenhoek</i> , 2017, 110, 313-320.	0.7	48
2276	Characterization of <i>Phaeoacremonium</i> isolates associated with Petri disease of table grape in Northeastern Brazil, with description of <i>Phaeoacremonium nordesticola</i> sp. nov.. <i>European Journal of Plant Pathology</i> , 2017, 149, 695-709.	0.8	18
2277	Phylogenomic Insights into the Evolution of Stinging Wasps and the Origins of Ants and Bees. <i>Current Biology</i> , 2017, 27, 1019-1025.	1.8	329
2278	Young inversion with multiple linked QTLs under selection in a hybrid zone. <i>Nature Ecology and Evolution</i> , 2017, 1, 119.	3.4	94
2279	Morphological and Molecular Identification of the Invasive <i>Xylosandrus crassiusculus</i> (Coleoptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 Annals of the Entomological Society of America, 2017, 110, 344-349.	1.3	23
2280	Phylogenomic Systematics of Ostariophysan Fishes: Ultraconserved Elements Support the Surprising Non-Monophyly of Characiformes. <i>Systematic Biology</i> , 2017, 66, 881-895.	2.7	74
2281	Why Do Phylogenomic Data Sets Yield Conflicting Trees? Data Type Influences the Avian Tree of Life more than Taxon Sampling. <i>Systematic Biology</i> , 2017, 66, 857-879.	2.7	242
2282	Molecular phylogeny of Didemnidae (Ascidiacea: Tunicata). <i>Zoological Journal of the Linnean Society</i> , 2017, 180, 603-612.	1.0	16
2283	Adaptive sequence evolution is driven by biotic stress in a pair of orchid species (<i>Dactylorhiza</i>) with distinct ecological optima. <i>Molecular Ecology</i> , 2017, 26, 3649-3662.	2.0	25
2284	Intra- and interspecific genetic diversity of New Zealand hairworms (Nematomorpha). <i>Parasitology</i> , 2017, 144, 1026-1040.	0.7	14
2285	Niche partitioning of diverse sulfur-oxidizing bacteria at hydrothermal vents. <i>ISME Journal</i> , 2017, 11, 1545-1558.	4.4	168
2286	A Nonsynonymous SNP Catalog of <i>Mycobacterium tuberculosis</i> Virulence Genes and Its Use for Detecting New Potentially Virulent Sublineages. <i>Genome Biology and Evolution</i> , 2017, 9, 887-899.	1.1	37
2287	Origin and Evolutionary Alteration of the Mitochondrial Import System in Eukaryotic Lineages. <i>Molecular Biology and Evolution</i> , 2017, 34, 1574-1586.	3.5	52
2288	The Influence of HIV on the Evolution of <i>Mycobacterium tuberculosis</i> . <i>Molecular Biology and Evolution</i> , 2017, 34, 1654-1668.	3.5	27
2289	Use of municipal solid wastes for chemical and microbiological recovery of soils contaminated with metal(loid)s. <i>Soil Biology and Biochemistry</i> , 2017, 111, 25-35.	4.2	47
2290	Deep reticulation and incomplete lineage sorting obscure the diploid phylogeny of rain-lilies and allies (Amaryllidaceae tribe Hippeastreae). <i>Molecular Phylogenetics and Evolution</i> , 2017, 111, 231-247.	1.2	88

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2291	Convergent Reversion to Single Mating in a Wasp Social Parasite. <i>American Naturalist</i> , 2017, 189, E138-E151.	1.0	6
2292	Phenotypic diversity and genotypic flexibility of <i>Burkholderia cenocepacia</i> during long-term chronic infection of cystic fibrosis lungs. <i>Genome Research</i> , 2017, 27, 650-662.	2.4	64
2293	Grass plastomes reveal unexpected paraphyly with endemic species of Micraioideae from India and new haplotype markers in Arundinoideae. <i>American Journal of Botany</i> , 2017, 104, 286-295.	0.8	9
2294	Sequential displacement of Type VI Secretion System effector genes leads to evolution of diverse immunity gene arrays in <i>Vibrio cholerae</i> . <i>Scientific Reports</i> , 2017, 7, 45133.	1.6	90
2295	Conflicting phylogenomic signals reveal a pattern of reticulate evolution in a recent high-Andean diversification (Asteraceae: Astereae: <i>Diplostephium</i>). <i>New Phytologist</i> , 2017, 214, 1736-1750.	3.5	201
2296	Evolution of group I introns in Porifera: new evidence for intron mobility and implications for DNA barcoding. <i>BMC Evolutionary Biology</i> , 2017, 17, 82.	3.2	33
2297	Whence river blindness? The domestication of mammals and host-parasite co-evolution in the nematode genus <i>Onchocerca</i> . <i>International Journal for Parasitology</i> , 2017, 47, 457-470.	1.3	36
2298	On the importance of geographic and taxonomic sampling in phylogeography: A reevaluation of diversification and species limits in a Neotropical thrush (Aves, Turdidae). <i>Molecular Phylogenetics and Evolution</i> , 2017, 111, 87-97.	1.2	23
2299	Characterization of the complete chloroplast genome of <i>Xanthoceras sorbifolium</i> , an endangered oil tree. <i>Conservation Genetics Resources</i> , 2017, 9, 595-598.	0.4	6
2300	Comparative genomics of <i>Vibrio campbellii</i> strains and core species of the <i>Vibrio Harveyi</i> clade. <i>Scientific Reports</i> , 2017, 7, 41394.	1.6	42
2301	Decay of the glycolytic pathway and adaptation to intranuclear parasitism within Enterocytozoonidae microsporidia. <i>Environmental Microbiology</i> , 2017, 19, 2077-2089.	1.8	74
2302	Systematics of the genus <i>Halimeda</i> (Bryopsidales, Chlorophyta) in Brazil including the description of <i>Halimeda jolyana</i> sp. nov. <i>Phycologia</i> , 2017, 56, 369-381.	0.6	6
2303	Ancestral Protein Reconstruction and Circular Permutation for Improving the Stability and Dynamic Range of FRET Sensors. <i>Methods in Molecular Biology</i> , 2017, 1596, 71-87.	0.4	9
2304	Genome-wide data delimits multiple climate-determined species ranges in a widespread Australian fish, the golden perch (<i>Macquaria ambigua</i>). <i>Molecular Phylogenetics and Evolution</i> , 2017, 111, 65-75.	1.2	42
2305	Macrocycle peptides delineate locked-open inhibition mechanism for microorganism phosphoglycerate mutases. <i>Nature Communications</i> , 2017, 8, 14932.	5.8	41
2306	Origin and Evolution of the Kiwifruit Canker Pandemic. <i>Genome Biology and Evolution</i> , 2017, 9, 932-944.	1.1	106
2307	Gene Tree Discordance Does Not Explain Away the Temporal Decline of Convergence in Mammalian Protein Sequence Evolution. <i>Molecular Biology and Evolution</i> , 2017, 34, 1682-1688.	3.5	10
2308	New insights into Plutonium, one of the largest and least known European centipedes (Chilopoda): distribution, evolution and morphology. <i>Zoological Journal of the Linnean Society</i> , 2017, 180, 887-909.	1.0	4

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2309	KNOTTED1 Cofactors, BLH12 and BLH14, Regulate Internode Patterning and Vein Anastomosis in Maize. <i>Plant Cell</i> , 2017, 29, 1105-1118.	3.1	64
2310	The taxonomic status of two <i>Telmatobius</i> frog species (Anura: Telmatobiidae) from the western Andean slopes of northernmost Chile. <i>Zootaxa</i> , 2017, 4250, 301-314.	0.2	8
2311	The complete chloroplast genome of wild shaddock, <i>Citrus maxima</i> (Burm.) Merr.. <i>Conservation Genetics Resources</i> , 2017, 9, 599-601.	0.4	2
2312	Using relatedness networks to infer contemporary dispersal: Application to the endangered mammal <i>Galemys pyrenaicus</i> . <i>Molecular Ecology</i> , 2017, 26, 3343-3357.	2.0	30
2313	High-quality genome assembly of <i>Capsella bursa-pastoris</i> reveals asymmetry of regulatory elements at early stages of polyploid genome evolution. <i>Plant Journal</i> , 2017, 91, 278-291.	2.8	40
2314	A Genome-Scale Model of <i>Shewanella piezotolerans</i> Simulates Mechanisms of Metabolic Diversity and Energy Conservation. <i>MSystems</i> , 2017, 2, .	1.7	14
2315	Carbon dating cancer: defining the chronology of metastatic progression in colorectal cancer. <i>Annals of Oncology</i> , 2017, 28, 1243-1249.	0.6	25
2316	Diversity of fungus-growing termites (<i>Macrotermes</i>) and their fungal symbionts (<i>Termitomyces</i>) in the semi-arid Tsavo Ecosystem, Kenya. <i>Biotropica</i> , 2017, 49, 402-412.	0.8	21
2317	Evolution of the endomembrane systems of trypanosomatids: conservation and specialisation. <i>Journal of Cell Science</i> , 2017, 130, 1421-1434.	1.2	23
2318	When different contact zones tell different stories: putative ring species in the <i>Megachile concinna</i> species complex (Hymenoptera: Megachilidae). <i>Biological Journal of the Linnean Society</i> , 2017, 121, 815-832.	0.7	18
2319	A Pan-Genomic Approach to Understand the Basis of Host Adaptation in <i>Achromobacter</i> . <i>Genome Biology and Evolution</i> , 2017, 9, 1030-1046.	1.1	40
2320	A phylogenomic perspective on the biogeography of skinks in the <i>Plestiodon brevirostris</i> group inferred from target enrichment of ultraconserved elements. <i>Journal of Biogeography</i> , 2017, 44, 2033-2044.	1.4	24
2321	Mitochondrial genome of the nematode endoparasitic fungus <i>Hirsutella vermicola</i> reveals a high level of synteny in the family Ophiocordycipitaceae. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 3295-3304.	1.7	55
2322	The complete mitochondrial genome of <i>Etheostoma okaloosae</i> (Perciformes: Percidae). <i>Conservation Genetics Resources</i> , 2017, 9, 591-593.	0.4	1
2323	Using phylogenomics to understand the link between biogeographic origins and regional diversification in ratsnakes. <i>Molecular Phylogenetics and Evolution</i> , 2017, 111, 206-218.	1.2	36
2324	Molecular phylogenetics and historical biogeography of <i>Sorbus sensu stricto</i> (Rosaceae). <i>Molecular Phylogenetics and Evolution</i> , 2017, 111, 76-86.	1.2	27
2325	Genomic characterization of Nontuberculous Mycobacteria. <i>Scientific Reports</i> , 2017, 7, 45258.	1.6	176
2326	Molecular phylogenetic diversity in the widespread lizard <i>Cercosaura ocellata</i> (Reptilia: Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.5	5

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2327	All roads lead to weediness: Patterns of genomic divergence reveal extensive recurrent weedy rice origins from South Asian <i>Oryza</i> . <i>Molecular Ecology</i> , 2017, 26, 3151-3167.	2.0	51
2328	Convergent adaptation to dangerous prey proceeds through the same first-step mutation in the garter snake <i>Thamnophis sirtalis</i> . <i>Evolution; International Journal of Organic Evolution</i> , 2017, 71, 1504-1518.	1.1	22
2329	Dynamic microbiome evolution in social bees. <i>Science Advances</i> , 2017, 3, e1600513.	4.7	349
2330	Phylogenomic inferences from reference-mapped and de novo assembled short-read sequence data using RADseq sequencing of California white oaks (<i>Quercus</i> section <i>Quercus</i>). <i>Genome</i> , 2017, 60, 743-755.	0.9	50
2331	The influence of O ₂ availability and Fe(III) mineralogy on Fe metabolism by an acidophilic bacterial culture. <i>Chemical Geology</i> , 2017, 457, 107-117.	1.4	5
2332	A phylogeny of open-habitat lizards (Squamata: Lacertidae: <i>Ophisops</i>) supports the antiquity of Indian grassy biomes. <i>Journal of Biogeography</i> , 2017, 44, 2021-2032.	1.4	36
2333	Phylogenomic analysis of <i>Picramnia</i> , <i>Alvaradoa</i> , and <i>Leitneria</i> supports the independent Picramniales. <i>Journal of Systematics and Evolution</i> , 2017, 55, 171-176.	1.6	7
2334	Molecular taxonomy and morphological characterization reveal new species and new host records of <i>Torula</i> species (Torulaceae, Pleosporales). <i>Mycological Progress</i> , 2017, 16, 447-461.	0.5	22
2335	Saprobic Dothideomycetes in Thailand: <i>Neoquastroma</i> gen. nov. (Parabambusicolaceae) introduced based on morphological and molecular data. <i>Phytotaxa</i> , 2017, 302, 133.	0.1	11
2336	An integrative systematic framework helps to reconstruct skeletal evolution of glass sponges (Porifera, Hexactinellida). <i>Frontiers in Zoology</i> , 2017, 14, 18.	0.9	25
2337	Reduction of antinutritional glucosinolates in Brassica oilseeds by mutation of genes encoding transporters. <i>Nature Biotechnology</i> , 2017, 35, 377-382.	9.4	84
2338	Microevolution of Serial Clinical Isolates of <i>Cryptococcus neoformans</i> var. <i>grubii</i> and <i>C. Gattii</i> . <i>MBio</i> , 2017, 8, .	1.8	69
2339	<i>Entoloma chamaemori</i> (Entolomataceae, Basidiomycota) a new boreal species, with isolated phylogenetic position. <i>Phytotaxa</i> , 2017, 298, 289.	0.1	6
2340	Phylogeny, classification and diversity of <i>Choreotrichia</i> and <i>Oligotrichia</i> (Ciliophora, Spirotrichea). <i>Molecular Phylogenetics and Evolution</i> , 2017, 112, 12-22.	1.2	53
2341	The assembly of ant-farmed gardens: mutualism specialization following host broadening. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20161759.	1.2	26
2342	The acacia ants revisited: convergent evolution and biogeographic context in an iconic ant/plant mutualism. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20162569.	1.2	49
2343	Taxonomy-free molecular diatom index for high-throughput eDNA biomonitoring. <i>Molecular Ecology Resources</i> , 2017, 17, 1231-1242.	2.2	140
2344	Phylogenetic systematics of <i>Syncephalis</i> (Zoopagales, Zoopagomycotina), a genus of ubiquitous mycoparasites. <i>Mycologia</i> , 2017, 109, 333-349.	0.8	20

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2345	Plasmid diversity and phylogenetic consistency in the Lyme disease agent <i>Borrelia burgdorferi</i> . <i>BMC Genomics</i> , 2017, 18, 165.	1.2	72
2346	Phylogenetic analyses of Chaetopteridae (Annelida). <i>Zoologica Scripta</i> , 2017, 46, 596-610.	0.7	10
2347	The complete chloroplast genome of the endangered Chinese paperbark maple, <i>Acer griseum</i> (Sapindaceae). <i>Conservation Genetics Resources</i> , 2017, 9, 527-529.	0.4	13
2348	Based on DNA sequences of ITS and rpb 2, <i>Amylostereum orientale</i> is reported for the first time in Japan. <i>Mycoscience</i> , 2017, 58, 169-173.	0.3	1
2349	Species delimitation and phylogenetic reconstruction of the sinipercids (Perciformes: Siniperidae) based on target enrichment of thousands of nuclear coding sequences. <i>Molecular Phylogenetics and Evolution</i> , 2017, 111, 44-55.	1.2	33
2350	Phylogenetic analysis of proteins involved in the stringent response in plant cells. <i>Journal of Plant Research</i> , 2017, 130, 625-634.	1.2	31
2351	Characterization of the complete chloroplast genome of <i>Carpinus tientaiensis</i> . <i>Conservation Genetics Resources</i> , 2017, 9, 339-341.	0.4	5
2352	Molecular phylogeny and taxonomic revision of the genus <i>Wittrockiella</i> (Pithophoraceae, Tj ETQq1 1 0.784314 rgBT /Overlock 1 nov.. <i>Journal of Phycology</i> , 2017, 53, 522-540.	1.0	4
2353	Museum archives revisited: Central Asiatic hawkmoths reveal exceptionally high late Pliocene species diversification (Lepidoptera, Sphingidae). <i>Zoologica Scripta</i> , 2017, 46, 552-570.	0.7	15
2354	A New Species of Cotton from Wake Atoll, <i>Gossypium stephensii</i> (Malvaceae). <i>Systematic Botany</i> , 2017, 42, 115-123.	0.2	94
2355	Parasites dominate hyperdiverse soil protist communities in Neotropical rainforests. <i>Nature Ecology and Evolution</i> , 2017, 1, 91.	3.4	262
2356	<i>Metschnikowia</i> cf. <i>typographi</i> and other pathogens from the bark beetle <i>Ips sexdentatus</i> – Prevalence, histological and ultrastructural evidence, and molecular characterization. <i>Journal of Invertebrate Pathology</i> , 2017, 143, 69-78.	1.5	2
2357	The apicoplast genomes of two taxonomic units of <i>Babesia</i> from sheep. <i>Veterinary Parasitology</i> , 2017, 233, 123-128.	0.7	10
2358	Reconstruction of molecular phylogeny of closely related <i>Amorphophallus</i> species of India using plastid DNA marker and fingerprinting approaches. <i>Physiology and Molecular Biology of Plants</i> , 2017, 23, 155-167.	1.4	12
2359	Integrative data helps the assessment of a butterfly within the <i>Udranomia kikkawai</i> species complex (Lepidoptera: Hesperidae): Immature stages, natural history, and molecular evidence. <i>Zoologischer Anzeiger</i> , 2017, 266, 169-176.	0.4	4
2360	Exploring the shell-based taxonomy of the Sri Lankan land snail <i>Corilla</i> H. and A. Adams, 1855 (Pulmonata: Corillidae) using mitochondrial DNA. <i>Molecular Phylogenetics and Evolution</i> , 2017, 107, 609-618.	1.2	6
2361	Revising the phylogenetic position of the extinct Mascarene Parrot <i>Mascarinus mascarin</i> (Linnaeus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.2	5
2362	New CRISPR-Cas systems from uncultivated microbes. <i>Nature</i> , 2017, 542, 237-241.	13.7	471

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2363	Comparative genomics provides a timeframe for Wolbachia evolution and exposes a recent biotin synthesis operon transfer. <i>Nature Microbiology</i> , 2017, 2, 16241.	5.9	113
2364	Functional relatedness in the Inv/Mxi- ϵ spa type III secretion system family. <i>Molecular Microbiology</i> , 2017, 103, 973-991.	1.2	11
2365	Geographical structure, narrow species ranges, and Cenozoic diversification in a pantropical clade of epiphyllous leafy liverworts. <i>Ecology and Evolution</i> , 2017, 7, 638-653.	0.8	37
2366	Supermatrix phylogeny and biogeography of the Australasian Meliphagides radiation (Aves: Tj ETQq1 1 0.784314 rgBT / Overlock 10 Tf 50 502 Td	1.2	77
2367	Systematics and biogeography of the <i>Automolus infuscatus</i> complex (Aves; Furnariidae): Cryptic diversity reveals western Amazonia as the origin of a transcontinental radiation. <i>Molecular Phylogenetics and Evolution</i> , 2017, 107, 503-515.	1.2	22
2368	Elucidation of the first definitively identified life cycle for a marine turtle blood fluke (Trematoda: Tj ETQq1 1 0.784314 rgBT / Overlock 1	1.3	38
2369	Multilocus and multiregional phylogeny reconstruction of the genus <i>Sarcophaga</i> (Diptera,) Tj ETQq0 0 0 rgBT / Overlock 10 Tf 50 502 Td	1.2	22
2370	Molecular determination of kleptoplast origins from the sea slug <i>Plakobranthus ocellatus</i> (Sacoglossa, Gastropoda) reveals cryptic bryopsidalean (Chlorophyta) diversity in the Hawaiian Islands. <i>Journal of Phycology</i> , 2017, 53, 467-475.	1.0	20
2371	By how much do we underestimate species diversity of liverworts using morphological evidence? An example from Australasian <i>Plagiochila</i> (Plagiochilaceae: Jungermanniopsida). <i>Molecular Phylogenetics and Evolution</i> , 2017, 107, 576-593.	1.2	52
2372	Community structure of fern-affiliated endophytes in three neotropical forests. <i>Journal of Tropical Ecology</i> , 2017, 33, 60-73.	0.5	18
2373	Mitochondrial phylogenomics illuminates the evolutionary history of Neuropterida. <i>Cladistics</i> , 2017, 33, 617-636.	1.5	117
2374	Global phylogeography of <i>Oithona similis</i> s.l. (Crustacea, Copepoda, Oithonidae) – A cosmopolitan plankton species or a complex of cryptic lineages?. <i>Molecular Phylogenetics and Evolution</i> , 2017, 107, 473-485.	1.2	49
2375	Genome sequence and genetic diversity of European ash trees. <i>Nature</i> , 2017, 541, 212-216.	18.7	166
2376	Phylogeny and biogeography of the genus <i>Cephalenchus</i> (Tylenchomorpha, Nematoda). <i>Zoologica Scripta</i> , 2017, 46, 506-520.	0.7	10
2377	<i>Burkholderia humptydoensis</i> sp. nov., a New Species Related to <i>Burkholderia thailandensis</i> and the Fifth Member of the <i>Burkholderia pseudomallei</i> Complex. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	45
2378	Emergence of Ceftazidime-Avibactam Resistance Due to Plasmid-Borne bla _{KPC-3} Mutations during Treatment of Carbapenem-Resistant <i>Klebsiella pneumoniae</i> Infections. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	334
2379	Population genetic structure of Grauer's Swamp Warbler <i>Bradypterus graueri</i> , an Albertine Rift endemic. <i>Ibis</i> , 2017, 159, 415-429.	1.0	36
2380	Two for one: inadvertent introduction of <i>Euglandina</i> species during failed bio-control efforts in Hawaii. <i>Biological Invasions</i> , 2017, 19, 1399-1405.	1.2	20

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2381	Comparative Genome Analysis and Global Phylogeny of the Toxin Variant <i>Clostridium difficile</i> PCR Ribotype 017 Reveals the Evolution of Two Independent Sublineages. <i>Journal of Clinical Microbiology</i> , 2017, 55, 865-876.	1.8	50
2382	Ancient and Recent Duplications Support Functional Diversity of <i>Daphnia</i> Opsins. <i>Journal of Molecular Evolution</i> , 2017, 84, 12-28.	0.8	14
2383	First plastid phylogenomic study reveals potential cyto-nuclear discordance in the evolutionary history of <i>Ficus</i> L. (Moraceae). <i>Molecular Phylogenetics and Evolution</i> , 2017, 109, 93-104.	1.2	75
2384	Characterization of the complete chloroplast genome of <i>Camptotheca acuminata</i> . <i>Conservation Genetics Resources</i> , 2017, 9, 241-243.	0.4	5
2385	Characterization of <i>CYCLOIDEA</i> -like genes in Proteaceae, a basal eudicot family with multiple shifts in floral symmetry. <i>Annals of Botany</i> , 2017, 119, 367-378.	1.4	37
2386	Asynchronous Non-Generational Model to Parallelize Metaheuristics: A Bioinformatics Case Study. <i>IEEE Transactions on Parallel and Distributed Systems</i> , 2017, 28, 1825-1838.	4.0	7
2387	Complete gene sequence of spider attachment silk protein (PySp1) reveals novel linker regions and extreme repeat homogenization. <i>Insect Biochemistry and Molecular Biology</i> , 2017, 81, 80-90.	1.2	48
2388	Prospective use of whole genome sequencing (WGS) detected a multi-country outbreak of <i>Salmonella</i> Enteritidis. <i>Epidemiology and Infection</i> , 2017, 145, 289-298.	1.0	106
2389	Steppingâ€stones across space and time: repeated radiation of Pacific flightless broadâ€nosed weevils (Coleoptera: Curculionidae: Entiminae: <i>Rhyncogonus</i>). <i>Journal of Biogeography</i> , 2017, 44, 784-796.	1.4	17
2390	Arbuscular mycorrhizal fungal community composition is altered by longâ€term litter removal but not litter addition in a lowland tropical forest. <i>New Phytologist</i> , 2017, 214, 455-467.	3.5	45
2391	A molecular approach to arthrotardigrade phylogeny (Heterotardigrada, Tardigrada). <i>Zoologica Scripta</i> , 2017, 46, 496-505.	0.7	30
2392	Insidious Risk of Severe <i>Mycobacterium chimaera</i> Infection in Cardiac Surgery Patients. <i>Clinical Infectious Diseases</i> , 2017, 64, 335-342.	2.9	129
2393	In the shadows: Phylogenomics and coalescent species delimitation unveil cryptic diversity in a Cerrado endemic lizard (Squamata: Tropicurus). <i>Molecular Phylogenetics and Evolution</i> , 2017, 107, 455-465.	1.2	37
2394	Improved sampling at the subspecies level solves a taxonomic dilemma â€“ A case study of two enigmatic Chinese tit species (Aves, Passeriformes, Paridae, Poecile). <i>Molecular Phylogenetics and Evolution</i> , 2017, 107, 538-550.	1.2	13
2395	<i>Hyperspora aquatica</i> n.g.n., n.sp. (Microsporidia), hyperparasitic in <i>Marteilia cochillia</i> (Paramyxida), is closely related to crustacean-infecting microsporidian taxa. <i>Parasitology</i> , 2017, 144, 186-199.	0.7	34
2396	Searching for the glacial refugia of <i>Erebia euryale</i> (Lepidoptera, Nymphalidae) - insights from mtDNA- and nDNA-based phylogeography in the Western Carpathians. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2017, 55, 118-128.	0.6	4
2397	Novel DNA coding regions and protein arginylation reveal unexplored <i>T. cruzi</i> proteome and PTMs. <i>International Journal of Mass Spectrometry</i> , 2017, 418, 51-66.	0.7	4
2398	Outbreak of <i>Klebsiella pneumoniae</i> Carbapenemaseâ€Producing <i>Citrobacter freundii</i> at a Tertiary Acute Care Facility in Miami, Florida. <i>Infection Control and Hospital Epidemiology</i> , 2017, 38, 320-326.	1.0	21

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2399	Diverse manganese(II)-oxidizing bacteria are prevalent in drinking water systems. <i>Environmental Microbiology Reports</i> , 2017, 9, 120-128.	1.0	52
2400	The spider tree of life: phylogeny of Araneae based on targeted gene analyses from an extensive taxon sampling. <i>Cladistics</i> , 2017, 33, 574-616.	1.5	341
2401	Can functional traits account for phylogenetic signal in community composition?. <i>New Phytologist</i> , 2017, 214, 607-618.	3.5	39
2402	Phylogeographic patterns of a lower intertidal isopod in the Gulf of California and the Caribbean and comparison with other intertidal isopods. <i>Ecology and Evolution</i> , 2017, 7, 346-357.	0.8	12
2403	Enzootic origins for clinical manifestations of Lyme borreliosis. <i>Infection, Genetics and Evolution</i> , 2017, 49, 48-54.	1.0	19
2404	Molecular phylogeny and morphological analysis resolve a long-standing controversy over generic concepts in <i>Ecdyonurinae</i> mayflies (<i>Ecdyonoptera</i> : <i>Hemiptera</i> : <i>Eptageniidae</i>). <i>Systematic Entomology</i> , 2017, 42, 182-193.	1.7	17
2405	Hitchhikers at the dinner table: a revisionary study of a group of ant parasitoids (<i>Hymenoptera</i> : <i>Eucharitidae</i>) specializing in the use of extrafloral nectaries for host access. <i>Systematic Entomology</i> , 2017, 42, 204-229.	1.7	12
2406	Multilocus molecular phylogeny of the ornamental wood-eating catfishes (<i>Siluriformes</i> , <i>Loricariidae</i>). <i>Tj ETQq1 1 0.784314 rgBT /Over</i> and <i>Evolution</i> , 2017, 109, 321-336.	1.2	15
2407	Phylogenetic Tools for Generalized HIV-1 Epidemics: Findings from the PANGEA-HIV Methods Comparison. <i>Molecular Biology and Evolution</i> , 2017, 34, 185-203.	3.5	53
2408	Identification of <i>Escherichia coli</i> and <i>Shigella</i> Species from Whole-Genome Sequences. <i>Journal of Clinical Microbiology</i> , 2017, 55, 616-623.	1.8	103
2409	Description of a new anaerobic thermophilic bacterium, <i>Thermoanaerobacterium butyriciformans</i> sp. nov.. <i>Systematic and Applied Microbiology</i> , 2017, 40, 86-91.	1.2	14
2410	Evolution of floral diversity: genomics, genes and γ . <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017, 372, 20150509.	1.8	41
2411	Molecular Phylogeny of <i>Paraphelidium letcheri</i> sp. nov. (<i>Aphelida</i> , <i>Opisthosporidia</i>). <i>Journal of Eukaryotic Microbiology</i> , 2017, 64, 573-578.	0.8	21
2412	From Eastern Arc Mountains to extreme sexual dimorphism: systematics of the enigmatic assassin bug genus <i>Xenocaucus</i> (<i>Hemiptera</i> : <i>Reduviidae</i> : <i>Tribelocephalinae</i>). <i>Organisms Diversity and Evolution</i> , 2017, 17, 421-445.	0.7	5
2413	Redescription and molecular phylogeny of the type species for two main metopid genera, <i>Metopus es</i> (Müller, 1776) <i>Lauterborn</i> , 1916 and <i>Brachonella contorta</i> (Levander, 1894) <i>Jankowski</i> , 1964 (<i>Metopida</i>). <i>Tj ETQq1 0 0 rgBT /Over</i>	0.5	8
2414	The phylogeny of <i>Heliconia</i> (<i>Heliconiaceae</i>) and the evolution of floral presentation. <i>Molecular Phylogenetics and Evolution</i> , 2017, 117, 150-167.	1.2	16
2415	Towards a multigene phylogeny of the <i>Cymatosiraceae</i> (<i>Bacillariophyta</i> , <i>Mediophyceae</i>) I: novel taxa within the subfamily <i>cymatosiroideae</i> based on molecular and morphological data. <i>Journal of Phycology</i> , 2017, 53, 342-360.	1.0	14
2416	Sybr Green- and TaqMan-Based Quantitative PCR Approaches Allow Assessment of the Abundance and Relative Distribution of <i>Frankia</i> Clusters in Soils. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	10

#	ARTICLE	IF	CITATIONS
2417	Phylogenetic relationships of Burmeistera (Campanulaceae: Lobelioideae): Combining whole plastome with targeted loci data in a recent radiation. <i>Molecular Phylogenetics and Evolution</i> , 2017, 107, 551-563.	1.2	31
2418	A Proposal for a Genome Similarity-Based Taxonomy for Plant-Pathogenic Bacteria that Is Sufficiently Precise to Reflect Phylogeny, Host Range, and Outbreak Affiliation Applied to <i>Pseudomonas syringae sensu lato</i> as a Proof of Concept. <i>Phytopathology</i> , 2017, 107, 18-28.	1.1	26
2419	Novel domain architectures and functional determinants in atypical annexins revealed by phylogenomic analysis. <i>Biological Chemistry</i> , 2017, 398, 751-763.	1.2	8
2420	The ultimate and proximate mechanisms driving the evolution of long tails in forest deer mice. <i>Evolution; International Journal of Organic Evolution</i> , 2017, 71, 261-273.	1.1	34
2421	In and out of the Qinghai-Tibet Plateau: divergence time estimation and historical biogeography of the large arctic-alpine genus <i>Saxifraga</i> L.. <i>Journal of Biogeography</i> , 2017, 44, 900-910.	1.4	117
2422	What causes flag smut of wheat?. <i>Plant Pathology</i> , 2017, 66, 1139-1148.	1.2	5
2423	Markers to differentiate species of anthracnose fungi identify <i>Colletotrichum fructicola</i> as the predominant virulent species in strawberry plants in Chiba Prefecture of Japan. <i>Journal of General Plant Pathology</i> , 2017, 83, 14-22.	0.6	33
2424	Phylogenetic relationships in <i>Kerkia</i> and introgression between <i>Hauffenia</i> and <i>Kerkia</i> (Caenogastropoda: Hydrobiidae). <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2017, 55, 106-117.	0.6	26
2425	Protracted Regional Dissemination of GIM-1-Producing <i>Serratia marcescens</i> in Western Germany. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	6
2426	Beta diversity of macroalgal communities around St. Eustatius, Dutch Caribbean. <i>Marine Biodiversity</i> , 2017, 47, 123-138.	0.3	10
2427	Biogeography and radiation of the land snail genus <i>Xerocrassa</i> (Geomitridae) in the Balearic Islands. <i>Journal of Biogeography</i> , 2017, 44, 760-772.	1.4	19
2428	<i>Riptortus pedestris</i> and <i>Burkholderia</i> symbiont: an ideal model system for insect-microbe symbiotic associations. <i>Research in Microbiology</i> , 2017, 168, 175-187.	1.0	86
2429	Genomewide variation provides insight into evolutionary relationships in a monkeyflower species complex (<i>Mimulus</i> sect. <i>Diplacus</i>). <i>American Journal of Botany</i> , 2017, 104, 1510-1521.	0.8	18
2430	Population Genomics in Wild Tomatoes—The Interplay of Divergence and Admixture. <i>Genome Biology and Evolution</i> , 2017, 9, 3023-3038.	1.1	33
2431	Using Molecules and Morphology to Unravel the Systematics of Neotropical Preponine Butterflies (Lepidoptera: Charaxinae: Preponini). <i>Insect Systematics and Diversity</i> , 2017, 1, 48-56.	0.7	4
2432	Longitudinal genomic surveillance of MRSA in the UK reveals transmission patterns in hospitals and the community. <i>Science Translational Medicine</i> , 2017, 9, .	5.8	103
2433	Molecular phylogeny and divergence times of <i>Astragalus</i> section <i>Hymenostegis</i> : An analysis of a rapidly diversifying species group in Fabaceae. <i>Scientific Reports</i> , 2017, 7, 14033.	1.6	47
2434	Coordinated Functional Divergence of Genes after Genome Duplication in <i>Arabidopsis thaliana</i> . <i>Plant Cell</i> , 2017, 29, 2786-2800.	3.1	46

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2435	Obstruction of pilus retraction stimulates bacterial surface sensing. <i>Science</i> , 2017, 358, 535-538.	6.0	231
2436	Comparative analysis of complete chloroplast genome sequences of two subtropical trees, <i>Phoebe sheareri</i> and <i>Phoebe omeiensis</i> (Lauraceae). <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	30
2437	Complete chloroplast genome sequences contribute to plant species delimitation: A case study of the <i>Anemopaegma</i> species complex. <i>American Journal of Botany</i> , 2017, 104, 1493-1509.	0.8	54
2438	The evolution and diversification of the red oaks of the California Floristic Province (<i>Quercus</i>) Tj ETQq1 1 0.784314 rgBT / Overlock 10 T	0.8	27
2439	Evolutionary Analysis of Pectin Lyases of the Genus <i>Colletotrichum</i> . <i>Journal of Molecular Evolution</i> , 2017, 85, 120-136.	0.8	5
2440	Keeping it complicated: Mitochondrial genome plasticity across diplomonads. <i>Scientific Reports</i> , 2017, 7, 14166.	1.6	18
2441	Molecular Evolution of Spider Vision: New Opportunities, Familiar Players. <i>Biological Bulletin</i> , 2017, 233, 21-38.	0.7	53
2442	Linking micro- and macroevolutionary perspectives to evaluate the role of Quaternary sea level oscillations in island diversification. <i>Evolution; International Journal of Organic Evolution</i> , 2017, 71, 2901-2917.	1.1	25
2443	Plastome Evolution in the Sole Hemiparasitic Genus Laurel Dodder (<i>Cassytha</i>) and Insights into the Plastid Phylogenomics of Lauraceae. <i>Genome Biology and Evolution</i> , 2017, 9, 2604-2614.	1.1	36
2444	Comparative Genomics of Apomictic Root-Knot Nematodes: Hybridization, Ploidy, and Dynamic Genome Change. <i>Genome Biology and Evolution</i> , 2017, 9, 2844-2861.	1.1	98
2445	Evolution and Spatiotemporal Dynamics of Enterovirus A71 Subgenogroups in Vietnam. <i>Journal of Infectious Diseases</i> , 2017, 216, 1371-1379.	1.9	19
2446	Biologically induced formation of realgar deposits in soil. <i>Geochimica Et Cosmochimica Acta</i> , 2017, 218, 237-256.	1.6	23
2447	The evolutionary history of two lizards (Squamata: Lacertidae) is linked to the geological development of Iran. <i>Zoologischer Anzeiger</i> , 2017, 270, 49-56.	0.4	9
2448	Convergence of plasmid architectures drives emergence of multi-drug resistance in a clonally diverse <i>Escherichia coli</i> population from a veterinary clinical care setting. <i>Veterinary Microbiology</i> , 2017, 211, 6-14.	0.8	15
2449	<i>Rhizocarpon smaragdulum</i> , a new monosporic yellow-thalline species and some additional species of the genus <i>Rhizocarpon</i> from the Altai Mountains (Siberia). <i>Lichenologist</i> , 2017, 49, 457-466.	0.5	12
2450	Comparative mitogenomic analysis of <i>Aposthonia borneensis</i> and <i>Aposthonia japonica</i> (Embioptera:) Tj ETQq1 1 0.784314 rgBT / Overlock 10 T	1.6	3
2451	Whole genome-based phylogeny of reptile-associated <i>Helicobacter</i> indicates independent niche adaptation followed by diversification in a poikilothermic host. <i>Scientific Reports</i> , 2017, 7, 8387.	1.6	19
2452	Complete genomic characterisation of two novel poxviruses (WKPV and EKPV) from western and eastern grey kangaroos. <i>Virus Research</i> , 2017, 242, 106-121.	1.1	8

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2453	A unique cysteine-rich zinc finger domain present in a majority of class II ribonucleotide reductases mediates catalytic turnover. <i>Journal of Biological Chemistry</i> , 2017, 292, 19044-19054.	1.6	14
2454	Metagenomic assessment of the interplay between the environment and the genetic diversification of <i>Acinetobacter</i> . <i>Environmental Microbiology</i> , 2017, 19, 5010-5024.	1.8	24
2455	Historical biogeography and phylogeny of the pantropical Psychotriaceae alliance (Rubiaceae), with particular emphasis on the Western Indian Ocean Region. <i>American Journal of Botany</i> , 2017, 104, 1407-1423.	0.8	22
2456	Diversity and bioactivities of nostocacean cyanobacteria isolated from paddy soil in Vietnam. <i>Systematic and Applied Microbiology</i> , 2017, 40, 470-481.	1.2	16
2457	A communal catalogue reveals Earth's multiscale microbial diversity. <i>Nature</i> , 2017, 551, 457-463.	13.7	1,942
2458	The asparagus genome sheds light on the origin and evolution of a young Y chromosome. <i>Nature Communications</i> , 2017, 8, 1279.	5.8	240
2459	PhyloNetworks: A Package for Phylogenetic Networks. <i>Molecular Biology and Evolution</i> , 2017, 34, 3292-3298.	3.5	250
2460	Population genomics of the Asian tiger mosquito, <i>Aedes albopictus</i> : insights into the recent worldwide invasion. <i>Ecology and Evolution</i> , 2017, 7, 10143-10157.	0.8	89
2461	Shaping the evolutionary tree of green plants: evidence from the GST family. <i>Scientific Reports</i> , 2017, 7, 14363.	1.6	17
2462	The genetic variation in the R1a clade among the Ashkenazi Levites' Y chromosome. <i>Scientific Reports</i> , 2017, 7, 14969.	1.6	13
2463	Adaptability as the key to success for the ubiquitous marine nitrite oxidizer <i>Nitrococcus</i> . <i>Science Advances</i> , 2017, 3, e1700807.	4.7	74
2464	Ancient genomes show social and reproductive behavior of early Upper Paleolithic foragers. <i>Science</i> , 2017, 358, 659-662.	6.0	263
2465	Development of single-copy nuclear intron markers for species-level phylogenetics: Case study with Paullinieae (Sapindaceae). <i>Applications in Plant Sciences</i> , 2017, 5, 1700051.	0.8	5
2466	Insights into Land Plant Evolution Garnered from the <i>Marchantia polymorpha</i> Genome. <i>Cell</i> , 2017, 171, 287-304.e15.	13.5	973
2467	Natural product diversity associated with the nematode symbionts <i>Photorhabdus</i> and <i>Xenorhabdus</i> . <i>Nature Microbiology</i> , 2017, 2, 1676-1685.	5.9	136
2468	Ant-infecting <i>Ophiocordyceps</i> genomes reveal a high diversity of potential behavioral manipulation genes and a possible major role for enterotoxins. <i>Scientific Reports</i> , 2017, 7, 12508.	1.6	52
2469	The chromosomal organization of horizontal gene transfer in bacteria. <i>Nature Communications</i> , 2017, 8, 841.	5.8	184
2470	Ctenophore relationships and their placement as the sister group to all other animals. <i>Nature Ecology and Evolution</i> , 2017, 1, 1737-1746.	3.4	202

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2471	Multiple Geographical Origins of Environmental Sex Determination enhanced the diversification of Darwin's Favourite Orchids. <i>Scientific Reports</i> , 2017, 7, 12878.	1.6	20
2472	Minimal and RNA-free RNase P in <i>Aquifex aeolicus</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 11121-11126.	3.3	46
2473	A sister of <i>NANOG</i> regulates genes expressed in pre-implantation human development. <i>Open Biology</i> , 2017, 7, 170027.	1.5	13
2474	Beneath the hairy look: the hidden reproductive diversity of the <i>Gibsmithia hawaiiensis</i> complex (Dumontiaceae, Rhodophyta). <i>Journal of Phycology</i> , 2017, 53, 1171-1192.	1.0	11
2475	Two new species of <i>Ripella</i> (Amoebozoa, Vannellida) and unusual intragenomic variability in the SSU rRNA gene of this genus. <i>European Journal of Protistology</i> , 2017, 61, 92-106.	0.5	19
2476	Membrane Trafficking Modulation during <i>Entamoeba</i> Encystation. <i>Scientific Reports</i> , 2017, 7, 12854.	1.6	12
2477	Phylogenetic relationships of millipedes in the subclass Penicillata (Diplopoda) with a key to the genera. <i>Journal of Natural History</i> , 2017, 51, 2443-2461.	0.2	10
2478	Bayesian and likelihood phylogenetic reconstructions of morphological traits are not discordant when taking uncertainty into consideration: a comment on Puttick <i>et al.</i> .. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20170986.	1.2	30
2479	Depth Distribution and Assembly of Sulfate-Reducing Microbial Communities in Marine Sediments of Aarhus Bay. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	53
2480	Metabolic Roles of Uncultivated Bacterioplankton Lineages in the Northern Gulf of Mexico "Dead Zone". <i>MBio</i> , 2017, 8, .	1.8	80
2481	Genomic adaptation to polyphagy and insecticides in a major East Asian noctuid pest. <i>Nature Ecology and Evolution</i> , 2017, 1, 1747-1756.	3.4	269
2482	Comparative Genomics of Soybean and Other Legumes. <i>Compendium of Plant Genomes</i> , 2017, , 83-93.	0.3	1
2483	Enhancing Searches for Optimal Trees Using SIESTA. <i>Lecture Notes in Computer Science</i> , 2017, , 232-255.	1.0	0
2484	Occurrence and effect of trematode metacercariae in two endangered killifishes from Greece. <i>Parasitology Research</i> , 2017, 116, 3007-3018.	0.6	2
2485	The complete mitochondrial genome of <i>Apis nuluensis</i> Tingek, an Asian honey bee (Insecta: Tj ETQq0 0 0 rgBT /Overlqck 10 Tf 50	0.2	1
2486	Mitochondrial genome of <i>Taiwania circumdata</i> (Coleoptera: Chrysomelidae: Cassidinae) and phylogenetic analysis. <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 674-675.	0.2	0
2487	Insights into the Impact of CD8 ⁺ Immune Modulation on Human Immunodeficiency Virus Evolutionary Dynamics in Distinct Anatomical Compartments by Using Simian Immunodeficiency Virus-Infected Macaque Models of AIDS Progression. <i>Journal of Virology</i> , 2017, 91, .	1.5	8
2488	ASTRAL-III: Increased Scalability and Impacts of Contracting Low Support Branches. <i>Lecture Notes in Computer Science</i> , 2017, , 53-75.	1.0	129

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2489	A Cretaceous-aged Palaeotropical dispersal established an endemic lineage of Caribbean praying mantises. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20171280.	1.2	19
2490	A functional zeaxanthin epoxidase from red algae shedding light on the evolution of light-harvesting carotenoids and the xanthophyll cycle in photosynthetic eukaryotes. <i>Plant Journal</i> , 2017, 92, 879-891.	2.8	52
2492	Description of <i>Neoparamoeba longipodia</i> n. sp. and a new strain of <i>Neoparamoeba aestuarina</i> (Page,.) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf</i> 107-121.	0.5	15
2493	Effective purifying selection in ancient asexual oribatid mites. <i>Nature Communications</i> , 2017, 8, 873.	5.8	32
2494	Single-cell sequencing data reveal widespread recurrence and loss of mutational hits in the life histories of tumors. <i>Genome Research</i> , 2017, 27, 1885-1894.	2.4	156
2495	An evolutionary timescale for terrestrial isopods and a lack of molecular support for the monophyly of Oniscidea (Crustacea: Isopoda). <i>Organisms Diversity and Evolution</i> , 2017, 17, 813-820.	0.7	43
2496	A new large species of gecko of the genus <i>Hemidactylus</i> Oken, 1817 (Reptilia: Sauria: Gekkonidae) from the Eastern Ghats, India. <i>Comptes Rendus - Biologies</i> , 2017, 340, 531-540.	0.1	10
2497	<i>Echinochloa crus-galli</i> genome analysis provides insight into its adaptation and invasiveness as a weed. <i>Nature Communications</i> , 2017, 8, 1031.	5.8	138
2498	Evidence for a conserved inhibitory binding mode between the membrane fusion assembly factors Munc18 and syntaxin in animals. <i>Journal of Biological Chemistry</i> , 2017, 292, 20449-20460.	1.6	11
2499	Evolutionary History of Saber-Toothed Cats Based on Ancient Mitogenomics. <i>Current Biology</i> , 2017, 27, 3330-3336.e5.	1.8	45
2500	Delimiting species of <i>Protaphorura</i> (Collembola: Onychiuridae): integrative evidence based on morphology, DNA sequences and geography. <i>Scientific Reports</i> , 2017, 7, 8261.	1.6	16
2501	Evolutionary mechanisms of runaway chromosome number change in <i>Agrodiaetus</i> butterflies. <i>Scientific Reports</i> , 2017, 7, 8199.	1.6	28
2502	<i>Panax ginseng</i> genome examination for ginsenoside biosynthesis. <i>GigaScience</i> , 2017, 6, 1-15.	3.3	150
2503	Whole-Genome Next-Generation Sequencing to Study Within-Host Evolution of Norovirus (NoV) Among Immunocompromised Patients With Chronic NoV Infection. <i>Journal of Infectious Diseases</i> , 2017, 216, 1513-1524.	1.9	36
2504	Genetic Mapping and Phylogenetic Analysis Reveal Intraspecific Variation in Sex Chromosomes of the Virginian Strawberry. <i>Journal of Heredity</i> , 2017, 108, 731-739.	1.0	14
2505	Genomic differentiation and patterns of gene flow between two long-tailed tit species (<i>Aegithalos</i>). <i>Molecular Ecology</i> , 2017, 26, 6654-6665.	2.0	11
2506	Genome skimming and plastid microsatellite profiling of alder trees (<i>Alnus</i> spp., Betulaceae): phylogenetic and phylogeographical prospects. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	17
2507	Genome-Guided Phylo-Transcriptomic Methods and the Nuclear Phylogenetic Tree of the Paniceae Grasses. <i>Scientific Reports</i> , 2017, 7, 13528.	1.6	27

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2508	Phylogenetics, phylogeography and vicariance of polyphyletic Grammosciadium (Apiaceae: Careae) in Anatolia. <i>Botanical Journal of the Linnean Society</i> , 2017, 185, 168-188.	0.8	13
2509	Fragmentary Gene Sequences Negatively Impact Gene Tree and Species Tree Reconstruction. <i>Molecular Biology and Evolution</i> , 2017, 34, 3279-3291.	3.5	73
2510	Integrative taxonomy of the <i>Felimare californiensis</i> and <i>F. ghiselini</i> species complex (Nudibranchia: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50). <i>Biological Journal of the Linnean Society</i> , 2017, 83, 461-475.	0.4	7
2511	The non-visual opsins: eighteen in the ancestor of vertebrates, astonishing increase in ray-finned fish, and loss in amniotes. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2017, 328, 685-696.	0.6	30
2512	Population genomics of Wolbachia and mtDNA in <i>Drosophila simulans</i> from California. <i>Scientific Reports</i> , 2017, 7, 13369.	1.6	14
2513	Development of functional ectopic compound eyes in scarabaeid beetles by knockdown of <i>orthodenticle</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 12021-12026.	3.3	12
2514	A Broad-Spectrum Inhibitor of CRISPR-Cas9. <i>Cell</i> , 2017, 170, 1224-1233.e15.	13.5	211
2515	Out of Asia: Biogeography of fungal populations reveals Asian origin of diversification of the <i>Laccaria amethystina</i> complex, and two new species of violet <i>Laccaria</i> . <i>Fungal Biology</i> , 2017, 121, 939-955.	1.1	24
2516	Arsenic Methylation Dynamics in a Rice Paddy Soil Anaerobic Enrichment Culture. <i>Environmental Science & Technology</i> , 2017, 51, 10546-10554.	4.6	61
2517	Large-scale comparative metagenomics of <i>Blastocystis</i> , a common member of the human gut microbiome. <i>ISME Journal</i> , 2017, 11, 2848-2863.	4.4	136
2518	Cryptic diversity of marine gastropod <i>Monodonta labio</i> (Trochidae): did the early Pleistocene glacial isolation and sea surface temperature gradient jointly drive diversification of sister species and/or subspecies in the Northwestern Pacific?. <i>Marine Ecology</i> , 2017, 38, e12443.	0.4	26
2519	Investigating Difficult Nodes in the Placental Mammal Tree with Expanded Taxon Sampling and Thousands of Ultraconserved Elements. <i>Genome Biology and Evolution</i> , 2017, 9, 2308-2321.	1.1	102
2520	IDXL: Species Tree Inference Using Internode Distance and Excess Gene Leaf Count. <i>Journal of Molecular Evolution</i> , 2017, 85, 57-78.	0.8	1
2521	Proteogenomic Investigation of Strain Variation in Clinical <i>Mycobacterium tuberculosis</i> Isolates. <i>Journal of Proteome Research</i> , 2017, 16, 3841-3851.	1.8	27
2522	First global molecular phylogeny and biogeographical analysis of two arachnid orders (Schizomida). <i>Biogeography</i> , 2017, 44, 2660-2672.	1.4	37
2523	Resurrection of <i>Cortinarius coalescens</i> : taxonomy, chemistry, and ecology. <i>Mycological Progress</i> , 2017, 16, 927-939.	0.5	7
2524	Spatial and phylogeographical analyses of <i>nosZ</i> genes underscore niche differentiation amongst terrestrial N ₂ O reducing communities. <i>Soil Biology and Biochemistry</i> , 2017, 115, 82-91.	4.2	52
2525	Host-derived viral transporter protein for nitrogen uptake in infected marine phytoplankton. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E7489-E7498.	3.3	74

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2526	Genome-wide signatures of complex introgression and adaptive evolution in the big cats. <i>Science Advances</i> , 2017, 3, e1700299.	4.7	142
2527	Postnatal Identification of Zika Virus Peptides from Saliva. <i>Journal of Dental Research</i> , 2017, 96, 1078-1084.	2.5	37
2528	Bioinformatics for NGS-based metagenomics and the application to biogas research. <i>Journal of Biotechnology</i> , 2017, 261, 10-23.	1.9	84
2529	The confounding effects of hybridization on phylogenetic estimation in the New Zealand cicada genus <i>Kikihia</i> . <i>Molecular Phylogenetics and Evolution</i> , 2017, 116, 172-181.	1.2	12
2530	The systematics and biogeography of the mite harvestman family Sironidae (Arachnida : Opiliones :). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5</i>	0.5	3
2531	Phylogenetic analyses of plastid DNA suggest a different interpretation of morphological evolution than those used as the basis for previous classifications of Dipterocarpaceae (Malvales). <i>Botanical Journal of the Linnean Society</i> , 2017, 185, 1-26.	0.8	37
2532	Torix group <i>Rickettsia</i> are widespread in <i>Culicoides</i> biting midges (Diptera:). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 507 Td (</i> <i>Microbiology</i> , 2017, 19, 4238-4255.	1.8	41
2533	Evolutionarily Conserved Alternative Splicing Across Monocots. <i>Genetics</i> , 2017, 207, 465-480.	1.2	47
2534	Ancient Occasional Host Switching of Maternally Transmitted Bacterial Symbionts of Chemosynthetic Vesicomyid Clams. <i>Genome Biology and Evolution</i> , 2017, 9, 2226-2236.	1.1	21
2535	The genomic basis of cichlid fish adaptation within the deepwater "twilight zone" of Lake Malawi. <i>Evolution Letters</i> , 2017, 1, 184-198.	1.6	21
2536	An expanded mammal mitogenome dataset from Southeast Asia. <i>GigaScience</i> , 2017, 6, 1-8.	3.3	27
2537	Genomic Characterization of VIM Metallo- β -Lactamase-Producing <i>Alcaligenes faecalis</i> from Gaza, Palestine. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	17
2538	Large-Scale Phylogenomics of the <i>Lactobacillus casei</i> Group Highlights Taxonomic Inconsistencies and Reveals Novel Clade-Associated Features. <i>MSystems</i> , 2017, 2, .	1.7	79
2539	<i>Mangleticornia</i> (<i>Amaranthaceae: Salicornioideae</i>) " a new sister for <i>Salicornia</i> from the Pacific coast of South America. <i>Willdenowia</i> , 2017, 47, 145-153.	0.5	10
2540	Whole-Genome Sequencing of Bacterial Pathogens: the Future of Nosocomial Outbreak Analysis. <i>Clinical Microbiology Reviews</i> , 2017, 30, 1015-1063.	5.7	310
2541	Metabolic Network Analysis and Metatranscriptomics Reveal Auxotrophies and Nutrient Sources of the Cosmopolitan Freshwater Microbial Lineage acl. <i>MSystems</i> , 2017, 2, .	1.7	21
2542	Phylogenetic Conflict in Bears Identified by Automated Discovery of Transposable Element Insertions in Low-Coverage Genomes. <i>Genome Biology and Evolution</i> , 2017, 9, 2862-2878.	1.1	14
2543	A Key Regulator of the Glycolytic and Gluconeogenic Central Metabolic Pathways in <i>Sinorhizobium meliloti</i> . <i>Genetics</i> , 2017, 207, 961-974.	1.2	15

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2544	The evolutionary history of <i>Senna</i> ser. <i>Aphyllae</i> (Leguminosae“Caesalpinioideae), an endemic clade of southern South America. <i>Plant Systematics and Evolution</i> , 2017, 303, 1351-1366.	0.3	3
2546	Development of chloroplast genome resources for peanut (<i>Arachis hypogaea</i> L.) and other species of <i>Arachis</i> . <i>Scientific Reports</i> , 2017, 7, 11649.	1.6	44
2547	Habitat Association Predicts Genetic Diversity and Population Divergence in Amazonian Birds. <i>American Naturalist</i> , 2017, 190, 631-648.	1.0	73
2548	Cytochrome P450 diversification and hostplant utilization patterns in specialist and generalist moths: Birth, death and adaptation. <i>Molecular Ecology</i> , 2017, 26, 6021-6035.	2.0	68
2549	Genomic Characterization of Urethritis-Associated <i>Neisseria meningitidis</i> Shows that a Wide Range of <i>N. meningitidis</i> Strains Can Cause Urethritis. <i>Journal of Clinical Microbiology</i> , 2017, 55, 3374-3383.	1.8	24
2550	Parallel Evolution of Group B <i>Streptococcus</i> Hypervirulent Clonal Complex 17 Unveils New Pathoadaptive Mutations. <i>MSystems</i> , 2017, 2, .	1.7	31
2551	First record of <i>Albatrellus</i> (Russulales, Albatrellaceae) from Thailand. <i>Phytotaxa</i> , 2017, 317, 104.	0.1	4
2552	Sectional Relationships in the Eurasian Bearded Iris (subgen. <i>Iris</i>) Based on Phylogenetic Analyses of Sequence Data. <i>Systematic Botany</i> , 2017, 42, 392-401.	0.2	12
2553	Evolution of the 3-hydroxypropionate bicycle and recent transfer of anoxygenic photosynthesis into the Chloroflexi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 10749-10754.	3.3	108
2554	Plate pattern clarification of the marine dinophyte <i>Heterocapsa triquetra</i> sensu Stein (Dinophyceae) collected at the Kiel Fjord (Germany). <i>Journal of Phycology</i> , 2017, 53, 1305-1324.	1.0	23
2555	Relatedness of wildlife and livestock avian isolates of the nosocomial pathogen <i>Acinetobacter baumannii</i> to lineages spread in hospitals worldwide. <i>Environmental Microbiology</i> , 2017, 19, 4349-4364.	1.8	64
2556	The complete genome sequence of human adenovirus 84, a highly recombinant new Human mastadenovirus D type with a unique fiber gene. <i>Virus Research</i> , 2017, 242, 79-84.	1.1	16
2557	Complete mitochondrial genome of <i>Zeuzera multistrigata</i> Moore, 1881 (Lepidoptera: Cossidae). <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 502-503.	0.2	2
2558	Molecular phylogeny of the genus <i>Apatrobus</i> (Coleoptera: Carabidae: Patrobinae) in western Japan. <i>Entomological Science</i> , 2017, 20, 462-469.	0.3	2
2559	Ryanodine receptor and FK506 binding protein 1 in the Atlantic killifish (<i>Fundulus heteroclitus</i>): A phylogenetic and population-based comparison. <i>Aquatic Toxicology</i> , 2017, 192, 105-115.	1.9	13
2560	Characteristics of 29 novel atypical solute carriers of major facilitator superfamily type: evolutionary conservation, predicted structure and neuronal co-expression. <i>Open Biology</i> , 2017, 7, 170142.	1.5	49
2561	Taxonomy assignment approach determines the efficiency of identification of OTUs in marine nematodes. <i>Royal Society Open Science</i> , 2017, 4, 170315.	1.1	36
2562	Low hepatitis E virus RNA prevalence in a large scale survey of United States source plasma donors. <i>Transfusion</i> , 2017, 57, 2958-2964.	0.8	37

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2563	Forensic Human Identification Using Skin Microbiomes. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	74
2564	Pathogenic lineage of <i>Perkinsea</i> associated with mass mortality of frogs across the United States. <i>Scientific Reports</i> , 2017, 7, 10288.	1.6	34
2565	Uniqueness of <i>Entamoeba</i> sulfur metabolism: sulfolipid metabolism that plays pleiotropic roles in the parasitic life cycle. <i>Molecular Microbiology</i> , 2017, 106, 479-491.	1.2	24
2566	Two new <i>Tylophilus</i> species (Boletaceae) from Northeastern Atlantic Forest, Brazil. <i>Phytotaxa</i> , 2017, 316, 250.	0.1	15
2567	Molecular analysis of <i>Sargassum</i> from the northern China seas. <i>Phytotaxa</i> , 2017, 319, 71.	0.1	11
2568	Diversity of two widespread Indo-Pacific demosponge species revisited. <i>Marine Biodiversity</i> , 2017, 47, 1035-1043.	0.3	13
2569	Validation of DNA barcoding markers in common <i>Mucuna</i> species of India for taxonomy and pharmacognosy applications. <i>Plant Gene</i> , 2017, 12, 98-104.	1.4	4
2570	Community-like genome in single cells of the sulfur bacterium <i>Achromatium oxaliferum</i> . <i>Nature Communications</i> , 2017, 8, 455.	5.8	31
2571	Genomic and Molecular Characterization of Clinical Isolates of Enterobacteriaceae Harboring <i>mcr-1</i> in Colombia, 2002 to 2016. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	56
2572	Five distinct reassortants of H5N6 highly pathogenic avian influenza A viruses affected Japan during the winter of 2016–2017. <i>Virology</i> , 2017, 512, 8-20.	1.1	42
2573	The <i>Apostasia</i> genome and the evolution of orchids. <i>Nature</i> , 2017, 549, 379-383.	13.7	305
2574	The Landscape of Type VI Secretion across Human Gut Microbiomes Reveals Its Role in Community Composition. <i>Cell Host and Microbe</i> , 2017, 22, 411-419.e4.	5.1	137
2575	The parabasalid symbiont community of <i>Heterotermes aureus</i> : Molecular and morphological characterization of four new species and reestablishment of the genus <i>Cononympha</i> . <i>European Journal of Protistology</i> , 2017, 61, 48-63.	0.5	20
2576	Genetic analysis of ID1-DBL2X predicts its validity as a vaccine candidate in Colombia and supports at least two independently introduced <i>Plasmodium falciparum</i> populations in the region. <i>Infection, Genetics and Evolution</i> , 2017, 55, 175-185.	1.0	3
2577	Phylogenomic analyses of more than 4000 nuclear loci resolve the origin of snakes among lizard families. <i>Biology Letters</i> , 2017, 13, 20170393.	1.0	79
2578	A Neolithic expansion, but strong genetic structure, in the independent history of New Guinea. <i>Science</i> , 2017, 357, 1160-1163.	6.0	45
2579	Genetic differentiation and inferred dynamics of a hybrid zone between Northern Spotted Owls (<i>Strix occidentalis caurina</i>) and California Spotted Owls (<i>S. occidentalis</i>) in northern California. <i>Ecology and Evolution</i> , 2017, 7, 6871-6883.	0.8	7
2580	Combined genotyping strategy reveals structural differences between <i>Aspergillus flavus</i> lineages from different habitats impacting human health. <i>Journal of Basic Microbiology</i> , 2017, 57, 899-909.	1.8	2

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2581	Genome Architecture and Evolution of a Unichromosomal Asexual Nematode. <i>Current Biology</i> , 2017, 27, 2928-2939.e6.	1.8	56
2582	Enabling the democratization of the genomics revolution with a fully integrated web-based bioinformatics platform. <i>Nucleic Acids Research</i> , 2017, 45, 67-80.	6.5	147
2583	<scp>iDNA</scp> screening: Disease vectors as vertebrate samplers. <i>Molecular Ecology</i> , 2017, 26, 6478-6486.	2.0	57
2584	Evolutionarily significant units of the critically endangered leaf frog <i>Pithecopus ayeaye</i> (Anura, Phyllomedusidae) are not effectively preserved by the Brazilian protected areas network. <i>Ecology and Evolution</i> , 2017, 7, 8812-8828.	0.8	20
2585	Phylogeography of the sand dollar genus <i>Encope</i> : implications regarding the Central American Isthmus and rates of molecular evolution. <i>Scientific Reports</i> , 2017, 7, 11520.	1.6	15
2586	Old Yellow Enzyme homologues in <i>Mucor circinelloides</i> : expression profile and biotransformation. <i>Scientific Reports</i> , 2017, 7, 12093.	1.6	8
2587	Dihydrofolate Reductase/Thymidylate Synthase Fine-Tunes the Folate Status and Controls Redox Homeostasis in Plants. <i>Plant Cell</i> , 2017, 29, 2831-2853.	3.1	64
2588	The complete mitochondrial genome of an east African honey bee, <i>Apis mellifera monticola</i> Smith (Insecta: Hymenoptera: Apidae). <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 589-590.	0.2	9
2589	Biogeographic conservation of the cytosine epigenome in the globally important marine, nitrogen-fixing cyanobacterium <i>Trichodesmium</i> . <i>Environmental Microbiology</i> , 2017, 19, 4700-4713.	1.8	13
2590	Complete mitochondrial genomes of <i>Anopheles stephensi</i> and <i>An. dirus</i> and comparative evolutionary mitochondriomics of 50 mosquitoes. <i>Scientific Reports</i> , 2017, 7, 7666.	1.6	47
2591	Field-based species identification of closely-related plants using real-time nanopore sequencing. <i>Scientific Reports</i> , 2017, 7, 8345.	1.6	68
2592	Complete Chloroplast Genome Sequence of <i>Decaisnea insignis</i> : Genome Organization, Genomic Resources and Comparative Analysis. <i>Scientific Reports</i> , 2017, 7, 10073.	1.6	68
2593	The extraordinary variation of the organellar genomes of the <i>Aneura pinguis</i> revealed advanced cryptic speciation of the early land plants. <i>Scientific Reports</i> , 2017, 7, 9804.	1.6	34
2594	Phylogenetic revision of <i>Camarosporium</i> (<i>Pleosporineae</i>, <i>Dothideomycetes</i>) and allied genera. <i>Studies in Mycology</i> , 2017, 87, 207-256.	4.5	65
2595	Genomic insights into the ancient spread of Lyme disease across North America. <i>Nature Ecology and Evolution</i> , 2017, 1, 1569-1576.	3.4	39
2596	Field Pathogenomics: An Advanced Tool for Wheat Rust Surveillance. <i>Methods in Molecular Biology</i> , 2017, 1659, 13-28.	0.4	6
2597	Discovery of the skull of <i>Stephanorhinus kirchbergensis</i> (Jäger, 1839) above the Arctic Circle. <i>Quaternary Research</i> , 2017, 88, 537-550.	1.0	20
2598	Genomic signatures of evolution in <i>Nautilus</i>—An endangered living fossil. <i>Molecular Ecology</i> , 2017, 26, 5923-5938.	2.0	30

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2599	KinFin: Software for Taxon-Aware Analysis of Clustered Protein Sequences. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3349-3357.	0.8	72
2600	Recurrent horizontal transfer of arsenite methyltransferase genes facilitated adaptation of life to arsenic. <i>Scientific Reports</i> , 2017, 7, 7741.	1.6	60
2601	Two new and one known species of <i>Tergestia</i> Stossich, 1899 (Trematoda: Fellodistomidae) with novel molecular characterisation for the genus. <i>Systematic Parasitology</i> , 2017, 94, 861-874.	0.5	13
2602	Transcriptome and target DNA enrichment sequence data provide new insights into the phylogeny of vespid wasps (Hymenoptera: Aculeata: Vespidae). <i>Molecular Phylogenetics and Evolution</i> , 2017, 116, 213-226.	1.2	87
2603	Ecological niche comparison and molecular phylogeny segregate the invasive moss species <i>Campylopus introflexus</i> (Leucobryaceae, Bryophyta) from its closest relatives. <i>Ecology and Evolution</i> , 2017, 7, 8017-8031.	0.8	14
2604	Tapping the woodpecker tree for evolutionary insight. <i>Molecular Phylogenetics and Evolution</i> , 2017, 116, 182-191.	1.2	54
2605	Deep-level phylogeny of Cicadomorpha inferred from mitochondrial genomes sequenced by NGS. <i>Scientific Reports</i> , 2017, 7, 10429.	1.6	52
2606	Genome reconstruction in <i>Cynara cardunculus</i> taxa gains access to chromosome-scale DNA variation. <i>Scientific Reports</i> , 2017, 7, 5617.	1.6	30
2607	Barcoding utility in a mega-diverse, cross-continental genus: keeping pace with <i>Cyrtodactylus</i> geckos. <i>Scientific Reports</i> , 2017, 7, 5592.	1.6	24
2608	Genotypic diversity in root-endophytic fungi reflects efficient dispersal and environmental adaptation. <i>Molecular Ecology</i> , 2017, 26, 4618-4630.	2.0	12
2609	Complete mitochondrial genome of the smallmouth hardyhead (<i>Atherinosoma microstoma</i>) and its phylogenetic position among the Atheriniform fishes. <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 318-320.	0.2	0
2610	Molecular phylogeny, frequent parallel evolution and new system of Japanese clausiliid land snails (Gastropoda: Stylommatophora). <i>Zoological Journal of the Linnean Society</i> , 2017, 181, 795-845.	1.0	21
2611	An <i>In Vitro</i> Chicken Gut Model Demonstrates Transfer of a Multidrug Resistance Plasmid from <i>Salmonella</i> to Commensal <i>Escherichia coli</i> . <i>MBio</i> , 2017, 8, .	1.8	60
2612	Morphologic and molecular characterization of seven species of the remarkably diverse and widely distributed metopid genus <i>Lrostomides</i> Jankowski, 1964 (Armophorea, Ciliophora). <i>European Journal of Protistology</i> , 2017, 61, 194-232.	0.5	21
2613	Evolutionary Dynamics of Cryptophyte Plastid Genomes. <i>Genome Biology and Evolution</i> , 2017, 9, 1859-1872.	1.1	51
2614	Archaic Hominin Introgression in Africa Contributes to Functional Salivary MUC7 Genetic Variation. <i>Molecular Biology and Evolution</i> , 2017, 34, 2704-2715.	3.5	57
2615	Inferring the phylogenetic position of the <i>Drosophila flavopilosa</i> group: Incongruence within and between mitochondrial and nuclear multilocus datasets. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2017, 55, 208-221.	0.6	7
2616	Discrimination and Characterization of Two Mediterranean Species from the <i>Laurencia</i> Complex (Rhodomelaceae) Using an ¹ H-NMR-Based Metabolomic Approach. <i>Chemistry and Biodiversity</i> , 2017, 14, e1700226.	1.0	3

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2617	Conioscypha nakagirii, a new species from naturally submerged wood in Thailand based on morphological and molecular data. Mycoscience, 2017, 58, 424-431.	0.3	9
2618	Neo- and Paleopolyploidy contribute to the species diversity of <i>Asplenium</i> the most species-rich genus of ferns. Journal of Systematics and Evolution, 2017, 55, 353-364.	1.6	51
2619	Dissecting the "bacon and eggs" phenotype: transcriptomics of post-anthesis colour change in Lotus. Annals of Botany, 2017, 120, 563-575.	1.4	1
2620	Population structure and cryptic species in the cosmopolitan rotifer Euchlanis dilatata. Zoological Journal of the Linnean Society, 2017, 181, 757-777.	1.0	18
2621	Disguised as a Sulfate Reducer: Growth of the Deltaproteobacterium <i>Desulfurivibrio alkaliphilus</i> by Sulfide Oxidation with Nitrate. MBio, 2017, 8, .	1.8	122
2622	Intercontinental and intracontinental biogeography of the eastern Asian " Eastern North American disjunct Panax (the ginseng genus, Araliaceae), emphasizing its diversification processes in eastern Asia. Molecular Phylogenetics and Evolution, 2017, 117, 60-74.	1.2	38
2623	Resolving the <i>Melampsora epitea</i> complex. Mycologia, 2017, 109, 391-407.	0.8	11
2624	Phylogenomics reveals a complex evolutionary history of lobed-leaf white oaks in western North America. Genome, 2017, 60, 733-742.	0.9	39
2625	<i>Ramalina europaea</i> and <i>R. labiosorediata</i> , two new species of the <i>R. pollinaria</i> group (Ascomycota: Ramalinaceae), and new typifications for <i>Lichen pollinarius</i> and <i>L. squarrosus</i> . Lichenologist, 2017, 49, 301-319.	0.5	13
2626	Molecular phylogeny and morphology of Pseudomallada (Neuroptera: Chrysopidae), one of the largest genera within Chrysopidae. Zoological Journal of the Linnean Society, 2017, 180, 556-569.	1.0	13
2627	Developing integrative systematics in the informatics and genomic era, and calling for a global Biodiversity Cyberbank. Journal of Systematics and Evolution, 2017, 55, 308-321.	1.6	43
2628	Dissecting functions of <i>SEPALLATA</i> -like <i>MADS</i> box genes in patterning of the pseudanthial inflorescence of <i>Gerbera hybrida</i> . New Phytologist, 2017, 216, 939-954.	3.5	46
2629	Genome-wide analysis of carbohydrate-active enzymes in <i>Pyramimonas parkeae</i> (Prasinophyceae). Journal of Phycology, 2017, 53, 1072-1086.	1.0	7
2630	Increasing phylogenetic support for explosively radiating taxa: The promise of high-throughput sequencing for <i>Oxytropis</i> (Fabaceae). Journal of Systematics and Evolution, 2017, 55, 385-404.	1.6	39
2631	The Discovery of Wild Date Palms in Oman Reveals a Complex Domestication History Involving Centers in the Middle East and Africa. Current Biology, 2017, 27, 2211-2218.e8.	1.8	63
2632	Maullinia braseltonii sp. nov. (Rhizaria, Phytomyxea, Phagomyxida): A Cyst-forming Parasite of the Bull Kelp Durvillaea spp. (Stramenopila, Phaeophyceae, Fucales). Protist, 2017, 168, 468-480.	0.6	30
2633	Divergent copies of the large inverted repeat in the chloroplast genomes of ulvophycean green algae. Scientific Reports, 2017, 7, 994.	1.6	77
2634	Nuclear genomes distinguish cryptic species suggested by their DNA barcodes and ecology. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 8313-8318.	3.3	89

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2635	Accelerated Evolution and Functional Divergence of the Dim Light Visual Pigment Accompanies Cichlid Colonization of Central America. <i>Molecular Biology and Evolution</i> , 2017, 34, 2650-2664.	3.5	39
2636	Phenetic Comparison of Prokaryotic Genomes Using k-mers. <i>Molecular Biology and Evolution</i> , 2017, 34, 2716-2729.	3.5	20
2637	Freshwater planarian diversity (Platyhelminthes: Tricladida: Dugesiidae) in Madagascar: new species, cryptic species, with a redefinition of character states. <i>Zoological Journal of the Linnean Society</i> , 2017, 181, 727-756.	1.0	13
2638	Analysis of large 16S rRNA Illumina data sets: Impact of singleton read filtering on microbial community description. <i>Molecular Ecology Resources</i> , 2017, 17, e122-e132.	2.2	55
2639	Dynamics of genetic and morphological diversification in an incipient intra-island radiation of Philippine rodents (Muridae: <i>Bullimus</i>). <i>Journal of Biogeography</i> , 2017, 44, 2585-2594.	1.4	9
2640	The Compositae Tree of Life in the age of phylogenomics. <i>Journal of Systematics and Evolution</i> , 2017, 55, 405-410.	1.6	61
2641	Insights into the historical assembly of East Asian subtropical evergreen broadleaved forests revealed by the temporal history of the tea family. <i>New Phytologist</i> , 2017, 215, 1235-1248.	3.5	119
2642	Structure and evolution of ENTH and VHS/ENTH-like domains in tepsin. <i>Traffic</i> , 2017, 18, 590-603.	1.3	9
2643	Phylogenetic relationships of diurnal, phytotelm-breeding <i>Melanophryniscus</i> (Anura: Bufonidae) based on mitogenomic data. <i>Gene</i> , 2017, 628, 194-199.	1.0	3
2644	Inferring the shallow phylogeny of true salamanders (<i>Salamandra</i>) by multiple phylogenomic approaches. <i>Molecular Phylogenetics and Evolution</i> , 2017, 115, 16-26.	1.2	44
2645	Phylogeny of saprobic microfungi from Southern Europe. <i>Studies in Mycology</i> , 2017, 86, 53-97.	4.5	126
2646	Streptophage-mediated control of off-flavour taint producing streptomycetes isolated from barramundi ponds. <i>Synthetic and Systems Biotechnology</i> , 2017, 2, 105-112.	1.8	11
2647	Molecular phylogeny of Miltogramminae (Diptera: Sarcophagidae): Implications for classification, systematics and evolution of larval feeding strategies. <i>Molecular Phylogenetics and Evolution</i> , 2017, 116, 49-60.	1.2	39
2648	The phylogeny of extant starfish (Asteroidea: Echinodermata) including <i>Xyloplax</i> , based on comparative transcriptomics. <i>Molecular Phylogenetics and Evolution</i> , 2017, 115, 161-170.	1.2	40
2649	Rates and relations of mitochondrial genome evolution across the Echinoidea, with special focus on the superfamily Odontophora. <i>Ecology and Evolution</i> , 2017, 7, 4543-4551.	0.8	11
2650	Continuity and Admixture in the Last Five Millennia of Levantine History from Ancient Canaanite and Present-Day Lebanese Genome Sequences. <i>American Journal of Human Genetics</i> , 2017, 101, 274-282.	2.6	102
2651	Molecular phylogeny of Pasiphaeidae (Crustacea, Decapoda, Caridea) reveals systematic incongruence of the current classification. <i>Molecular Phylogenetics and Evolution</i> , 2017, 115, 171-180.	1.2	19
2652	Molecular phylogeny of the lower acorn barnacle families (Bathylasmataceae, Chionelasmataceae, Tj ETQq1 1 0.784314 rgBT /Overlock family classification. <i>Zoological Journal of the Linnean Society</i> , 2017, 180, 542-555.	1.0	14

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2653	Genome-scale data reveal that endemic <i>Poecilia</i> populations from small sulphidic springs display no evidence of inbreeding. <i>Molecular Ecology</i> , 2017, 26, 4920-4934.	2.0	8
2654	Cool Geckos: Does Plesiomorphy Explain Morphological Similarities between Geckos from the Southern Cone?. <i>Journal of Herpetology</i> , 2017, 51, 330.	0.2	13
2655	Discovery and genomic analyses of hybridization between divergent lineages of <i>Trypanosoma congolense</i> , causative agent of Animal African Trypanosomiasis. <i>Molecular Ecology</i> , 2017, 26, 6524-6538.	2.0	50
2656	Diversity of Diptera families that pollinate <i>Ceropegia</i> (Apocynaceae) trap flowers: An update in light of new data and phylogenetic analyses. <i>Flora: Morphology, Distribution, Functional Ecology of Plants</i> , 2017, 234, 233-244.	0.6	21
2657	Foreign Plastid Sequences in Plant Mitochondria are Frequently Acquired Via Mitochondrion-to-Mitochondrion Horizontal Transfer. <i>Scientific Reports</i> , 2017, 7, 43402.	1.6	64
2658	Divergent evolution and niche differentiation within the common peatmoss <i>Sphagnum magellanicum</i> . <i>American Journal of Botany</i> , 2017, 104, 1060-1072.	0.8	28
2659	Evolutionary history of the extant amphioxus lineage with shallow-branching diversification. <i>Scientific Reports</i> , 2017, 7, 1157.	1.6	27
2660	Evolution of sex-dependent mtDNA transmission in freshwater mussels (<i>Bivalvia</i> : Unionida). <i>Scientific Reports</i> , 2017, 7, 1551.	1.6	40
2661	Regulation of chloroplast and nucleomorph replication by the cell cycle in the cryptophyte <i>Guillardia theta</i> . <i>Scientific Reports</i> , 2017, 7, 2345.	1.6	9
2662	The importance of naming cryptic species and the conservation of endemic subterranean amphipods. <i>Scientific Reports</i> , 2017, 7, 3391.	1.6	140
2663	Origin and evolutionary history of freshwater Rhodophyta: further insights based on phylogenomic evidence. <i>Scientific Reports</i> , 2017, 7, 2934.	1.6	25
2664	Molecular Phylogenies indicate a Paleo-Tibetan Origin of Himalayan Lazy Toads (<i>Scutiger</i>). <i>Scientific Reports</i> , 2017, 7, 3308.	1.6	25
2665	Functional variants of the melanocortin-4 receptor associated with the Odontoceti and Mysticeti suborders of cetaceans. <i>Scientific Reports</i> , 2017, 7, 5684.	1.6	4
2666	A genomic glance through the fog of plasticity and diversification in <i>Pocillopora</i> . <i>Scientific Reports</i> , 2017, 7, 5991.	1.6	87
2667	Comparative genomic analysis of <i>Paenibacillus</i> sp. SSG-1 and its closely related strains reveals the effect of glycometabolism on environmental adaptation. <i>Scientific Reports</i> , 2017, 7, 5720.	1.6	9
2668	Genomic epidemiology of global <i>Klebsiella pneumoniae</i> carbapenemase (KPC)-producing <i>Escherichia coli</i> . <i>Scientific Reports</i> , 2017, 7, 5917.	1.6	108
2669	Molecular diversity of benthic ctenophores (<i>Coeloplanidae</i>). <i>Scientific Reports</i> , 2017, 7, 6365.	1.6	21
2670	Metabolic pathway and cell adaptation mechanisms revealed through genomic, proteomic and transcription analysis of a <i>Sphingomonas haloaromaticamans</i> strain degrading ortho-phenylphenol. <i>Scientific Reports</i> , 2017, 7, 6449.	1.6	25

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2671	Global biogeography, cryptic species and systematic issues in the shrimp genus <i>Hippolyte</i> Leach, 1814 (Decapoda: Caridea: Hippolytidae) by multimarker analyses. <i>Scientific Reports</i> , 2017, 7, 6697.	1.6	16
2672	Recent increased identification and transmission of HIV-1 unique recombinant forms in Sweden. <i>Scientific Reports</i> , 2017, 7, 6371.	1.6	13
2673	A First Phylogeny of the Genus <i>Dimocarpus</i> and Suggestions for Revision of Some Taxa Based on Molecular and Morphological Evidence. <i>Scientific Reports</i> , 2017, 7, 6716.	1.6	8
2674	Two new species of <i>Endocarpon</i> (Verrucariaceae, Ascomycota) from China. <i>Scientific Reports</i> , 2017, 7, 7193.	1.6	6
2675	Long-spurred <i>Angraecum</i> orchids and long-tongued sphingid moths on Madagascar: a time frame for Darwin's predicted <i>Xanthopan/Angraecum</i> coevolution. <i>Biological Journal of the Linnean Society</i> , 2017, 122, 469-478.	0.7	13
2676	Taxonomy and Phylogeny of <i>Aspiciliella</i> , a Resurrected genus of Megasporaceae, Including the New Species <i>A. portosantana</i> . <i>Herzogia</i> , 2017, 30, 166-176.	0.1	13
2677	Plastome sequences of an ancient fern lineage reveal remarkable changes in gene content and architecture. <i>American Journal of Botany</i> , 2017, 104, 1008-1018.	0.8	25
2678	Phylogeography of freshwater fishes of the Qilian Mountains area (<i>Triplophysa leptosoma</i> , Cobitidae:). <i>Tj ETQq1 1 0,784314 rgBT /Over</i>	0.4	1
2679	Three partial mitochondrial genomes from <i>Ips</i> (Coleoptera: Curculionidae, Scolytinae) contribute to the phylogeny of Scolytinae. <i>Journal of Asia-Pacific Entomology</i> , 2017, 20, 1007-1013.	0.4	5
2680	Phylogenetics of Australasian gall flies (Diptera: Fergusoninidae): Evolutionary patterns of host-shifting and gall morphology. <i>Molecular Phylogenetics and Evolution</i> , 2017, 115, 140-160.	1.2	4
2681	Generic recircumscription of <i>Parasenecio</i> (Asteraceae: Senecioneae) based on nuclear ribosomal and plastid DNA sequences, with descriptions of two new genera. <i>Botanical Journal of the Linnean Society</i> , 2017, 184, 418-443.	0.8	12
2682	Cuticle micromorphology and the evolution of characters in leaves of <i>Taxaceae</i> s.l.. <i>Botanical Journal of the Linnean Society</i> , 2017, 184, 503-517.	0.8	8
2683	Molecular phylogeography of endangered Cuban hutias within the Caribbean radiation of capromyid rodents. <i>Journal of Mammalogy</i> , 2017, 98, 950-963.	0.6	19
2684	Large-Scale Identification of <i>Wolbachia pipientis</i> Effectors. <i>Genome Biology and Evolution</i> , 2017, 9, 1925-1937.	1.1	58
2685	Phylogenetic evaluation of <i>Amyntas</i> earthworms from South China reveals the initial ancestral state of spermathecae. <i>Molecular Phylogenetics and Evolution</i> , 2017, 115, 106-114.	1.2	11
2686	Factors contributing to the accumulation of reproductive isolation: A mixed model approach. <i>Ecology and Evolution</i> , 2017, 7, 5808-5820.	0.8	13
2687	A re-evaluation of diversity of the <i>Aporocotylidae</i> Odhner, 1912 in <i>Siganus fuscescens</i> (Houttuyn) (Perciformes: Siganidae) and associated species. <i>Systematic Parasitology</i> , 2017, 94, 717-737.	0.5	14
2688	Evolution of mitochondrial energy metabolism genes associated with hydrothermal vent adaption of <i>Alvinocaridid</i> shrimps. <i>Genes and Genomics</i> , 2017, 39, 1367-1376.	0.5	21

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2689	Redescription of the halophile ciliate, <i>Blepharisma halophilum</i> Ruinen, 1938 (Ciliophora,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 747 Td (h Journal of Protistology, 2017, 61, 20-28.	0.5	16
2690	Whole genome sequencing of <i>Mycobacterium bovis</i> to obtain molecular fingerprints in human and cattle isolates from Baja California, Mexico. <i>International Journal of Infectious Diseases</i> , 2017, 63, 48-56.	1.5	37
2691	<i>Syndesmis aethopharynx</i> (Umagillidae, Rhabdocoela, Platyhelminthes) from the sea urchin <i>Paracentrotus lividus</i> : First record from the Eastern Mediterranean, phylogenetic position and intraspecific morphological variation. <i>Parasitology International</i> , 2017, 66, 848-858.	0.6	3
2692	Characterization and phylogenetic analysis of a <i>Cunninghamella bertholletiae</i> isolate from a bottlenose dolphin (<i>Tursiops truncatus</i>). <i>Revista Iberoamericana De Micologia</i> , 2017, 34, 215-219.	0.4	4
2693	The first complete genomes of <i>Metalmarks</i> and the classification of butterfly families. <i>Genomics</i> , 2017, 109, 485-493.	1.3	20
2694	In search of the phylogenetic affinity of the temperate woody bamboos from Madagascar, with description of a new species (Bambusoideae, Poaceae). <i>Journal of Systematics and Evolution</i> , 2017, 55, 453-465.	1.6	10
2695	Phylogeny and taxonomy of the genus <i>Ilyodon</i> Eigenmann, 1907 (Teleostei: Goodeidae), based on mitochondrial and nuclear DNA sequences. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2017, 55, 340-355.	0.6	13
2696	A Prospective Cohort Multicenter Study of Molecular Epidemiology and Phylogenomics of <i>Staphylococcus aureus</i> Bacteremia in Nine Latin American Countries. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	95
2697	Methane-Fueled Syntrophy through Extracellular Electron Transfer: Uncovering the Genomic Traits Conserved within Diverse Bacterial Partners of Anaerobic Methanotrophic Archaea. <i>MBio</i> , 2017, 8, .	1.8	62
2698	Mitochondrial Genomes of Two Pygmy Grasshoppers (Orthoptera: Tetrigoidea) and a Comparative Analysis of Caelifera Mitogenomes. <i>Zoological Science</i> , 2017, 34, 287.	0.3	2
2700	Evolution of novel mimicry rings facilitated by adaptive introgression in tropical butterflies. <i>Molecular Ecology</i> , 2017, 26, 5160-5172.	2.0	70
2701	Genomic timetree and historical biogeography of Caribbean island ameiva lizards (<i>Pholidoscelis</i> : Teiidae). <i>Ecology and Evolution</i> , 2017, 7, 7080-7090.	0.8	25
2702	<i>Viridivalis adhaerens</i> gen. et sp. nov., a novel colony-forming chlorarachniophyte. <i>Journal of Plant Research</i> , 2017, 130, 999-1012.	1.2	3
2703	Present-day sympatry belies the evolutionary origin of a high-order polyploid. <i>New Phytologist</i> , 2017, 216, 279-290.	3.5	13
2704	Systematics and evolution of the whirligig beetle tribe Dineutini (Coleoptera: Gyrinidae: Gyrininae). <i>Zoological Journal of the Linnean Society</i> , 2017, 181, 118-150.	1.0	20
2705	The Divided Bacterial Genome: Structure, Function, and Evolution. <i>Microbiology and Molecular Biology Reviews</i> , 2017, 81, .	2.9	190
2706	Transitions from distyly to homostyly are associated with floral evolution in the buckwheat genus (<i>Fagopyrum</i>). <i>American Journal of Botany</i> , 2017, 104, 1232-1240.	0.8	17
2707	Genome-wide screening of <i>Oryza sativa</i> ssp. japonica and indica reveals a complex family of proteins with ribosome-inactivating protein domains. <i>Phytochemistry</i> , 2017, 143, 87-97.	1.4	8

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2708	The draft genome sequence of a desert tree <i>Populus pruinosa</i> . <i>GigaScience</i> , 2017, 6, 1-7.	3.3	61
2709	Phylogenetic evidence from freshwater crayfishes that cave adaptation is not an evolutionary dead-end. <i>Evolution; International Journal of Organic Evolution</i> , 2017, 71, 2522-2532.	1.1	38
2710	Grape pomace compost harbors organohalide-respiring <i>Dehalogenimonas</i> species with novel reductive dehalogenase genes. <i>ISME Journal</i> , 2017, 11, 2767-2780.	4.4	118
2711	Third time lucky? Another substantially revised sectional classification for Australasian <i>Plagiochila</i> (<i>Plagiochilaceae</i> : <i>Jungermanniopsida</i>). <i>Australian Systematic Botany</i> , 2017, 30, 70.	0.3	5
2712	Succession of arbuscular mycorrhizal fungi along a 52-years agricultural recultivation chronosequence. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	1.3	19
2713	The Zhenya Mammoth (<i>Mammuthus primigenius</i> (Blum.)): Taphonomy, geology, age, morphology and ancient DNA of a 48,000 year old frozen mummy from western Taimyr, Russia. <i>Quaternary International</i> , 2017, 445, 104-134.	0.7	20
2714	Molecular phylogenetics and definition of the <i>Acrapex minima</i> Janse group (Lepidoptera, Noctuidae). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5</i> <i>Societe Entomologique De France</i> , 2017, 53, 219-235.	0.4	4
2715	Molecular Tracing of the Geographical Origin of Human Immunodeficiency Virus Type 1 Infection and Patterns of Epidemic Spread Among Migrants Who Inject Drugs in Athens. <i>Clinical Infectious Diseases</i> , 2017, 65, 2078-2084.	2.9	19
2716	Release from prey preservation behavior via prey switch allowed diversification of cuticular hydrocarbon profiles in digger wasps. <i>Evolution; International Journal of Organic Evolution</i> , 2017, 71, 2562-2571.	1.1	5
2717	Isolation, fatty acid profiles and cryopreservation of marine thraustochytrids from mangrove habitats in Thailand. <i>Botanica Marina</i> , 2017, 60, .	0.6	19
2718	Population structure of a widespread bat (<i>Tadarida brasiliensis</i>) in an island system. <i>Ecology and Evolution</i> , 2017, 7, 7585-7598.	0.8	24
2719	Phylogenomic Resolution of the Phylogeny of Laurasiatherian Mammals: Exploring Phylogenetic Signals within Coding and Noncoding Sequences. <i>Genome Biology and Evolution</i> , 2017, 9, 1998-2012.	1.1	65
2720	Cophylogenetic analyses reveal extensive host-shift speciation in a highly specialized and host-specific symbiont system. <i>Molecular Phylogenetics and Evolution</i> , 2017, 115, 190-196.	1.2	46
2721	Can asexuality confer a short-term advantage? Investigating apparent biogeographic success in the apomictic triploid fern <i>Myriopteris gracilis</i> . <i>American Journal of Botany</i> , 2017, 104, 1254-1265.	0.8	7
2722	Evaluation of the Systematic Status of Geographical Variations in <i>Arcuphantes hibanus</i> (Arachnida:). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5</i>	0.3	2
2723	Characterization of influenza A(H1N1)pdm09 viruses isolated from Nepalese and Indian outbreak patients in early 2015. <i>Influenza and Other Respiratory Viruses</i> , 2017, 11, 399-403.	1.5	11
2724	Carbonyl reduction by YmfI in <i>Bacillus subtilis</i> prevents accumulation of an inhibitory EF- ϵ P modification state. <i>Molecular Microbiology</i> , 2017, 106, 236-251.	1.2	26
2725	Comparative Genomics of <i>Bacillus thuringiensis</i> Reveals a Path to Specialized Exploitation of Multiple Invertebrate Hosts. <i>MBio</i> , 2017, 8, .	1.8	43

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2726	Feathermoss and epiphytic <i>Nostoc</i> cooperate differently: expanding the spectrum of plant-cyanobacteria symbiosis. <i>ISME Journal</i> , 2017, 11, 2821-2833.	4.4	69
2727	Genomics of the new species <i>Kingella negevensis</i> : diagnostic issues and identification of a locus encoding a RTX toxin. <i>Microbes and Infection</i> , 2017, 19, 546-552.	1.0	24
2728	The genome analysis of <i>Oleiphilus messinensis</i> ME102 (DSM 13489 T) reveals backgrounds of its obligate alkane-devouring marine lifestyle. <i>Marine Genomics</i> , 2017, 36, 41-47.	0.4	18
2729	Parallel genome reduction in symbionts descended from closely related free-living bacteria. <i>Nature Ecology and Evolution</i> , 2017, 1, 1160-1167.	3.4	62
2730	Phylotranscriptomic consolidation of the jawed vertebrate timetree. <i>Nature Ecology and Evolution</i> , 2017, 1, 1370-1378.	3.4	247
2731	The mitochondrial genomes of the acoelomorph worms <i>Paratomella rubra</i> , <i>Isodiametra pulchra</i> and <i>Archaphanostoma ylva</i> . <i>Scientific Reports</i> , 2017, 7, 1847.	1.6	22
2732	Population genetics and dispersal of the flatworm, <i>Polycelis coronata</i> : a test of the habitat stability hypothesis. <i>Journal of Freshwater Ecology</i> , 2017, 32, 179-192.	0.5	7
2733	The complete mitochondrial genome of the "solar-powered" sea slug <i>Plakobranthus cf. ocellatus</i> (Heterobranchia: Panpulmonata: Sacoglossa). <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 130-131.	0.2	4
2734	The complete mitochondrial genome of a cryptic amphipod species from the <i>Gammarus fossarum</i> complex. <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 17-18.	0.2	12
2735	The complete mitochondrial genome of a yeti crab <i>Kiwa tyleri</i> (Crustacea: Decapod: Tj ETQq1 1 0.784314 rgBT / Overlock 10 Tf 50 34 141-142.	0.2	6
2736	The complete mitogenome of the Emerald Ash Borer (EAB), <i>Agrilus planipennis</i> (Insecta: Tj ETQq0 0 0 rgBT / Overlock 10 Tf 50 34 0.2	0.2	10
2737	The complete mitochondrial genome of <i>Cerion uva uva</i> (Gastropoda: Panpulmonata: Tj ETQq1 1 0.784314 rgBT / Overlock 10 Tf 50 34 0.2	0.2	4
2738	The complete mitochondrial genome of <i>Xiphister atropurpureus</i> (Perciformes: Stichaeidae). <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 161-162.	0.2	7
2739	Complete mitochondrial genome and the phylogenetic position of the Lake Eyre hardyhead (<i>Craterocephalus eyresii</i>), a freshwater atherinid fish endemic to Lake Eyre Basin, South Australia. <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 315-317.	0.2	0
2740	The complete mitochondrial genome of <i>Tringa semipalmata inornata</i> (Charadriiformes; Tj ETQq0 0 0 rgBT / Overlock 10 Tf 50 182 0.2	0.2	1
2741	Complete chloroplast genomes of the <i>Chlamydomonas reinhardtii</i> nonphotosynthetic mutants CC-1375, CC-373, CC-4199, CC-2359 and CC-1051. <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 405-407.	0.2	2
2742	The complete mitochondrial genome of <i>Axis porcinus</i> (Mammalia: Cervidae) from Victoria, Australia, using MiSeq sequencing. <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 453-454.	0.2	2
2743	Endemic diversification in an isolated archipelago with few endemics: an example from a cleaner shrimp species complex in the Tropical Western Atlantic. <i>Biological Journal of the Linnean Society</i> , 2017, 122, 98-112.	0.7	8

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2744	<i>Drosophila melanogaster</i> rhodopsin Rh7 is a UV-to-visible light sensor with an extraordinarily broad absorption spectrum. <i>Scientific Reports</i> , 2017, 7, 7349.	1.6	22
2745	<i>Bifiguratus adelaidae</i> , gen. et sp. nov., a new member of Mucoromycotina in endophytic and soil-dwelling habitats. <i>Mycologia</i> , 2017, 109, 363-378.	0.8	27
2746	Mechanisms of Surface Antigenic Variation in the Human Pathogenic Fungus <i>Pneumocystis jirovecii</i> . <i>MBio</i> , 2017, 8, .	1.8	24
2747	Conserved Gene Microsynteny Unveils Functional Interaction Between Protein Disulfide Isomerase and Rho Guanine-Dissociation Inhibitor Families. <i>Scientific Reports</i> , 2017, 7, 17262.	1.6	16
2748	A genomic perspective of the pink-headed duck <i>Rhodonessa caryophyllacea</i> suggests a long history of low effective population size. <i>Scientific Reports</i> , 2017, 7, 16853.	1.6	8
2749	A novel type I cystatin of parasite origin with atypical legumain-binding domain. <i>Scientific Reports</i> , 2017, 7, 17526.	1.6	17
2750	<i>Polyozellus multiplex</i> (Thelephorales) is a species complex containing four new species. <i>Mycologia</i> , 2017, 109, 975-992.	0.8	6
2751	Subspecies in the global human gut microbiome. <i>Molecular Systems Biology</i> , 2017, 13, 960.	3.2	115
2752	Metagenomics of bolidophyceae in plankton and ice of the White Sea. <i>Biochemistry (Moscow)</i> , 2017, 82, 1538-1548.	0.7	9
2753	Complete chloroplast genome of <i>Pluchea indica</i> (L.) Less. (Asteraceae) and its phylogenetic analysis. <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 918-919.	0.2	3
2754	Genomic Variation and Evolution of <i>Vibrio parahaemolyticus</i> ST36 over the Course of a Transcontinental Epidemic Expansion. <i>MBio</i> , 2017, 8, .	1.8	53
2755	Multilocus DNA barcoding – Species Identification with Multilocus Data. <i>Scientific Reports</i> , 2017, 7, 16601.	1.6	33
2756	Towards a natural classification of <i>Ophiobolus</i> and ophiobolus-like taxa; introducing three novel genera <i>Ophiobolopsis</i> , <i>Paraophiobolus</i> and <i>Pseudoophiobolus</i> in Phaeosphaeriaceae (Pleosporales). <i>Fungal Diversity</i> , 2017, 87, 299-339.	4.7	35
2757	Genetic evolution of influenza H9N2 viruses isolated from various hosts in China from 1994 to 2013. <i>Emerging Microbes and Infections</i> , 2017, 6, 1-11.	3.0	56
2758	Opsins and Their Expression Patterns in the Xiphosuran <i>Limulus polyphemus</i> . <i>Biological Bulletin</i> , 2017, 233, 3-20.	0.7	7
2759	Complete mitochondrial genome of the freshwater red alga <i>Lympha mucosa</i> (Rhodophyta). <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 707-708.	0.2	2
2760	Taxonomy and molecular phylogeny of three marine benthic species of <i>Haslea</i> (Bacillariophyceae), with transfer of two species to <i>Navicula</i> . <i>Diatom Research</i> , 2017, 32, 451-463.	0.5	14
2761	Genomic analyses reveal low mitochondrial and high nuclear diversity in the cyclosporin-producing fungus <i>Tolypocladium inflatum</i> . <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 8517-8531.	1.7	34

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2762	Amphitropical disjunctions in New World Menthinae: Three Pliocene dispersals to South America following late Miocene dispersal to North America from the Old World. <i>American Journal of Botany</i> , 2017, 104, 1695-1707.	0.8	22
2763	Comparative functional genomics of the TPR gene family in <i>Arabidopsis</i> , rice and maize. <i>Molecular Breeding</i> , 2017, 37, 1.	1.0	10
2764	<i>Arambarria</i> the pathogen involved in canker rot of <i>Eucalyptus</i> , native trees wood rots and grapevine diseases in the Southern Hemisphere. <i>Forest Pathology</i> , 2017, 47, e12397.	0.5	14
2765	Parallel Pleistocene amphitropical disjunctions of a parasitic plant and its host. <i>American Journal of Botany</i> , 2017, 104, 1745-1755.	0.8	17
2766	Mitochondrial genome of <i>Dinophilus gyrocilatus</i> (Annelida: Dinophilidae). <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 831-832.	0.2	3
2767	Phylogenetic Profiling of Mitochondrial Proteins and Integration Analysis of Bacterial Transcription Units Suggest Evolution of F1Fo ATP Synthase from Multiple Modules. <i>Journal of Molecular Evolution</i> , 2017, 85, 219-233.	0.8	11
2768	Tuberculosis in Swiss captive Asian elephants: microevolution of <i>Mycobacterium tuberculosis</i> characterized by multilocus variable-number tandem-repeat analysis and whole-genome sequencing. <i>Scientific Reports</i> , 2017, 7, 14647.	1.6	14
2769	Evolutionary history of enigmatic bears in the Tibetan Plateau—Himalaya region and the identity of the yeti. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20171804.	1.2	62
2770	Molecular and phylogenetic analyses of <i>Salmonella Gallinarum</i> trace the origin and diversification of recent outbreaks of fowl typhoid in poultry farms. <i>Veterinary Microbiology</i> , 2017, 212, 80-86.	0.8	16
2771	Different diversity-dependent declines in speciation rate unbalances species richness in terrestrial slugs. <i>Scientific Reports</i> , 2017, 7, 16198.	1.6	6
2772	Multimodal sensorimotor system in unicellular zoospores of a fungus. <i>Journal of Experimental Biology</i> , 2018, 221, .	0.8	13
2773	A workflow of massive identification and application of intron markers using snakes as a model. <i>Ecology and Evolution</i> , 2017, 7, 10042-10055.	0.8	10
2774	The Plastid Genome in Cladophorales Green Algae Is Encoded by Hairpin Chromosomes. <i>Current Biology</i> , 2017, 27, 3771-3782.e6.	1.8	45
2775	Improved Modeling of Compositional Heterogeneity Supports Sponges as Sister to All Other Animals. <i>Current Biology</i> , 2017, 27, 3864-3870.e4.	1.8	244
2776	Memoirs of a frequent flier: Phylogenomics reveals 18 long-distance dispersals between North America and South America in the popcorn flowers (Amsinckiinae). <i>American Journal of Botany</i> , 2017, 104, 1717-1728.	0.8	16
2777	Comparative ecological transcriptomics and the contribution of gene expression to the evolutionary potential of a threatened fish. <i>Molecular Ecology</i> , 2017, 26, 6841-6856.	2.0	30
2778	Mind the gap! Integrating taxonomic approaches to assess ant diversity at the southern extreme of the Atlantic Forest. <i>Ecology and Evolution</i> , 2017, 7, 10451-10466.	0.8	12
2779	Novel Microbial Diversity and Functional Potential in the Marine Mammal Oral Microbiome. <i>Current Biology</i> , 2017, 27, 3752-3762.e6.	1.8	82

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2780	Microdiversity of an Abundant Terrestrial Bacterium Encompasses Extensive Variation in Ecologically Relevant Traits. <i>MBio</i> , 2017, 8, .	1.8	49
2781	Methanogenesis in oxygenated soils is a substantial fraction of wetland methane emissions. <i>Nature Communications</i> , 2017, 8, 1567.	5.8	195
2782	Global population structure and adaptive evolution of aflatoxin-producing fungi. <i>Ecology and Evolution</i> , 2017, 7, 9179-9191.	0.8	25
2783	Colorful seashells: Identification of haem pathway genes associated with the synthesis of porphyrin shell color in marine snails. <i>Ecology and Evolution</i> , 2017, 7, 10379-10397.	0.8	34
2784	A New Lineage of Eukaryotes Illuminates Early Mitochondrial Genome Reduction. <i>Current Biology</i> , 2017, 27, 3717-3724.e5.	1.8	109
2785	A Peptide Signaling System that Rapidly Enforces Paternity in the <i>Aedes aegypti</i> Mosquito. <i>Current Biology</i> , 2017, 27, 3734-3742.e5.	1.8	43
2786	Preliminary phylogeny of <i>Coemansia</i> (Kickxellales), with descriptions of four new species from Taiwan. <i>Mycologia</i> , 2017, 109, 1-17.	0.8	4
2787	Integrated genomic and interfacility patient-transfer data reveal the transmission pathways of multidrug-resistant <i>Klebsiella pneumoniae</i> in a regional outbreak. <i>Science Translational Medicine</i> , 2017, 9, .	5.8	47
2788	Reconstructing Yeasts Phylogenies and Ancestors from Whole Genome Data. <i>Scientific Reports</i> , 2017, 7, 15209.	1.6	16
2789	<i>Ardissonea crystallina</i> has a type of sexual reproduction that is unusual for centric diatoms. <i>Scientific Reports</i> , 2017, 7, 14670.	1.6	16
2790	Global phylogenetic analysis of <i>Escherichia coli</i> and plasmids carrying the <i>mcr-1</i> gene indicates bacterial diversity but plasmid restriction. <i>Scientific Reports</i> , 2017, 7, 15364.	1.6	230
2791	Assigning chemoreceptors to chemosensory pathways in <i>Pseudomonas aeruginosa</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 12809-12814.	3.3	72
2792	Genomic and epidemiological characterisation of a dengue virus outbreak among blood donors in Brazil. <i>Scientific Reports</i> , 2017, 7, 15216.	1.6	40
2794	Resurrecting ancestral genes in bacteria to interpret ancient biosignatures. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2017, 375, 20160352.	1.6	19
2795	Associations among Antibiotic and Phage Resistance Phenotypes in Natural and Clinical <i>Escherichia coli</i> Isolates. <i>MBio</i> , 2017, 8, .	1.8	37
2796	A phylogenetic framework for the <i>Hylocereeae</i> (Cactaceae) and implications for the circumscription of the genera. <i>Phytotaxa</i> , 2017, 327, 1.	0.1	52
2797	Pushing the limits of photoreception in twilight conditions: The rod-like cone retina of the deep-sea pearlsides. <i>Science Advances</i> , 2017, 3, eaao4709.	4.7	55
2798	Testing hypotheses on suprageneric relationships and morphological evolution in the <i>Leucobryaceae</i> (Bryophyta). <i>Plant Systematics and Evolution</i> , 2017, 303, 1383-1397.	0.3	12

#	ARTICLE	IF	CITATIONS
2799	Idiosyncratic Genome Degradation in a Bacterial Endosymbiont of Periodical Cicadas. <i>Current Biology</i> , 2017, 27, 3568-3575.e3.	1.8	37
2800	Integrated view of <i>Vibrio cholerae</i> in the Americas. <i>Science</i> , 2017, 358, 789-793.	6.0	128
2801	<i>Psychonectria hyperantarctica</i> , gen. nov., comb. nov., epitypification and phylogenetic position of an Antarctic bryophilous ascomycete. <i>Mycologia</i> , 2017, 109, 1-7.	0.8	7
2802	Trunk dental tissue evolved independently from underlying dermal bony plates but is associated with surface bones in living odontode-bearing catfish. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20171831.	1.2	17
2803	Molecular phylogenetics and taxonomy in <i>Melanoleuca excissa</i> group, (Tricholomataceae, Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 587 T	0.3	9
2804	Phylogenetic study of the <i>Colletotrichum</i> species on imported citrus fruits uncovers a low diversity and a new species in the <i>Colletotrichum gigasporum</i> complex. <i>Fungal Biology</i> , 2017, 121, 858-868.	1.1	23
2805	Molecular phylogenetics and biogeography of the ambush bugs (Hemiptera: Reduviidae: Phymatinae). <i>Molecular Phylogenetics and Evolution</i> , 2017, 114, 225-233.	1.2	15
2806	Tracing the epidemic history of HIV-1 CRF01_AE clusters using near-complete genome sequences. <i>Scientific Reports</i> , 2017, 7, 4024.	1.6	42
2807	The inclusion of <i>Anogeissus</i> , <i>Buchenavia</i> and <i>Pteleopsis</i> in <i>Terminalia</i> (Combretaceae: Terminaliinae). <i>Botanical Journal of the Linnean Society</i> , 2017, 184, 312-325.	0.8	14
2808	Primordial-like enzymes from bacteria with reduced genomes. <i>Molecular Microbiology</i> , 2017, 105, 508-524.	1.2	28
2809	<i>Dominikia emiratia</i> and <i>Rhizoglosum dunense</i> , two new species in the Glomeromycota. <i>Botany</i> , 2017, 95, 629-639.	0.5	8
2810	<i>Sedum danjoense</i> (Crassulaceae), a new species of succulent plants from the Danjo Islands in Japan. <i>Phytotaxa</i> , 2017, 309, 23.	0.1	8
2811	Threatened but understudied: supporting conservation by understanding the genetic structure of the flat-headed cat. <i>Conservation Genetics</i> , 2017, 18, 1423-1433.	0.8	12
2812	An analysis of Echinacea chloroplast genomes: Implications for future botanical identification. <i>Scientific Reports</i> , 2017, 7, 216.	1.6	52
2813	Phylogenetic relationships of Brazilian <i>Mikania</i> species (Asteraceae, Eupatorieae) based on multilocus DNA markers. <i>Botanical Journal of the Linnean Society</i> , 2017, 184, 326-346.	0.8	10
2814	Macroclimatic niche limits and the evolution of C4 photosynthesis in Gomphrenoideae (Amaranthaceae). <i>Botanical Journal of the Linnean Society</i> , 2017, 184, 283-297.	0.8	11
2815	Malagasy cichlids differentially limit impacts of body shape evolution on oral jaw functional morphology. <i>Evolution; International Journal of Organic Evolution</i> , 2017, 71, 2219-2229.	1.1	19
2816	<i>Streptomyces asenjonii</i> sp. nov., isolated from hyper-arid Atacama Desert soils and emended description of <i>Streptomyces viridosporus</i> Pridham et al. 1958. <i>Antonie Van Leeuwenhoek</i> , 2017, 110, 1133-1148.	0.7	42

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2817	Morphological and molecular analysis of <i>Paratrichodorus teres</i> (Hooper 1962) (Nematoda): Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 747 To <i>Paratrichodorus</i> species. <i>European Journal of Plant Pathology</i> , 2017, 148, 907-917.	0.8	4
2818	<i>Olpidiopsis porphyrae</i> var. <i>koreanae</i> , an endemic endoparasite infecting cultivated <i>Pyropia yezoensis</i> in Korea. <i>Journal of Applied Phycology</i> , 2017, 29, 2003-2012.	1.5	19
2819	Comparative analysis of <i>Dendrobium</i> plastomes and utility of plastomic mutational hotspots. <i>Scientific Reports</i> , 2017, 7, 2073.	1.6	45
2820	The complete mitochondrial genome of northern grasshopper mouse (<i>Onychomys leucogaster</i>). <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 393-394.	0.2	7
2821	Sex-specific evolution during the diversification of live-bearing fishes. <i>Nature Ecology and Evolution</i> , 2017, 1, 1185-1191.	3.4	18
2822	The calmodulin fused kinase novel gene family is the major system in plants converting Ca ²⁺ signals to protein phosphorylation responses. <i>Scientific Reports</i> , 2017, 7, 4127.	1.6	12
2823	Use of whole-genome sequencing and evaluation of the apparent sensitivity and specificity of antemortem tuberculosis tests in the investigation of an unusual outbreak of <i>Mycobacterium bovis</i> infection in a Michigan dairy herd. <i>Journal of the American Veterinary Medical Association</i> , 2017, 251, 206-216.	0.2	26
2824	Spring and early summer species of <i>Cortinarius</i> , subgenus <i>Telamonia</i> , section <i>Colymbadini</i> and <i>Flavobasilis</i> , in the mountains of western North America. <i>Mycologia</i> , 2017, 109, 443-458.	0.8	8
2825	Detection of misidentifications of species from the <i>Burkholderia cepacia</i> complex and description of a new member, the soil bacterium <i>Burkholderia catarinensis</i> sp. nov.. <i>Pathogens and Disease</i> , 2017, 75, .	0.8	70
2826	Sulfide Generation by Dominant <i>Halanaerobium</i> Microorganisms in Hydraulically Fractured Shales. <i>MSphere</i> , 2017, 2, .	1.3	62
2827	Widespread paleopolyploidy, gene tree conflict, and recalcitrant relationships among the carnivorous <i>Caryophyllales</i> . <i>American Journal of Botany</i> , 2017, 104, 858-867.	0.8	62
2828	Comparative landscape of alternative splicing in fruit plants. <i>Current Plant Biology</i> , 2017, 9-10, 29-36.	2.3	16
2829	CTCF binding landscape in jawless fish with reference to Hox cluster evolution. <i>Scientific Reports</i> , 2017, 7, 4957.	1.6	35
2830	Genomic Epidemiology of NDM-1-Encoding Plasmids in Latin American Clinical Isolates Reveals Insights into the Evolution of Multidrug Resistance. <i>Genome Biology and Evolution</i> , 2017, 9, 1725-1741.	1.1	48
2831	Specificity in diversity: single origin of a widespread ciliate-bacteria symbiosis. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20170764.	1.2	34
2832	Whole Genome Sequence of the Heterozygous Clinical Isolate <i>Candida krusei</i> 81-B-5. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2883-2889.	0.8	31
2833	Phylogeography of <i>Petrolisthes armatus</i> , an invasive species with low dispersal ability. <i>Scientific Reports</i> , 2017, 7, 3359.	1.6	17
2835	Life at the beach: comparative phylogeography of a sandhopper and its nematode parasite reveals extreme lack of parasite mtDNA variation. <i>Biological Journal of the Linnean Society</i> , 2017, 122, 113-132.	0.7	12

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2836	Molecular phylogeny of the Haplospalchnata Olson, Cribb, Tkach, Bray and Littlewood, 2003, with a description of <i>Schikhobalotrema huffmanii</i> n. sp.. <i>Acta Parasitologica</i> , 2017, 62, 502-512.	0.4	7
2837	Genome-Wide Sequence and Expression Analysis of the NAC Transcription Factor Family in Polyploid Wheat. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3019-3029.	0.8	59
2838	Genome analysis of <i>Diploscapter coronatus</i> : insights into molecular peculiarities of a nematode with parthenogenetic reproduction. <i>BMC Genomics</i> , 2017, 18, 478.	1.2	30
2839	Molecular phylogenetic studies unmask overlooked diversity in the tropical lichenized fungal genus <i>Bulbothrix</i> s.l. (Parmeliaceae, Ascomycota). <i>Botanical Journal of the Linnean Society</i> , 2017, 184, 387-399.	0.8	8
2840	Biting midges (Ceratopogonidae) as vectors of avian trypanosomes. <i>Parasites and Vectors</i> , 2017, 10, 224.	1.0	31
2841	Data on the time of integration of the human mitochondrial pseudogenes (NUMTs) into the nuclear genome. <i>Data in Brief</i> , 2017, 13, 536-544.	0.5	4
2842	Floral micromorphology and anatomy and its systematic application to Neotropical <i>Bulbophyllum</i> section <i>Micranthae</i> (Orchidaceae). <i>Botanical Journal of the Linnean Society</i> , 2017, 183, 294-315.	0.8	8
2843	Diet-induced reconstruction of mucosal microbiota associated with alterations of epithelium lectin expression and regulation in the maintenance of rumen homeostasis. <i>Scientific Reports</i> , 2017, 7, 3941.	1.6	5
2844	Genetic variation and phylogenetic relationships of the ectomycorrhizal <i>Floccularia luteovirens</i> on the Qinghai-Tibet Plateau. <i>Journal of Microbiology</i> , 2017, 55, 600-606.	1.3	12
2845	A Critical Review on the Use of Support Values in Tree Viewers and Bioinformatics Toolkits. <i>Molecular Biology and Evolution</i> , 2017, 34, 1535-1542.	3.5	28
2846	Contrasting Rates of Molecular Evolution and Patterns of Selection among Gymnosperms and Flowering Plants. <i>Molecular Biology and Evolution</i> , 2017, 34, 1363-1377.	3.5	164
2847	Single Cell Transcriptomics, Mega-Phylogeny, and the Genetic Basis of Morphological Innovations in Rhizaria. <i>Molecular Biology and Evolution</i> , 2017, 34, 1557-1573.	3.5	35
2848	Convergence of Domain Architecture, Structure, and Ligand Affinity in Animal and Plant RNA-Binding Proteins. <i>Molecular Biology and Evolution</i> , 2017, 34, 1429-1444.	3.5	13
2849	Tracing Genetic Exchange and Biogeography of <i>Cryptococcus neoformans</i> var. <i>grubii</i> at the Global Population Level. <i>Genetics</i> , 2017, 207, 327-346.	1.2	105
2850	Plastid genome structure and phylogenomics of Nymphaeales: conserved gene order and new insights into relationships. <i>Plant Systematics and Evolution</i> , 2017, 303, 1251-1270.	0.3	41
2851	Andean Mountain Building Did not Preclude Dispersal of Lowland Epiphytic Orchids in the Neotropics. <i>Scientific Reports</i> , 2017, 7, 4919.	1.6	35
2852	The complete chloroplast genome of <i>Cupressus chengiana</i> . <i>Conservation Genetics Resources</i> , 2017, 9, 347-349.	0.4	1
2853	Characterization of the complete chloroplast genome of the golden crane butterfly, <i>Euonymus schensianus</i> (Celastraceae). <i>Conservation Genetics Resources</i> , 2017, 9, 545-547.	0.4	6

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2854	The complete mitochondrial genome of the copperhead (<i>Agkistrodon contortrix</i>) and phylogenetic analyses of Crotalinae (Serpentes; Colubroidea; Viperidae). <i>Conservation Genetics Resources</i> , 2017, 9, 607-611.	0.4	0
2855	The complete chloroplast genomes of <i>Adenolobus garipensis</i> and <i>Cercis glabra</i> (Cercidoideae.) <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10</i>	0.4	17
2856	Resurrecting the Dead (Molecules). <i>Computational and Structural Biotechnology Journal</i> , 2017, 15, 351-358.	1.9	4
2857	DNA barcoding of the Thai species of terrestrial earthworms in the genera <i>Amyntas</i> and <i>Metaphire</i> (Haplotaxida: Megascolecidae). <i>European Journal of Soil Biology</i> , 2017, 81, 39-47.	1.4	21
2858	An L-threonine transaldolase is required for L-threo- β -hydroxy- β -amino acid assembly during obafluorin biosynthesis. <i>Nature Communications</i> , 2017, 8, 15935.	5.8	70
2859	A mitogenomic timetree for Darwin's enigmatic South American mammal <i>Macrauchenia patachonica</i> . <i>Nature Communications</i> , 2017, 8, 15951.	5.8	71
2860	Unexplored diversity and strain-level structure of the skin microbiome associated with psoriasis. <i>Npj Biofilms and Microbiomes</i> , 2017, 3, 14.	2.9	159
2861	A novel plant E3 ligase stabilizes <i>Escherichia coli</i> heat shock factor σ 32. <i>Scientific Reports</i> , 2017, 7, 4045.	1.6	3
2862	Resolution and reconciliation of non-binary gene trees with transfers, duplications and losses. <i>Bioinformatics</i> , 2017, 33, 980-987.	1.8	24
2863	Transcript variations, phylogenetic tree and chromosomal localization of porcine aryl hydrocarbon receptor (AhR) and AhR nuclear translocator (ARNT) genes. <i>Journal of Genetics</i> , 2017, 96, 75-85.	0.4	1
2864	Molecular phylogeny reveals food plasticity in the evolution of true ladybird beetles (Coleoptera:) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 3</i>	3.2	52
2865	The wolf reference genome sequence (<i>Canis lupus lupus</i>) and its implications for <i>Canis</i> spp. population genomics. <i>BMC Genomics</i> , 2017, 18, 495.	1.2	73
2866	Molecular Evidence of <i>Apatococcus</i> , including <i>A. fuscidae</i> sp. nov., as Photobiont in the Genus <i>Fuscidea</i> . <i>Protist</i> , 2017, 168, 425-438.	0.6	12
2867	Impact of species delimitation and sampling on niche models and phylogeographical inference: A case study of the East African reed frog <i>Hyperolius substriatus</i> Ahl, 1931. <i>Molecular Phylogenetics and Evolution</i> , 2017, 114, 261-270.	1.2	8
2868	Phylogenomics reveals rapid, simultaneous diversification of three major clades of Gondwanan frogs at the Cretaceous-Paleogene boundary. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E5864-E5870.	3.3	261
2869	Do plant-eating insect lineages pass through phases of host-use generalism during speciation and host switching? Phylogenetic evidence. <i>Evolution; International Journal of Organic Evolution</i> , 2017, 71, 2100-2109.	1.1	20
2870	TreeToReads - a pipeline for simulating raw reads from phylogenies. <i>BMC Bioinformatics</i> , 2017, 18, 178.	1.2	16
2871	OrthoReD: a rapid and accurate orthology prediction tool with low computational requirement. <i>BMC Bioinformatics</i> , 2017, 18, 310.	1.2	27

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2872	Comparative analyses of glycerotoxin expression unveil a novel structural organization of the bloodworm venom system. <i>BMC Evolutionary Biology</i> , 2017, 17, 64.	3.2	17
2873	Correlated duplications and losses in the evolution of palmitoylation writer and eraser families. <i>BMC Evolutionary Biology</i> , 2017, 17, 83.	3.2	4
2874	Evolutionary origin and function of NOX4-art, an arthropod specific NADPH oxidase. <i>BMC Evolutionary Biology</i> , 2017, 17, 92.	3.2	14
2875	Distinct genetic differentiation and species diversification within two marine nematodes with different habitat preference in Antarctic sediments. <i>BMC Evolutionary Biology</i> , 2017, 17, 120.	3.2	21
2876	Phylogenomic analyses of Crassicitellata support major Northern and Southern Hemisphere clades and a Pangaean origin for earthworms. <i>BMC Evolutionary Biology</i> , 2017, 17, 123.	3.2	27
2877	Ixora (Rubiaceae) on the Philippines - crossroad or cradle?. <i>BMC Evolutionary Biology</i> , 2017, 17, 131.	3.2	5
2878	The conquering of North America: dated phylogenetic and biogeographic inference of migratory behavior in bee hummingbirds. <i>BMC Evolutionary Biology</i> , 2017, 17, 126.	3.2	26
2879	MARS: improving multiple circular sequence alignment using refined sequences. <i>BMC Genomics</i> , 2017, 18, 86.	1.2	35
2880	Three novel Pseudomonas phages isolated from composting provide insights into the evolution and diversity of tailed phages. <i>BMC Genomics</i> , 2017, 18, 346.	1.2	32
2881	No evidence for a bovine mastitis Escherichia coli pathotype. <i>BMC Genomics</i> , 2017, 18, 359.	1.2	85
2882	Whole genome sequencing reveals within-host genetic changes in paired meningococcal carriage isolates from Ethiopia. <i>BMC Genomics</i> , 2017, 18, 407.	1.2	25
2883	Comparative transcriptomic analysis of the evolution and development of flower size in <i>Saltugilia</i> (Polemoniaceae). <i>BMC Genomics</i> , 2017, 18, 475.	1.2	18
2884	Competition assays and physiological experiments of soil and phyllosphere yeasts identify <i>Candida subhashii</i> as a novel antagonist of filamentous fungi. <i>BMC Microbiology</i> , 2017, 17, 4.	1.3	77
2885	Comparative genomics and evolution of the amylase-binding proteins of oral streptococci. <i>BMC Microbiology</i> , 2017, 17, 94.	1.3	13
2886	Emergence and spread of a new community-genotype methicillin-resistant <i>Staphylococcus aureus</i> clone in Colombia. <i>BMC Infectious Diseases</i> , 2017, 17, 108.	1.3	6
2887	Nuclear genetic codes with a different meaning of the UAG and the UAA codon. <i>BMC Biology</i> , 2017, 15, 8.	1.7	25
2888	Cleavage modification did not alter blastomere fates during bryozoan evolution. <i>BMC Biology</i> , 2017, 15, 33.	1.7	29
2889	Assessment of contemporary genetic diversity and inter-taxa/inter-region exchange of avian paramyxovirus serotype 1 in wild birds sampled in North America. <i>Virology Journal</i> , 2017, 14, 43.	1.4	17

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2890	Complete genome sequence of Tâ€™Ho virus, a novel putative flavivirus from the Yucatan Peninsula of Mexico. <i>Virology Journal</i> , 2017, 14, 110.	1.4	3
2891	The evolution of CHROMOMETHYLASES and gene body DNA methylation in plants. <i>Genome Biology</i> , 2017, 18, 65.	3.8	124
2892	Genome-wide characterization of cellulases from the hemi-biotrophic plant pathogen, <i>Bipolaris sorokiniana</i> , reveals the presence of a highly stable GH7 endoglucanase. <i>Biotechnology for Biofuels</i> , 2017, 10, 135.	6.2	23
2893	New var reconstruction algorithm exposes high var sequence diversity in a single geographic location in Mali. <i>Genome Medicine</i> , 2017, 9, 30.	3.6	13
2894	<i>Caenorhabditis monodelphis</i> sp. n.: defining the stem morphology and genomics of the genus <i>Caenorhabditis</i> . <i>BMC Zoology</i> , 2017, 2, .	0.3	33
2895	The chordate ancestor possessed a single copy of the <i>Brachyury</i> gene for notochord acquisition. <i>Zoological Letters</i> , 2017, 3, 4.	0.7	13
2896	The phylogenetic position of dicyemid mesozoans offers insights into spiralian evolution. <i>Zoological Letters</i> , 2017, 3, 6.	0.7	37
2897	Newly recorded species of the genus <i>Synura</i> (Synurophyceae) from Korea. <i>Journal of Ecology and Environment</i> , 2017, 41, .	1.6	15
2898	Unmatched DNA preservation prove arctic hare and sheep wool in Norse Greenlandic textile from âœœThe Farm Beneath the Sandâœ. <i>Journal of Archaeological Science: Reports</i> , 2017, 14, 603-608.	0.2	6
2899	Phylogenomics and comparative genomic studies delineate six main clades within the family Enterobacteriaceae and support the reclassification of several polyphyletic members of the family. <i>Infection, Genetics and Evolution</i> , 2017, 54, 108-127.	1.0	112
2900	Phylogenetic analysis of <i>Placobdella</i> (Hirudinea: Rhynchobdellida: Glossiphoniidae) with consideration of COI variation. <i>Molecular Phylogenetics and Evolution</i> , 2017, 114, 234-248.	1.2	30
2901	A phylogeny of Southern Hemisphere whelks (Gastropoda: Buccinulidae) and concordance with the fossil record. <i>Molecular Phylogenetics and Evolution</i> , 2017, 114, 367-381.	1.2	26
2902	Novel approaches for Spatial and Molecular Surveillance of Porcine Reproductive and Respiratory Syndrome Virus (PRRSv) in the United States. <i>Scientific Reports</i> , 2017, 7, 4343.	1.6	27
2903	Mitogenomic analyses support the recent division of the genus <i>Orthotrichum</i> (Orthotrichaceae,) Tj ETQq1 1 0.784314 rgBT /Overlock 1.6 31	1.6	31
2904	MRSA Transmission Dynamics Among Interconnected Acute, Intermediate-Term, and Long-Term Healthcare Facilities in Singapore. <i>Clinical Infectious Diseases</i> , 2017, 64, S76-S81.	2.9	33
2905	Unravelling diversity of deep-sea copepods using integrated morphological and molecular techniques. <i>Journal of Plankton Research</i> , 2017, 39, 600-617.	0.8	31
2906	Taxonomic reassessment of the freshwater mussel genus <i>Unio</i> (Bivalvia: Unionidae) in Russia and Ukraine based on morphological and molecular data. <i>Zootaxa</i> , 2017, 4286, .	0.2	36
2907	A new genus and new species of freshwater crab (Decapoda: Brachyura: Potamidae Ortman, 1896) from Yunnan Province, China. <i>Zootaxa</i> , 2017, 4286, .	0.2	16

#	ARTICLE	IF	CITATIONS
2908	Cross species selection scans identify components of C ₄ photosynthesis in the grasses. <i>Journal of Experimental Botany</i> , 2017, 68, 127-135.	2.4	61
2909	Detection of Diazotrophy in the Acetylene-Fermenting Anaerobe <i>Pelobacter</i> sp. Strain SFB93. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	15
2910	Description of a new <i>Notocomplana</i> species (Platyhelminthes: Acotylea), new combination and new records of Polycladida from the northeastern Sea of Japan, with a comparison of two different barcoding markers. <i>Zootaxa</i> , 2017, 4282, .	0.2	21
2911	Computational Functional Analysis of Lipid Metabolic Enzymes. <i>Methods in Molecular Biology</i> , 2017, 1609, 195-216.	0.4	2
2912	Nitrogen fixation in a chemoautotrophic lucinid symbiosis. <i>Nature Microbiology</i> , 2017, 2, 16193.	5.9	56
2913	Expanded molecular phylogeny of the genus <i>Bicyclus</i> (Lepidoptera: Nymphalidae) shows the importance of increased sampling for detecting semi-cryptic species and highlights potentials for future studies. <i>Systematics and Biodiversity</i> , 2017, 15, 115-130.	0.5	15
2914	Talpids Mole Phylogeny Unites Shrew Moles and Illuminates Overlooked Cryptic Species Diversity. <i>Molecular Biology and Evolution</i> , 2017, 34, 78-87.	3.5	36
2915	Conservatism and variability of gene expression profiles among homeologous transcription factors in <i>Xenopus laevis</i> . <i>Developmental Biology</i> , 2017, 426, 301-324.	0.9	24
2916	The Genomes of Two Bat Species with Long Constant Frequency Echolocation Calls. <i>Molecular Biology and Evolution</i> , 2017, 34, 20-34.	3.5	38
2917	Mutually exclusive phylogenomic inferences at the root of the angiosperms: <i>Amborella</i> is supported as sister and Observed Variability is biased. <i>Cladistics</i> , 2017, 33, 488-512.	1.5	16
2918	Weak coordination between leaf structure and function among closely related tomato species. <i>New Phytologist</i> , 2017, 213, 1642-1653.	3.5	40
2919	Using mixed mode programming to parallelize an indicator-based evolutionary algorithm for inferring multiobjective phylogenetic histories. <i>Soft Computing</i> , 2017, 21, 5601-5620.	2.1	4
2920	Defensive traits exhibit an evolutionary trade-off and drive diversification in ants. <i>Evolution; International Journal of Organic Evolution</i> , 2017, 71, 315-328.	1.1	77
2921	Sexual reproduction in <i>Schizostauron</i> (Bacillariophyta) and a preliminary phylogeny of the genus. <i>Phycologia</i> , 2017, 56, 77-93.	0.6	19
2922	Multilocus approaches reveal underestimated species diversity and inter-specific gene flow in pikas (<i>Ochotona</i>) from southwestern China. <i>Molecular Phylogenetics and Evolution</i> , 2017, 107, 239-245.	1.2	32
2923	A family-level Tree of Life for bivalves based on a Sanger-sequencing approach. <i>Molecular Phylogenetics and Evolution</i> , 2017, 107, 191-208.	1.2	117
2924	Complete mitochondrial genome and evolutionary analysis of <i>Turritopsis dohrnii</i> , the "immortal" jellyfish with a reversible life-cycle. <i>Molecular Phylogenetics and Evolution</i> , 2017, 107, 232-238.	1.2	13
2925	Arbuscular mycorrhizal interactions of mycoheterotrophic <i>Thismia</i> are more specialized than in autotrophic plants. <i>New Phytologist</i> , 2017, 213, 1418-1427.	3.5	32

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2926	Differences in the expression profile of endo- β -(1,6)-D-galactanase in pathogenic and non-pathogenic races of <i>Colletotrichum lindemuthianum</i> grown in the presence of arabinogalactan, xylan or <i>Phaseolus vulgaris</i> cell walls. <i>Physiological and Molecular Plant Pathology</i> , 2017, 99, 75-86.	1.3	1
2927	Phylogenomic analysis of yellowjackets and hornets (Hymenoptera: Vespidae, Vespinae). <i>Molecular Phylogenetics and Evolution</i> , 2017, 107, 10-15.	1.2	11
2928	Colonization and diversification of aquatic insects on three Macaronesian archipelagos using 59 nuclear loci derived from a draft genome. <i>Molecular Phylogenetics and Evolution</i> , 2017, 107, 27-38.	1.2	32
2929	Phylogenetic analysis of two <i>Plectus</i> mitochondrial genomes (Nematoda: Plectida) supports a sister group relationship between Plectida and Rhabditida within Chromadorea. <i>Molecular Phylogenetics and Evolution</i> , 2017, 107, 90-102.	1.2	39
2930	Deep sequencing reveals persistence of cell-associated mumps vaccine virus in chronic encephalitis. <i>Acta Neuropathologica</i> , 2017, 133, 139-147.	3.9	41
2931	The complete chloroplast genome sequence of the leafy bladderwort, <i>Utricularia foliosa</i> L. (Lentibulariaceae). <i>Conservation Genetics Resources</i> , 2017, 9, 213-216.	0.4	5
2932	A whole genome gene content phylogenetic analysis of anopheline mosquitoes. <i>Molecular Phylogenetics and Evolution</i> , 2017, 107, 266-269.	1.2	6
2933	Transcriptome-based phylogeny of endemic Lake Baikal amphipod species flock: fast speciation accompanied by frequent episodes of positive selection. <i>Molecular Ecology</i> , 2017, 26, 536-553.	2.0	55
2934	Nuclear DNA content correlates with depth, body size, and diversification rate in amphipod crustaceans from ancient Lake Baikal, Russia. <i>Genome</i> , 2017, 60, 303-309.	0.9	22
2935	Draft Genome Sequence of <i>Mentha longifolia</i> and Development of Resources for Mint Cultivar Improvement. <i>Molecular Plant</i> , 2017, 10, 323-339.	3.9	79
2936	Microsympatry in cryptic lowland salamanders (Caudata): <i>Triturus cristatus</i> and <i>T. cristatus</i> (Plethodontidae: <i>Bolitoglossa</i>) implications for taxonomy and regional biogeography. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2017, 55, 150-155.	0.6	1
2937	Microbial Nursery Production of High-Quality Biological Soil Crust Biomass for Restoration of Degraded Dryland Soils. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	55
2938	Microbiome analysis shows enrichment for specific bacteria in separate anatomical regions of the deep-sea carnivorous sponge <i>Chondrocladia grandis</i> . <i>FEMS Microbiology Ecology</i> , 2017, 93, fiw214.	1.3	22
2939	Phylogenetic relationships, song and distribution of the endangered Rufous-headed Robin <i>Larvivora ruficeps</i> . <i>Ibis</i> , 2017, 159, 204-216.	1.0	9
2940	Molecular Evolution of Human Coronavirus Genomes. <i>Trends in Microbiology</i> , 2017, 25, 35-48.	3.5	591
2941	Differential Infection Patterns and Recent Evolutionary Origins of Equine Hepaciviruses in Donkeys. <i>Journal of Virology</i> , 2017, 91, .	1.5	45
2942	DNA barcoding of tuberous Orchidoideae: a resource for identification of orchids used in Salep. <i>Molecular Ecology Resources</i> , 2017, 17, 342-352.	2.2	31
2943	High phylogenetic utility of an ultraconserved element probe set designed for Arachnida. <i>Molecular Ecology Resources</i> , 2017, 17, 812-823.	2.2	99

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2944	HSV-1 clinical isolates with unique in vivo and in vitro phenotypes and insight into genomic differences. <i>Journal of NeuroVirology</i> , 2017, 23, 171-185.	1.0	4
2945	The genome of serotype VI <i>Streptococcus agalactiae</i> serotype VI and comparative analysis. <i>Gene</i> , 2017, 597, 59-65.	1.0	10
2946	Genomic Basis of Adaptive Evolution: The Survival of <i>Amurella</i> (<i>Leuciscus waleckii</i>) in an Extremely Alkaline Environment. <i>Molecular Biology and Evolution</i> , 2017, 34, 145-159.	3.5	66
2947	Evolutionary history of the thicket rats (genus <i>Grammomys</i>) mirrors the evolution of African forests since late Miocene. <i>Journal of Biogeography</i> , 2017, 44, 182-194.	1.4	47
2948	Morphology and phylogeny of a new wall-less freshwater volvoclean flagellate, <i>Hapalochloris nozakii</i> gen. et sp. nov. (Volvocales, Chlorophyceae). <i>Journal of Phycology</i> , 2017, 53, 108-117.	1.0	4
2949	Chemosynthetic symbionts of marine invertebrate animals are capable of nitrogen fixation. <i>Nature Microbiology</i> , 2017, 2, 16195.	5.9	151
2950	Genome Dynamics and Molecular Infection Epidemiology of Multidrug-Resistant <i>Helicobacter pullorum</i> Isolates Obtained from Broiler and Free-Range Chickens in India. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	28
2951	Diversity of formyltetrahydrofolate synthetase genes in the rumens of roe deer (<i>Capreolus pygargus</i>) and sika deer (<i>Cervus nippon</i>) fed different diets. <i>Canadian Journal of Microbiology</i> , 2017, 63, 11-19.	0.8	10
2952	Analysis of the complete plastomes of three species of Membranoptera (Ceramiaceae, Rhodophyta) from Pacific North America. <i>Journal of Phycology</i> , 2017, 53, 32-43.	1.0	12
2953	Convergent evolution of social hybridogenesis in <i>Messor</i> harvester ants. <i>Molecular Ecology</i> , 2017, 26, 1108-1117.	2.0	27
2954	<code>ggtree</code> : an <code>r</code> package for visualization and annotation of phylogenetic trees with their covariates and other associated data. <i>Methods in Ecology and Evolution</i> , 2017, 8, 28-36.	2.2	2,998
2955	Postzygotic isolation varies by ploidy level within a polyploid complex. <i>New Phytologist</i> , 2017, 213, 404-412.	3.5	66
2956	Morphologically tortured: taxonomic placement of an Antarctic springtail (Collembola: Isotomidae) misguided by morphology and ecology. <i>Zoologica Scripta</i> , 2017, 46, 180-187.	0.7	14
2957	<i>Copromyxa laresi</i> n. sp. (Amoebozoa: Tubulinea) and Transfer of <i>Cashia limacoides</i> (Page, Tj ETQq1 1.0.784314 rgBT /Ove	0.8	5
2958	Phylogeny, taxonomy and diversification events in the Caliciaceae. <i>Fungal Diversity</i> , 2017, 82, 221-238.	4.7	41
2959	Morphological and Genetic Diversity of Opisthosporidia: New Aphelid <i>Paraphelidium tribonemae</i> gen. et sp. nov.. <i>Journal of Eukaryotic Microbiology</i> , 2017, 64, 204-212.	0.8	25
2960	Phylogenomics of tubeworms (Siboglinidae, Annelida) and comparative performance of different reconstruction methods. <i>Zoologica Scripta</i> , 2017, 46, 200-213.	0.7	33
2961	Metazoan evolution of the armadillo repeat superfamily. <i>Cellular and Molecular Life Sciences</i> , 2017, 74, 525-541.	2.4	37

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2962	Tackling relationships and species circumscriptions of <i>Octoblepharum</i> , an enigmatic genus of haplolepidous mosses (Dicranidae, Bryophyta). <i>Systematics and Biodiversity</i> , 2017, 15, 16-24.	0.5	11
2963	A new Antarctic heterobranch clade is sister to all other Cephalaspidea (Mollusca: Gastropoda). <i>Zoologica Scripta</i> , 2017, 46, 127-137.	0.7	11
2964	<scp>discomark</scp>: nuclear marker discovery from orthologous sequences using draft genome data. <i>Molecular Ecology Resources</i> , 2017, 17, 257-266.	2.2	9
2965	Population genomics identifies the origin and signatures of selection of Korean weedy rice. <i>Plant Biotechnology Journal</i> , 2017, 15, 357-366.	4.1	51
2966	Phylogeny of the most species-rich freshwater bivalve family (Bivalvia: Unionida: Unionidae): Defining modern subfamilies and tribes. <i>Molecular Phylogenetics and Evolution</i> , 2017, 106, 174-191.	1.2	133
2967	Molecular characterization and evolution of carnivorous sundew (<i>Drosera rotundifolia</i> L.) class V Î²-1,3-glucanase. <i>Planta</i> , 2017, 245, 77-91.	1.6	6
2968	Age estimates of <i>Frullania</i> (<i>Frullaniaceae</i> , Porellales) main lineages: another example of rapid and recent diversification in liverwort evolution. <i>Systematics and Biodiversity</i> , 2017, 15, 156-165.	0.5	13
2969	Verdant: automated annotation, alignment and phylogenetic analysis of whole chloroplast genomes. <i>Bioinformatics</i> , 2017, 33, 130-132.	1.8	48
2970	Monophyly of Anthozoa (Cnidaria): why do nuclear and mitochondrial phylogenies disagree?. <i>Zoologica Scripta</i> , 2017, 46, 363-371.	0.7	25
2971	Molecular phylogenies challenge the classification of Polymastiidae (Porifera, Demospongiae) based on morphology. <i>Organisms Diversity and Evolution</i> , 2017, 17, 45-66.	0.7	13
2972	Identification of a Lineage D Betacoronavirus in Cave Nectar Bats (<i>Eonycteris spelaea</i>) in Singapore and an Overview of Lineage D Reservoir Ecology in SE Asian Bats. <i>Transboundary and Emerging Diseases</i> , 2017, 64, 1790-1800.	1.3	22
2973	Morphological assessment of the <i>Octopus vulgaris</i> species complex evaluated in light of molecular-based phylogenetic inferences. <i>Zoologica Scripta</i> , 2017, 46, 275-288.	0.7	81
2974	The first complete plastome sequence of the basal asterid family Styracaceae (Ericales) reveals a large inversion. <i>Plant Systematics and Evolution</i> , 2017, 303, 61-70.	0.3	18
2975	Characterization of the complete chloroplast genome of an endangered species dwarf birch (<i>Betula</i>) Tj ETQq1 1 0.784314 rgBT /Over 0.4	0.4	6
2976	Gene duplication and concerted evolution of mitochondrial DNA in crane species. <i>Molecular Phylogenetics and Evolution</i> , 2017, 106, 158-163.	1.2	23
2977	<i>Botryosphaeria dothidea</i> : a latent pathogen of global importance to woody plant health. <i>Molecular Plant Pathology</i> , 2017, 18, 477-488.	2.0	202
2978	A molecular phylogeny and revised higher-level classification for the leaf-mining moth family <scp>G</scp>racillariidae and its implications for larval host-use evolution. <i>Systematic Entomology</i> , 2017, 42, 60-81.	1.7	61
2979	Rapid Functional and Sequence Differentiation of a Tandemly Repeated Species-Specific Multigene Family in <i>Drosophila</i> . <i>Molecular Biology and Evolution</i> , 2017, 34, 51-65.	3.5	11

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2980	Morphology and phylogeny of two new ciliates, <i>Sterkiella sinica</i> sp. nov. and <i>Rubrioxytricha tsinlingensis</i> sp. nov. (Protozoa, Ciliophora, Hypotrichia) from north-west China. <i>Systematics and Biodiversity</i> , 2017, 15, 131-142.	0.5	20
2981	Moorean and Tahitian <i>Partula</i> tree snail survival after a mass extinction: New genomic insights using museum specimens. <i>Molecular Phylogenetics and Evolution</i> , 2017, 106, 151-157.	1.2	10
2982	Comparative transcriptomics reveal host-specific nucleotide variation in entomophthoralean fungi. <i>Molecular Ecology</i> , 2017, 26, 2092-2110.	2.0	33
2983	An orthologue of the host-defense protein psoriasin (S100A7) is expressed in frog skin. <i>Developmental and Comparative Immunology</i> , 2017, 67, 395-403.	1.0	5
2984	Host range and salinity tolerance of <i>Pythium porphyrae</i> may indicate its terrestrial origin. <i>Journal of Applied Phycology</i> , 2017, 29, 371-379.	1.5	23
2985	Characterization of the complete chloroplast genome of <i>Carpinus putoensis</i> . <i>Conservation Genetics Resources</i> , 2017, 9, 127-129.	0.4	2
2986	Characterization of the whole chloroplast genome of an endangered species <i>Primula kwangtungensis</i> (Primulaceae). <i>Conservation Genetics Resources</i> , 2017, 9, 87-89.	0.4	3
2987	Phylogenomics and species delimitation in the knob-scaled lizards of the genus <i>Xenosaurus</i> (Squamata: Xenosauridae) using ddRADseq data reveal a substantial underestimation of diversity. <i>Molecular Phylogenetics and Evolution</i> , 2017, 106, 241-253.	1.2	63
2988	Transmission between Archaic and Modern Human Ancestors during the Evolution of the Oncogenic Human Papillomavirus 16. <i>Molecular Biology and Evolution</i> , 2017, 34, 4-19.	3.5	103
2989	Crown group Oxyphotobacteria postdate the rise of oxygen. <i>Geobiology</i> , 2017, 15, 19-29.	1.1	153
2990	Species delimitation and phylogeographic analyses in the <i>Ectocarpus</i> subgroup <i>siliculosi</i> (Ectocarpales, Phaeophyceae). <i>Journal of Phycology</i> , 2017, 53, 17-31.	1.0	54
2991	From a lost world: an integrative phylogenetic analysis of <i>Ansonia Stoliczka</i> , 1870 (Lissamphibia: Tj ETQq1 1 0.784314 rgBT /Overlap 10 Tf 50) 287-303.	0.7	10
2992	Species delimitation for cryptic species complexes: case study of <i>Pyramidula</i> (Gastropoda, Tj ETQq0 0 0 rgBT /Overlap 10 Tf 50) 0.7 36	0.7	36
2993	Metagenomic covariation along densely sampled environmental gradients in the Red Sea. <i>ISME Journal</i> , 2017, 11, 138-151.	4.4	40
2994	Multiple origins of Hawaiian drosophilids: Phylogeography of <i>Scaptomyza</i> Hardy (Diptera: Tj ETQq0 0 0 rgBT /Overlap 10 Tf 50) 0.3 23	0.3	23
2995	The genome of <i>Onchocerca volvulus</i> , agent of river blindness. <i>Nature Microbiology</i> , 2017, 2, 16216.	5.9	107
2996	Genomic diversity in <i>Onchocerca volvulus</i> and its <i>Wolbachia</i> endosymbiont. <i>Nature Microbiology</i> , 2017, 2, 16207.	5.9	53
2997	High genetic diversity of <i>Vibrio cholerae</i> in the European lake Neusiedler See is associated with intensive recombination in the reed habitat and the long-distance transfer of strains. <i>Environmental Microbiology</i> , 2017, 19, 328-344.	1.8	41

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2998	Quest for Ancestors of Eukaryal Cells Based on Phylogenetic Analyses of Aminoacyl-tRNA Synthetases. <i>Journal of Molecular Evolution</i> , 2017, 84, 51-66.	0.8	21
2999	The LBD12-1 Transcription Factor Suppresses Apical Meristem Size by Repressing Argonaute 10 Expression. <i>Plant Physiology</i> , 2017, 173, 801-811.	2.3	25
3000	Metagenomics of Two Severe Foodborne Outbreaks Provides Diagnostic Signatures and Signs of Coinfection Not Attainable by Traditional Methods. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	54
3001	Coastal marine habitats harbor novel early-diverging fungal diversity. <i>Fungal Ecology</i> , 2017, 25, 1-13.	0.7	116
3002	Genomic data reveals potential for hybridization, introgression, and incomplete lineage sorting to confound phylogenetic relationships in an adaptive radiation of narrow-mouth frogs. <i>Evolution; International Journal of Organic Evolution</i> , 2017, 71, 475-488.	1.1	40
3003	Nonreciprocal complementation of KNOX gene function in land plants. <i>New Phytologist</i> , 2017, 216, 591-604.	3.5	44
3004	Continental-level population differentiation and environmental adaptation in the mushroom <i>Sclerotium brevipes</i> . <i>Molecular Ecology</i> , 2017, 26, 2063-2076.	2.0	55
3005	Antimicrobial resistance surveillance in the genomic age. <i>Annals of the New York Academy of Sciences</i> , 2017, 1388, 78-91.	1.8	71
3006	Phylotranscriptomics resolves ancient divergences in the Lepidoptera. <i>Systematic Entomology</i> , 2017, 42, 305-316.	1.7	38
3007	Kisspeptin system in pejerrey fish (<i>Odontesthes bonariensis</i>). Characterization and gene expression pattern during early developmental stages. <i>Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology</i> , 2017, 204, 146-156.	0.8	31
3008	Families, genera, and species of Botryosphaerales. <i>Fungal Biology</i> , 2017, 121, 322-346.	1.1	134
3009	Hidden diversity in the <i>Podarcis tauricus</i> (Sauria, Lacertidae) species subgroup in the light of multilocus phylogeny and species delimitation. <i>Molecular Phylogenetics and Evolution</i> , 2017, 106, 6-17.	1.2	34
3010	G α and regulator of G α protein signaling (RGS) protein pairs maintain functional compatibility and conserved interaction interfaces throughout evolution despite frequent loss of RGS proteins in plants. <i>New Phytologist</i> , 2017, 216, 562-575.	3.5	46
3011	Plastid phylogenomic study of species within the genus <i>Zea</i> : rates and patterns of three classes of microstructural changes. <i>Current Genetics</i> , 2017, 63, 311-323.	0.8	14
3012	Characterization of the complete chloroplast genome of <i>Cycas panzhihuaensis</i> . <i>Conservation Genetics Resources</i> , 2017, 9, 21-23.	0.4	3
3013	Lineage diversification of fringe-toed lizards (Phrynosomatidae: <i>Uma notata</i> complex) in the Colorado Desert: Delimiting species in the presence of gene flow. <i>Molecular Phylogenetics and Evolution</i> , 2017, 106, 103-117.	1.2	28
3014	MetaMLST: multi-locus strain-level bacterial typing from metagenomic samples. <i>Nucleic Acids Research</i> , 2017, 45, e7-e7.	6.5	88
3015	Mitochondrial DNA and two Y-chromosome genes of common long-tailed macaques (<i>Macaca</i>) Tj ETQq1 1 0.784314 rgBT /Ove 2017, 79, 1-13.	0.8	64

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3016	Leapfrogging into new territory: How Mascarene ridged frogs diversified across Africa and Madagascar to maintain their ecological niche. <i>Molecular Phylogenetics and Evolution</i> , 2017, 106, 254-269.	1.2	44
3017	The complete mitochondrial genome of the scorpion <i>Centruroides vittatus</i> (Arachnida: Scorpiones). <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 841-842.	0.2	0
3018	<i>Didymium azorellae</i> , a new myxomycete from cushion plants of cold arid areas of South America. <i>Mycologia</i> , 2017, 109, 993-1002.	0.8	12
3019	Multi-rate Poisson tree processes for single-locus species delimitation under maximum likelihood and Markov chain Monte Carlo. <i>Bioinformatics</i> , 2017, 33, 1630-1638.	1.8	580
3020	Dry season characteristics in western Amazonia underlie the divergence of <i>Astrocaryum</i> section Huicungo (Arecaceae) and evaluation of potential anatomical adaptations. <i>Botanical Journal of the Linnean Society</i> , 2017, 185, 291-306.	0.8	3
3021	Diversification in a biodiversity hotspot: genomic variation in the river frog <i>Amietia nutti</i> across the Ethiopian Highlands. <i>Biological Journal of the Linnean Society</i> , 2017, 122, 801-813.	0.7	10
3022	The plastid genome sequence of the invasive plant common Ragweed (<i>Ambrosia artemisiifolia</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T	0.2	14
3023	<i>Thiersianthus</i> (Marchantiophyta: Lejeuneaceae), a new genus from lowland rainforests in Borneo. <i>Bryologist</i> , 2017, 120, 511.	0.1	16
3024	Expanded Taxonomic Sampling Coupled with Gene Genealogy Interrogation Provides Unambiguous Resolution for the Evolutionary Root of Angiosperms. <i>Genome Biology and Evolution</i> , 2017, 9, 3154-3161.	1.1	18
3025	Anchored Hybrid Enrichment-Based Phylogenomics of Leafhoppers and Treehoppers (Hemiptera:) Tj ETQq1 1 0.784314 rgBT /Overlock 110	0.7	110
3026	Popmarker: Identifying Phylogenetic Markers at the Population Level. <i>Evolutionary Bioinformatics</i> , 2017, 13, 117693431772440.	0.6	2
3027	Genomic Differentiation and Demographic Histories of Atlantic and Indo-Pacific Yellowfin Tuna (<i>Thunnus albacares</i>) Populations. <i>Genome Biology and Evolution</i> , 2017, 9, 1084-1098.	1.1	46
3028	Introducing the new Indian mangrove species, <i>Vaginatispora microarmatispora</i> (Lophiostomataceae) based on morphology and multigene phylogenetic analysis. <i>Phytotaxa</i> , 2017, 329, 139.	0.1	21
3029	Genome Sequences Reveal Cryptic Speciation in the Human Pathogen <i>Histoplasma capsulatum</i> . <i>MBio</i> , 2017, 8, .	1.8	112
3030	Towards a complete generic-level plastid phylogeny of the paleotropical woody bamboos (Poaceae:) Tj ETQq0 0 0 rgBT /Overlock 10 T	0.4	24
3031	Comparison of methods for phylogenetic B-cell lineage inference using time-resolved antibody repertoire simulations (AbSim). <i>Bioinformatics</i> , 2017, 33, 3938-3946.	1.8	50
3032	Evolution of the 3R-MYB Gene Family in Plants. <i>Genome Biology and Evolution</i> , 2017, 9, 1013-1029.	1.1	50
3033	Structured Populations of <i>Sulfolobus acidocaldarius</i> with Susceptibility to Mobile Genetic Elements. <i>Genome Biology and Evolution</i> , 2017, 9, 1699-1710.	1.1	17

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3034	Variation in DNA Methylation Is Not Consistently Reflected by Sociality in Hymenoptera. <i>Genome Biology and Evolution</i> , 2017, 9, 1687-1698.	1.1	46
3035	Evolutionary Dynamics of Pathoadaptation Revealed by Three Independent Acquisitions of the VirB/D4 Type IV Secretion System in <i>Bartonella</i> . <i>Genome Biology and Evolution</i> , 2017, 9, 761-776.	1.1	50
3036	<i>Pseudotriconympha leei</i> , <i>Pseudotriconympha lifesoni</i> , and <i>Pseudotriconympha pearti</i> , new species of parabasal flagellates and the description of a rotating subcellular structure. <i>Scientific Reports</i> , 2017, 7, 16349.	1.6	5
3037	Molecular phylogeny of <i>Neodevriesia</i> , with two new species and several new combinations. <i>Mycologia</i> , 2017, 109, 965-974.	0.8	20
3038	<i>Hedera caerulescens</i> (Alcyonacea : Alcyoniidae), a new genus and species of soft coral from the temperate North Atlantic: invasive in its known range?. <i>Invertebrate Systematics</i> , 2017, 31, 723.	0.5	4
3039	De novo assembling and primary analysis of genome and transcriptome of gray whale <i>Eschrichtius robustus</i> . <i>BMC Evolutionary Biology</i> , 2017, 17, 258.	3.2	11
3040	The Emergence of Earliest Angiosperms May be Earlier than Fossil Evidence Indicates. <i>Systematic Botany</i> , 2017, 42, 607-619.	0.2	21
3041	A Worldwide Molecular Phylogeny Provides New Insight on Cryptic Diversity Within the Moonworts (<i>Botrychium</i> s. s., Ophioglossaceae). <i>Systematic Botany</i> , 2017, 42, 620-639.	0.2	23
3042	Comparative analysis of the genomes of <i>Stylophora pistillata</i> and <i>Acropora digitifera</i> provides evidence for extensive differences between species of corals. <i>Scientific Reports</i> , 2017, 7, 17583.	1.6	121
3043	Complete mitochondrial genome and phylogenetic position of <i>Chaenodraco wilsoni</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 579-580.	0.2	2
3044	The plastid genome of <i>Vanillon</i> (<i>Vanilla pompona</i> , Orchidaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 689-691.	0.2	14
3045	Complete mitochondrial genomes of three Neotropical sleeper gobies: <i>Eleotris amblyopsis</i> , <i>E. picta</i> and <i>Hemieleotris latifasciata</i> (Gobiiformes: Eleotridae). <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 747-750.	0.2	4
3046	Characterization of the complete chloroplast genome of longan (<i>Dimocarpus longan</i> Lour.) using illumina paired-end sequencing. <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 904-906.	0.2	4
3047	RNA sequencing provides insights into the evolution of lettuce and the regulation of flavonoid biosynthesis. <i>Nature Communications</i> , 2017, 8, 2264.	5.8	133
3048	<i>Aspergillus</i> subgenus <i>Polypaecilum</i> from the built environment. <i>Studies in Mycology</i> , 2017, 88, 237-267.	4.5	23
3049	Draft genome of the reindeer (<i>Rangifer tarandus</i>). <i>GigaScience</i> , 2017, 6, 1-5.	3.3	41
3050	Genome-wide Screening for Lectin Motifs in <i>Arabidopsis thaliana</i> . <i>Plant Genome</i> , 2017, 10, plantgenome2017.02.0010.	1.6	49
3051	Monadic composition for deterministic, parallel batch processing. , 2017, 1, 1-26.		3

#	ARTICLE	IF	CITATIONS
3052	Reconstructing evolutionary trees in parallel for massive sequences. <i>BMC Systems Biology</i> , 2017, 11, 100.	3.0	15
3053	Origins of the fern genus <i>Hymenophyllum</i> (Hymenophyllaceae) in New Caledonia: Multiple independent colonizations from surrounding territories and limited in situ diversification. <i>Taxon</i> , 2017, 66, 1041-1064.	0.4	17
3054	Molecular data, based on an exhaustive species sampling of the fern genus <i>Rumohra</i> (Dryopteridaceae), reveal a biogeographical history mostly shaped by dispersal and several cryptic species in the widely distributed <i>Rumohra adiantiformis</i> . <i>Botanical Journal of the Linnean Society</i> , 2017, 185, 463-481.	0.8	21
3055	Bioinformatics in Microbiome Analysis. <i>Methods in Microbiology</i> , 2017, 44, 1-18.	0.4	4
3056	A Poissonian Model of Indel Rate Variation for Phylogenetic Tree Inference. <i>Systematic Biology</i> , 2017, 66, 698-714.	2.7	4
3057	Phylogeny of Anophelinae using mitochondrial protein coding genes. <i>Royal Society Open Science</i> , 2017, 4, 170758.	1.1	83
3058	<i>Magnaporthiopsis meyeri-festucaae</i> , sp. nov., associated with a summer patch-like disease of fine fescue turfgrasses. <i>Mycologia</i> , 2017, 109, 1-10.	0.8	10
3059	Two new <i>Geosmithia</i> species in <i>G. pallida</i> species complex from bark beetles in eastern USA. <i>Mycologia</i> , 2017, 109, 1-14.	0.8	9
3060	Genome-scale detection of positive selection in nine primates predicts human-virus evolutionary conflicts. <i>Nucleic Acids Research</i> , 2017, 45, 10634-10648.	6.5	76
3061	An integrative taxonomic study of European <i>Eupelmus</i> (Macroneura) (Hymenoptera: Chalcidoidea): <i>Tj ETQq1 1 0.784314 rgBT /Overl</i> species hiding under one name for 240 years. <i>Zoological Journal of the Linnean Society</i> , 2017, 181, 519-603.	1.0	40
3062	Comparative Genomics of the Dual-Obligate Symbionts from the Treehopper, <i>Entylia carinata</i> (Hemiptera: Membracidae), Provide Insight into the Origins and Evolution of an Ancient Symbiosis. <i>Genome Biology and Evolution</i> , 2017, 9, 1803-1815.	1.1	44
3063	New Mitogenomes of Two Chinese Stag Beetles (Coleoptera, Lucanidae) and Their Implications for Systematics. <i>Journal of Insect Science</i> , 2017, 17, .	0.6	15
3064	<i>scp>RAD</scp></i> seq dataset with 90% missing data fully resolves recent radiation of <i>Petalidium</i> (Acanthaceae) in the ultra-arid deserts of Namibia. <i>Ecology and Evolution</i> , 2017, 7, 7920-7936.	0.8	91
3065	Variation in reproductive isolation across a species range. <i>Ecology and Evolution</i> , 2017, 7, 9347-9357.	0.8	22
3066	Extensive gene content variation in the <i>Brachypodium distachyon</i> pan-genome correlates with population structure. <i>Nature Communications</i> , 2017, 8, 2184.	5.8	269
3067	Habitat Predicts Levels of Genetic Admixture in <i>Saccharomyces cerevisiae</i> . <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2919-2929.	0.8	19
3068	<i>Vittaria graminifolia</i> (Pteridaceae) and <i>Didymoglossum petersii</i> (Hymenophyllaceae) in Broxton Rocks, GA. <i>American Fern Journal</i> , 2017, 107, 257-264.	0.2	5
3069	VCFToTree: a user-friendly tool to construct locus-specific alignments and phylogenies from thousands of anthropologically relevant genome sequences. <i>BMC Bioinformatics</i> , 2017, 18, 426.	1.2	14

#	ARTICLE	IF	CITATIONS
3070	Complete chloroplast genome sequence of Coyote tobacco (<i>Nicotiana attenuata</i> , Solanaceae). Mitochondrial DNA Part B: Resources, 2017, 2, 761-762.	0.2	1
3071	Molecular phylogenetic relationships among Anatolian-Hyrcanian brown frog taxa (Ranidae: <i>Rana</i>). Amphibia - Reptilia, 2017, 38, 339-350.	0.1	8
3072	Confirmation that <i>Phytophthora insolita</i> (Peronosporaceae) is present as a marine saprotroph on mangrove leaves and first report of the species for the Philippines. Nova Hedwigia, 2017, 105, 185-196.	0.2	6
3073	Phylogeny and systematics of African Melastomateae (Melastomataceae). Taxon, 2017, 66, 584-614.	0.4	53
3074	New endophytic <i>Toxicocladosporium</i> species from cacti in Brazil, and description of <i>Neocladosporium</i> gen. nov.. IMA Fungus, 2017, 8, 77-97.	1.7	33
3075	Resolving Generic Boundaries in Indian&Australasian Cleomaceae: Circumscription of <i>Areocleome</i> , <i>Arivela</i> , and <i>Coryandra</i> as Distinct Genera. Systematic Botany, 2017, 42, 694-708.	0.2	14
3076	Suggested mechanisms for Zika virus causing microcephaly: what do the genomes tell us?. BMC Bioinformatics, 2017, 18, 471.	1.2	20
3077	Genomic insights into potential interdependencies in microbial hydrocarbon and nutrient cycling in hydrothermal sediments. Microbiome, 2017, 5, 106.	4.9	168
3078	Comparative Genomics of Pathogenic and Nonpathogenic Beetle-Vectored Fungi in the Genus <i>Geosmithia</i> . Genome Biology and Evolution, 2017, 9, 3312-3327.	1.1	18
3079	The <i>Huperzia selago</i> Shoot Tip Transcriptome Sheds New Light on the Evolution of Leaves. Genome Biology and Evolution, 2017, 9, 2444-2460.	1.1	22
3080	<i>Femsjonia uniseptata</i> (Dacrymycetes, Basidiomycota), a new species collected from <i>Pinus densiflora</i> forests in Japan. Phytotaxa, 2017, 312, 271.	0.1	5
3081	<i>Esteya Vermicola</i> , a Nematophagous Fungus Attacking the Pine Wood Nematode, Harbors a Bacterial Endosymbiont Affiliated with <i>Gammaproteobacteria</i> . Microbes and Environments, 2017, 32, 201-209.	0.7	11
3082	Clarifying the identity of <i>Geastrum campestre</i> var. <i>famatinum</i> (Geastrales, Basidiomycota). Phytotaxa, 2017, 328, 159.	0.1	1
3083	Global Kinetoplastea phylogeny inferred from a large-scale multigene alignment including parasitic species for better understanding transitions from a free-living to a parasitic lifestyle. Genes and Genetic Systems, 2017, 92, 35-42.	0.2	27
3084	Synthesizing Species Trees from Unrooted Gene Trees. , 2017, , .		2
3085	Genome-Based Analyses of Six Hexacorallian Species Reject the "Naked Coral" Hypothesis. Genome Biology and Evolution, 2017, 9, 2626-2634.	1.1	8
3086	Insights into origin and evolution of λ -proteobacterial gene transfer agents. Virus Evolution, 2017, 3, vex036.	2.2	53
3087	Insights into the Existence of Isomeric Plastomes in Cupressoideae (Cupressaceae). Genome Biology and Evolution, 2017, 9, 1110-1119.	1.1	53

#	ARTICLE	IF	CITATIONS
3088	Genome sequence of the small brown planthopper, <i>Laodelphax striatellus</i> . <i>GigaScience</i> , 2017, 6, 1-12.	3.3	106
3089	Inhibition of Degranulation of RBL-2H3 Cells by Extracts and Compounds from <i>Armillaria ostoyae</i> . <i>Planta Medica International Open</i> , 2017, 4, e1-e7.	0.3	8
3090	Fates of angiosperm species following long-distance dispersal: Examples from American amphitropical Polemoniaceae. <i>American Journal of Botany</i> , 2017, 104, 1729-1744.	0.8	12
3091	The complete chloroplast genome sequence of <i>Barthea barthei</i> (Melastomataceae), a shrub endemic to southern China. <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 810-811.	0.2	3
3092	Data-Aware Modeling of Elastic Processes for Elasticity Strategies Evaluation. , 2017, , .		2
3093	Towards a balanced view of the bacterial tree of life. <i>Microbiome</i> , 2017, 5, 140.	4.9	102
3094	Genomic characterization reconfirms the taxonomic status of <i>Lactobacillus parakefiri</i> . <i>Bioscience of Microbiota, Food and Health</i> , 2017, 36, 129-134.	0.8	2
3095	An <i>Arabidopsis</i> introgression zone studied at high spatio-temporal resolution: interglacial and multiple genetic contact exemplified using whole nuclear and plastid genomes. <i>BMC Genomics</i> , 2017, 18, 810.	1.2	37
3096	<i>Tuber griseolivaceum</i> sp. nov., a new olive-gray truffle species from China based on morphological and DNA data. <i>Phytotaxa</i> , 2017, 309, 166.	0.1	1
3097	Causes and Consequences of Rapidly Evolving mtDNA in a Plant Lineage. <i>Genome Biology and Evolution</i> , 2017, 9, 323-336.	1.1	64
3098	<i>Fistulinella ruschii</i> , sp. nov., and a new record of <i>Fistulinella campinaranae</i> var. <i>scrobiculata</i> for the Atlantic Forest, Brazil. <i>Mycologia</i> , 2017, 109, 1003-1013.	0.8	12
3099	High-throughput structural modeling of the HIV transmission bottleneck. , 2017, , .		3
3100	Sub-Paratethyan origin and Middle to Late Miocene principal diversification of the Lactucinae (Compositae: Cichorieae) inferred from molecular phylogenetics, divergence dating and biogeographic analysis. <i>Taxon</i> , 2017, 66, 675-703.	0.4	39
3101	Spatial phylogenetics of the native California flora. <i>BMC Biology</i> , 2017, 15, 96.	1.7	104
3102	The complete chloroplast genome of <i>Mentha spicata</i> , an endangered species native to South Europe. <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 907-909.	0.2	10
3103	Six new <i>Phytophthora</i> species from ITS Clade 7a including two sexually functional heterothallic hybrid species detected in natural ecosystems in Taiwan. <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2017, 38, 100-135.	1.6	67
3104	Genetic diversity and population genetic analysis of <i>Donax vittatus</i> (Mollusca: Bivalvia) and phylogeny of the genus with mitochondrial and nuclear markers. <i>Estuarine, Coastal and Shelf Science</i> , 2017, 197, 126-135.	0.9	17
3105	Importance of Beringia for the divergence of two northern Pacific alpine plants, <i>Phyllodoce aleutica</i> and <i>Phyllodoce glanduliflora</i> (Ericaceae). <i>Biological Journal of the Linnean Society</i> , 2017, 122, 249-257.	0.7	2

#	ARTICLE	IF	CITATIONS
3106	Comparative Genome Analysis Reveals Adaptation to the Ectophytic Lifestyle of Sooty Blotch and Flyspeck Fungi. <i>Genome Biology and Evolution</i> , 2017, 9, 3137-3151.	1.1	11
3107	Increased Affinity for RNA Targets Evolved Early in Animal and Plant Dicer Lineages through Different Structural Mechanisms. <i>Molecular Biology and Evolution</i> , 2017, 34, 3047-3063.	3.5	14
3108	Draft genome of the Marco Polo Sheep (<i>Ovis ammon polii</i>). <i>GigaScience</i> , 2017, 6, 1-7.	3.3	25
3109	Comparative Genomic Analysis of <i>Acanthamoeba</i> Endosymbionts Highlights the Role of Amoebae as a "Melting Pot" Shaping the Rickettsiales Evolution. <i>Genome Biology and Evolution</i> , 2017, 9, 3214-3224.	1.1	36
3110	A review of carnivorous sponges (Porifera: Cladorhizidae) from the Boreal North Atlantic and Arctic. <i>Zoological Journal of the Linnean Society</i> , 2017, 181, 1-69.	1.0	35
3111	Taxonomic evaluation of selected <i>Ganoderma</i> species and database sequence validation. <i>PeerJ</i> , 2017, 5, e3596.	0.9	44
3112	A molecular portrait of maternal sepsis from Byzantine Troy. <i>ELife</i> , 2017, 6, .	2.8	46
3113	A novel caulimovirus associated with a complete fruit drop symptom in "Bluecrop" blueberry. <i>Acta Horticulturae</i> , 2017, , 39-44.	0.1	1
3114	Nuevo registro de <i>Ulva australis</i> (Ulvaceae, Chlorophyta) en el norte de Chile. <i>Revista De Biología Marina Y Oceanografía</i> , 2017, 52, 621-630.	0.1	4
3115	Phylogeny of the popcorn flowers: Use of genome skimming to evaluate monophyly and interrelationships in subtribe Amsinckiinae (Boraginaceae). <i>Taxon</i> , 2017, 66, 1406-1420.	0.4	22
3116	Determination of Nucleopolyhedrovirus™ Taxonomic Position. , 2017, , .		1
3117	Morphological and molecular analyses support the ampho-Atlantic distribution and taxonomic status of the snapping shrimp <i>Alpheus intricatus</i> Spence Bate, 1888 (Crustacea: Decapoda: Alpheidae). <i>Zootaxa</i> , 2017, 4303, .	0.2	7
3118	New species of <i>Chimaera</i> (Chondrichthyes: Holocephali: Chimaeriformes: Chimaeridae) from the Southwestern Indian Ocean. <i>Zootaxa</i> , 2017, 4312, .	0.2	8
3119	<i>Hemibates koningsi</i> spec. nov: a new deep-water cichlid (Teleostei: Cichlidae) from Lake Tanganyika. <i>Zootaxa</i> , 2017, 4312, .	0.2	4
3120	Revision of the Genus <i>Leptogomphus</i> Selys in Borneo, including gene trees and a two marker molecular phylogeny (Odonata: Anisoptera: Gomphidae). <i>Zootaxa</i> , 2017, 4358, 201-257.	0.2	1
3121	A new species of <i>Plestiodon</i> (Squamata: Scincidae) from the Balsas Basin, Mexico. <i>Zootaxa</i> , 2017, 4365, 149-172.	0.2	7
3122	Genome sequencing of 39 <i>Akkermansia muciniphila</i> isolates reveals its population structure, genomic and functional diversity, and global distribution in mammalian gut microbiotas. <i>BMC Genomics</i> , 2017, 18, 800.	1.2	111
3123	Mitochondrial genomes of blister beetles (Coleoptera, Meloidae) and two large intergenic spacers in <i>Hycleus</i> genera. <i>BMC Genomics</i> , 2017, 18, 698.	1.2	34

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3124	Genome-Wide Characterization and Expression Profiling of Sugar Transporter Family in the Whitefly, <i>Bemisia tabaci</i> (Gennadius) (Hemiptera: Aleyrodidae). <i>Frontiers in Physiology</i> , 2017, 8, 322.	1.3	15
3125	Distinct Subfamilies of Odorant Binding Proteins in Locust (Orthoptera, Acrididae): Molecular Evolution, Structural Variation, and Sensilla-Specific Expression. <i>Frontiers in Physiology</i> , 2017, 8, 734.	1.3	51
3126	Completion of the Chloroplast Genomes of Five Chinese Juglans and Their Contribution to Chloroplast Phylogeny. <i>Frontiers in Plant Science</i> , 2016, 7, 1955.	1.7	110
3127	Population Structure and Phylogenetic Relationships in a Diverse Panel of <i>Brassica rapa</i> L.. <i>Frontiers in Plant Science</i> , 2017, 8, 321.	1.7	53
3128	The Chloroplast Genome of <i>Passiflora edulis</i> (Passifloraceae) Assembled from Long Sequence Reads: Structural Organization and Phylogenomic Studies in Malpighiales. <i>Frontiers in Plant Science</i> , 2017, 8, 334.	1.7	79
3129	Altered Expression of Genes Implicated in Xylan Biosynthesis Affects Penetration Resistance against Powdery Mildew. <i>Frontiers in Plant Science</i> , 2017, 8, 445.	1.7	30
3130	Comparative Genomics and Phylogenomics of East Asian Tulips (<i>Amana</i> , Liliaceae). <i>Frontiers in Plant Science</i> , 2017, 8, 451.	1.7	65
3131	Robust Phylogeny of <i>Tetrastigma</i> (Vitaceae) Based on Ten Plastid DNA Regions: Implications for Infrageneric Classification and Seed Character Evolution. <i>Frontiers in Plant Science</i> , 2017, 8, 590.	1.7	22
3132	The Complete Plastome Sequences of Four Orchid Species: Insights into the Evolution of the Orchidaceae and the Utility of Plastomic Mutational Hotspots. <i>Frontiers in Plant Science</i> , 2017, 8, 715.	1.7	95
3133	Population Genetic Differentiation and Taxonomy of Three Closely Related Species of <i>Saxifraga</i> (Saxifragaceae) from Southern Tibet and the Hengduan Mountains. <i>Frontiers in Plant Science</i> , 2017, 8, 1325.	1.7	30
3134	Unveiling the Identity of Wenwan Walnuts and Phylogenetic Relationships of Asian Juglans Species Using Restriction Site-Associated DNA-Sequencing. <i>Frontiers in Plant Science</i> , 2017, 8, 1708.	1.7	15
3135	Comparative Analysis of the Complete Plastomes of <i>Apostasia wallichii</i> and <i>Neuwiedia singaporeana</i> (Apostasioideae) Reveals Different Evolutionary Dynamics of IR/SSC Boundary among Photosynthetic Orchids. <i>Frontiers in Plant Science</i> , 2017, 8, 1713.	1.7	29
3136	Plastome Rearrangements in the <i>Adenocalymma-Neojobertia</i> Clade (Bignoniaceae, Bignoniaceae) and Its Phylogenetic Implications. <i>Frontiers in Plant Science</i> , 2017, 8, 1875.	1.7	29
3137	Evolution of mobile genetic element composition in an epidemic methicillin-resistant <i>Staphylococcus aureus</i> : temporal changes correlated with frequent loss and gain events. <i>BMC Genomics</i> , 2017, 18, 684.	1.2	43
3138	Comparative Study of Lectin Domains in Model Species: New Insights into Evolutionary Dynamics. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1136.	1.8	40
3139	<i>Sycidiphaga</i> , a new genus of Sycophaginae Walker, 1975 (Hymenoptera, Chalcidoidea, Agaonidae) associated with <i>Ficus</i> subgenus <i>Sycidium</i> in southern China. <i>Zootaxa</i> , 2017, 4306, 91.	0.2	0
3140	Complete plastome sequencing of both living species of Circaeasteraceae (Ranunculales) reveals unusual rearrangements and the loss of the <i>ndh</i> gene family. <i>BMC Genomics</i> , 2017, 18, 592.	1.2	51
3141	Pathogenic <i>Elizabethkingia miricola</i> Infection in Cultured Black-Spotted Frogs, China, 2016. <i>Emerging Infectious Diseases</i> , 2017, 23, 2055-2059.	2.0	45

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3142	Next-Generation Sequencing, Bioinformatics, and Infectious Diseases. , 2017, , 405-420.		0
3143	Research Article Full-length genomic and molecular characterization of Canine parvovirus in dogs from North of Brazil.. Genetics and Molecular Research, 2017, 16, .	0.3	12
3144	A new family and genus in Dothideales for Aureobasidium-like species isolated from house dust. IMA Fungus, 2017, 8, 299-315.	1.7	24
3145	Pan-genome Analyses of the Species Salmonella enterica, and Identification of Genomic Markers Predictive for Species, Subspecies, and Serovar. Frontiers in Microbiology, 2017, 8, 1345.	1.5	74
3146	Determination of <i>Elizabethkingia</i> Diversity by MALDI-TOF Mass Spectrometry and Whole-Genome Sequencing. Emerging Infectious Diseases, 2017, 23, 320-323.	2.0	28
3147	Draft sequencing and assembly of the genome of the world's largest fish, the whale shark: <i>Rhincodon typus</i> Smith 1828. BMC Genomics, 2017, 18, 532.	1.2	91
3148	Chemosensory genes in the antennal transcriptome of two syrphid species, <i>Episyrphus balteatus</i> and <i>Eupeodes corollae</i> (Diptera: Syrphidae). BMC Genomics, 2017, 18, 586.	1.2	64
3149	Genome-wide characterization, evolution, and expression analysis of the leucine-rich repeat receptor-like protein kinase (LRR-RLK) gene family in Rosaceae genomes. BMC Genomics, 2017, 18, 763.	1.2	62
3150	The complete mitochondrial genome of parasitic nematode <i>Camallanus cotti</i> : extreme discontinuity in the rate of mitogenomic architecture evolution within the Chromadorea class. BMC Genomics, 2017, 18, 840.	1.2	60
3151	Molecular evidence supporting the expansion of the geographical distribution of the Brazilian cownose ray <i>Rhinoptera brasiliensis</i> (Myliobatiformes: Rhinopteridae) in the western Atlantic. Zootaxa, 2017, 4341, 593-600.	0.2	10
3152	Molecular Characterization of <i>Corynebacterium diphtheriae</i> Outbreak Isolates, South Africa, March–June 2015. Emerging Infectious Diseases, 2017, 23, 1308-1315.	2.0	36
3153	Bioinformatic Analyses of Whole-Genome Sequence Data in a Public Health Laboratory. Emerging Infectious Diseases, 2017, 23, 1441-1445.	2.0	40
3154	Highly Conserved Elements and Chromosome Structure Evolution in Mitochondrial Genomes in Ciliates. Life, 2017, 7, 9.	1.1	3
3155	Genome-Wide Identification and Evolutionary Analysis of <i>Sarcocystis neurona</i> Protein Kinases. Pathogens, 2017, 6, 12.	1.2	4
3156	Variation in the Genetic Repertoire of Viruses Infecting <i>Micromonas pusilla</i> Reflects Horizontal Gene Transfer and Links to Their Environmental Distribution. Viruses, 2017, 9, 116.	1.5	15
3157	Characterization and Temperature Dependence of Arctic <i>Micromonas polaris</i> Viruses. Viruses, 2017, 9, 134.	1.5	59
3158	Re-Assembly and Analysis of an Ancient Variola Virus Genome. Viruses, 2017, 9, 253.	1.5	14
3159	The <i>Operophtera brumata</i> Nucleopolyhedrovirus (OpbuNPV) Represents an Early, Divergent Lineage within Genus <i>Alphabaculovirus</i> . Viruses, 2017, 9, 307.	1.5	20

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3160	Molecular Phylogeny of Acerentomidae (Protura), with Description of <i>Acerentuloides bernardi</i> sp. nov. from North America. <i>Florida Entomologist</i> , 2017, 100, 433-443.	0.2	2
3161	The complete chloroplast genome sequence of the CAM epiphyte Spanish moss (<i>Tillandsia usneoides</i>), <i>Tj ETQq1 1 0.784314 ggBT /Over</i>	1.1	48
3162	Two new genera of Australian dung beetles (Coleoptera: Scarabaeidae: Scarabaeinae) with the description of six new species and transfer of six described species. <i>Zootaxa</i> , 2017, 4290, 201.	0.2	4
3163	A new family, Pervetustaceae with a new genus, Pervetustus, and <i>P. simplex</i> sp. nov. (Paraglomerales), and a new genus, Innospora with <i>I. majewskii</i> comb. nov. (Paraglomeraceae) in the Glomeromycotina. <i>Nova Hedwigia</i> , 2017, 105, 397-410.	0.2	13
3164	The Chloroplast Genome Sequence of <i>Scutellaria baicalensis</i> Provides Insight into Intraspecific and Interspecific Chloroplast Genome Diversity in <i>Scutellaria</i> . <i>Genes</i> , 2017, 8, 227.	1.0	79
3165	The Transcriptomes of <i>Xiphinema index</i> and <i>Longidorus elongatus</i> Suggest Independent Acquisition of Some Plant Parasitism Genes by Horizontal Gene Transfer in Early-Branching Nematodes. <i>Genes</i> , 2017, 8, 287.	1.0	19
3166	Ancient DNA Resolves the History of Tetragnatha (Araneae, Tetragnathidae) Spiders on Rapa Nui. <i>Genes</i> , 2017, 8, 403.	1.0	14
3167	First Mitochondrial Genome from Nemouridae (Plecoptera) Reveals Novel Features of the Elongated Control Region and Phylogenetic Implications. <i>International Journal of Molecular Sciences</i> , 2017, 18, 996.	1.8	33
3168	Six new species of Heteropriapulid (Monogenea: Dactylogyridae) from South American fishes with an amended diagnosis to the genus. <i>Zootaxa</i> , 2017, 4290, .	0.2	25
3169	Dynamics of genomic innovation in the unicellular ancestry of animals. <i>ELife</i> , 2017, 6, .	2.8	121
3170	Genome Dynamics of <i>Escherichia coli</i> during Antibiotic Treatment: Transfer, Loss, and Persistence of Genetic Elements In situ of the Infant Gut. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 126.	1.8	46
3171	Nuclear and Mitochondrial Gene Data Support Recent Radiation within the Sea Spider Species Complex <i>Pallenopsis patagonica</i> . <i>Frontiers in Ecology and Evolution</i> , 2017, 4, .	1.1	14
3172	Evolinc: A Tool for the Identification and Evolutionary Comparison of Long Intergenic Non-coding RNAs. <i>Frontiers in Genetics</i> , 2017, 8, 52.	1.1	32
3173	Adaptive Evolution of Energy Metabolism-Related Genes in Hypoxia-Tolerant Mammals. <i>Frontiers in Genetics</i> , 2017, 8, 205.	1.1	34
3174	Seasonal and Interannual Changes in Ciliate and Dinoflagellate Species Assemblages in the Arctic Ocean (Amundsen Gulf, Beaufort Sea, Canada). <i>Frontiers in Marine Science</i> , 2017, 4, .	1.2	35
3175	Zoantharians (Hexacorallia: Zoantharia) Associated with Cold-Water Corals in the Azores Region: New Species and Associations in the Deep Sea. <i>Frontiers in Marine Science</i> , 2017, 4, .	1.2	26
3176	Integrative Taxonomy of Amazon Reefs' Arenosclera spp.: A New Clade in the Haplosclerida (Demospongiae). <i>Frontiers in Marine Science</i> , 2017, 4, .	1.2	10
3177	Abyssal Solenogastres (Mollusca, Aplousobranchia) from the Northwest Pacific: Scratching the Surface of Deep-Sea Diversity Using Integrative Taxonomy. <i>Frontiers in Marine Science</i> , 2017, 4, .	1.2	9

#	ARTICLE	IF	CITATIONS
3178	Characterization of the Genomic Diversity of Norovirus in Linked Patients Using a Metagenomic Deep Sequencing Approach. <i>Frontiers in Microbiology</i> , 2017, 8, 73.	1.5	34
3179	Freshwater Recirculating Aquaculture System Operations Drive Biofilter Bacterial Community Shifts around a Stable Nitrifying Consortium of Ammonia-Oxidizing Archaea and Comammox Nitrospira. <i>Frontiers in Microbiology</i> , 2017, 8, 101.	1.5	178
3180	<i>Staphylococcus aureus</i> Enterotoxin C and Enterotoxin-Like L Associated with Post-partum Mastitis. <i>Frontiers in Microbiology</i> , 2017, 8, 173.	1.5	16
3181	Diversity and Distribution of Freshwater Aerobic Anoxygenic Phototrophic Bacteria across a Wide Latitudinal Gradient. <i>Frontiers in Microbiology</i> , 2017, 8, 175.	1.5	44
3182	Genotypes Associated with <i>Listeria monocytogenes</i> Isolates Displaying Impaired or Enhanced Tolerances to Cold, Salt, Acid, or Desiccation Stress. <i>Frontiers in Microbiology</i> , 2017, 8, 369.	1.5	147
3183	A Comparative Analysis of the Lyve-SET Phylogenomics Pipeline for Genomic Epidemiology of Foodborne Pathogens. <i>Frontiers in Microbiology</i> , 2017, 8, 375.	1.5	137
3184	Mosquito Microbiome Dynamics, a Background for Prevalence and Seasonality of West Nile Virus. <i>Frontiers in Microbiology</i> , 2017, 8, 526.	1.5	114
3185	Pan-Genomic Analysis Permits Differentiation of Virulent and Non-virulent Strains of <i>Xanthomonas arboricola</i> That Cohabit <i>Prunus</i> spp. and Elucidate Bacterial Virulence Factors. <i>Frontiers in Microbiology</i> , 2017, 8, 573.	1.5	38
3186	Comparative Genomic Analysis of the Class Epsilonproteobacteria and Proposed Reclassification to Epsilonbacteraeota (phyl. nov.). <i>Frontiers in Microbiology</i> , 2017, 8, 682.	1.5	409
3187	Temporal Genomic Phylogeny Reconstruction Indicates a Geospatial Transmission Path of <i>Salmonella</i> Cerro in the United States and a Clade-Specific Loss of Hydrogen Sulfide Production. <i>Frontiers in Microbiology</i> , 2017, 8, 737.	1.5	31
3188	Spatial Structure of the Mormon Cricket Gut Microbiome and its Predicted Contribution to Nutrition and Immune Function. <i>Frontiers in Microbiology</i> , 2017, 8, 801.	1.5	37
3189	Global Diversity of Desert Hypolithic Cyanobacteria. <i>Frontiers in Microbiology</i> , 2017, 8, 867.	1.5	61
3190	Evaluating the Detection of Hydrocarbon-Degrading Bacteria in 16S rRNA Gene Sequencing Surveys. <i>Frontiers in Microbiology</i> , 2017, 8, 896.	1.5	25
3191	Replications of Two Closely Related Groups of Jumbo Phages Show Different Level of Dependence on Host-encoded RNA Polymerase. <i>Frontiers in Microbiology</i> , 2017, 8, 1010.	1.5	26
3192	Unexpected Dominance of Elusive Acidobacteria in Early Industrial Soft Coal Slags. <i>Frontiers in Microbiology</i> , 2017, 8, 1023.	1.5	32
3193	<i>Clostridium chauvoei</i> , an Evolutionary Dead-End Pathogen. <i>Frontiers in Microbiology</i> , 2017, 8, 1054.	1.5	33
3194	Antimicrobial Potential of Bacteria Associated with Marine Sea Slugs from North Sulawesi, Indonesia. <i>Frontiers in Microbiology</i> , 2017, 8, 1092.	1.5	46
3195	Genome Data Provides High Support for Generic Boundaries in <i>Burkholderia</i> Sensu Lato. <i>Frontiers in Microbiology</i> , 2017, 8, 1154.	1.5	122

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3196	Nutrient and Rainfall Additions Shift Phylogenetically Estimated Traits of Soil Microbial Communities. <i>Frontiers in Microbiology</i> , 2017, 8, 1271.	1.5	25
3197	Novel Pelagic Iron-Oxidizing Zetaproteobacteria from the Chesapeake Bay Oxic-Anoxic Transition Zone. <i>Frontiers in Microbiology</i> , 2017, 8, 1280.	1.5	72
3198	The Physiological Functions and Structural Determinants of Catalytic Bias in the [FeFe]-Hydrogenases Cpl and Cpll of <i>Clostridium pasteurianum</i> Strain W5. <i>Frontiers in Microbiology</i> , 2017, 8, 1305.	1.5	30
3199	Complete Mitochondrial Genome of <i>Phytophthora nicotianae</i> and Identification of Molecular Markers for the Oomycetes. <i>Frontiers in Microbiology</i> , 2017, 8, 1484.	1.5	22
3200	Seed and Root Endophytic Fungi in a Range Expanding and a Related Plant Species. <i>Frontiers in Microbiology</i> , 2017, 8, 1645.	1.5	77
3201	Whole-Genome Sequencing for National Surveillance of <i>Shigella flexneri</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 1700.	1.5	29
3202	Bacterial, Archaeal, and Eukaryotic Diversity across Distinct Microhabitats in an Acid Mine Drainage. <i>Frontiers in Microbiology</i> , 2017, 8, 1756.	1.5	88
3203	The Composite 259-kb Plasmid of <i>Marteella mediterranea</i> DSM 17316: A Natural Replicon with Functional RepABC Modules from Rhodobacteraceae and Rhizobiaceae. <i>Frontiers in Microbiology</i> , 2017, 8, 1787.	1.5	18
3204	Pathogenicity of Human ST23 <i>Streptococcus agalactiae</i> to Fish and Genomic Comparison of Pathogenic and Non-pathogenic Isolates. <i>Frontiers in Microbiology</i> , 2017, 8, 1933.	1.5	8
3205	Remarkable Diversity of <i>Escherichia coli</i> Carrying <i>mcr-1</i> from Hospital Sewage with the Identification of Two New <i>mcr-1</i> Variants. <i>Frontiers in Microbiology</i> , 2017, 8, 2094.	1.5	63
3206	Evolutionary Analysis of HIV-1 Pol Proteins Reveals Representative Residues for Viral Subtype Differentiation. <i>Frontiers in Microbiology</i> , 2017, 8, 2151.	1.5	13
3207	Distribution of Abundant and Active Planktonic Ciliates in Coastal and Slope Waters Off New England. <i>Frontiers in Microbiology</i> , 2017, 8, 2178.	1.5	14
3208	An Assessment of Different Genomic Approaches for Inferring Phylogeny of <i>Listeria monocytogenes</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 2351.	1.5	66
3209	Niche Partitioning of the N Cycling Microbial Community of an Offshore Oxygen Deficient Zone. <i>Frontiers in Microbiology</i> , 2017, 8, 2384.	1.5	60
3210	Fight Fungi with Fungi: Antifungal Properties of the Amphibian Mycobiome. <i>Frontiers in Microbiology</i> , 2017, 8, 2494.	1.5	56
3211	Aerobic and Anaerobic Methanotrophic Communities Associated with Methane Hydrates Exposed on the Seafloor: A High-Pressure Sampling and Stable Isotope-Incubation Experiment. <i>Frontiers in Microbiology</i> , 2017, 8, 2569.	1.5	18
3212	Comprehensive Analysis Reveals Two Distinct Evolution Patterns of <i>Salmonella</i> Flagellin Gene Clusters. <i>Frontiers in Microbiology</i> , 2017, 8, 2604.	1.5	14
3213	Deconstruction of the Ras switching cycle through saturation mutagenesis. <i>ELife</i> , 2017, 6, .	2.8	95

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3214	Severe infections emerge from commensal bacteria by adaptive evolution. <i>ELife</i> , 2017, 6, .	2.8	93
3215	Molecular phylogeny reveals strong biogeographic signal and two new species in a Cape Biodiversity Hotspot endemic mini-radiation, the pygmy geckos (Gekkonidae: Goggia). <i>Zootaxa</i> , 2017, 4312, 449.	0.2	12
3216	A new species of Andinobates (Anura: Dendrobatidae) from the Urabá region of Colombia. <i>Zootaxa</i> , 2017, 4290, 531.	0.2	4
3217	Population Structure of Pathogenic Bacteria. , 2017, , 51-70.		25
3218	Molecular Phylogeny and Morphological Distinctions of Two Popular Bivalves, <i>Ctenoides scaber</i> and <i>Ctenoides mitis</i> . <i>Journal of Marine Biology</i> , 2017, 2017, 1-9.	1.0	2
3219	A revision of the <i>Paracanthocobitis zonalternans</i> (Cypriniformes: Nemacheilidae) species complex with descriptions of three new species. <i>Zootaxa</i> , 2017, 4324, 85.	0.2	6
3220	A cybertaxonomic revision of the new dung beetle tribe Parachoriini (Coleoptera: Scarabaeidae). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 50</i> 4329, 101-149.	0.2	10
3221	Complete Chloroplast Genome Sequence of <i>Coptis chinensis</i> Franch. and Its Evolutionary History. <i>BioMed Research International</i> , 2017, 2017, 1-7.	0.9	6
3222	Evolution of an intricate J-protein network driving protein disaggregation in eukaryotes. <i>ELife</i> , 2017, 6, .	2.8	60
3223	Resolution of a Global Mango and Fig Pest Identity Crisis. <i>Insect Systematics and Diversity</i> , 2017, 1, .	0.7	9
3224	<i>Amphioxus Sp5</i> is a member of a conserved Specificity Protein complement and is modulated by Wnt/β-catenin signalling. <i>International Journal of Developmental Biology</i> , 2017, 61, 723-732.	0.3	7
3225	The genome of the Antarctic-endemic copepod, <i>Tigriopus kingsejongensis</i> . <i>GigaScience</i> , 2017, 6, 1-9.	3.3	12
3226	Support for Lungfish as the Closest Relative of Tetrapods by Using Slowly Evolving Ray-finned fish as the Outgroup. <i>Genome Biology and Evolution</i> , 2017, 9, eww288.	1.1	11
3227	A compendium of transcription factor and Transcriptionally active protein coding gene families in cowpea (<i>Vigna unguiculata</i> L.). <i>BMC Genomics</i> , 2017, 18, 898.	1.2	12
3228	Comparative genomics of <i>Coniophora olivacea</i> reveals different patterns of genome expansion in Boletales. <i>BMC Genomics</i> , 2017, 18, 883.	1.2	20
3229	Molecular phylogenetics of cool-season grasses in the subtribes Agrostidinae, Anthoxanthinae, Aveninae, Brizinae, Calothecinae, Koeleriinae and Phalaridinae (Poaceae, Pooideae, Poaeae, Poaeae) <i>Tj ETQq1 1 0.784614 rgBT /Overlock 10</i>	1.4	13
3230	Evolutionary Context of Non-Sorbitol-Fermenting Shiga Toxin-Producing <i>Escherichia coli</i> O55:H7. <i>Emerging Infectious Diseases</i> , 2017, 23, 1966-1973.	2.0	24
3231	<i>Nothophytophthora</i> gen. nov., a new sister genus of <i>Phytophthora</i> from natural and semi-natural ecosystems. <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2017, 39, 143-174.	1.6	30

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3232	An rbcl mRNA-binding protein is associated with C3 to C4 evolution and light-induced production of Rubisco in <i>Flaveria</i> . <i>Journal of Experimental Botany</i> , 2017, 68, 4635-4649.	2.4	7
3233	Asexual-sexual morph connection in the type species of <i>Berkleasium</i> . <i>IMA Fungus</i> , 2017, 8, 99-105.	1.7	12
3234	The Complete Maternally and Paternally Inherited Mitochondrial Genomes of a Freshwater Mussel <i>Potamilus alatus</i> (Bivalvia: Unionidae). <i>PLoS ONE</i> , 2017, 12, e0169749.	1.1	16
3235	Molecular Analysis of Chinese <i>Celastrus</i> and <i>Tripterygium</i> and Implications in Medicinal and Pharmacological Studies. <i>PLoS ONE</i> , 2017, 12, e0169973.	1.1	5
3236	Whole-genome duplication and molecular evolution in <i>Cornus</i> L. (Cornaceae) – Insights from transcriptome sequences. <i>PLoS ONE</i> , 2017, 12, e0171361.	1.1	17
3237	Within-host whole genome analysis of an antibiotic resistant <i>Pseudomonas aeruginosa</i> strain sub-type in cystic fibrosis. <i>PLoS ONE</i> , 2017, 12, e0172179.	1.1	31
3238	Historic DNA for taxonomy and conservation: A case-study of a century-old Hawaiian hawkmoth type (Lepidoptera: Sphingidae). <i>PLoS ONE</i> , 2017, 12, e0173255.	1.1	4
3239	The mitochondrial genome of pin-tailed snipe <i>Gallinago stenura</i> , and its implications for the phylogeny of Charadriiformes. <i>PLoS ONE</i> , 2017, 12, e0175244.	1.1	15
3240	AS3MT-mediated tolerance to arsenic evolved by multiple independent horizontal gene transfers from bacteria to eukaryotes. <i>PLoS ONE</i> , 2017, 12, e0175422.	1.1	29
3241	The Agassiz's desert tortoise genome provides a resource for the conservation of a threatened species. <i>PLoS ONE</i> , 2017, 12, e0177708.	1.1	33
3242	Discovery of a new hypotrich ciliate from petroleum contaminated soil. <i>PLoS ONE</i> , 2017, 12, e0178657.	1.1	20
3243	The emerging GII.P16-GII.4 Sydney 2012 norovirus lineage is circulating worldwide, arose by late-2014 and contains polymerase changes that may increase virus transmission. <i>PLoS ONE</i> , 2017, 12, e0179572.	1.1	63
3244	Northward dispersal of sea kraits (<i>Laticauda semifasciata</i>) beyond their typical range. <i>PLoS ONE</i> , 2017, 12, e0179871.	1.1	14
3245	<i>Ijuhya vitellina</i> sp. nov., a novel source for chaetoglobosin A, is a destructive parasite of the cereal cyst nematode <i>Heterodera filipjevi</i> . <i>PLoS ONE</i> , 2017, 12, e0180032.	1.1	45
3246	<i>Myotis rufoniger</i> genome sequence and analyses: <i>M. rufoniger</i> 's genomic feature and the decreasing effective population size of <i>Myotis</i> bats. <i>PLoS ONE</i> , 2017, 12, e0180418.	1.1	10
3247	The mitochondrial genome of the terrestrial carnivorous plant <i>Utricularia reniformis</i> (Lentibulariaceae): Structure, comparative analysis and evolutionary landmarks. <i>PLoS ONE</i> , 2017, 12, e0180484.	1.1	24
3248	Characterization of the emerging zoonotic pathogen <i>Arcobacter</i> <i>thereius</i> by whole genome sequencing and comparative genomics. <i>PLoS ONE</i> , 2017, 12, e0180493.	1.1	21
3249	Analysis of aquaporins from the euryhaline barnacle <i>Balanus improvisus</i> reveals differential expression in response to changes in salinity. <i>PLoS ONE</i> , 2017, 12, e0181192.	1.1	27

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3250	Sexual reproduction in plagiogrammecean diatoms: First insights into the early pennates. PLoS ONE, 2017, 12, e0181413.	1.1	9
3251	Molecular phylogeny and systematics of native North American lumbricid earthworms (Clitellata: Tj ETQq1 1 0.784314 rgBT /Overloc	1.1	30
3252	Diversity and phylogenetic relationships among Bartonella strains from Thai bats. PLoS ONE, 2017, 12, e0181696.	1.1	30
3253	Sequencing of the complete mitochondrial genomes of eight freshwater snail species exposes pervasive paraphyly within the Viviparidae family (Caenogastropoda). PLoS ONE, 2017, 12, e0181699.	1.1	29
3254	First fossil of an oestroid fly (Diptera: Calyptratae: Oestroidea) and the dating of oestroid divergences. PLoS ONE, 2017, 12, e0182101.	1.1	37
3255	Study of three interesting Amanita species from Thailand: Morphology, multiple-gene phylogeny and toxin analysis. PLoS ONE, 2017, 12, e0182131.	1.1	26
3256	Whole-genome sequencing illuminates the evolution and spread of multidrug-resistant tuberculosis in Southwest Nigeria. PLoS ONE, 2017, 12, e0184510.	1.1	27
3257	Grape microbiome as a reliable and persistent signature of field origin and environmental conditions in Cannonau wine production. PLoS ONE, 2017, 12, e0184615.	1.1	90
3258	Plant DNA barcodes and assessment of phylogenetic community structure of a tropical mixed dipterocarp forest in Brunei Darussalam (Borneo). PLoS ONE, 2017, 12, e0185861.	1.1	15
3259	Novel calpain families and novel mechanisms for calpain regulation in Aplysia. PLoS ONE, 2017, 12, e0186646.	1.1	9
3260	Spoligotyping and whole-genome sequencing analysis of lineage 1 strains of Mycobacterium tuberculosis in Da Nang, Vietnam. PLoS ONE, 2017, 12, e0186800.	1.1	8
3261	A continuous morphological approach to study the evolution of pollen in a phylogenetic context: An example with the order Myrtales. PLoS ONE, 2017, 12, e0187228.	1.1	28
3262	Archigregarines of the English Channel revisited: New molecular data on Selenidium species including early described and new species and the uncertainties of phylogenetic relationships. PLoS ONE, 2017, 12, e0187430.	1.1	14
3263	Molecular and epidemiological characterization of carbapenemase-producing Enterobacteriaceae in Norway, 2007 to 2014. PLoS ONE, 2017, 12, e0187832.	1.1	53
3264	Molecular detection of tick-borne pathogens in cattle from Southwestern Ethiopia. PLoS ONE, 2017, 12, e0188248.	1.1	60
3265	Deep sequencing of near full-length HIV-1 genomes from plasma identifies circulating subtype C and infrequent occurrence of AC recombinant form in Southern India. PLoS ONE, 2017, 12, e0188603.	1.1	6
3266	Modern-day SIV viral diversity generated by extensive recombination and cross-species transmission. PLoS Pathogens, 2017, 13, e1006466.	2.1	52
3267	Adaptive HIV-1 evolutionary trajectories are constrained by protein stability. Virus Evolution, 2017, 3, vex019.	2.2	10

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3268	Unique genome organization of non-mammalian papillomaviruses provides insights into the evolution of viral early proteins. <i>Virus Evolution</i> , 2017, 3, vex027.	2.2	51
3269	Patterns and Processes of <i>Mycobacterium bovis</i> Evolution Revealed by Phylogenomic Analyses. <i>Genome Biology and Evolution</i> , 2017, 9, 521-535.	1.1	31
3270	Phylogenetic relationships of <i>Limonium</i> (Plumbaginaceae) inferred from multiple chloroplast and nuclear loci. <i>Taxon</i> , 2017, 66, 1128-1146.	0.4	16
3271	Umbilicariaceae (lichenized Ascomycota) – Trait evolution and a new generic concept. <i>Taxon</i> , 2017, 66, 1282-1303.	0.4	30
3272	An updated phylogeny and infrageneric classification of the genus <i>Sisyrrinchium</i> (Iridaceae): Challenges of molecular and morphological evidence. <i>Taxon</i> , 2017, 66, 1317-1348.	0.4	12
3273	Fungal Planet description sheets: 625–715. <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2017, 39, 270-467.	1.6	148
3274	Unraveling relationships in the morphologically diverse and taxonomically challenging –justicioid– lineage (Acanthaceae: Justicieae). <i>Taxon</i> , 2017, 66, 645-674.	0.4	39
3275	Drivers of genetic diversity in secondary metabolic gene clusters within a fungal species. <i>PLoS Biology</i> , 2017, 15, e2003583.	2.6	187
3276	Phylogeny of the order <i>Phyllachorales</i> (<i>Ascomycota</i> , <i>Sordariomycetes</i>): among and within order relationships based on five molecular loci. <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2017, 39, 74-90.	1.6	28
3277	<i>Amanita cingulata</i> , a new annulate species of <i>Amanita</i> sect. <i>Vaginatae</i> from subtropical China. <i>Phytotaxa</i> , 2017, 326, 41.	0.1	9
3278	<i>Phallus aureolatus</i> (Phallaceae, Agaricomycetes), a new species from the Brazilian Atlantic Forest. <i>Phytotaxa</i> , 2017, 327, 223.	0.1	4
3279	Introducing <i>Ophiocordyceps thanathonensis</i> , a new species of entomogenous fungi on ants, and a reference specimen for <i>O. pseudolloydii</i> . <i>Phytotaxa</i> , 2017, 328, 115.	0.1	10
3280	<i>Lecanora stanislai</i> , a new, sterile, usnic acid containing lichen species from Eurasia and North America. <i>Phytotaxa</i> , 2017, 329, 201.	0.1	18
3281	<i>Alfaria avenellae</i> sp. nov. from Italy. <i>Phytotaxa</i> , 2017, 332, 67.	0.1	0
3282	Phylogeny and biogeography of <i>Artemisia</i> subgenus <i>Seriphidium</i> (Asteraceae: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 182 T	0.4	30
3283	The sea cucumber genome provides insights into morphological evolution and visceral regeneration. <i>PLoS Biology</i> , 2017, 15, e2003790.	2.6	202
3284	Comparative chloroplast genomes of eleven <i>Schima</i> (Theaceae) species: Insights into DNA barcoding and phylogeny. <i>PLoS ONE</i> , 2017, 12, e0178026.	1.1	34
3285	A multi-gene phylogeny of <i>Lactifluus</i> (<i>Basidiomycota</i> , <i>Russulales</i>) translated into a new infrageneric classification of the genus. <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2017, 38, 58-80.	1.6	57

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3286	Study in <i>Agaricus</i> subgenus <i>Minores</i> and allied clades reveals a new American subgenus and contrasting phylogenetic patterns in Europe and Greater Mekong Subregion. <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2017, 38, 170-196.	1.6	26
3287	Morphological reassessment and molecular phylogenetic analyses of <i>Amauroderma</i> s.lat. raised new perspectives in the generic classification of the <i>Ganodermataceae</i> family. <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2017, 39, 254-269.	1.6	26
3288	<i>Agaricus globocystidiatus</i> : a new neotropical species with pleurocystidia in <i>Agaricus</i> subg. <i>Minoriopsis</i> . <i>Phytotaxa</i> , 2017, 314, 64.	0.1	3
3289	<i>Bisifusarium tonghuanum</i> (Nectriaceae), a novel species of <i>Fusarium</i> -like fungi from two desert oasis plants. <i>Phytotaxa</i> , 2017, 317, 123.	0.1	2
3290	A new marine alga, <i>Pterocliadiella andresii</i> sp. nov. (Gelidiales, Rhodophyta) and its relationship to <i>P. caloglossoides</i> from Pacific South America. <i>Phytotaxa</i> , 2017, 319, 139.	0.1	5
3291	Mutation Accumulation in an Asexual Relative of <i>Arabidopsis</i> . <i>PLoS Genetics</i> , 2017, 13, e1006550.	1.5	54
3292	Carbapenem-resistance and pathogenicity of bovine <i>Acinetobacter indicus</i> -like isolates. <i>PLoS ONE</i> , 2017, 12, e0171986.	1.1	22
3293	Demystifying the <i>Capitella capitata</i> complex (Annelida, Capitellidae) diversity by morphological and molecular data along the Brazilian coast. <i>PLoS ONE</i> , 2017, 12, e0177760.	1.1	22
3294	Analysis of intra-host genetic diversity of <i>Prunus necrotic ringspot virus</i> (PNRSV) using amplicon next generation sequencing. <i>PLoS ONE</i> , 2017, 12, e0179284.	1.1	28
3295	Identification of benthic diatoms isolated from the eastern tidal flats of the Yellow Sea: Comparison between morphological and molecular approaches. <i>PLoS ONE</i> , 2017, 12, e0179422.	1.1	15
3296	Ultraconserved elements (UCEs) resolve the phylogeny of Australasian smurf-weevils. <i>PLoS ONE</i> , 2017, 12, e0188044.	1.1	51
3297	Cut from the same cloth: The convergent evolution of dwarf morphotypes of the <i>Carex flava</i> group (Cyperaceae) in Circum-Mediterranean mountains. <i>PLoS ONE</i> , 2017, 12, e0189769.	1.1	14
3298	Comparative genomics of the tardigrades <i>Hypsibius dujardini</i> and <i>Ramazzottius varieornatus</i> . <i>PLoS Biology</i> , 2017, 15, e2002266.	2.6	170
3299	Estimating the Respective Contributions of Human and Viral Genetic Variation to HIV Control. <i>PLoS Computational Biology</i> , 2017, 13, e1005339.	1.5	28
3300	Rearrangement moves on rooted phylogenetic networks. <i>PLoS Computational Biology</i> , 2017, 13, e1005611.	1.5	15
3301	Systematic identification and characterization of regulatory elements derived from human endogenous retroviruses. <i>PLoS Genetics</i> , 2017, 13, e1006883.	1.5	132
3302	Whole Genome Amplification and Reduced-Representation Genome Sequencing of <i>Schistosoma japonicum</i> Miracidia. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005292.	1.3	23
3303	Minimal genetic change in <i>Vibrio cholerae</i> in Mozambique over time: Multilocus variable number tandem repeat analysis and whole genome sequencing. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005671.	1.3	31

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3304	Phylogenetics and Phylogenomics of Rust Fungi. <i>Advances in Genetics</i> , 2017, 100, 267-307.	0.8	68
3305	Do ampharetids take sedimented steps between vents and seeps? Phylogeny and habitat-use of Ampharetidae (Annelida, Terebelliformia) in chemosynthesis-based ecosystems. <i>BMC Evolutionary Biology</i> , 2017, 17, 222.	3.2	21
3306	Pan-genome and phylogeny of <i>Bacillus cereus</i> sensu lato. <i>BMC Evolutionary Biology</i> , 2017, 17, 176.	3.2	92
3307	Rapid turnover of effectors in grass powdery mildew (<i>Blumeria graminis</i>). <i>BMC Evolutionary Biology</i> , 2017, 17, 223.	3.2	52
3308	The complete chloroplast genome of <i>Primulina</i> and two novel strategies for development of high polymorphic loci for population genetic and phylogenetic studies. <i>BMC Evolutionary Biology</i> , 2017, 17, 224.	3.2	18
3309	A new species of <i>Xenoturbella</i> from the western Pacific Ocean and the evolution of <i>Xenoturbella</i> . <i>BMC Evolutionary Biology</i> , 2017, 17, 245.	3.2	16
3310	From ground pools to treeholes: convergent evolution of habitat and phenotype in <i>Aedes</i> mosquitoes. <i>BMC Evolutionary Biology</i> , 2017, 17, 262.	3.2	39
3311	The molecular evolutionary dynamics of oxidative phosphorylation (OXPHOS) genes in Hymenoptera. <i>BMC Evolutionary Biology</i> , 2017, 17, 269.	3.2	40
3312	Origins and biogeography of the <i>Anolis crassulus</i> subgroup (Squamata: Dactyloidae) in the highlands of Nuclear Central America. <i>BMC Evolutionary Biology</i> , 2017, 17, 267.	3.2	14
3314	First gene-ontology enrichment analysis based on bacterial coregenome variants: insights into adaptations of <i>Salmonella</i> serovars to mammalian- and avian-hosts. <i>BMC Microbiology</i> , 2017, 17, 222.	1.3	41
3315	Phylogenetics of subtribe Orchidinae s.l. (Orchidaceae; Orchidoideae) based on seven markers (plastid) Tj ETQq0 0 0 rgBT /Overlock 10 Plant Biology, 2017, 17, 222.	1.6	41
3316	Genomic innovations, transcriptional plasticity and gene loss underlying the evolution and divergence of two highly polyphagous and invasive <i>Helicoverpa</i> pest species. <i>BMC Biology</i> , 2017, 15, 63.	1.7	238
3317	Genome sequencing of the staple food crop white Guinea yam enables the development of a molecular marker for sex determination. <i>BMC Biology</i> , 2017, 15, 86.	1.7	114
3318	HAlign-II: efficient ultra-large multiple sequence alignment and phylogenetic tree reconstruction with distributed and parallel computing. <i>Algorithms for Molecular Biology</i> , 2017, 12, 25.	0.3	30
3319	Whole-genome analysis of human papillomavirus genotypes 52 and 58 isolated from Japanese women with cervical intraepithelial neoplasia and invasive cervical cancer. <i>Infectious Agents and Cancer</i> , 2017, 12, 44.	1.2	16
3320	Methicillin-resistant <i>Staphylococcus aureus</i> emerged long before the introduction of methicillin into clinical practice. <i>Genome Biology</i> , 2017, 18, 130.	3.8	193
3321	Conservation and divergence of small RNA pathways and microRNAs in land plants. <i>Genome Biology</i> , 2017, 18, 158.	3.8	91
3322	Spatiotemporal regulation of nervous system development in the annelid <i>Capitella teleta</i> . <i>EvoDevo</i> , 2017, 8, 13.	1.3	22

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3323	Members of the Candidate Phyla Radiation are functionally differentiated by carbon- and nitrogen-cycling capabilities. <i>Microbiome</i> , 2017, 5, 112.	4.9	118
3324	Associations among dietary non-fiber carbohydrate, ruminal microbiota and epithelium G-protein-coupled receptor, and histone deacetylase regulations in goats. <i>Microbiome</i> , 2017, 5, 123.	4.9	74
3325	Bottled aqua incognita: microbiota assembly and dissolved organic matter diversity in natural mineral waters. <i>Microbiome</i> , 2017, 5, 126.	4.9	26
3326	<i>Circinella simplex</i> a misapplied name of <i>Mucor circinatus</i> sp. nov.. <i>Phytotaxa</i> , 2017, 329, 269.	0.1	7
3327	Genetic diversity of <i>Timarete punctata</i> (Annelida: Cirratulidae): Detection of pseudo-cryptic species and a potential biological invader. <i>Estuarine, Coastal and Shelf Science</i> , 2017, 197, 214-220.	0.9	14
3328	A Novel Heuristic for Data Distribution in Massively Parallel Phylogenetic Inference Using Site Repeats. , 2017, , .		3
3329	Characterization of the complete chloroplast genome of the Eastern gamagrass, <i>Tripsacum dactyloides</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 910-912.	0.2	2
3330	Reconstructing the Evolutionary History of Powdery Mildew Lineages (<i>Blumeria graminis</i>) at Different Evolutionary Time Scales with NGS Data. <i>Genome Biology and Evolution</i> , 2017, 9, 446-456.	1.1	34
3331	Comparative genomics analyses of alpha-keratins reveal insights into evolutionary adaptation of marine mammals. <i>Frontiers in Zoology</i> , 2017, 14, 41.	0.9	18
3332	The genomic study of an environmental isolate of <i>Scedosporium apiospermum</i> shows its metabolic potential to degrade hydrocarbons. <i>Standards in Genomic Sciences</i> , 2017, 12, 71.	1.5	25
3333	Genome sequence of the model plant pathogen <i>Pectobacterium carotovorum</i> SCC1. <i>Standards in Genomic Sciences</i> , 2017, 12, 87.	1.5	16
3334	Whole mitochondrial genomes provide increased resolution and indicate paraphyly in deer mice. <i>BMC Zoology</i> , 2017, 2, .	0.3	29
3335	Streptococcal toxic shock syndrome caused by the dissemination of an invasive emm3/ST15 strain of <i>Streptococcus pyogenes</i> . <i>BMC Infectious Diseases</i> , 2017, 17, 774.	1.3	4
3336	Myosin repertoire expansion coincides with eukaryotic diversification in the Mesoproterozoic era. <i>BMC Evolutionary Biology</i> , 2017, 17, 211.	3.2	50
3337	Pneumococcal 23B Molecular Subtype Identified Using Whole Genome Sequencing. <i>Genome Biology and Evolution</i> , 2017, 9, 2145-2158.	1.1	12
3338	Evolutionary thrift: mycobacteria repurpose plasmid diversity during adaptation of type VII secretion systems. <i>Genome Biology and Evolution</i> , 2017, 9, 398-413.	1.1	33
3339	Multigene phylogeny of Endogonales, an early diverging lineage offungi associated with plants. <i>IMA Fungus</i> , 2017, 8, 245-257.	1.7	45
3340	Venomics of Remipede Crustaceans Reveals Novel Peptide Diversity and Illuminates the Venom's Biological Role. <i>Toxins</i> , 2017, 9, 234.	1.5	27

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3341	Polyphasic characterization of <i>Westiellopsis prolifica</i> (Hapalosiphonaceae, Cyanobacteria) from the El-Farafra Oasis (Western Desert, Egypt). <i>Phycologia</i> , 2017, 56, 697-709.	0.6	10
3342	Burrowers from the Past: Mitochondrial Signatures of Ordovician Bivalve Infaunalization. <i>Genome Biology and Evolution</i> , 2017, 9, 956-967.	1.1	14
3343	SpartaABC: a web server to simulate sequences with indel parameters inferred using an approximate Bayesian computation algorithm. <i>Nucleic Acids Research</i> , 2017, 45, W453-W457.	6.5	5
3344	Molecular analyses reveal the occurrence of three new sympatric lineages of velvet worms (<i>Onychophora</i> : <i>Peripatidae</i>) in the eastern Amazon basin. <i>Genetics and Molecular Biology</i> , 2017, 40, 147-152.	0.6	4
3345	Highly Pathogenic Avian Influenza A(H7N9) Virus, Tennessee, USA, March 2017. <i>Emerging Infectious Diseases</i> , 2017, 23, 1860-1863.	2.0	52
3346	The monophyly of the Claurocarini (Diptera: Tachinidae: Tachininae) with the description of a new species of <i>Semisuturia</i> from Australia. <i>Insect Systematics and Evolution</i> , 2017, 49, 1-22.	0.2	1
3347	Molecular Characterization of Copepod Photoreception. <i>Biological Bulletin</i> , 2017, 233, 96-110.	0.7	14
3348	The evolutionary history of plant T2/S-type ribonucleases. <i>PeerJ</i> , 2017, 5, e3790.	0.9	64
3349	An expanded phylogeny for the genus <i>Phytophthora</i> . <i>IMA Fungus</i> , 2017, 8, 355-384.	1.7	170
3350	Phylogenetic relationships of eight new <i>Dacrymycetes</i> collected from new Zealand. <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2017, 38, 156-169.	1.6	13
3351	New species of <i>Auritella</i> (Inocybaceae) from Cameroon, with a worldwide key to the known species. <i>IMA Fungus</i> , 2017, 8, 287-298.	1.7	8
3352	Multiple introductions and recent spread of the emerging human pathogen <i>Mycobacterium ulcerans</i> across Africa. <i>Genome Biology and Evolution</i> , 2017, 9, evx003.	1.1	32
3353	<i>Pleiocarpon</i> gen. nov. and a new species of <i>Ilyonectria</i> causing basal rot of <i>Strelitzia reginae</i> in Italy. <i>IMA Fungus</i> , 2017, 8, 65-76.	1.7	19
3354	Parallel Miocene-dominated diversification of the lichen-forming fungal genus <i>Oropogon</i> (Ascomycota: Parmeliaceae) in different continents. <i>Taxon</i> , 2017, 66, 1269-1281.	0.4	6
3355	Swine Influenza Virus (H1N2) Characterization and Transmission in Ferrets, Chile. <i>Emerging Infectious Diseases</i> , 2017, 23, 241-251.	2.0	12
3356	Genomic characterisation of clinical and environmental <i>Pseudomonas putida</i> group strains and determination of their role in the transfer of antimicrobial resistance genes to <i>Pseudomonas aeruginosa</i> . <i>BMC Genomics</i> , 2017, 18, 859.	1.2	48
3357	phyloSkeleton: taxon selection, data retrieval and marker identification for phylogenomics. <i>Bioinformatics</i> , 2017, 33, 1230-1232.	1.8	18
3358	Fatal Outbreak in Tonkean Macaques Caused by Possibly Novel Orthopoxvirus, Italy, January 20151. <i>Emerging Infectious Diseases</i> , 2017, 23, 1941-1949.	2.0	27

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3359	Phylogenomic Insights into Mouse Evolution Using a Pseudoreference Approach. <i>Genome Biology and Evolution</i> , 2017, 9, 726-739.	1.1	47
3360	Adaptation in a Fibronectin Binding Autolysin of <i>Staphylococcus saprophyticus</i> . <i>MSphere</i> , 2017, 2, .	1.3	9
3361	Multiple new cryptic pathogenic <i>Phytophthora</i> species from Fagaceae forests in Austria, Italy and Portugal. <i>IMA Fungus</i> , 2017, 8, 219-244.	1.7	65
3362	Molecular dating of phylogenetic divergence between <i>Urochloa</i> species based on complete chloroplast genomes. <i>BMC Genomics</i> , 2017, 18, 516.	1.2	40
3363	Genomic Analysis of <i>Salmonella enterica</i> Serovar Typhimurium DT160 Associated with a 14-Year Outbreak, New Zealand, 1998–2012. <i>Emerging Infectious Diseases</i> , 2017, 23, 906-913.	2.0	31
3364	Invasive Serotype 35B Pneumococci Including an Expanding Serotype Switch Lineage, United States, 2015–2016. <i>Emerging Infectious Diseases</i> , 2017, 23, 922-930.	2.0	52
3365	Extremely low genomic diversity of <i>Rickettsia japonica</i> distributed in Japan. <i>Genome Biology and Evolution</i> , 2017, 9, evw304.	1.1	16
3366	Anion-selective Formate/nitrite transporters: taxonomic distribution, phylogenetic analysis and subfamily-specific conservation pattern in prokaryotes. <i>BMC Genomics</i> , 2017, 18, 560.	1.2	24
3367	Preliminary comparative genomics revealed pathogenic potential and international spread of <i>Staphylococcus argenteus</i> . <i>BMC Genomics</i> , 2017, 18, 808.	1.2	44
3368	Analysis of the genome of the New Zealand giant collembolan (<i>Holacanthella duospinosa</i>) sheds light on hexapod evolution. <i>BMC Genomics</i> , 2017, 18, 795.	1.2	28
3369	Identification of the Sex-Biased Gene Expression and Putative Sex-Associated Genes in <i>Eucommia ulmoides</i> Oliver Using Comparative Transcriptome Analyses. <i>Molecules</i> , 2017, 22, 2255.	1.7	16
3370	<i>Pterocliadiella</i> (<i>Gelidiales</i> , <i>Rhodophyta</i>) species of Brazil including morphological studies of <i>Pterocliadiella media</i> and a reassessment of <i>Pterocliadiella taylorii</i> . <i>Phycologia</i> , 2017, 56, 624-637.	0.6	12
3371	DNA Barcoding analysis of seafood accuracy in Washington, D.C. restaurants. <i>PeerJ</i> , 2017, 5, e3234.	0.9	15
3372	Collagen IV and basement membrane at the evolutionary dawn of metazoan tissues. <i>ELife</i> , 2017, 6, .	2.8	139
3373	<i>Selaginella guihai</i> (<i>Selaginellaceae</i>): A new spikemoss species from southern China and northern Vietnam around the Gulf of Tonkin. <i>PhytoKeys</i> , 2017, 80, 41-52.	0.4	5
3374	Phylogeny of Viruses . . . , 2017, . . .		13
3375	Origin and evolution of transporter substrate specificity within the NPF family. <i>ELife</i> , 2017, 6, .	2.8	100
3376	The <i>Phyllophoraceae</i> (<i>Gigartinales</i> , <i>Rhodophyta</i>) from Peru with descriptions of <i>Acletoa tarazonae</i> gen. nov. & sp. nov. and <i>Gymnogongrus caespitosus</i> sp. nov. <i>Phycologia</i> , 2017, 56, 686-696.	0.6	9

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3377	Three new cryptogenic species in the tribes Polysiphoniae and Streblocladiae (Rhodomelaceae,) Tj ETQq0 0 0 rgBTj/Overlock 10 Tf 50	0.6	19
3378	Introducing EzBioCloud: a taxonomically united database of 16S rRNA gene sequences and whole-genome assemblies. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 1613-1617.	0.8	5,862
3379	The evolutionary history of Stomatopoda (Crustacea: Malacostraca) inferred from molecular data. PeerJ, 2017, 5, e3844.	0.9	29
3380	Helobdella blinni sp. n. (Hirudinida, Glossiphoniidae) a new species inhabiting Montezuma Well, Arizona, USA. ZooKeys, 2017, 661, 137-155.	0.5	6
3381	Utility of Combining Whole Genome Sequencing with Traditional Investigational Methods To Solve Foodborne Outbreaks of Salmonella Infections Associated with Chicken: A New Tool for Tackling This Challenging Food Vehicle. Journal of Food Protection, 2017, 80, 654-660.	0.8	23
3382	<i>Lactifluus persicinus</i> sp. nov. from the gallery forests of West Cameroon. Mycotaxon, 2017, 132, 471-483.	0.1	7
3383	A Fast Algorithm for Reconstructing Multiple Sequence Alignment and Phylogeny Simultaneously. Current Bioinformatics, 2017, 12, .	0.7	1
3384	Metabolic phenotype of clinical and environmental <i>Mycobacterium avium</i> subsp. <i>hominissuis</i> isolates. PeerJ, 2017, 5, e2833.	0.9	2
3385	The presence of genes encoding enzymes that digest carbohydrates in coral genomes and analysis of their activities. PeerJ, 2017, 5, e4087.	0.9	7
3386	The complete mitochondrial genome of <i>Engyodontium album</i> and comparative analyses with Ascomycota mitogenomes. Genetics and Molecular Biology, 2017, 40, 844-854.	0.6	5
3387	Expression of G Proteins in the Eyes and Parietovisceral Ganglion of the Bay Scallop <i>Argopecten irradians</i> . Biological Bulletin, 2017, 233, 83-95.	0.7	11
3388	Neurologic Complications of Influenza B Virus Infection in Adults, Romania. Emerging Infectious Diseases, 2017, 23, 574-581.	2.0	33
3389	Palaeogenomes of Eurasian straight-tusked elephants challenge the current view of elephant evolution. ELife, 2017, 6, .	2.8	50
3390	<i>Opisthotropis</i> sp. nov. Zoological Research, 2017, 38, 251-263.	0.9	4
3391	A new species of <i>Scutellaria</i> (Scutellarioideae, Lamiaceae) from Sichuan Province in southwest China. PeerJ, 2017, 5, e3624.	0.9	10
3392	A new species of <i>Ophryotrocha</i> (Annelida, Eunicida, Dorvilleidae) from hydrothermal vents on the Southwest Indian Ridge. ZooKeys, 2017, 687, 1-9.	0.5	14
3393	Complete mitochondrial genomes from two species of Chinese freshwater crabs of the genus <i>Sinopotamon</i> recovered using next-generation sequencing reveal a novel gene order (Brachyura,) Tj ETQq0 0 0 rgBTj/Overlock 10 Tf 50	0.6	19
3394	Encoding Data Using Biological Principles: The Multisample Variant Format for Phylogenomics and Population Genomics. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 1231-1238.	1.9	23

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3395	The complete genome sequence of CrRV-Ch01, a new member of the family Rhabdoviridae in the parasitic copepod <i>Caligus rogercresseyi</i> present on farmed Atlantic salmon (<i>Salmo salar</i>) in Chile. <i>Archives of Virology</i> , 2018, 163, 1657-1661.	0.9	7
3396	NaPi/S<sub>g</sub>X</sub>-RNase segregates as a functional S-RNase and is induced under phosphate deficiency in <i>Nicotiana glauca</i> . <i>Biologia Plantarum</i> , 2018, 62, 261-268.	1.9	14
3397	Specialized plant biochemistry drives gene clustering in fungi. <i>ISME Journal</i> , 2018, 12, 1694-1705.	4.4	20
3398	Isoniazid resistance levels of <i>Mycobacterium tuberculosis</i> can largely be predicted by high-confidence resistance-conferring mutations. <i>Scientific Reports</i> , 2018, 8, 3246.	1.6	87
3399	The timescale of early land plant evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E2274-E2283.	3.3	654
3400	Spatiotemporal Characteristics of the HIV-1 CRF02_AG/CRF63_02A1 Epidemic in Russia and Central Asia. <i>AIDS Research and Human Retroviruses</i> , 2018, 34, 415-420.	0.5	19
3401	Emergence of an Extensively Drug-Resistant <i>Salmonella enterica</i> Serovar Typhi Clone Harboring a Promiscuous Plasmid Encoding Resistance to Fluoroquinolones and Third-Generation Cephalosporins. <i>MBio</i> , 2018, 9, .	1.8	434
3402	Constructing a broadly inclusive seed plant phylogeny. <i>American Journal of Botany</i> , 2018, 105, 302-314.	0.8	647
3403	You stay, but I Hop: Host shifting near and far dominated the evolution of <i>Enchenopa</i> treehoppers. <i>Ecology and Evolution</i> , 2018, 8, 1954-1965.	0.8	10
3404	Comparative phylogeography of diadromous and freshwater daces of the genus <i>Tribolodon</i> (Cyprinidae). <i>Ichthyological Research</i> , 2018, 65, 383-397.	0.5	18
3405	Unraveling the genetic history of the European wild goats. <i>Quaternary Science Reviews</i> , 2018, 185, 189-198.	1.4	21
3406	Antigenic and genetic evolution of contemporary swine H1 influenza viruses in the United States. <i>Virology</i> , 2018, 518, 45-54.	1.1	64
3407	Hidden diversity of forest birds in Madagascar revealed using integrative taxonomy. <i>Molecular Phylogenetics and Evolution</i> , 2018, 124, 16-26.	1.2	24
3408	ViCTree: an automated framework for taxonomic classification from protein sequences. <i>Bioinformatics</i> , 2018, 34, 2195-2200.	1.8	6
3409	Expanded diversity of microbial groups that shape the dissimilatory sulfur cycle. <i>ISME Journal</i> , 2018, 12, 1715-1728.	4.4	347
3410	Ancient genomes revisit the ancestry of domestic and Przewalski's horses. <i>Science</i> , 2018, 360, 111-114.	6.0	241
3411	Two new species of the <i>Ophisops microlepis</i> (Squamata: Lacertidae) complex from northwestern India with a key to Indian <i>Ophisops</i> . <i>Journal of Natural History</i> , 2018, 52, 819-847.	0.2	7
3412	New <i>Cortinarius</i> (Agaricales) species described from New Zealand. <i>New Zealand Journal of Botany</i> , 2018, 56, 163-182.	0.8	9

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3413	New data, same story: phylogenomics does not support Syrphoidea (Diptera: Syrphidae, Pipunculidae). <i>Systematic Entomology</i> , 2018, 43, 447-459.	1.7	53
3414	Avian Influenza A (H7N9) Virus in a Wild Land Bird in Central China, Late 2015. <i>Virologica Sinica</i> , 2018, 33, 96-99.	1.2	7
3415	SubRecon: ancestral reconstruction of amino acid substitutions along a branch in a phylogeny. <i>Bioinformatics</i> , 2018, 34, 2297-2299.	1.8	4
3416	Molecular phylogenetics and species limits in a cryptically coloured radiation of Australo-Papuan passerine birds (Pachycephalidae: Colluricincla). <i>Molecular Phylogenetics and Evolution</i> , 2018, 124, 100-105.	1.2	16
3417	Using floristics, modern systematics and phylogenetics for disentangling biodiversity hotspots across scales: a Mediterranean case study. <i>Plant Biosystems</i> , 2018, 152, 1293-1310.	0.8	6
3418	Molecular Phylogeny and Dating Reveal a Terrestrial Origin in the Early Carboniferous for Ascaridoid Nematodes. <i>Systematic Biology</i> , 2018, 67, 888-900.	2.7	75
3419	Lineage-specific plasmid acquisition and the evolution of specialized pathogens in <i>Bacillus thuringiensis</i> and the <i>Bacillus cereus</i> group. <i>Molecular Ecology</i> , 2018, 27, 1524-1540.	2.0	43
3420	Appearance of reassortant European avian-origin H1 influenza A viruses of swine in Vietnam. <i>Transboundary and Emerging Diseases</i> , 2018, 65, 1110-1116.	1.3	6
3421	<i>Mycoplasma</i> -related endobacteria within Mortierellomycotina fungi: diversity, distribution and functional insights into their lifestyle. <i>ISME Journal</i> , 2018, 12, 1743-1757.	4.4	48
3422	The first known virus isolates from Antarctic sea ice have complex infection patterns. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	20
3423	Culture-Facilitated Comparative Genomics of the Facultative Symbiont <i>Hamiltonella defensa</i> . <i>Genome Biology and Evolution</i> , 2018, 10, 786-802.	1.1	37
3424	Rates of Mutation and Recombination in Siphoviridae Phage Genome Evolution over Three Decades. <i>Molecular Biology and Evolution</i> , 2018, 35, 1147-1159.	3.5	61
3425	Long-Term Microevolution of <i>Pseudomonas aeruginosa</i> Differs between Mildly and Severely Affected Cystic Fibrosis Lungs. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2018, 59, 246-256.	1.4	42
3426	Recombinant type Human mastadenovirus D85 associated with epidemic keratoconjunctivitis since 2015 in Japan. <i>Journal of Medical Virology</i> , 2018, 90, 881-889.	2.5	53
3427	Convergent evolution of high elevation plant growth forms and geographically structured variation in Andean <i>Lupinus</i> (Fabaceae). <i>Botanical Journal of the Linnean Society</i> , 2018, 187, 118-136.	0.8	48
3428	Two new species of <i>Pustula</i> (Albuginales, Oomycota) from Junggar Basin in China based on morphology and molecular data. <i>Mycological Progress</i> , 2018, 17, 501-508.	0.5	2
3429	Genome-wide nucleotide diversity and associations with geography, ploidy level and glucosinolate profiles in <i>Aethionema arabicum</i> (Brassicaceae). <i>Plant Systematics and Evolution</i> , 2018, 304, 619-630.	0.3	13
3430	Conservation of Dynamics Associated with Biological Function in an Enzyme Superfamily. <i>Structure</i> , 2018, 26, 426-436.e3.	1.6	52

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3431	Sympatric occurrence of three leaf beetle species of <i>Macrolea</i> Samouelle, 1819 (Coleoptera, Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 39, 21-42.	0.6	1
3432	Whole genome analysis of cephalosporin-resistant <i>Escherichia coli</i> from bloodstream infections in Australia, New Zealand and Singapore: high prevalence of CMY-2 producers and ST131 carrying blaCTX-M-15 and blaCTX-M-27. <i>Journal of Antimicrobial Chemotherapy</i> , 2018, 73, 634-642.	1.3	56
3433	The phylogenetic position of the extinct Cuban Macaw <i>Ara tricolor</i> based on complete mitochondrial genome sequences. <i>Ibis</i> , 2018, 160, 666-672.	1.0	5
3434	A phylogenomic analysis of Culicomorpha (Diptera) resolves the relationships among the eight constituent families. <i>Systematic Entomology</i> , 2018, 43, 434-446.	1.7	22
3435	Exploring species boundaries with multiple genetic loci using empirical data from non-biting midges. <i>Zoologica Scripta</i> , 2018, 47, 325-341.	0.7	18
3436	Horizontal gene cluster transfer increased hallucinogenic mushroom diversity. <i>Evolution Letters</i> , 2018, 2, 88-101.	1.6	73
3437	MtDNA allows the sensitive detection and haplotyping of the crayfish plague disease agent <i>Aphanomyces astaci</i> showing clues about its origin and migration. <i>Parasitology</i> , 2018, 145, 1210-1218.	0.7	39
3438	Complete chloroplast genome of an Endangered mangrove plant <i>Hernandia nymphiifolia</i> (C. Presl) Kubitzki (Hernandiaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 231-232.	0.2	1
3439	Large Blooms of <i>Bacillales</i> (<i>Firmicutes</i>) Underlie the Response to Wetting of Cyanobacterial Biocrusts at Various Stages of Maturity. <i>MBio</i> , 2018, 9, .	1.8	28
3440	Genotyping-by-sequencing reveals the origin of the Tunisian relatives of cultivated carrot (<i>Daucus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 0,8	0.8	14
3441	Conservation implications of spatial genetic structure in two species of oribatid mites from the Antarctic Peninsula and the Scotia Arc. <i>Antarctic Science</i> , 2018, 30, 105-114.	0.5	12
3442	Mitochondrial OXPHOS genes provides insights into genetics basis of hypoxia adaptation in anchialine cave shrimps. <i>Genes and Genomics</i> , 2018, 40, 1169-1180.	0.5	8
3443	West meets East: How do rainforest beetles become circum-Pacific? Evolutionary origin of <i>Callipogon relictus</i> and allied species (Cerambycidae: Prioninae) in the New and Old Worlds. <i>Molecular Phylogenetics and Evolution</i> , 2018, 125, 163-176.	1.2	17
3444	Large-scale phylogenetic analyses provide insights into unrecognized diversity and historical biogeography of Asian leaf-litter frogs, genus <i>Leptotalax</i> (Anura: Megophryidae). <i>Molecular Phylogenetics and Evolution</i> , 2018, 124, 162-171.	1.2	68
3445	Comprehensive molecular phylogeny of barn owls and relatives (Family: Tytonidae), and their six major Pleistocene radiations. <i>Molecular Phylogenetics and Evolution</i> , 2018, 125, 127-137.	1.2	38
3446	The complete mitochondrial genomes of five lichenized fungi in the genus <i>Usnea</i> (Ascomycota) Tj ETQq1 1 0.784314 rgBT /Overlock 0,2 16	0.2	16
3447	Molecular evolution and diversification of the SMXL gene family. <i>Journal of Experimental Botany</i> , 2018, 69, 2367-2378.	2.4	41
3448	Phylogenetic Characterization of <i>Salmonella enterica</i> Serovar Typhimurium and Its Monophasic Variant Isolated from Food Animals in Japan Revealed Replacement of Major Epidemic Clones in the Last 4 Decades. <i>Journal of Clinical Microbiology</i> , 2018, 56, .	1.8	38

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3449	Studying AMPK in an Evolutionary Context. <i>Methods in Molecular Biology</i> , 2018, 1732, 111-142.	0.4	3
3450	A preliminary molecular phylogeny shows Japanese and Austrian populations of the red mite <i>Balaustium murorum</i> (Acari: Trombidiformes: Erythraeidae) to be closely related. <i>Experimental and Applied Acarology</i> , 2018, 74, 225-238.	0.7	3
3451	Phylogenetic systematics of subtribe <i>Spiranthinae</i> (Orchidaceae: Orchidoideae: Cranichideae) based on nuclear and plastid DNA sequences of a nearly complete generic sample. <i>Botanical Journal of the Linnean Society</i> , 2018, 186, 273-303.	0.8	25
3452	Unravelling the complicated evolutionary and dissemination history of HIV-1M subtype A lineages. <i>Virus Evolution</i> , 2018, 4, vey003.	2.2	12
3453	Genome-reconstruction for eukaryotes from complex natural microbial communities. <i>Genome Research</i> , 2018, 28, 569-580.	2.4	163
3454	The complete chloroplast genome of the common self-heal, <i>Prunella vulgaris</i> (Lamiaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 125-126.	0.2	1
3455	Frequent Undetected Ward-Based Methicillin-Resistant <i>Staphylococcus aureus</i> Transmission Linked to Patient Sharing Between Hospitals. <i>Clinical Infectious Diseases</i> , 2018, 66, 840-848.	2.9	25
3456	Gene Flow between Divergent Cereal- and Grass-Specific Lineages of the Rice Blast Fungus <i>Magnaporthe oryzae</i> . <i>MBio</i> , 2018, 9, .	1.8	163
3457	UBCG: Up-to-date bacterial core gene set and pipeline for phylogenomic tree reconstruction. <i>Journal of Microbiology</i> , 2018, 56, 280-285.	1.3	1,010
3458	Cladogenesis and Genomic Streamlining in Extracellular Endosymbionts of Tropical Stink Bugs. <i>Genome Biology and Evolution</i> , 2018, 10, 680-693.	1.1	21
3459	Electron Transfer to Nitrogenase in Different Genomic and Metabolic Backgrounds. <i>Journal of Bacteriology</i> , 2018, 200, .	1.0	85
3460	Improved heterologous expression of the membrane-bound quinoprotein quinate dehydrogenase from <i>Gluconobacter oxydans</i> . <i>Protein Expression and Purification</i> , 2018, 145, 100-107.	0.6	13
3461	Multiple origins and strong phenotypic convergence in fish-cleaning palaemonid shrimp lineages. <i>Molecular Phylogenetics and Evolution</i> , 2018, 124, 71-81.	1.2	21
3462	Phylogeny, molecular dating and zoogeographic history of the titi monkeys (<i>Callicebus</i> , Pitheciidae) of eastern Brazil. <i>Molecular Phylogenetics and Evolution</i> , 2018, 124, 10-15.	1.2	9
3463	Discovery and Biosynthesis of the Antibiotic Bicyclomycin in Distantly Related Bacterial Classes. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	36
3464	Remodeling the Specificity of an Endosomal CORVET Tether Underlies Formation of Regulated Secretory Vesicles in the Ciliate <i>Tetrahymena thermophila</i> . <i>Current Biology</i> , 2018, 28, 697-710.e13.	1.8	25
3465	Molecular characterization of a novel algal glutamine synthetase (GS) and an algal glutamate synthase (GOGAT) from the colorful outer mantle of the giant clam, <i>Tridacna squamosa</i> , and the putative GS-GOGAT cycle in its symbiotic zooxanthellae. <i>Gene</i> , 2018, 656, 40-52.	1.0	16
3466	Feeding and grazing impact by the bloom-forming euglenophyte <i>Eutreptiella eupharyngea</i> on marine eubacteria and cyanobacteria. <i>Harmful Algae</i> , 2018, 73, 98-109.	2.2	10

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3467	Phylogeny and Morphology of New Diplonemids from Japan. <i>Protist</i> , 2018, 169, 158-179.	0.6	44
3468	Novel and interesting <i>Ophiocordyceps</i> spp. (<i>Ophiocordycipitaceae</i> , <i>Hypocreales</i>) with superficial perithecia from Thailand. <i>Studies in Mycology</i> , 2018, 89, 125-142.	4.5	42
3469	Mitochondrial phylogeny, divergence history and high-altitude adaptation of grassland caterpillars (Lepidoptera: Lymantriinae: Gynaephora) inhabiting the Tibetan Plateau. <i>Molecular Phylogenetics and Evolution</i> , 2018, 122, 116-124.	1.2	43
3470	Pseudo-parallel patterns of disjunctions in an Arctic-alpine plant lineage. <i>Molecular Phylogenetics and Evolution</i> , 2018, 123, 88-100.	1.2	34
3471	Loss of metagenesis and evolution of a parasitic life style in a group of open-ocean jellyfish. <i>Molecular Phylogenetics and Evolution</i> , 2018, 124, 50-59.	1.2	20
3472	Pneumonia and Renal Replacement Therapy Are Risk Factors for Ceftazidime-Avibactam Treatment Failures and Resistance among Patients with Carbapenem-Resistant Enterobacteriaceae Infections. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	1.4	203
3473	Evidence of exposure of domestic pigs to Highly Pathogenic Avian Influenza H5N1 in Nigeria. <i>Scientific Reports</i> , 2018, 8, 5900.	1.6	27
3474	Triplicate parallel life cycle divergence despite gene flow in periodical cicadas. <i>Communications Biology</i> , 2018, 1, 26.	2.0	9
3475	Draft genome of the milu (<i>Elaphurus davidianus</i>). <i>GigaScience</i> , 2018, 7, .	3.3	22
3476	Taxonomy, phylogeny, and divergence time estimation for <i>Apiosphaeria guaranitica</i> , a Neotropical parasite on bignoniaceous hosts. <i>Mycologia</i> , 2018, 110, 526-545.	0.8	6
3477	Resolving the psyllid tree of life: phylogenomic analyses of the superfamily Psylloidea (Hemiptera). <i>Systematic Entomology</i> , 2018, 43, 762-776.	1.7	61
3478	Parallel evolution of Batesian mimicry supergene in two <i>Papilio</i> butterflies, <i>P. polytes</i> and <i>P. memnon</i> . <i>Science Advances</i> , 2018, 4, eaao5416.	4.7	48
3479	Partnerships Between Ambrosia Beetles and Fungi: Lineage-Specific Promiscuity Among Vectors of the Laurel Wilt Pathogen, <i>Raffaelea lauricola</i> . <i>Microbial Ecology</i> , 2018, 76, 925-940.	1.4	28
3480	Molecular phylogenetics of the genus <i>Costularia</i> (Schoeneae, Cyperaceae) reveals multiple distinct evolutionary lineages. <i>Molecular Phylogenetics and Evolution</i> , 2018, 126, 196-209.	1.2	19
3481	The role of natural selection in shaping genetic variation in a promising Chagas disease drug target: <i>Trypanosoma cruzi</i> trans-sialidase. <i>Infection, Genetics and Evolution</i> , 2018, 62, 151-159.	1.0	4
3482	<i>Vibrio</i> Ecology in the Neuse River Estuary, North Carolina, Characterized by Next-Generation Amplicon Sequencing of the Gene Encoding Heat Shock Protein 60 (<i>hsp60</i>). <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	48
3483	Molecular detection and quantification of viable probiotic strains in animal feedstuffs using the commercial direct fed microbial <i>Lactobacillus animalis</i> NP51 as a model. <i>Journal of Microbiological Methods</i> , 2018, 149, 36-43.	0.7	5
3484	Phylogeny and evolutionary radiation of the marine mussels (Bivalvia: Mytilidae) based on mitochondrial and nuclear genes. <i>Molecular Phylogenetics and Evolution</i> , 2018, 126, 233-240.	1.2	39

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3485	Comparative genomics provides insights into the lifestyle and reveals functional heterogeneity of dark septate endophytic fungi. <i>Scientific Reports</i> , 2018, 8, 6321.	1.6	138
3486	Thylakoid membranes contain a non-selective channel permeable to small organic molecules. <i>Journal of Biological Chemistry</i> , 2018, 293, 7777-7785.	1.6	3
3487	Pollination along an elevational gradient mediated both by floral scent and pollinator compatibility in the fig and fig-wasp mutualism. <i>Journal of Ecology</i> , 2018, 106, 2256-2273.	1.9	37
3488	Diversification of African tree frogs (genus <i>Leptopelis</i>) in the highlands of Ethiopia. <i>Molecular Ecology</i> , 2018, 27, 2256-2270.	2.0	14
3489	The Evolution of Polymorphic Hybrid Incompatibilities in House Mice. <i>Genetics</i> , 2018, 209, 845-859.	1.2	50
3490	Whole-Genome Analysis of an Extensively Drug-Resistance <i>Empedobacter falsenii</i> Strain Reveals Distinct Features and the Presence of a Novel Metallo- β -Lactamase (EBR-2). <i>Current Microbiology</i> , 2018, 75, 1084-1089.	1.0	6
3491	An annotated transcriptome of highly inbred <i>Thuja plicata</i> (Cupressaceae) and its utility for gene discovery of terpenoid biosynthesis and conifer defense. <i>Tree Genetics and Genomes</i> , 2018, 14, 1.	0.6	17
3492	Deep mitochondrial origin outside the sampled alphaproteobacteria. <i>Nature</i> , 2018, 557, 101-105.	13.7	278
3493	Genomic Characterization of Nonclonal <i>mcr-1</i> -Positive Multidrug-Resistant <i>Klebsiella pneumoniae</i> from Clinical Samples in Thailand. <i>Microbial Drug Resistance</i> , 2018, 24, 403-410.	0.9	38
3494	Genomic insights into the evolution and ecology of botulinum neurotoxins. <i>Pathogens and Disease</i> , 2018, 76, .	0.8	30
3495	Molecular Analysis of Human Immunodeficiency Virus Type 1 (HIV-1)â€“Infected Individuals in a Network-Based Intervention (Transmission Reduction Intervention Project): Phylogenetics Identify HIV-1â€“Infected Individuals With Social Links. <i>Journal of Infectious Diseases</i> , 2018, 218, 707-715.	1.9	18
3496	Global diversity and distribution of close relatives of apicomplexan parasites. <i>Environmental Microbiology</i> , 2018, 20, 2824-2833.	1.8	50
3497	Reconquering the water: Evolution and systematics of South and Central American aquatic lizards (Gymnophthalmidae). <i>Zoologica Scripta</i> , 2018, 47, 255-265.	0.7	12
3498	Successive duplication-divergence mechanisms at the <i>RCO</i> locus contributed to leaf shape diversity in the Brassicaceae. <i>Development (Cambridge)</i> , 2018, 145, .	1.2	11
3499	Population genomics and geographical parthenogenesis in Japanese harvestmen (Opiliones.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 182 T	0.8	11
3500	The Egyptian Roussette Genome Reveals Unexpected Features of Bat Antiviral Immunity. <i>Cell</i> , 2018, 173, 1098-1110.e18.	13.5	220
3501	Genetic and evolutionary analysis of emerging H3N2 canine influenza virus. <i>Emerging Microbes and Infections</i> , 2018, 7, 1-15.	3.0	34
3502	The complete chloroplast genome of <i>Cibotium barometz</i> (Cibotiaceae), an endangered CITES medicinal fern. <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 464-465.	0.2	3

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3503	Restoration of short chain fatty acid and bile acid metabolism following fecal microbiota transplantation in patients with recurrent <i>Clostridium difficile</i> infection. <i>Anaerobe</i> , 2018, 53, 64-73.	1.0	144
3504	High genetic diversity of extended-spectrum β -lactamases producing <i>Escherichia coli</i> in feces of horses. <i>Veterinary Microbiology</i> , 2018, 219, 117-122.	0.8	14
3505	Molecular evolution of key metabolic genes during transitions to C ₄ and CAM photosynthesis. <i>American Journal of Botany</i> , 2018, 105, 602-613.	0.8	24
3506	A revised phylogeny of macropathine cave crickets (Orthoptera: Rhaphidophoridae) uncovers a paraphyletic Australian fauna. <i>Molecular Phylogenetics and Evolution</i> , 2018, 126, 153-161.	1.2	9
3507	Impact of the tree prior on estimating clock rates during epidemic outbreaks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 4200-4205.	3.3	35
3508	The complete chloroplast genome of hemi-parasitic <i>Pedicularis hallaisanensis</i> (Orobanchaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 235-236.	0.2	6
3509	Rhizarian "Novel Clade 10" Revealed as Abundant and Diverse Planktonic and Terrestrial Flagellates, including <i>Aquavolon</i> n. gen.. <i>Journal of Eukaryotic Microbiology</i> , 2018, 65, 828-842.	0.8	29
3510	Next-Generation Sequencing of the Complete Mitochondrial Genome of the Endangered Species Black Lion Tamarin <i>Leontopithecus chrysopygus</i> (Primates) and Mitogenomic Phylogeny Focusing on the Callitrichidae Family. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 1985-1991.	0.8	6
3511	Correlated evolution between climate and suites of traits along a fast-slow continuum in the radiation of <i>Protea</i> . <i>Ecology and Evolution</i> , 2018, 8, 1853-1866.	0.8	12
3512	Transcriptome of the bivalve <i>Limecola balthica</i> L. from Western Pacific: A new resource for studies of European populations. <i>Marine Genomics</i> , 2018, 40, 58-63.	0.4	4
3513	Genome-wide analyses of the bHLH superfamily in crustaceans: reappraisal of higher-order groupings and evidence for lineage-specific duplications. <i>Royal Society Open Science</i> , 2018, 5, 172433.	1.1	5
3514	Survival in northern microrefugia in an endemic Carpathian gammarid (Crustacea: Amphipoda). <i>Zoologica Scripta</i> , 2018, 47, 357-372.	0.7	18
3515	Coexistence of Multiple Endemic and Pandemic Lineages of the Rice Blast Pathogen. <i>MBio</i> , 2018, 9, .	1.8	59
3516	Molecular phylogeny and comparative morphology indicate that odontostomatids (Alveolata, Tj ETQq1 1 0.784314 rgBT /Overlock 107 Evolution, 2018, 126, 382-389.	1.2	25
3517	The complete plastid genome of <i>Suaeda malacosperma</i> (Amaranthaceae/Chenopodiaceae), a vulnerable halophyte in coastal regions of Korea and Japan. <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 382-383.	0.2	9
3518	Consequences of Asexuality in Natural Populations: Insights from Stick Insects. <i>Molecular Biology and Evolution</i> , 2018, 35, 1668-1677.	3.5	63
3519	Phylogenomics reveals an extensive history of genome duplication in diatoms (Bacillariophyta). <i>American Journal of Botany</i> , 2018, 105, 330-347.	0.8	64
3520	New <i>Penicillium</i> and <i>Talaromyces</i> species from honey, pollen and nests of stingless bees. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 1883-1912.	0.7	63

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3521	A Gene Constellation in Avian Influenza A (H7N9) Viruses May Have Facilitated the Fifth Wave Outbreak in China. <i>Cell Reports</i> , 2018, 23, 909-917.	2.9	33
3522	The species of <i>Coleosporium</i> (Pucciniales) on <i>Solidago</i> in North America. <i>Fungal Biology</i> , 2018, 122, 800-809.	1.1	25
3523	Morphological and molecular taxonomy of <i>Jahnula dianchia</i> sp. nov. (Jahnulales) from submerged wood in Dianchi Lake, Yunnan China. <i>Mycological Progress</i> , 2018, 17, 547-555.	0.5	11
3524	Comprehensive molecular phylogeny of the grassbirds and allies (Locustellidae) reveals extensive non-monophyly of traditional genera, and a proposal for a new classification. <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 367-375.	1.2	19
3525	Phylogeny and biogeography of <i>Phyllomys</i> (Rodentia: Echimyidae) reveal a new species from the Cerrado and suggest Miocene connections of the Amazon and Atlantic Forest. <i>Journal of Mammalogy</i> , 2018, 99, 377-396.	0.6	19
3526	Phylogenomic analyses reveal a deep history of hybridization and polyploidy in the Neotropical genus <i>Lachemilla</i> (Rosaceae). <i>New Phytologist</i> , 2018, 218, 1668-1684.	3.5	141
3527	Sequence Type 273 Carbapenem-Resistant <i>Klebsiella pneumoniae</i> Carrying <i>bla</i> _{NDM-1} and <i>bla</i> _{IMP-4} . <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	1.4	17
3528	Phylogenomics of palearctic <i>Formica</i> species suggests a single origin of temporary parasitism and gives insights to the evolutionary pathway toward slave-making behaviour. <i>BMC Evolutionary Biology</i> , 2018, 18, 40.	3.2	15
3529	Phylotranscriptomic analysis and genome evolution of the Cyripedioideae (Orchidaceae). <i>American Journal of Botany</i> , 2018, 105, 631-640.	0.8	25
3530	Identification of novel enzymes to enhance the ruminal digestion of barley straw. <i>Bioresource Technology</i> , 2018, 260, 76-84.	4.8	13
3531	<i>Halioticida noduliformans</i> infection in eggs of lobster (<i>Homarus gammarus</i>) reveals its generalist parasitic strategy in marine invertebrates. <i>Journal of Invertebrate Pathology</i> , 2018, 154, 109-116.	1.5	10
3532	Filtering nucleotide sites by phylogenetic signal to noise ratio increases confidence in the Neoaves phylogeny generated from ultraconserved elements. <i>Molecular Phylogenetics and Evolution</i> , 2018, 126, 116-128.	1.2	19
3533	<i>dsr</i> : A curated dinoflagellate (Dinophyceae) reference database for the 18S rRNA gene. <i>Molecular Ecology Resources</i> , 2018, 18, 974-987.	2.2	40
3534	Group-specific environmental sequencing reveals high levels of ecological heterogeneity across the microsporidian radiation. <i>Environmental Microbiology Reports</i> , 2018, 10, 328-336.	1.0	28
3535	Clarifying the Relationships between Microsporidia and Cryptomycota. <i>Journal of Eukaryotic Microbiology</i> , 2018, 65, 773-782.	0.8	98
3536	Revision of Corallinaceae (Corallinales, Rhodophyta): recognizing <i>Dawsoniolithon</i> gen. nov., <i>Parvicellularium</i> gen. nov. and Chamberlainoideae subfam. nov. containing <i>Chamberlainium</i> gen. nov. and <i>Pneophyllum</i> . <i>Journal of Phycology</i> , 2018, 54, 391-409.	1.0	61
3537	Novel green algal isolates from the Egyptian hyper-arid desert oases: a polyphasic approach with a description of <i>Pharao desertorum</i> gen. et sp. nov. (Chlorophyceae, Chlorophyta). <i>Journal of Phycology</i> , 2018, 54, 342-357.	1.0	13
3538	Phylogenetic and phylodynamic analyses of hepatitis C virus subtype 1a in Okinawa, Japan. <i>Journal of Viral Hepatitis</i> , 2018, 25, 976-985.	1.0	3

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3539	Nematode-associated microbial taxa do not correlate with host phylogeny, geographic region or feeding morphology in marine sediment habitats. <i>Molecular Ecology</i> , 2018, 27, 1930-1951.	2.0	49
3540	Regulation of early endosomes across eukaryotes: Evolution and functional homology of Vps9 proteins. <i>Traffic</i> , 2018, 19, 546-563.	1.3	12
3541	Whole-genome sequencing of the blue whale and other rorquals finds signatures for introgressive gene flow. <i>Science Advances</i> , 2018, 4, eaap9873.	4.7	112
3542	A Kinesin-14 Motor Activates Neocentromeres to Promote Meiotic Drive in Maize. <i>Cell</i> , 2018, 173, 839-850.e18.	13.5	104
3543	A Family of Vertebrate-Specific Polycombs Encoded by the LCOR/LCORL Genes Balance PRC2 Subtype Activities. <i>Molecular Cell</i> , 2018, 70, 408-421.e8.	4.5	121
3544	Analyses of HIV-1 integrase sequences prior to South African national HIV-treatment program and availability of integrase inhibitors in Cape Town, South Africa. <i>Scientific Reports</i> , 2018, 8, 4709.	1.6	21
3545	Hybridization and gene flow in the mega-pest lineage of moth, <i>Helicoverpa</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 5034-5039.	3.3	113
3546	DNA data and morphology suggest an occurrence of <i>Dendrolimus sibiricus</i> Tschetverikov, 1908 (Lepidoptera: Lasiocampidae) instead of <i>D. superans</i> Butler, 1877, in South Korea. <i>Entomological Research</i> , 2018, 48, 108-121.	0.6	4
3547	Rapid divergence of mussel populations despite incomplete barriers to dispersal. <i>Molecular Ecology</i> , 2018, 27, 1556-1571.	2.0	29
3548	Measuring inferential importance of taxa using taxon influence indices. <i>Ecology and Evolution</i> , 2018, 8, 4484-4494.	0.8	5
3549	On the phylogenetic position of the genus <i>Raphidocystis</i> (Haptista: Centroplasthelida) with notes on the dimorphism in centrohelid life cycle. <i>European Journal of Protistology</i> , 2018, 64, 82-90.	0.5	22
3550	Molecular mechanisms underlying intraspecific variation in snake venom. <i>Journal of Proteomics</i> , 2018, 181, 60-72.	1.2	54
3551	Phylogenetic relationships of rollers (Coraciidae) based on complete mitochondrial genomes and fifteen nuclear genes. <i>Molecular Phylogenetics and Evolution</i> , 2018, 126, 17-22.	1.2	4
3552	The origins of the Psechridae: Web-building lycosoid spiders. <i>Molecular Phylogenetics and Evolution</i> , 2018, 125, 213-219.	1.2	17
3553	A phylotranscriptomic backbone of the orb-weaving spider family Araneidae (Arachnida, Araneae) supported by multiple methodological approaches. <i>Molecular Phylogenetics and Evolution</i> , 2018, 126, 129-140.	1.2	35
3554	Pervasive contingency and entrenchment in a billion years of Hsp90 evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 4453-4458.	3.3	93
3555	Phylogenetic relationships within the New World subfamily Larreoideae (Zygophyllaceae) confirm polyphyly of the disjunct genus <i>Bulnesia</i> . <i>Systematics and Biodiversity</i> , 2018, 16, 453-468.	0.5	7
3556	Coestimating Reticulate Phylogenies and Gene Trees from Multilocus Sequence Data. <i>Systematic Biology</i> , 2018, 67, 439-457.	2.7	124

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3557	Complex Models of Sequence Evolution Require Accurate Estimators as Exemplified with the Invariable Site Plus Gamma Model. <i>Systematic Biology</i> , 2018, 67, 552-558.	2.7	11
3558	RecQ Helicases Function in Development, DNA Repair, and Gene Targeting in <i>Physcomitrella patens</i> . <i>Plant Cell</i> , 2018, 30, 717-736.	3.1	44
3559	Genome Sequences of <i>Apibacter</i> spp., Gut Symbionts of Asian Honey Bees. <i>Genome Biology and Evolution</i> , 2018, 10, 1174-1179.	1.1	27
3560	Draft genome of the Peruvian scallop <i>Argopecten purpuratus</i> . <i>GigaScience</i> , 2018, 7, .	3.3	60
3561	Increasing the utility of barcode databases through high-throughput sequencing of amplicons from dried museum specimens, an example on parasitic hymenoptera (Braconidae). <i>Biological Control</i> , 2018, 122, 93-100.	1.4	10
3562	Accelerated diversification is related to life history and locomotion in a hyperdiverse lineage of microbial eukaryotes (Diatoms, Bacillariophyta). <i>New Phytologist</i> , 2018, 219, 462-473.	3.5	104
3563	Molecular phylogeny and temporal diversification of <i>Tanytarsus</i> van der Wulp (Diptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 50 Entomology, 2018, 43, 659-677.	1.7	23
3564	Description of a New Subfamily, Astrocloninae (Ophiuroidea: Euryalida: Gorgonocephalidae), Based on Molecular Phylogeny and Morphological Observations. <i>Zoological Science</i> , 2018, 35, 179-187.	0.3	6
3565	Genetic Structure of <i>Dytiscus sharpi</i> in North and South Hokuriku in Japan Inferred from Mitochondrial and Nuclear Gene Sequence. <i>Zoological Science</i> , 2018, 35, 134-139.	0.3	1
3566	Role of a membrane-bound aldehyde dehydrogenase complex AldFGH in acetic acid fermentation with <i>Acetobacter pasteurianus</i> SKU1108. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 4549-4561.	1.7	16
3567	A large-scale phylogeny of Microhylidae inferred from a combined dataset of 121 genes and 427 taxa. <i>Molecular Phylogenetics and Evolution</i> , 2018, 126, 85-91.	1.2	35
3568	Molecular phylogeny of <i>Galium</i> L. of the tribe Rubieae (Rubiaceae) – Emphasis on Chinese species and recognition of a new genus <i>Pseudogalium</i> . <i>Molecular Phylogenetics and Evolution</i> , 2018, 126, 221-232.	1.2	11
3569	Wild birds in Chile Harbor diverse avian influenza A viruses. <i>Emerging Microbes and Infections</i> , 2018, 7, 1-4.	3.0	20
3570	Resolving relationships and phylogeographic history of the <i>Nyssa sylvatica</i> complex using data from RAD-seq and species distribution modeling. <i>Molecular Phylogenetics and Evolution</i> , 2018, 126, 1-16.	1.2	39
3571	Morphological, ontogenetic and molecular data support strongylidiids as being closely related to Dorsomarginalia (Protozoa, Ciliophora) and reactivation of the family Strongylidiidae Faur�-Fremiet, 1961. <i>Zoological Journal of the Linnean Society</i> , 2018, 184, 237-254.	1.0	38
3572	Multiple shifts to open habitats in Melastomateae (Melastomataceae) congruent with the increase of African Neogene climatic aridity. <i>Journal of Biogeography</i> , 2018, 45, 1420-1431.	1.4	51
3573	Comparison of taxon-specific versus general locus sets for targeted sequence capture in plant phylogenomics. <i>Applications in Plant Sciences</i> , 2018, 6, e1032.	0.8	55
3574	A giant virus infecting green algae encodes key fermentation genes. <i>Virology</i> , 2018, 518, 423-433.	1.1	92

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3575	Mitochondrial introgression obscures phylogenetic relationships among manakins of the genus <i>Lepidothrix</i> (Aves: Pipridae). <i>Molecular Phylogenetics and Evolution</i> , 2018, 126, 314-320.	1.2	21
3576	Two genetically diverse H7N7 avian influenza viruses isolated from migratory birds in central China. <i>Emerging Microbes and Infections</i> , 2018, 7, 1-12.	3.0	11
3577	SUMOylation is required for fungal development and pathogenicity in the rice blast fungus <i>Magnaporthe oryzae</i> . <i>Molecular Plant Pathology</i> , 2018, 19, 2134-2148.	2.0	22
3578	Insight into the Significance of <i>Aspergillus fumigatus</i> cyp51A Polymorphisms. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	1.4	57
3579	Single colony genetic analysis of epilithic stream algae of the genus <i>Chamaesiphon</i> spp.. <i>Hydrobiologia</i> , 2018, 811, 61-75.	1.0	19
3580	Reconciling Conflicting Phylogenies in the Origin of Sweet Potato and Dispersal to Polynesia. <i>Current Biology</i> , 2018, 28, 1246-1256.e12.	1.8	133
3581	Phylogeny of a cosmopolitan family of morphologically conserved trapdoor spiders (Mygalomorphae.) <i>Tj ETQq0 0 0 rgBT /Overlock 10 TF Pocock 1901</i> . <i>Molecular Phylogenetics and Evolution</i> , 2018, 126, 303-313.	1.2	33
3582	How single mutations affect viral escape from broad and narrow antibodies to H1 influenza hemagglutinin. <i>Nature Communications</i> , 2018, 9, 1386.	5.8	123
3583	Global and local DNA (meta)barcoding reveal new biogeography patterns in tintinnid ciliates. <i>Journal of Plankton Research</i> , 2018, 40, 209-221.	0.8	30
3584	HiMAP: Robust phylogenomics from highly multiplexed amplicon sequencing. <i>Molecular Ecology Resources</i> , 2018, 18, 1000-1019.	2.2	30
3585	The complete mitochondrial genomes of two schizothoracine fishes (Teleostei, Cypriniformes): A novel minisatellite in fish mitochondrial genomes. <i>Journal of Applied Ichthyology</i> , 2018, 34, 1028-1034.	0.3	3
3586	Evolutionary relationships of two balitorids (Cypriniformes, Balitoridae) revealed by comparative mitogenomics. <i>Zoologica Scripta</i> , 2018, 47, 300-310.	0.7	9
3587	Revision of the taxonomic status of the genus <i>Gloeoporus</i> (Polyporales, Basidiomycota) reveals two new species. <i>Mycological Progress</i> , 2018, 17, 855-863.	0.5	9
3588	Phylogeny and evolution of the cholesterol transporter NPC1 in insects. <i>Journal of Insect Physiology</i> , 2018, 107, 157-166.	0.9	13
3589	Morphological and phylogenetic analyses of <i>Rhipicephalus microplus</i> ticks from Bangladesh, Pakistan and Myanmar. <i>Ticks and Tick-borne Diseases</i> , 2018, 9, 1069-1079.	1.1	49
3590	The reduced genome of <i>Candidatus</i> <i>Kinetoplastibacterium sorsogonicusi</i> , the endosymbiont of <i>Kentomonas sorsogonicus</i> (Trypanosomatidae): loss of the haem-synthesis pathway. <i>Parasitology</i> , 2018, 145, 1287-1293.	0.7	20
3591	Species identification and mitochondrial genomes of ancient fish bones from the Riverine Kachemak tradition of the Kenai Peninsula, Alaska. <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 409-411.	0.2	9
3592	Carrot Juice Fermentations as Man-Made Microbial Ecosystems Dominated by Lactic Acid Bacteria. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	62

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3593	Character evolution and missing (morphological) data across <i>Asteridae</i> . <i>American Journal of Botany</i> , 2018, 105, 470-479.	0.8	19
3594	Conserved association of Argonaute 1 and 2 proteins with miRNA and siRNA pathways throughout insect evolution, from cockroaches to flies. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2018, 1861, 554-560.	0.9	18
3595	Oligocene origin and drivers of diversification in the genus <i>Sticta</i> (Lobariaceae, Ascomycota). <i>Molecular Phylogenetics and Evolution</i> , 2018, 126, 58-73.	1.2	19
3596	Oat evolution revealed in the maternal lineages of 25 <i>Avena</i> species. <i>Scientific Reports</i> , 2018, 8, 4252.	1.6	28
3597	Description of <i>Myolaimus mycophilus</i> Slos & Bert sp. n. (Rhabditida: Myolaimidae). <i>Nematology</i> , 2018, 20, 175-186.	0.2	3
3598	Genome-wide comparisons reveal evidence for a species complex in the black-lip pearl oyster <i>Pinctada margaritifera</i> (Bivalvia: Pteriidae). <i>Scientific Reports</i> , 2018, 8, 191.	1.6	7
3599	HIV-1 Infection in Cyprus, the Eastern Mediterranean European Frontier: A Densely Sampled Transmission Dynamics Analysis from 1986 to 2012. <i>Scientific Reports</i> , 2018, 8, 1702.	1.6	24
3600	Chloroplast genomes of <i>Byrsonima</i> species (Malpighiaceae): comparative analysis and screening of high divergence sequences. <i>Scientific Reports</i> , 2018, 8, 2210.	1.6	108
3601	To be serrate or pinnate: diverse leaf forms of yarrows (<i>Achillea</i>) are linked to differential expression patterns of NAM genes. <i>Annals of Botany</i> , 2018, 121, 255-266.	1.4	5
3602	Comparison of Methods for Molecular Species Delimitation Across a Range of Speciation Scenarios. <i>Systematic Biology</i> , 2018, 67, 830-846.	2.7	277
3603	Grass diversification in Madagascar: In situ radiation of two large C_{3} shade clades and support for a Miocene to Pliocene origin of C_{4} grassy biomes. <i>Journal of Biogeography</i> , 2018, 45, 750-761.	1.4	72
3604	Tethyan closure drove tropical marine biodiversity: Vicariant diversification of intertidal crustaceans. <i>Journal of Biogeography</i> , 2018, 45, 941-951.	1.4	18
3605	Insights into the Fundamental Physiology of the Uncultured Fe-Oxidizing Bacterium <i>Leptothrix ochracea</i> . <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	19
3606	Resolving taxonomic ambiguity and cryptic speciation of <i>Hypotrigena</i> species through morphometrics and DNA barcoding. <i>Journal of Apicultural Research</i> , 2018, 57, 354-363.	0.7	13
3607	Convergent Amino Acid Signatures in Polyphyletic <i>Campylobacter jejuni</i> Subpopulations Suggest Human Niche Tropism. <i>Genome Biology and Evolution</i> , 2018, 10, 763-774.	1.1	12
3608	Evidence that <i>Myotis lucifugus</i> "Subspecies" are Five Nonsister Species, Despite Gene Flow. <i>Systematic Biology</i> , 2018, 67, 756-769.	2.7	37
3609	Bacterial Gall of <i>Loropetalum chinense</i> caused by <i>Pseudomonas amygdali</i> pv. <i>loropetali</i> pv. nov.. <i>Plant Disease</i> , 2018, 102, 799-806.	0.7	7
3610	An improved method for PCR-based detection and routine monitoring of geosmin-producing cyanobacterial blooms. <i>Water Research</i> , 2018, 136, 34-40.	5.3	20

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3611	The complete mitochondrial genome of <i>Psychomantis borneensis</i> (Mantodea: Hymenopodidae). Mitochondrial DNA Part B: Resources, 2018, 3, 42-43.	0.2	11
3612	DNA stable-isotope probing identifies uncultivated members of Pseudonocardia associated with biodegradation of pyrene in agricultural soil. FEMS Microbiology Ecology, 2018, 94, .	1.3	25
3613	Genomic perspectives of spider silk genes through target capture sequencing: Conservation of stabilization mechanisms and homology-based structural models of spidroin terminal regions. International Journal of Biological Macromolecules, 2018, 113, 829-840.	3.6	57
3614	Gene-based predictive models of trophic modes suggest Asgard archaea are not phagocytotic. Nature Ecology and Evolution, 2018, 2, 697-704.	3.4	59
3615	Characterization of p57, a Stage-Specific Antigen of Pneumocystis murina. Journal of Infectious Diseases, 2018, 218, 282-290.	1.9	11
3616	Phylogeny and salt-tolerance of freshwater Nostocales strains: Contribution to their systematics and evolution. Harmful Algae, 2018, 73, 58-71.	2.2	11
3617	What lies beneath? Fungal diversity at the bottom of Lake Michigan and Lake Superior. Journal of Great Lakes Research, 2018, 44, 263-270.	0.8	29
3618	A complex of the blood fluke genus Psettarium (Digenea: Apocotylidae) infecting tetraodontiform fishes of east Queensland waters. Parasitology International, 2018, 67, 321-340.	0.6	17
3619	A Deep Hidden Diversity of Dictyostelia. Protist, 2018, 169, 64-78.	0.6	10
3620	Atlantic forests to the all Americas: Biogeographical history and divergence times of Neotropical Ficus (Moraceae). Molecular Phylogenetics and Evolution, 2018, 122, 46-58.	1.2	27
3621	Plastid phylogenomics with broad taxon sampling further elucidates the distinct evolutionary origins and timing of secondary green plastids. Scientific Reports, 2018, 8, 1523.	1.6	66
3622	A novel framework for evaluating the performance of codon usage bias metrics. Journal of the Royal Society Interface, 2018, 15, 20170667.	1.5	9
3623	Evolution of the Plastid Genomes in Diatoms. Advances in Botanical Research, 2018, 85, 129-155.	0.5	51
3624	Gall Inducers Arose from Inquillines: Phylogenetic Position of a Gall-Inducing Species and Its Relatives in the Inquilline Tribe Synergini (Hymenoptera: Cynipidae). Annals of the Entomological Society of America, 2018, 111, 6-12.	1.3	18
3625	The genomes of two Eutrema species provide insight into plant adaptation to high altitudes. DNA Research, 2018, 25, 307-315.	1.5	38
3626	The Complete Phylogeny of Pangolins: Scaling Up Resources for the Molecular Tracing of the Most Trafficked Mammals on Earth. Journal of Heredity, 2018, 109, 347-359.	1.0	64
3627	Conservation Below the Species Level: Suitable Evolutionarily Significant Units among Mountain Vipers (the Montivipera raddei complex) in Iran. Journal of Heredity, 2018, 109, 416-425.	1.0	6
3628	Comparative genome analysis and characterization of the <i>Salmonella</i> Typhimurium strain CCRJ_26 isolated from swine carcasses using whole-genome sequencing approach. Letters in Applied Microbiology, 2018, 66, 352-359.	1.0	15

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3629	Species delimitation in the morphologically conserved <i>Coecobrya</i> (Collembola): Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 747 Td (Entomol. exp. appl.) taxonomy. Zoologica Scripta, 2018, 47, 342-356.	0.7	33
3630	Genetically distinct lineages of Salmonella Typhimurium ST313 and ST19 are present in Brazil. International Journal of Medical Microbiology, 2018, 308, 306-316.	1.5	29
3631	Plastid phylogenomics resolves infrafamilial relationships of the Styracaceae and sheds light on the backbone relationships of the Ericales. Molecular Phylogenetics and Evolution, 2018, 121, 198-211.	1.2	42
3632	A jungle tale: Molecular phylogeny and divergence time estimates of the Desmopsis-Stenanona clade (Annonaceae) in Mesoamerica. Molecular Phylogenetics and Evolution, 2018, 122, 80-94.	1.2	16
3633	Transoceanic Dispersal and Plate Tectonics Shaped Global Cockroach Distributions: Evidence from Mitochondrial Phylogenomics. Molecular Biology and Evolution, 2018, 35, 970-983.	3.5	73
3634	Phylogenetic relationships and biogeography of <i>Ptilophora</i> (Gelidiales, Rhodophyta) with descriptions of <i>P. aureolusa</i> , <i>P. Amalagasya</i> , and <i>P. Spongiophila</i> from Madagascar. Journal of Phycology, 2018, 54, 249-263.	1.0	8
3635	A New Species of Long-glanded Coralsnake of the Genus <i>Calliophis</i> (Squamata: Elapidae) from Dinagat Island, with Notes on the Biogeography and Species Diversity of Philippine <i>Calliophis</i> and <i>Hemibungarus</i> . Herpetologica, 2018, 74, 89-104.	0.2	10
3636	Strain Tracking Reveals the Determinants of Bacterial Engraftment in the Human Gut Following Fecal Microbiota Transplantation. Cell Host and Microbe, 2018, 23, 229-240.e5.	5.1	292
3637	Genomic Analyses Yield Markers for Identifying Agronomically Important Genes in Potato. Molecular Plant, 2018, 11, 473-484.	3.9	73
3638	Combining high-throughput sequencing and targeted loci data to infer the phylogeny of the <i>Adenocalymma-Neojobertia</i> clade (Bignoniaceae). Molecular Phylogenetics and Evolution, 2018, 123, 1-15.	1.2	37
3639	Evolution of Hypolimnas butterflies (Nymphalidae): Out-of-Africa origin and Wolbachia-mediated introgression. Molecular Phylogenetics and Evolution, 2018, 123, 50-58.	1.2	25
3640	Filtering of target sequence capture individuals facilitates species tree construction in the plant subtribe Iochrominae (Solanaceae). Molecular Phylogenetics and Evolution, 2018, 123, 26-34.	1.2	9
3641	An ant genus-group (<i>Prenolepis</i>) illuminates the biogeography and drivers of insect diversification in the Indo-Pacific. Molecular Phylogenetics and Evolution, 2018, 123, 16-25.	1.2	28
3642	SeagrassDB: An open-source transcriptomics landscape for phylogenetically profiled seagrasses and aquatic plants. Scientific Reports, 2018, 8, 2749.	1.6	12
3643	Unmasking hidden species diversity within the <i>Ramazzottius oberhaeuseri</i> complex, with an integrative redescription of the nominal species for the family Ramazzottiidae (Tardigrada): Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 177 Td	1.1	30
3644	Are Fireworms Venomous? Evidence for the Convergent Evolution of Toxin Homologs in Three Species of Fireworms (Annelida, Amphinomidae). Genome Biology and Evolution, 2018, 10, 249-268.	1.1	30
3645	Whole genome duplication and transposable element proliferation drive genome expansion in Corydoradinae catfishes. Proceedings of the Royal Society B: Biological Sciences, 2018, 285, 20172732.	1.2	32
3646	Can social partnerships influence the microbiome? Insights from ant farmers and their trophobiont mutualists. Molecular Ecology, 2018, 27, 1898-1914.	2.0	42

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3647	Azithromycin Resistance in <i>Shigella</i> spp. in Southeast Asia. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	1.4	37
3648	Incipient speciation in a neotropical Gesneriaceae: <i>Columnea kucyniakii</i> is nested within <i>C. strigosa</i> . <i>Plant Systematics and Evolution</i> , 2018, 304, 511-519.	0.3	6
3649	A Comprehensive and Dated Phylogenomic Analysis of Butterflies. <i>Current Biology</i> , 2018, 28, 770-778.e5.	1.8	249
3650	<i>Clydonella sawyeri</i> n. sp. (Amoebozoa, Vannellida): Morphological and molecular study and a re-definition of the genus <i>Clydonella</i> Sawyer, 1975. <i>European Journal of Protistology</i> , 2018, 63, 62-71.	0.5	4
3651	<i>Mortierella sugadairana</i> , a new homothallic species related to the firstly described heterothallic species in the genus. <i>Mycoscience</i> , 2018, 59, 200-205.	0.3	6
3652	Phylogenomic Analysis of <i>Nassula variabilis</i> n. sp., <i>Furgasonia blochmanni</i> , and <i>Pseudomicrothorax dubius</i> Confirms a Nassophorean Clade. <i>Protist</i> , 2018, 169, 180-189.	0.6	22
3653	<i>Abditibacterium utsteinense</i> sp. nov., the first cultivated member of candidate phylum FBP, isolated from ice-free Antarctic soil samples. <i>Systematic and Applied Microbiology</i> , 2018, 41, 279-290.	1.2	58
3654	Multiple losses of photosynthesis and convergent reductive genome evolution in the colourless green algae <i>Prototheca</i> . <i>Scientific Reports</i> , 2018, 8, 940.	1.6	46
3655	<i>Saurogobio punctatus</i> sp. nov., a new cyprinid gudgeon (Teleostei: Cypriniformes) from the Yangtze River, based on both morphological and molecular data. <i>Journal of Fish Biology</i> , 2018, 92, 347-364.	0.7	3
3656	The Birth and Demise of the IS <i>Apl1</i> - <i>mcr-1</i> -IS <i>Apl1</i> Composite Transposon: the Vehicle for Transferable Colistin Resistance. <i>MBio</i> , 2018, 9, .	1.8	103
3657	<i>Bacidina mendax</i> sp. nov., a new widespread species in Central Europe, together with a new combination within the genus <i>Bacidina</i> . <i>Lichenologist</i> , 2018, 50, 43-57.	0.5	15
3658	A new species-level taxonomy for <i>Trapelia</i> (Trapeliaceae, Ostropomycetidae) with special reference to Great Britain and the Falkland Islands. <i>Lichenologist</i> , 2018, 50, 3-42.	0.5	12
3659	<i>Myriospora</i> , a genus newly reported for Antarctica with a worldwide key to the species. <i>Lichenologist</i> , 2018, 50, 101-112.	0.5	2
3660	Phylogenomic reclassification of the world's most venomous spiders (Mygalomorphae, Atracinae), with implications for venom evolution. <i>Scientific Reports</i> , 2018, 8, 1636.	1.6	53
3661	Use of whole genome sequencing to investigate an increase in <i>Neisseria gonorrhoeae</i> infection among women in urban areas of Australia. <i>Scientific Reports</i> , 2018, 8, 1503.	1.6	23
3662	Mitogenomic divergence between three pairs of putative geminate fishes from Panama. <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 1-5.	0.2	1
3663	An ancient Sec10 formin fusion provides insights into actin-mediated regulation of exocytosis. <i>Journal of Cell Biology</i> , 2018, 217, 945-957.	2.3	23
3664	The systematic analysis of ultraconserved genomic regions in the budding yeast. <i>Bioinformatics</i> , 2018, 34, 361-366.	1.8	1

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3666	Systematic revision of the Southeast Asian macrophagous leeches, with the description of two new gastrostomobdellid species (Hirudinida: Arhynchobdellida: Erpobdelliformes). <i>Zoological Journal of the Linnean Society</i> , 2018, 184, 1-30.	1.0	5
3667	A new genus, <i>Desertispora</i> , and a new species, <i>Diversispora sabulosa</i> , in the family <i>Diversisporaceae</i> (order <i>Diversisporales</i> , subphylum <i>Glomeromycotina</i>). <i>Mycological Progress</i> , 2018, 17, 437-449.	0.5	17
3668	Comammox Functionality Identified in Diverse Engineered Biological Wastewater Treatment Systems. <i>Environmental Science and Technology Letters</i> , 2018, 5, 110-116.	3.9	118
3669	The State of Software for Evolutionary Biology. <i>Molecular Biology and Evolution</i> , 2018, 35, 1037-1046.	3.5	36
3670	Phenotypic and Genetic Structure Support Gene Flow Generating Gene Tree Discordances in an Amazonian Floodplain Endemic Species. <i>Systematic Biology</i> , 2018, 67, 700-718.	2.7	60
3671	<i>Wolbachia</i> infections in Australian ichneumonid parasitoid wasps (Hymenoptera: Ichneumonidae): evidence for adherence to the global equilibrium hypothesis. <i>Biological Journal of the Linnean Society</i> , 2018, 123, 518-534.	0.7	8
3672	<i>Halomonas tabrizica</i> sp. nov., a novel moderately halophilic bacterium isolated from Urmia Lake in Iran. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 1139-1148.	0.7	16
3673	Evolutionary history of the angiosperm flora of China. <i>Nature</i> , 2018, 554, 234-238.	13.7	321
3674	<i>Lactobacillus backii</i> and <i>Pediococcus damnosus</i> isolated from 170-year-old beer recovered from a shipwreck lack the metabolic activities required to grow in modern lager beer. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	8
3675	Comparative Genomics Reveals Accelerated Evolution in Conserved Pathways during the Diversification of Anole Lizards. <i>Genome Biology and Evolution</i> , 2018, 10, 489-506.	1.1	43
3676	Multiple Acquisitions of Pathogen-Derived <i>Francisella</i> Endosymbionts in Soft Ticks. <i>Genome Biology and Evolution</i> , 2018, 10, 607-615.	1.1	46
3677	Diversity of Translation Initiation Mechanisms across Bacterial Species Is Driven by Environmental Conditions and Growth Demands. <i>Molecular Biology and Evolution</i> , 2018, 35, 582-592.	3.5	24
3678	Complex coevolution of wing, tail, and vocal sounds of courting male bee hummingbirds. <i>Evolution; International Journal of Organic Evolution</i> , 2018, 72, 630-646.	1.1	35
3679	A model species for agricultural pest genomics: the genome of the Colorado potato beetle, <i>Leptinotarsa decemlineata</i> (Coleoptera: Chrysomelidae). <i>Scientific Reports</i> , 2018, 8, 1931.	1.6	215
3680	Extensive mitochondrial heteroplasmy in the neotropical ants of the <i>Ectatomma ruidum</i> complex (Formicidae: Ectatomminae). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2018, 29, 1203-1214.	0.7	31
3681	Dating phototrophic microbial lineages with reticulate gene histories. <i>Geobiology</i> , 2018, 16, 179-189.	1.1	80
3682	A primordial and reversible TCA cycle in a facultatively chemolithoautotrophic thermophile. <i>Science</i> , 2018, 359, 559-563.	6.0	155
3683	In search of a meaningful classification for Amazonian marmosets: Should dwarf marmosets be considered <i>Mico</i> congeners?. <i>Zoologica Scripta</i> , 2018, 47, 133-143.	0.7	9

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3684	Incomplete Co-cladogenesis Between Zootermopsis Termites and Their Associated Protists. <i>Environmental Entomology</i> , 2018, 47, 184-195.	0.7	19
3685	Reassessment of the species <i>Stigeoclonium polyrhizum</i> (Chaetophoraceae, Chaetophorales) based on morphological and molecular data. <i>Phytotaxa</i> , 2018, 333, 86.	0.1	2
3686	Genetic and biometric variation across the fragmented range of Jerdon's Babbler, <i>Chrysomma altirostre</i> , a threatened Oriental grassland specialist. <i>Journal of Ornithology</i> , 2018, 159, 575-579.	0.5	3
3687	Swarm incursions of reassortants of highly pathogenic avian influenza virus strains H5N8 and H5N5, clade 2.3.4.4b, Germany, winter 2016/17. <i>Scientific Reports</i> , 2018, 8, 15.	1.6	57
3688	The characterization of the circadian clock in the olive fly <i>Bactrocera oleae</i> (Diptera: Tephritidae) reveals a <i>Drosophila</i> -like organization. <i>Scientific Reports</i> , 2018, 8, 816.	1.6	13
3689	Molecular epidemiology reveals the role of war in the spread of HIV in Ukraine. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 1051-1056.	3.3	65
3690	Evidence of Adaptive Evolution and Relaxed Constraints in Sex-Biased Genes of South American and West Indies Fruit Flies (Diptera: Tephritidae). <i>Genome Biology and Evolution</i> , 2018, 10, 380-395.	1.1	11
3691	Environmental Sequencing Fills the Gap Between Parasitic Haplosporidians and Free-living Giant Amoebae. <i>Journal of Eukaryotic Microbiology</i> , 2018, 65, 574-586.	0.8	21
3692	Large-scale phylogenomic analysis resolves a backbone phylogeny in ferns. <i>GigaScience</i> , 2018, 7, 1-11.	3.3	90
3693	Mode and Rate of Evolution of Haemosporidian Mitochondrial Genomes: Timing the Radiation of Avian Parasites. <i>Molecular Biology and Evolution</i> , 2018, 35, 383-403.	3.5	122
3694	The Genomes of Four <i>Meyerozyma caribbica</i> Isolates and Novel Insights into the <i>Meyerozyma guilliermondii</i> Species Complex. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 755-759.	0.8	20
3695	Taxonomic delimitation of <i>Fulvifomes robiniae</i> (Hymenochaetales, Basidiomycota) and related species in America: <i>F. squamosus</i> sp. nov.. <i>Plant Systematics and Evolution</i> , 2018, 304, 445-459.	0.3	18
3696	A multi-omics study of the grapevine-downy mildew (<i>Plasmopara viticola</i>) pathosystem unveils a complex protein coding- and noncoding-based arms race during infection. <i>Scientific Reports</i> , 2018, 8, 757.	1.6	70
3697	A Two-State Model of Tree Evolution and Its Applications to Alu Retrotransposition. <i>Systematic Biology</i> , 2018, 67, 475-489.	2.7	5
3698	Intraclade Variability in Toxin Production and Cytotoxicity of <i>Bacillus cereus</i> Group Type Strains and Dairy-Associated Isolates. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	74
3699	A case of biodiversity overestimation in the Balkan <i>Belgrandiella</i> A. J. Wagner, 1927 (Caenogastropoda: Hydrobiidae): molecular divergence not paralleled by high morphological variation. <i>Journal of Natural History</i> , 2018, 52, 323-344.	0.2	26
3700	Recent lineage diversification in a venomous snake through dispersal across the Amazon River. <i>Biological Journal of the Linnean Society</i> , 2018, 123, 651-665.	0.7	16
3701	Molecular Phylogenetic Positions and Ultrastructure of Marine Gregarines (Apicomplexa) <i>Cuspisella ishikariensis</i> n. gen., n. sp. and <i>Loxomorpha</i> cf. <i>harmothoe</i> from Western Pacific scaleworms (Polynoidae). <i>Journal of Eukaryotic Microbiology</i> , 2018, 65, 637-647.	0.8	3

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3702	A Tree of Trees: Using Campus Tree Diversity to Integrate Molecular, Organismal, and Evolutionary Biology. <i>American Biology Teacher</i> , 2018, 80, 144-151.	0.1	0
3703	Antibiotic resistance ABCF proteins reset the peptidyl transferase centre of the ribosome to counter translational arrest. <i>Nucleic Acids Research</i> , 2018, 46, 3753-3763.	6.5	71
3704	Genomic characteristics of vB_PpaP_PP74, a T7-like Autographivirinae bacteriophage infecting a potato pathogen of the newly proposed species <i>Pectobacterium parmentieri</i> . <i>Archives of Virology</i> , 2018, 163, 1691-1694.	0.9	9
3705	Reductions in complexity of mitochondrial genomes in lichen-forming fungi shed light on genome architecture of obligate symbioses. <i>Molecular Ecology</i> , 2018, 27, 1155-1169.	2.0	39
3706	<i>Amycolatopsis vastitatis</i> sp. nov., an isolate from a high altitude subsurface soil on Cerro Chajnantor, northern Chile. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 1523-1533.	0.7	16
3707	The complete chloroplast genome of the green algae <i>Hariotina reticulata</i> (Scenedesmaceae, Tj ETQq1 1 0.784314 rgBT / Overlock 10	0.5	6
3708	Phylogeny, historical biogeography, and diversification of angiosperm order Ericales suggest ancient Neotropical and East Asian connections. <i>Molecular Phylogenetics and Evolution</i> , 2018, 122, 59-79.	1.2	92
3709	Whole Mitochondrial Genomic and Y-Chromosomal Phylogenies of Burmese Long-Tailed Macaque (<i>Macaca fascicularis aurea</i>) Suggest Ancient Hybridization between <i>fascicularis</i> and <i>sinica</i> Species Groups. <i>Journal of Heredity</i> , 2018, 109, 360-371.	1.0	20
3710	Draft genome sequence of ramie, <i>Boehmeria nivea</i> (L.) Gaudich. <i>Molecular Ecology Resources</i> , 2018, 18, 639-645.	2.2	46
3711	Taxon sampling effects on the quantification and comparison of community phylogenetic diversity. <i>Molecular Ecology</i> , 2018, 27, 1296-1308.	2.0	34
3712	Identification of tumor-reactive B cells and systemic IgG in breast cancer based on clonal frequency in the sentinel lymph node. <i>Cancer Immunology, Immunotherapy</i> , 2018, 67, 729-738.	2.0	42
3713	Cloning and functional characterization of three new pheromone receptors from the diamondback moth, <i>Plutella xylostella</i> . <i>Journal of Insect Physiology</i> , 2018, 107, 14-22.	0.9	28
3714	Comparative genome analysis reveals a complex population structure of <i>Legionella pneumophila</i> subspecies. <i>Infection, Genetics and Evolution</i> , 2018, 59, 172-185.	1.0	15
3715	Accumulation and Dissolution of Magnetite Crystals in a Magnetically Responsive Ciliate. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	17
3716	Phylogenetic and Protein Sequence Analysis of Bacterial Chemoreceptors. <i>Methods in Molecular Biology</i> , 2018, 1729, 373-385.	0.4	3
3717	Digeneans of northern fur seals <i>Callorhinus ursinus</i> (Pinnipedia: Otariidae) from five subpopulations on St. Paul Island, Alaska. <i>Parasitology Research</i> , 2018, 117, 1079-1086.	0.6	15
3718	Two species of <i>Phyllodistomum</i> Braun, 1899 (Trematoda: Gorgoderidae) from Moreton Bay, Australia. <i>Systematic Parasitology</i> , 2018, 95, 325-336.	0.5	7
3719	Solution structure of sperm lysin yields novel insights into molecular dynamics of rapid protein evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 1310-1315.	3.3	14

#	ARTICLE	IF	CITATIONS
3720	The complete chloroplast genome of an aromatic Chinese pepper (<i>Zanthoxylum simulans</i>). Mitochondrial DNA Part B: Resources, 2018, 3, 26-27.	0.2	2
3721	The mycobiota of the sand fly <i>Phlebotomus perniciosus</i> : Involvement of yeast symbionts in uric acid metabolism. Environmental Microbiology, 2018, 20, 1064-1077.	1.8	14
3722	Muscular evolution of hemipenis in Imantodini snakes (Squamata: Dipsadidae). Zoological Journal of the Linnean Society, 2018, 183, 966-980.	1.0	0
3723	Machine Learning Leveraging Genomes from Metagenomes Identifies Influential Antibiotic Resistance Genes in the Infant Gut Microbiome. MSystems, 2018, 3, .	1.7	68
3724	High intraspecific genome diversity in the model arbuscular mycorrhizal symbiont <i>Rhizophagus irregularis</i> . New Phytologist, 2018, 220, 1161-1171.	3.5	206
3725	Chloroplast genomic resources for phylogeny and DNA barcoding: a case study on <i>Fritillaria</i> . Scientific Reports, 2018, 8, 1184.	1.6	120
3726	PhyloChromoMap, a Tool for Mapping Phylogenomic History along Chromosomes, Reveals the Dynamic Nature of Karyotype Evolution in <i>Plasmodium falciparum</i> . Genome Biology and Evolution, 2018, 10, 553-561.	1.1	8
3727	Three gene phylogeny of the Thoreales (Rhodophyta) reveals high species diversity. Journal of Phycology, 2018, 54, 159-170.	1.0	10
3728	The Ancient Link between G-Protein-Coupled Receptors and C-Terminal Phospholipid Kinase Domains. MBio, 2018, 9, .	1.8	16
3729	Complete mitochondrial genome sequence of the Thomson's gazelle (<i>Eudorcas thomsonii</i>). Conservation Genetics Resources, 2018, 10, 543-545.	0.4	0
3730	Evolutionary Genetics of Cytoplasmic Incompatibility Genes <i>cifA</i> and <i>cifB</i> in Prophage WO of <i>Wolbachia</i> . Genome Biology and Evolution, 2018, 10, 434-451.	1.1	143
3731	A major lineage of non-tailed dsDNA viruses as unrecognized killers of marine bacteria. Nature, 2018, 554, 118-122.	13.7	160
3732	Combining morphology and molecular data to improve <i>Drosophila paulistorum</i> (Diptera, Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 26 0,9 9		
3733	Further insights into the highly derived haptorids (Ciliophora, Litostomatea): Phylogeny based on multigene data. Zoologica Scripta, 2018, 47, 231-242.	0.7	33
3734	Convergent Evolution Driven by Rifampin Exacerbates the Global Burden of Drug-Resistant <i>Staphylococcus aureus</i> . MSphere, 2018, 3, .	1.3	55
3735	Phylogeography of the Ibero-Maghrebian red-eyed grass snake (<i>Natrix astreptophora</i>). Organisms Diversity and Evolution, 2018, 18, 143-150.	0.7	16
3736	Complete mitochondrial genome of <i>Saturnia jonasii</i> (Lepidoptera: Saturniidae): Genomic comparisons and phylogenetic inference among Bombycoidea. Genomics, 2018, 110, 274-282.	1.3	26
3737	The Combined Effect of Temperature and Host Clonal Line on the Microbiota of a Planktonic Crustacean. Microbial Ecology, 2018, 76, 506-517.	1.4	28

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3738	The complete chloroplast genome of vulnerable <i>Aesculus wangii</i> (Sapindaceae), a narrowly endemic tree in Yunnan, China. <i>Conservation Genetics Resources</i> , 2018, 10, 335-338.	0.4	9
3739	Reclassification of <i>Lamprotula rochechouartii</i> as <i>Margaritifera rochechouartii</i> comb. nov. (Bivalvia): Tj ETQq1 1 0.784314 rgBT /Overlo phylogenomics of Unionoida. <i>Molecular Phylogenetics and Evolution</i> , 2018, 120, 297-306.	1.2	24
3740	Genetic diversity and distribution differ between long-established and recently introduced populations in the invasive mosquito <i>Aedes albopictus</i> . <i>Infection, Genetics and Evolution</i> , 2018, 58, 145-156.	1.0	29
3741	Species diversity in the marine microturbellarian <i>Astrotrorhynchus bifidus sensu lato</i> (Platyhelminthes: Rhabdozoa) from the Northeast Pacific Ocean. <i>Molecular Phylogenetics and Evolution</i> , 2018, 120, 259-273.	1.2	16
3742	Two Novel Fungal Symbionts <i>Fusarium kuroshium</i> sp. nov. and <i>Graphium kuroshium</i> sp. nov. of Kuroshio Shot Hole Borer (<i>Euwallacea</i> sp. nr. <i>fornicatus</i>) Cause <i>Fusarium</i> Dieback on Woody Host Species in California. <i>Plant Disease</i> , 2018, 102, 1154-1164.	0.7	61
3743	Genome statistics and phylogenetic reconstructions for Southern Hemisphere whelks (Gastropoda): Tj ETQq1 1 0.784314 rgBT /Overlo 0.5	0.5	2
3744	Genome-wide searches and molecular analyses highlight the unique evolutionary path of flavone synthase I (FNSI) in Apiaceae. <i>Genome</i> , 2018, 61, 103-109.	0.9	7
3745	Whole-genome sequencing reveals the extent of heterozygosity in a preferentially self-fertilizing hermaphroditic vertebrate. <i>Genome</i> , 2018, 61, 241-247.	0.9	15
3746	Bioinformatic Approaches for Comparative Analysis of Viruses. <i>Methods in Molecular Biology</i> , 2018, 1704, 401-417.	0.4	1
3747	Comparative Genomics for Prokaryotes. <i>Methods in Molecular Biology</i> , 2018, 1704, 55-78.	0.4	15
3748	Phylogenomics. <i>Methods in Molecular Biology</i> , 2018, 1704, 103-187.	0.4	15
3749	A primer on microbial bioinformatics for nonbioinformaticians. <i>Clinical Microbiology and Infection</i> , 2018, 24, 342-349.	2.8	52
3750	Incongruence between molecules and morphology: A seven-gene phylogeny of Dacini fruit flies paves the way for reclassification (Diptera: Tephritidae). <i>Molecular Phylogenetics and Evolution</i> , 2018, 121, 139-149.	1.2	42
3751	Multiple origins of interdependent endosymbiotic complexes in a genus of cicadas. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E226-E235.	3.3	69
3752	Differing phylogeographic patterns within the Indo-West Pacific mangrove genus <i>Xylocarpus</i> (Meliaceae). <i>Journal of Biogeography</i> , 2018, 45, 676-689.	1.4	21
3753	<i>Reinerantha foliicola</i> , a new genus and species of Lejeuneaceae subtribe Cololejeuneinae (Marchantiophyta) from Ecuador. <i>Journal of Systematics and Evolution</i> , 2018, 56, 67-75.	1.6	12
3754	Prevalence and diversity of avian Haemosporida infecting songbirds in southwest Michigan. <i>Parasitology Research</i> , 2018, 117, 471-489.	0.6	14
3755	Evolution within the fungal genus <i>Verticillium</i> is characterized by chromosomal rearrangement and gene loss. <i>Environmental Microbiology</i> , 2018, 20, 1362-1373.	1.8	70

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3756	A Winteraceae pollen tetrad from the early Paleocene of western Greenland, and the fossil record of Winteraceae in Laurasia and Gondwana. <i>Journal of Biogeography</i> , 2018, 45, 567-581.	1.4	15
3757	Individual- and Species-Specific Skin Microbiomes in Three Different Estrildid Finch Species Revealed by 16S Amplicon Sequencing. <i>Microbial Ecology</i> , 2018, 76, 518-529.	1.4	29
3758	The first two mitochondrial genomes from Taeniopterygidae (Insecta: Plecoptera): Structural features and phylogenetic implications. <i>International Journal of Biological Macromolecules</i> , 2018, 111, 70-76.	3.6	33
3759	Molecular systematics and phylogenetic analysis of the Asian endemic freshwater sleepers (Gobiiformes: Odontobutidae). <i>Molecular Phylogenetics and Evolution</i> , 2018, 121, 1-11.	1.2	18
3760	Phylogenomic analysis of Fundulidae (Teleostei: Cyprinodontiformes) using RNA-sequencing data. <i>Molecular Phylogenetics and Evolution</i> , 2018, 121, 150-157.	1.2	19
3761	Cryptic lineage differentiation among Indo-Pacific bottlenose dolphins (<i>Tursiops aduncus</i>) in the northwest Indian Ocean. <i>Molecular Phylogenetics and Evolution</i> , 2018, 122, 1-14.	1.2	21
3762	Neobodonids are dominant kinetoplastids in the global ocean. <i>Environmental Microbiology</i> , 2018, 20, 878-889.	1.8	27
3763	Molecular cloning and characterization of APOBEC3 family in tree shrew. <i>Gene</i> , 2018, 646, 143-152.	1.0	6
3764	Retrieval of a million high-quality, full-length microbial 16S and 18S rRNA gene sequences without primer bias. <i>Nature Biotechnology</i> , 2018, 36, 190-195.	9.4	165
3765	The <i>ropAe</i> gene encodes a porin-like protein involved in copper transit in <i>Rhizobium etli</i> CFN42. <i>MicrobiologyOpen</i> , 2018, 7, e00573.	1.2	15
3766	Mitogenomic and nuclear diversity in the Mulga Parrot of the Australian arid zone: cryptic subspecies and tests for selection. <i>Emu</i> , 2018, 118, 22-35.	0.2	13
3767	Evidence for trophic transfer of <i>Inodosporus octospora</i> and <i>Ovipleistophora arlo</i> n. sp. (Microsporidia) between crustacean and fish hosts. <i>Parasitology</i> , 2018, 145, 1105-1117.	0.7	31
3768	The complex resistomes of Paenibacillaceae reflect diverse antibiotic chemical ecologies. <i>ISME Journal</i> , 2018, 12, 885-897.	4.4	15
3769	On the Monophyly of <i>Macrolobium</i> Schreb., an Ecologically Diverse Neotropical Tree Genus (Fabaceae-Detarioideae). <i>International Journal of Plant Sciences</i> , 2018, 179, 75-86.	0.6	8
3770	Cophylogenetic assessment of New World warblers (Parulidae) and their symbiotic feather mites (Proctophylloidae). <i>Journal of Avian Biology</i> , 2018, 49, jav-01580.	0.6	26
3771	An outbreak of Shiga toxin-producing <i>Escherichia coli</i> O157:H7 associated with contaminated salad leaves: epidemiological, genomic and food trace back investigations. <i>Epidemiology and Infection</i> , 2018, 146, 187-196.	1.0	54
3772	Morphological and molecular identification of <i>Carpophilus dimidiatus</i> (Coleoptera: Nitidulidae) associated with stored walnut in Northwestern Argentina. <i>Journal of Stored Products Research</i> , 2018, 76, 37-42.	1.2	9
3773	A phylogenomic analysis of lichen-feeding tiger moths uncovers evolutionary origins of host chemical sequestration. <i>Molecular Phylogenetics and Evolution</i> , 2018, 121, 23-34.	1.2	17

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3774	Methylation in <i>Mycobacterium tuberculosis</i> is lineage specific with associated mutations present globally. <i>Scientific Reports</i> , 2018, 8, 160.	1.6	31
3775	Deuterostome Genomics: Lineage-Specific Protein Expansions That Enabled Chordate Muscle Evolution. <i>Molecular Biology and Evolution</i> , 2018, 35, 914-924.	3.5	16
3776	PLAZA 4.0: an integrative resource for functional, evolutionary and comparative plant genomics. <i>Nucleic Acids Research</i> , 2018, 46, D1190-D1196.	6.5	460
3777	Genome-enabled metabolic reconstruction of dominant chemosynthetic colonizers in deep-sea massive sulfide deposits. <i>Environmental Microbiology</i> , 2018, 20, 862-877.	1.8	41
3778	Trait-specific processes of convergence and conservatism shape ecomorphological evolution in ground-dwelling squirrels. <i>Evolution; International Journal of Organic Evolution</i> , 2018, 72, 473-489.	1.1	22
3779	Phylogenetic placement of <i>Yunnanopilia</i> (Opiliaceae) inferred from molecular and morphological data. <i>Journal of Systematics and Evolution</i> , 2018, 56, 48-55.	1.6	1
3780	Role of cytochrome P450 2B sequence variation and gene copy number in facilitating dietary specialization in mammalian herbivores. <i>Molecular Ecology</i> , 2018, 27, 723-736.	2.0	17
3781	Molecular phylogeny of <i>Systellognatha</i> (Plecoptera: Arctoperlaria) inferred from mitochondrial genome sequences. <i>International Journal of Biological Macromolecules</i> , 2018, 111, 542-547.	3.6	32
3782	Bayesian Inference of Species Networks from Multilocus Sequence Data. <i>Molecular Biology and Evolution</i> , 2018, 35, 504-517.	3.5	158
3783	Using Phylogenomic Data to Explore the Effects of Relaxed Clocks and Calibration Strategies on Divergence Time Estimation: Primates as a Test Case. <i>Systematic Biology</i> , 2018, 67, 594-615.	2.7	143
3784	Species delimitation of the North American orchard-spider <i>Leucauge venusta</i> (Walckenaer, 1841) (Araneae, Tetragnathidae). <i>Molecular Phylogenetics and Evolution</i> , 2018, 121, 183-197.	1.2	14
3785	Transfer of a bla CTX-M-1-carrying plasmid between different <i>Escherichia coli</i> strains within the human gut explored by whole genome sequencing analyses. <i>Scientific Reports</i> , 2018, 8, 280.	1.6	28
3786	Genome-based classification of micromonosporae with a focus on their biotechnological and ecological potential. <i>Scientific Reports</i> , 2018, 8, 525.	1.6	102
3787	Speciation Generates Mosaic Genomes in Kangaroos. <i>Genome Biology and Evolution</i> , 2018, 10, 33-44.	1.1	26
3788	Tracheophyte genomes keep track of the deep evolution of the Caulimoviridae. <i>Scientific Reports</i> , 2018, 8, 572.	1.6	46
3789	The genome and microbiome of a dikaryotic fungus (<i>Inocybe terrigena</i> , Inocybaceae) revealed by metagenomics. <i>Environmental Microbiology Reports</i> , 2018, 10, 155-166.	1.0	17
3790	Population genomic footprints of host adaptation, introgression and recombination in coffee leaf rust. <i>Molecular Plant Pathology</i> , 2018, 19, 1742-1753.	2.0	35
3791	Evolutionary history of Coleoptera revealed by extensive sampling of genes and species. <i>Nature Communications</i> , 2018, 9, 205.	5.8	352

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3792	Ancient balancing selection on heterocyst function in a cosmopolitan cyanobacterium. <i>Nature Ecology and Evolution</i> , 2018, 2, 510-519.	3.4	24
3793	Variation and constraints in hybrid genome formation. <i>Nature Ecology and Evolution</i> , 2018, 2, 549-556.	3.4	69
3794	<i>Salmonella enterica</i> genomes from victims of a major sixteenth-century epidemic in Mexico. <i>Nature Ecology and Evolution</i> , 2018, 2, 520-528.	3.4	218
3795	Molecular phylogeny of Macrosiphini (Hemiptera: Aphididae): An evolutionary hypothesis for the Pterocomma-group habitat adaptation. <i>Molecular Phylogenetics and Evolution</i> , 2018, 121, 12-22.	1.2	20
3796	Fossil flowers from the early Palaeocene of Patagonia, Argentina, with affinity to Schizomerieae (Cunoniaceae). <i>Annals of Botany</i> , 2018, 121, 431-442.	1.4	25
3797	Herbarium collection-based phylogenetics of the ragweeds (<i>Ambrosia</i> , Asteraceae). <i>Molecular Phylogenetics and Evolution</i> , 2018, 120, 335-341.	1.2	28
3798	At the Origin of a Worldwide Invasion: Unraveling the Genetic Makeup of the Caribbean Bridgehead Populations of the Dengue Vector <i>Aedes aegypti</i> . <i>Genome Biology and Evolution</i> , 2018, 10, 56-71.	1.1	24
3799	Evaluating Fast Maximum Likelihood-Based Phylogenetic Programs Using Empirical Phylogenomic Data Sets. <i>Molecular Biology and Evolution</i> , 2018, 35, 486-503.	3.5	147
3800	Higher tRNA gene duplication in mitogenomes of praying mantises (Dictyoptera, Mantodea) and the phylogeny within Mantodea. <i>International Journal of Biological Macromolecules</i> , 2018, 111, 787-795.	3.6	42
3801	Noncontiguous finished genome sequence of <i>Megasphaera</i> sp. ASD88, isolated from faeces of a child with autism spectrum disorder. <i>New Microbes and New Infections</i> , 2018, 22, 13-16.	0.8	5
3802	Phylogenomics offers resolution of major tunicate relationships. <i>Molecular Phylogenetics and Evolution</i> , 2018, 121, 166-173.	1.2	56
3803	Morphological and Molecular Redefinition of <i>Euplotes platystoma</i> Dragesco & Dragesco-KernÁ©is, 1986 and <i>Aspidisca lynceus</i> (MÁ¼ller, 1773) Ehrenberg, 1859, with Reconsideration of a "Well-known" <i>Euplotes</i> Ciliate, <i>Euplotes harpa</i> Stein, 1859 (Ciliophora, Euplotida). <i>Journal of Eukaryotic Microbiology</i> , 2018, 65, 531-543.	0.8	14
3804	Positive selection on the mitochondrial <i>ATP synthase 6</i> and the <i>NADH dehydrogenase 2</i> genes across 22 hare species (genus <i>Lepus</i>). <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2018, 56, 428-443.	0.6	8
3805	Disturbance reduces the differentiation of mycorrhizal fungal communities in grasslands along a precipitation gradient. <i>Ecological Applications</i> , 2018, 28, 736-748.	1.8	45
3806	Long-distance dispersal or postglacial contraction? Insights into disjunction between Himalaya-Hengduan Mountains and Taiwan in a cold-adapted herbaceous genus, <i>Triplostegia</i> . <i>Nature Ecology and Evolution</i> , 2018, 8, 1131-1146.	0.8	23
3807	Characterization and phylogenetic analysis of the complete chloroplast genome of <i>Orinus thoroldii</i> (Poaceae). <i>Conservation Genetics Resources</i> , 2018, 10, 761-764.	0.4	3
3808	Complete mitochondrial genome of <i>Naemorhedus goral</i> (Caprinae), a threatened species from the Himalayan and Hindu Kush regions. <i>Conservation Genetics Resources</i> , 2018, 10, 855-858.	0.4	4
3809	A biogeographic and ecological perspective to the evolution of reproductive behaviour in the family Salamandridae. <i>Molecular Phylogenetics and Evolution</i> , 2018, 121, 98-109.	1.2	19

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3810	The evolution of substrate discrimination in macrolide antibiotic resistance enzymes. <i>Nature Communications</i> , 2018, 9, 112.	5.8	50
3811	Integrating restriction site-associated DNA sequencing (RAD-seq) with morphological cladistic analysis clarifies evolutionary relationships among major species groups of bee orchids. <i>Annals of Botany</i> , 2018, 121, 85-105.	1.4	48
3812	<i>Bacillus amyloliquefaciens</i> ssp. <i>plantarum</i> F11 isolated from Algerian salty lake as a source of biosurfactants and bioactive lipopeptides. <i>FEMS Microbiology Letters</i> , 2018, 365, .	0.7	16
3813	BUSCO Applications from Quality Assessments to Gene Prediction and Phylogenomics. <i>Molecular Biology and Evolution</i> , 2018, 35, 543-548.	3.5	1,844
3814	A Single Mutation Unlocks Cascading Exaptations in the Origin of a Potent Pitviper Neurotoxin. <i>Molecular Biology and Evolution</i> , 2018, 35, 887-898.	3.5	26
3815	Information Criteria for Comparing Partition Schemes. <i>Systematic Biology</i> , 2018, 67, 616-632.	2.7	17
3816	An AlgU-Regulated Antisense Transcript Encoded within the <i>Pseudomonas syringae</i> <i>flaQ</i> Gene Has a Positive Effect on Motility. <i>Journal of Bacteriology</i> , 2018, 200, .	1.0	11
3817	Taxonomic reassessment of the Indo-Pacific Scytosiphonaceae (Phaeophyceae): <i>Hydroclathrus rapanuii</i> sp. nov. and <i>Chnoospora minima</i> from Easter Island, with proposal of <i>Dactylosiphon</i> gen. nov. and <i>Pseudochnoospora</i> gen. nov.. <i>Botanica Marina</i> , 2018, 61, 47-64.	0.6	11
3818	An Iranian genomic sequence of Beet mosaic virus provides insights into diversity and evolution of the world population. <i>Virus Genes</i> , 2018, 54, 272-279.	0.7	8
3819	Colonization and diversification of the white-browed shortwing (Aves: Muscicapidae: Brachypteryx) Tj ETQq1 1 0.784314 rgBT /Overlock 1.2	1.2	32
3820	Light in the darkness: New perspective on lanternfish relationships and classification using genomic and morphological data. <i>Molecular Phylogenetics and Evolution</i> , 2018, 121, 71-85.	1.2	32
3821	The phylogeography of the cycad genus <i>Dioon</i> (Zamiaceae) clarifies its Cenozoic expansion and diversification in the Mexican transition zone. <i>Annals of Botany</i> , 2018, 121, 535-548.	1.4	42
3822	Phylogeographic analysis of the East Asian goldenrod (<i>Solidago virgaurea</i> complex, Asteraceae) reveals hidden ecological diversification with recurrent formation of ecotypes. <i>Annals of Botany</i> , 2018, 121, 489-500.	1.4	14
3823	<i>Salmonella enterica</i> Serotype 4,[5],12:i:- in Swine in the United States Midwest: An Emerging Multidrug-Resistant Clade. <i>Clinical Infectious Diseases</i> , 2018, 66, 877-885.	2.9	79
3824	Phylogenomic Data Yield New and Robust Insights into the Phylogeny and Evolution of Weevils. <i>Molecular Biology and Evolution</i> , 2018, 35, 823-836.	3.5	93
3825	Angular cartilage structure and variation in Neotropical freshwater stingrays (Chondrichthyes) Tj ETQq1 1 0.784314 rgBT /Overlock 1.0	1.0	8
3826	Sooty mangabey genome sequence provides insight into AIDS resistance in a natural SIV host. <i>Nature</i> , 2018, 553, 77-81.	13.7	81
3827	Morphological and molecular analysis of <i>Henricia</i> Gray, 1840 (Asterozoa: Echinodermata) from the Northern Atlantic Ocean. <i>Zoological Journal of the Linnean Society</i> , 2018, 182, 791-807.	1.0	10

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3828	Transcriptome sequence-based phylogeny of chalcidoid wasps (Hymenoptera: Chalcidoidea) reveals a history of rapid radiations, convergence, and evolutionary success. <i>Molecular Phylogenetics and Evolution</i> , 2018, 120, 286-296.	1.2	83
3829	Multiple origins of the Phaenonotum beetles in the Greater Antilles (Coleoptera: Hydrophilidae): phylogeny, biogeography and systematics. <i>Zoological Journal of the Linnean Society</i> , 2018, 183, 97-120.	1.0	8
3830	The systematics and biogeography of the Bearded Greenbul (Aves: Criniger) reveals the impact of Plio-Pleistocene forest fragmentation on Afro-tropical avian diversity. <i>Zoological Journal of the Linnean Society</i> , 2018, 183, 672-686.	1.0	8
3831	Island- and lake-like parallel adaptive radiations replicated in rivers. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018, 285, 20171762.	1.2	49
3832	Multiplexed gene synthesis in emulsions for exploring protein functional landscapes. <i>Science</i> , 2018, 359, 343-347.	6.0	102
3833	An integrative assessment of the taxonomic status of putative hybrid leopard frogs (Anura: Ranidae) from the ChortAs Highlands of Central America, with description of a new species. <i>Systematics and Biodiversity</i> , 2018, 16, 340-356.	0.5	9
3834	Co-invading symbiotic mutualists of <i>Medicago polymorpha</i> retain high ancestral diversity and contain diverse accessory genomes. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	6
3835	Genetic Competence Drives Genome Diversity in <i>Bacillus subtilis</i> . <i>Genome Biology and Evolution</i> , 2018, 10, 108-124.	1.1	67
3836	A new genus and species of vespertilionid bat from the Indomalayan Region. <i>Journal of Mammalogy</i> , 2018, 99, 209-222.	0.6	13
3837	Phylogenetic relationships of Aurantioideae (Rutaceae) based on RAD-Seq. <i>Tree Genetics and Genomes</i> , 2018, 14, 1.	0.6	24
3838	<scp>GPS</scp>it: An automated method for evolutionary analysis of nonculturable ciliated microeukaryotes. <i>Molecular Ecology Resources</i> , 2018, 18, 700-713.	2.2	36
3839	Laurobasidiaceae fam. nov. (Exobasidiales, Basidiomycota), a new family for fungi causing galls with aerial root-like outgrowths, with a new record from Thailand of <i>Laurobasidium hachijoense</i> on a new host, <i>Cinnamomum subavenium</i> . <i>Phytotaxa</i> , 2018, 347, 150.	0.1	3
3840	Phylogenetic relationships among <i>Ananas</i> and related taxa (Bromelioideae, Bromeliaceae) based on nuclear, plastid and AFLP data. <i>Plant Systematics and Evolution</i> , 2018, 304, 841-851.	0.3	19
3841	Species delimitation and sex associations in the bee genus <i>Thygater</i> , with the aid of molecular data, and the description of a new species. <i>Apidologie</i> , 2018, 49, 484-496.	0.9	9
3842	New insights into the phylogeny of the TMBIM superfamily across the tree of life: Comparative genomics and synteny networks reveal independent evolution of the BI and LFG families in plants. <i>Molecular Phylogenetics and Evolution</i> , 2018, 126, 266-278.	1.2	15
3843	A new phylogeny-based tribal classification of subfamily Detarioideae, an early branching clade of florally diverse tropical arborescent legumes. <i>Scientific Reports</i> , 2018, 8, 6884.	1.6	38
3844	Convergent Acquisition of Nonembryonic Development in Styelid Ascidiarians. <i>Molecular Biology and Evolution</i> , 2018, 35, 1728-1743.	3.5	35
3845	Genes for de novo biosynthesis of omega-3 polyunsaturated fatty acids are widespread in animals. <i>Science Advances</i> , 2018, 4, eaar6849.	4.7	252

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3846	Quantifying the Evolutionary Conservation of Genes Encoding Multidrug Efflux Pumps in the ESKAPE Pathogens To Identify Antimicrobial Drug Targets. <i>MSystems</i> , 2018, 3, .	1.7	20
3847	Phylogenetic approaches reveal a new sterile lichen in the genus <i>Loxospora</i> (Sarrameanales.) Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.1	11
3848	Evolutionary history of Mexican domesticated and wild <i>Meleagris gallopavo</i> . <i>Genetics Selection Evolution</i> , 2018, 50, 19.	1.2	10
3849	Tracing the evolution of the heterotrimeric G protein α subunit in Metazoa. <i>BMC Evolutionary Biology</i> , 2018, 18, 51.	3.2	17
3850	Disjunct distribution and distinct intraspecific diversification of <i>Eothenomys melanogaster</i> in South China. <i>BMC Evolutionary Biology</i> , 2018, 18, 50.	3.2	14
3851	Role of genetic introgression during the evolution of cultivated rice (<i>Oryza sativa</i> L.). <i>BMC Evolutionary Biology</i> , 2018, 18, 57.	3.2	34
3852	Genomic epidemiology and population structure of <i>Neisseria gonorrhoeae</i> from remote highly endemic Western Australian populations. <i>BMC Genomics</i> , 2018, 19, 165.	1.2	22
3853	Expansion of a urethritis-associated <i>Neisseria meningitidis</i> clade in the United States with concurrent acquisition of <i>N. gonorrhoeae</i> alleles. <i>BMC Genomics</i> , 2018, 19, 176.	1.2	61
3854	Primordial origin and diversification of plasmids in Lyme disease agent bacteria. <i>BMC Genomics</i> , 2018, 19, 218.	1.2	46
3855	Classification and phylogenetic analyses of the Arabidopsis and tomato G-type lectin receptor kinases. <i>BMC Genomics</i> , 2018, 19, 239.	1.2	35
3856	New insights into the phylogenetics and population structure of the prairie falcon (<i>Falco mexicanus</i>). <i>BMC Genomics</i> , 2018, 19, 233.	1.2	25
3857	Identification of a novel fused gene family implicates convergent evolution in eukaryotic calcium signaling. <i>BMC Genomics</i> , 2018, 19, 306.	1.2	4
3858	Genetic variability in the <i>sdrD</i> gene in <i>Staphylococcus aureus</i> from healthy nasal carriers. <i>BMC Microbiology</i> , 2018, 18, 34.	1.3	10
3859	The Antarctic sea ice alga <i>Chlamydomonas</i> sp. ICE-L provides insights into adaptive patterns of chloroplast evolution. <i>BMC Plant Biology</i> , 2018, 18, 53.	1.6	22
3860	Dominant integration locus drives continuous diversification of plant immune receptors with exogenous domain fusions. <i>Genome Biology</i> , 2018, 19, 23.	3.8	109
3861	â€œCandidatus <i>Paraporphyromonas polyenzymogenes</i> â€•encodes multi-modular cellulases linked to the type IX secretion system. <i>Microbiome</i> , 2018, 6, 44.	4.9	32
3862	Adaptive evolution of osmoregulatory-related genes provides insight into salinity adaptation in Chinese mitten crab, <i>Eriocheir sinensis</i> . <i>Genetica</i> , 2018, 146, 303-311.	0.5	14
3863	Morphological, histological and molecular characterization of three <i>Myxobolus</i> species (Cnidaria:) Tj ETQq1 1 0.784314 rgBT /Overlock 0.6	0.6	8
	Hypophthalmichthys nobilis Richardson in China. <i>Parasitology International</i> , 2018, 67, 509-516.		

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3864	Repeated evolution of self-compatibility for reproductive assurance. <i>Nature Communications</i> , 2018, 9, 1639.	5.8	19
3865	The prevalence of terraced treescapes in analyses of phylogenetic data sets. <i>BMC Evolutionary Biology</i> , 2018, 18, 46.	3.2	13
3866	<i>Ginkgo biloba</i> 's footprint of dynamic Pleistocene history dates back only 390,000 years ago. <i>BMC Genomics</i> , 2018, 19, 299.	1.2	35
3867	Factors driving metabolic diversity in the budding yeast subphylum. <i>BMC Biology</i> , 2018, 16, 26.	1.7	36
3868	OCTAL: Optimal Completion of gene trees in polynomial time. <i>Algorithms for Molecular Biology</i> , 2018, 13, 6.	0.3	12
3869	TREE2FASTA: a flexible Perl script for batch extraction of FASTA sequences from exploratory phylogenetic trees. <i>BMC Research Notes</i> , 2018, 11, 164.	0.6	10
3870	Biological invasions increase the richness of arbuscular mycorrhizal fungi from a Hawaiian subtropical ecosystem. <i>Biological Invasions</i> , 2018, 20, 2421-2437.	1.2	18
3871	<i>Cryptodiscus muriformis</i> and <i>Schizoxylon gilienstamii</i> , two new species of Stictidaceae (Ascomycota). <i>Mycological Progress</i> , 2018, 17, 295-305.	0.5	9
3872	First insights on the biogeographical history of <i>Phlegmariurus</i> (Lycopodiaceae), with a focus on Madagascar. <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 488-501.	1.2	25
3873	ANISEED 2017: extending the integrated ascidian database to the exploration and evolutionary comparison of genome-scale datasets. <i>Nucleic Acids Research</i> , 2018, 46, D718-D725.	6.5	90
3874	Two new species of <i>Rhodocollybia</i> from tropical India. <i>Phytotaxa</i> , 2018, 340, 157.	0.1	2
3875	A new species and a new record of <i>Clitopilus</i> and a description of <i>C. orientalis</i> from India based on morphology and molecular phylogeny. <i>Phytotaxa</i> , 2018, 343, 47.	0.1	13
3876	<i>Phylloporia minuta</i> sp. nov. (Basidiomycota, Hymenochaetales): a remarkable species discovered in a small protected urban area of Atlantic Forest. <i>Phytotaxa</i> , 2018, 348, 199.	0.1	5
3877	Signature of positive selection in mitochondrial DNA in <i>Cetartiodactyla</i> . <i>Genes and Genetic Systems</i> , 2018, 93, 65-73.	0.2	21
3878	The <i>Inocybe geophylla</i> group in North America: a revision of the lilac species surrounding <i>I. lilacina</i> . <i>Mycologia</i> , 2018, 110, 618-634.	0.8	12
3879	The complete mitochondrial genome of the common vole, <i>Microtus arvalis</i> (Rodentia: Arvicolinae). <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 446-447.	0.2	9
3880	Deciphering the genome and secondary metabolome of the plant pathogen <i>Fusarium culmorum</i> . <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	10
3881	DNA sequencing to clarify the taxonomical conundrum of the clinical coelomycetes. <i>Mycoses</i> , 2018, 61, 708-717.	1.8	11

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3882	The systematic position of <i>Microlejeunea ocellata</i> (Marchantiophyta: Lejeuneaceae), an extraordinary species endemic to Australia and New Zealand. <i>Bryologist</i> , 2018, 121, 158.	0.1	5
3883	Intra-host sequence variability in human papillomavirus. <i>Papillomavirus Research (Amsterdam,)</i> Tj ETQq1 1 0.784314 rgBT /Overlock 1000 4.5 35	4.5	35
3884	Expansion and systematics redefinition of the most threatened freshwater mussel family, the Margaritiferidae. <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 98-118.	1.2	53
3885	Macroecology and macroevolution of the latitudinal diversity gradient in ants. <i>Nature Communications</i> , 2018, 9, 1778.	5.8	133
3886	Diversity of the cyrtophorid genus <i>Chlamydodon</i> (Protista, Ciliophora): its systematics and geographic distribution, with taxonomic descriptions of three species. <i>Systematics and Biodiversity</i> , 2018, 16, 497-511.	0.5	8
3887	ComM is a hexameric helicase that promotes branch migration during natural transformation in diverse Gram-negative species. <i>Nucleic Acids Research</i> , 2018, 46, 6099-6111.	6.5	39
3888	The evolution of diapause in <i>Rivulus</i> (Laimosemion). <i>Zoological Journal of the Linnean Society</i> , 2018, 184, 773-790.	1.0	9
3889	Invasive Methicillin-Resistant <i>Staphylococcus aureus</i> USA500 Strains from the U.S. Emerging Infections Program Constitute Three Geographically Distinct Lineages. <i>MSphere</i> , 2018, 3, .	1.3	46
3890	Phylogenomic analyses reveal extensive gene flow within the magic flowers (<i>Achimenes</i>). <i>American Journal of Botany</i> , 2018, 105, 726-740.	0.8	11
3891	Targeting legume loci: A comparison of three methods for target enrichment bait design in Leguminosae phylogenomics. <i>Applications in Plant Sciences</i> , 2018, 6, e1036.	0.8	64
3892	Phylogenomics, Diversification Dynamics, and Comparative Transcriptomics across the Spider Tree of Life. <i>Current Biology</i> , 2018, 28, 1489-1497.e5.	1.8	198
3893	TreeTime: Maximum-likelihood phylodynamic analysis. <i>Virus Evolution</i> , 2018, 4, vex042.	2.2	883
3894	Does a plant-eating insect's diet govern the evolution of insecticide resistance? Comparative tests of the preadaptation hypothesis. <i>Evolutionary Applications</i> , 2018, 11, 739-747.	1.5	36
3895	A comparison of different methods for preserving plant molecular materials and the effect of degraded DNA on ddRAD sequencing. <i>Plant Diversity</i> , 2018, 40, 106-116.	1.8	8
3896	Transcriptional profiling of the CAM plant <i>Agave salmiana</i> reveals conservation of a genetic program for regeneration. <i>Developmental Biology</i> , 2018, 442, 28-39.	0.9	17
3897	Resolving the systematic positions of enigmatic taxa: Manipulating the chloroplast genome data of Saxifragales. <i>Molecular Phylogenetics and Evolution</i> , 2018, 126, 321-330.	1.2	67
3898	Ancestral Function and Diversification of a Horizontally Acquired Oomycete Carboxylic Acid Transporter. <i>Molecular Biology and Evolution</i> , 2018, 35, 1887-1900.	3.5	24
3899	Phylogeny and Evolution of the Neotropical Radiation of <i>Lachemilla</i> (Rosaceae): Uncovering a History of Reticulate Evolution and Implications for Infrageneric Classification. <i>Systematic Botany</i> , 2018, 43, 17-34.	0.2	33

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3900	The <i>Tetramerium</i> Lineage (Acanthaceae, Justicieae) Revisited: Phylogenetic Relationships Reveal Polyphyly of Many New World Genera Accompanied by Rampant Evolution of Floral Morphology. <i>Systematic Botany</i> , 2018, 43, 97-116.	0.2	15
3901	Multilocus Phylogenetics of New World Milkweed Vines (Apocynaceae, Asclepiadoideae, Gonolobinae). <i>Systematic Botany</i> , 2018, 43, 77-96.	0.2	13
3902	Reinstatement of the Southern Andean Genus <i>Stenodraba</i> (Brassicaceae) Based on Molecular Data and Insights from its Environmental and Geographic Distribution. <i>Systematic Botany</i> , 2018, 43, 35-52.	0.2	11
3903	Plastid Transcript Editing across Dinoflagellate Lineages Shows Lineage-Specific Application but Conserved Trends. <i>Genome Biology and Evolution</i> , 2018, 10, 1019-1038.	1.1	22
3904	Comparative Genomics Reveals Thousands of Novel Chemosensory Genes and Massive Changes in Chemoreceptor Repertoires across Chelicerates. <i>Genome Biology and Evolution</i> , 2018, 10, 1221-1236.	1.1	35
3905	Phylogenomics confirms monophyly of Nudipleura (Gastropoda: Heterobranchia). <i>Journal of Molluscan Studies</i> , 2018, 84, 259-265.	0.4	12
3906	<i>Gymnomonas nepalensis</i> gen. et sp. nov. for the naked flagellate strain "Nepal", formerly identified as <i>Dunaliella lateralis</i> (Volvocales, Chlorophyceae). <i>Phycological Research</i> , 2018, 66, 167-172.	0.8	3
3907	Madagopsina gen. n. and Gracilopsina gen. n. (Diptera: Diopsidae) from Madagascar with description of four new species. <i>Tijdschrift Voor Entomologie</i> , 2018, 160, 141-215.	0.1	3
3908	Multi-locus phylogenetics, lineage sorting, and reticulation in <i>Pinus</i> subsection <i>Australes</i> . <i>American Journal of Botany</i> , 2018, 105, 711-725.	0.8	51
3909	A matter of phylogenetic scale: Distinguishing incomplete lineage sorting from lateral gene transfer as the cause of gene tree discord in recent versus deep diversification histories. <i>American Journal of Botany</i> , 2018, 105, 376-384.	0.8	45
3910	Magnetic beads, a particularly effective novel method for extraction of NGS-ready DNA from macroalgae. <i>Algal Research</i> , 2018, 32, 308-313.	2.4	21
3911	Detection of reassortant H5N6 clade 2.3.4.4 highly pathogenic avian influenza virus in a black-faced spoonbill (<i>Platalea minor</i>) found dead, Taiwan, 2017. <i>Infection, Genetics and Evolution</i> , 2018, 62, 275-278.	1.0	12
3912	Morphological and molecular systematics of the <i>Monanchora arbuscula</i> complex (Poecilosclerida : Tj ETQq0 0 0 rgBT /Overlock the Tropical Western Atlantic. <i>Invertebrate Systematics</i> , 2018, 32, 457.	0.5	9
3913	Carbapenem-Resistant Hypervirulent <i>Klebsiella pneumoniae</i> of Sequence Type 36. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	1.4	66
3914	DNA barcoding reveals the Palaearctic species <i>Histeromerus mystacinus</i> (Hymenoptera: Braconidae: Tj ETQq0 0 0 rgBT /Overlock 10 Tf	0.4	1
3915	Gymnosperms on the EDGE. <i>Scientific Reports</i> , 2018, 8, 6053.	1.6	75
3916	Phylogenetic position and taxonomy of <i>Kusaghiporia usambarensis</i> gen. et sp. nov. (Polyporales). <i>Mycology</i> , 2018, 9, 136-144.	2.0	8
3917	Global species delimitation and phylogeography of the circumtropical "sexy shrimp" <i>Thor amboinensis</i> reveals a cryptic species complex and secondary contact in the Indo-West Pacific. <i>Journal of Biogeography</i> , 2018, 45, 1275-1287.	1.4	14

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3918	Morphological and phylogenetic evidence reveal <i>Fissuroma taiwanense</i> sp. nov. (Aigialaceae, Tj ETQq0 0 0 rgBT /Oyerlock 10, Tf 50 742	0.1	9
3919	<i>Ophiocordyceps neonutans</i> sp. nov., a new neotropical species from <i>O. nutans</i> complex (Ophiocordycipitaceae, Ascomycota). <i>Phytotaxa</i> , 2018, 344, 215.	0.1	9
3920	The genus <i>Agaricus</i> in the Caribbean. Nine new taxa mostly based on collections from the Dominican Republic. <i>Phytotaxa</i> , 2018, 345, 219.	0.1	23
3921	Quartet Sampling distinguishes lack of support from conflicting support in the green plant tree of life. <i>American Journal of Botany</i> , 2018, 105, 385-403.	0.8	194
3922	<i>Leucangium carthusianum</i> var. <i>purpureum</i> , a new purple truffle from China. <i>Phytotaxa</i> , 2018, 347, 165.	0.1	0
3923	Species limits in the Rusty-breasted Antpitta (<i>Grallaricula ferrugineipectus</i>) complex. <i>Wilson Journal of Ornithology</i> , 2018, 130, 152.	0.1	9
3924	Comparative genomic analysis of the "pseudofungus" <i>Hyphochytrium catenoides</i> . <i>Open Biology</i> , 2018, 8, 170184.	1.5	31
3925	New contribution to the species-rich genus <i>Euplotes</i> : Morphology, ontogeny and systematic position of two species (Ciliophora; Euplotia). <i>European Journal of Protistology</i> , 2018, 64, 20-39.	0.5	18
3926	Large-scale sequence analysis reveals novel human-adaptive markers in PB2 segment of seasonal influenza A viruses. <i>Emerging Microbes and Infections</i> , 2018, 7, 1-12.	3.0	13
3927	Detecting Signatures of Positive Selection along Defined Branches of a Population Tree Using LSD. <i>Molecular Biology and Evolution</i> , 2018, 35, 1520-1535.	3.5	25
3928	Phylogenetic insights on Mediterranean and Afrotropical <i>Rhipicephalus</i> species (Acari: Ixodida) based on mitochondrial DNA. <i>Experimental and Applied Acarology</i> , 2018, 75, 107-128.	0.7	17
3929	Structural Basis for Superoxide Activation of <i>Flavobacterium johnsoniae</i> Class I Ribonucleotide Reductase and for Radical Initiation by Its Dimanganese Cofactor. <i>Biochemistry</i> , 2018, 57, 2679-2693.	1.2	38
3930	Horizontal gene transfer constrains the timing of methanogen evolution. <i>Nature Ecology and Evolution</i> , 2018, 2, 897-903.	3.4	109
3931	Hagfish and lamprey Hox genes reveal conservation of temporal colinearity in vertebrates. <i>Nature Ecology and Evolution</i> , 2018, 2, 859-866.	3.4	55
3932	Genomics of Parallel Ecological Speciation in Lake Victoria Cichlids. <i>Molecular Biology and Evolution</i> , 2018, 35, 1489-1506.	3.5	103
3933	The phylogenetic position of <i>Choerodonicola</i> Cribb, 2005 (Digenea: Opecoelidae) with a partial life-cycle for a new species from the blue-barred parrotfish <i>Scarus ghobban</i> Forssk (Scaridae) in Moreton Bay, Australia. <i>Systematic Parasitology</i> , 2018, 95, 337-352.	0.5	9
3934	<i>Palaeocentroscomnus</i> (Chondrichthyes: Somniosidae), a new sleeper shark genus from Miocene deposits of Austria (Europe). <i>Palaontologische Zeitschrift</i> , 2018, 92, 443-456.	0.8	7
3935	<i>Collimyces mutans</i> gen. et sp. nov. (Rhizophydiales, Collimycetaceae fam. nov.), a New Chytrid Parasite of <i>Microglena</i> (Volvocales, clade Monadinia). <i>Protist</i> , 2018, 169, 507-520.	0.6	16

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3936	Phylogenetic analysis of trophic niche evolution reveals a latitudinal herbivory gradient in Clupeoidei (herrings, anchovies, and allies). <i>Molecular Phylogenetics and Evolution</i> , 2018, 124, 151-161.	1.2	37
3937	Carbonate-sensitive phytotransferrin controls high-affinity iron uptake in diatoms. <i>Nature</i> , 2018, 555, 534-537.	13.7	106
3938	Complete chloroplast genome of the tree fern <i>Alsophila podophylla</i> (Cyatheaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 48-49.	0.2	7
3939	A Model-Based Approach for Identifying Functional Intergenic Transcribed Regions and Noncoding RNAs. <i>Molecular Biology and Evolution</i> , 2018, 35, 1422-1436.	3.5	31
3940	New species and a molecular dating analysis of <i>Vetulina</i> Schmidt, 1879 (Porifera: Demospongiae: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 Society, 2018, 184, 585-604.	1.0	8
3941	Identification and characterisation of the cryptic Golgi apparatus in <i>Naegleria gruberi</i> . <i>Journal of Cell Science</i> , 2018, 131, .	1.2	6
3942	The first mitochondrial genome for Brahmin moths (Brahmaeidae) and implications for the higher phylogeny of Bombycoidea. <i>Journal of Asia-Pacific Entomology</i> , 2018, 21, 578-584.	0.4	1
3943	Cooption of an appendage-patterning gene cassette in the head segmentation of arachnids. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E3491-E3500.	3.3	36
3944	Inhabiting plant roots, nematodes, and trufflesâ€™ <i>Polyphilus</i> , a new helotialean genus with two globally distributed species. <i>Mycologia</i> , 2018, 110, 286-299.	0.8	25
3945	Mitonuclear discordance in wolf spiders: Genomic evidence for species integrity and introgression. <i>Molecular Ecology</i> , 2018, 27, 1681-1695.	2.0	55
3946	HybPhyloMaker: Target Enrichment Data Analysis From Raw Reads to Species Trees. <i>Evolutionary Bioinformatics</i> , 2018, 14, 117693431774261.	0.6	34
3947	Phyldynamic analysis and molecular diversity of the avian infectious bronchitis virus of chickens in Brazil. <i>Infection, Genetics and Evolution</i> , 2018, 61, 77-83.	1.0	15
3948	ViFi: accurate detection of viral integration and mRNA fusion reveals indiscriminate and unregulated transcription in proximal genomic regions in cervical cancer. <i>Nucleic Acids Research</i> , 2018, 46, 3309-3325.	6.5	47
3949	Using genomic analysis to identify tomato Tm-2 resistance-breaking mutations and their underlying evolutionary path in a new and emerging tobamovirus. <i>Archives of Virology</i> , 2018, 163, 1863-1875.	0.9	33
3950	Thyridariella, a novel marine fungal genus from India: morphological characterization and phylogeny inferred from multigene DNA sequence analyses. <i>Mycological Progress</i> , 2018, 17, 791-804.	0.5	31
3951	The complete mitochondrial genome of <i>Epeorus herklotsi</i> (Ephemeroptera: Heptageniidae) and its phylogeny. <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 303-304.	0.2	21
3952	Genomic insight into the taxonomy of <i>Rhizobium</i> genospecies that nodulate <i>Phaseolus vulgaris</i> . <i>Systematic and Applied Microbiology</i> , 2018, 41, 300-310.	1.2	44
3953	A survey of Type III restriction-modification systems reveals numerous, novel epigenetic regulators controlling phase-variable regulons; phasevarions. <i>Nucleic Acids Research</i> , 2018, 46, 3532-3542.	6.5	43

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3954	High Mitochondrial Diversity in a New Water Bear Species (Tardigrada: Eutardigrada) from Mountain Glaciers in Central Asia, with the Erection of a New Genus <i>Cryoconicus</i> . <i>Annales Zoologici</i> , 2018, 68, 179-201.	0.1	51
3955	The <i>Microtus</i> voles: Resolving the phylogeny of one of the most speciose mammalian genera using genomics. <i>Molecular Phylogenetics and Evolution</i> , 2018, 125, 85-92.	1.2	28
3956	Relentless spread and adaptation of non-typeable vanA vancomycin-resistant <i>Enterococcus faecium</i> : a genome-wide investigation. <i>Journal of Antimicrobial Chemotherapy</i> , 2018, 73, 1487-1491.	1.3	24
3957	New Threats from H7N9 Influenza Virus: Spread and Evolution of High- and Low-Pathogenicity Variants with High Genomic Diversity in Wave Five. <i>Journal of Virology</i> , 2018, 92, .	1.5	92
3958	Application of Chloroplast Phylogenomics to Resolve Species Relationships Within the Plant Genus <i>Amaranthus</i> . <i>Journal of Molecular Evolution</i> , 2018, 86, 216-239.	0.8	25
3959	Resolving complex phylogeographic patterns in the Balkan Peninsula using closely related wall-lizard species as a model system. <i>Molecular Phylogenetics and Evolution</i> , 2018, 125, 100-115.	1.2	29
3960	Photobiont switching causes changes in the reproduction strategy and phenotypic dimorphism in the Arthoniomycetes. <i>Scientific Reports</i> , 2018, 8, 4952.	1.6	41
3961	Phylogenetic relationships in <i>Bulbostylis</i> (Abildgaardieae: Cyperaceae) inferred from nuclear and plastid DNA sequence data. <i>Systematics and Biodiversity</i> , 2018, 16, 441-452.	0.5	7
3962	The first complete chloroplast genome of a traditional Chinese medicinal herb <i>Odontosoria chinensis</i> (Lindsaeaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 292-293.	0.2	3
3963	Variation Across Mitochondrial Gene Trees Provides Evidence for Systematic Error: How Much Gene Tree Variation Is Biological?. <i>Systematic Biology</i> , 2018, 67, 847-860.	2.7	51
3964	Formal description of <i>Mycobacterium neglectum</i> sp. nov. and <i>Mycobacterium palauense</i> sp. nov., rapidly growing actinobacteria. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 1209-1223.	0.7	12
3965	Phylogenetic framework for the phylum Tenericutes based on genome sequence data: proposal for the creation of a new order Mycoplasmodales ord. nov., containing two new families Mycoplasmodaceae fam. nov. and Metamycoplasmataceae fam. nov. harbouring Eperythrozoon, Ureaplasma and five novel genera. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 1583-1630.	0.7	488
3966	Phylogenetic analysis of cnidarian peroxiredoxins and stress-responsive expression in the estuarine sea anemone <i>Nematostella vectensis</i> . <i>Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology</i> , 2018, 221, 32-43.	0.8	8
3967	Captive individuals of endangered Philippine raptors maintain native feather mites (Acariformes: Tj ETQq1 1 0.784314 rgBT /Overlock 1 0.6 4	0.6	4
3968	A new cryptic species of <i>Asteronyx</i> MÅller and Troschel, 1842 (Echinodermata: Ophiuroidea), based on molecular phylogeny and morphology, from off Pacific Coast of Japan. <i>Zoologischer Anzeiger</i> , 2018, 274, 14-33.	0.4	9
3969	Targeted Sampling and Target Capture: Assessing Phylogeographic Concordance with Genome-wide Data. <i>Systematic Biology</i> , 2018, 67, 979-996.	2.7	26
3970	Preliminary assessment of community composition and phylogeographic relationships of the birds of the Meratus Mountains, south-east borneo, Indonesia. <i>Bulletin of the British Ornithologists' Club</i> , 2018, 138, 45-66.	0.1	8
3971	Evolutionary and expression analyses reveal a pattern of ancient duplications and functional specializations in the diversification of the Downstream of Kinase (DOK) genes. <i>Developmental and Comparative Immunology</i> , 2018, 84, 193-198.	1.0	2

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3972	A Novel <i>Glaesserella</i> sp. Isolated from Pigs with Severe Respiratory Infections Has a Mosaic Genome with Virulence Factors Putatively Acquired by Horizontal Transfer. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	17
3973	Homologous Recombination in Core Genomes Facilitates Marine Bacterial Adaptation. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	12
3974	Phylogenetic evidence for an ancestral coevolution between a major clade of coccidian parasites and elasmobranch hosts. <i>Systematic Parasitology</i> , 2018, 95, 367-371.	0.5	10
3975	Multilocus phylogeny and coalescent species delimitation in Kotschy's gecko, <i>Mediodactylus kotschyi</i> : Hidden diversity and cryptic species. <i>Molecular Phylogenetics and Evolution</i> , 2018, 125, 177-187.	1.2	42
3976	<i>Xanthomonas citri</i> jumbo phage XacN1 exhibits a wide host range and high complement of tRNA genes. <i>Scientific Reports</i> , 2018, 8, 4486.	1.6	47
3977	Adaptive evolution during the establishment of European avian H1N1 influenza A virus in swine. <i>Evolutionary Applications</i> , 2018, 11, 534-546.	1.5	12
3978	Heads up: evolution of exaggerated head length in the minute litter bug genus <i>Nannocoris</i> Reuter (Hemiptera: Schizopteridae). <i>Organisms Diversity and Evolution</i> , 2018, 18, 211-224.	0.7	3
3979	Early insularity and subsequent mountain uplift were complementary drivers of diversification in a Melanesian lizard radiation (Gekkonidae: <i>Cyrtodactylus</i>). <i>Molecular Phylogenetics and Evolution</i> , 2018, 125, 29-39.	1.2	33
3980	Phylogenomic evidence for a recent and rapid radiation of lizards in the Patagonian <i>Liolaemus fitzingerii</i> species group. <i>Molecular Phylogenetics and Evolution</i> , 2018, 125, 243-254.	1.2	25
3981	Dismantling a complex of anther smuts (<i>Microbotryum</i>) on carnivorous plants in the genus <i>Pinguicula</i> . <i>Mycologia</i> , 2018, 110, 361-374.	0.8	13
3982	Phylogeny of the subfamily Stelliferinae suggests speciation in <i>Ophioscion</i> Gill, 1863 (Sciaenidae: <i>Ophioscion</i> Gill, 1863). <i>Journal of Systematics and Evolutionary Biology</i> , 2018, 46, 1-10.	1.2	5
3983	<i>Taitaia</i> , a novel lichenicolous fungus in tropical montane forests in Kenya (East Africa). <i>Lichenologist</i> , 2018, 50, 173-184.	0.5	13
3984	Large Diversity of Nonstandard Genes and Dynamic Evolution of Chloroplast Genomes in Siphonous Green Algae (Bryopsidales, Chlorophyta). <i>Genome Biology and Evolution</i> , 2018, 10, 1048-1061.	1.1	27
3985	Innovative assembly strategy contributes to understanding the evolution and conservation genetics of the endangered <i>Solenodon paradoxus</i> from the island of Hispaniola. <i>GigaScience</i> , 2018, 7, .	3.3	12
3986	Two monorchiid species from the freckled goatfish, <i>Upeneus tragula</i> Richardson (Perciformes: <i>Upeneus</i> Richardson, 1845). <i>Journal of Parasitology</i> , 2018, 95, 353-365.	0.5	12
3987	Novel Collophorina and Coniochaeta species from <i>Euphorbia polycaulis</i> , an endemic plant in Iran. <i>Mycological Progress</i> , 2018, 17, 755-771.	0.5	16
3988	Horizontal gene transfer among rhizobia of the Core Cape Subregion of southern Africa. <i>South African Journal of Botany</i> , 2018, 118, 342-352.	1.2	8
3989	Inferring phylogenetic structure, hybridization and divergence times within Salmoninae (Teleostei: <i>Salmoninae</i>). <i>Molecular Phylogenetics and Evolution</i> , 2018, 125, 1-14.	1.2	70

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3990	Two new species of <i>Arthoniaceae</i> from old-growth European forests, <i>Arthonia thoriana</i> and <i>Inoderma solediatum</i> , and a new genus for <i>Schismatomma niveum</i> . <i>Lichenologist</i> , 2018, 50, 161-172.	0.5	19
3991	Discovery of enzymes for toluene synthesis from anoxic microbial communities. <i>Nature Chemical Biology</i> , 2018, 14, 451-457.	3.9	47
3992	<i>Haemophilus influenzae</i> genome evolution during persistence in the human airways in chronic obstructive pulmonary disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E3256-E3265.	3.3	57
3993	Lifting the blue-headed veil – integrative taxonomy of the <i>Acanthocercus atricollis</i> species complex (Squamata: Agamidae). <i>Journal of Natural History</i> , 2018, 52, 771-817.	0.2	5
3994	Genomic Changes Associated with the Evolutionary Transitions of Nostoc to a Plant Symbiont. <i>Molecular Biology and Evolution</i> , 2018, 35, 1160-1175.	3.5	54
3995	Revised classification of the righteye flounders (Teleostei: Pleuronectidae) based on multilocus phylogeny with complete taxon sampling. <i>Molecular Phylogenetics and Evolution</i> , 2018, 125, 147-162.	1.2	26
3996	Landscape-Scale Factors Affecting the Prevalence of <i>Escherichia coli</i> in Surface Soil Include Land Cover Type, Edge Interactions, and Soil pH. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	25
3997	High-throughput sequencing data clarify evolutionary relationships among North American <i>Vitis</i> species and improve identification in USDA <i>Vitis</i> germplasm collections. <i>American Journal of Botany</i> , 2018, 105, 215-226.	0.8	45
3998	The modules of <i>trans</i> -acyltransferase assembly lines redefined with a central acyl carrier protein. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 664-675.	1.5	49
3999	Evolution of the mating types and mating strategies in prominent genera in the Botryosphaeriaceae. <i>Fungal Genetics and Biology</i> , 2018, 114, 24-33.	0.9	17
4000	De novo synthesis of the sedative valerenic acid in <i>Saccharomyces cerevisiae</i> . <i>Metabolic Engineering</i> , 2018, 47, 94-101.	3.6	21
4001	A phylogenomic perspective on the robust capuchin monkey (<i>Sapajus</i>) radiation: First evidence for extensive population admixture across South America. <i>Molecular Phylogenetics and Evolution</i> , 2018, 124, 137-150.	1.2	35
4002	Explosive diversification of marine fishes at the Cretaceous–Palaeogene boundary. <i>Nature Ecology and Evolution</i> , 2018, 2, 688-696.	3.4	156
4003	Inhibition of strigolactone receptors by N-phenylanthranilic acid derivatives: Structural and functional insights. <i>Journal of Biological Chemistry</i> , 2018, 293, 6530-6543.	1.6	37
4004	A phylogeny and genus-level revision of the African file snakes <i>Gonionotophis</i> Boulenger (Squamata: Lamprophiidae). <i>African Journal of Herpetology</i> , 2018, 67, 43-60.	0.3	9
4005	Extended and Continuous Decline in Effective Population Size Results in Low Genomic Diversity in the World's Rarest Hyena Species, the Brown Hyena. <i>Molecular Biology and Evolution</i> , 2018, 35, 1225-1237.	3.5	72
4006	At the end of the line: independent overwater colonizations of the Solomon Islands by a hyperdiverse trans-Wallacean lizard lineage (<i>Cyrtodactylus</i> : <i>Gekkota</i> : Squamata). <i>Zoological Journal of the Linnean Society</i> , 2018, 182, 681-694.	1.0	21
4007	Populations of <i>Phytophthora rubi</i> Show Little Differentiation and High Rates of Migration Among States in the Western United States. <i>Molecular Plant-Microbe Interactions</i> , 2018, 31, 614-622.	1.4	23

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4008	Targeted resequencing reveals genomic signatures of barley domestication. <i>New Phytologist</i> , 2018, 218, 1247-1259.	3.5	77
4009	<i>Acricoactis brachyacontis</i> sp. nov. from Adak Island, Alaska, represents a new genus and family of metridioidean sea anemone (Anthozoa: Hexacorallia: Actiniaria). <i>Marine Biodiversity</i> , 2018, 48, 1583-1590.	0.3	3
4010	Whole genome sequencing reveals an outbreak of <i>Salmonella</i> Enteritidis associated with reptile feeder mice in the United Kingdom, 2012-2015. <i>Food Microbiology</i> , 2018, 71, 32-38.	2.1	51
4011	Identifying selectively important amino acid positions associated with alternative habitat environments in fish mitochondrial genomes. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2018, 29, 511-524.	0.7	4
4012	The complete chloroplast genome of the long blooming and critically endangered <i>Camellia azalea</i> . <i>Conservation Genetics Resources</i> , 2018, 10, 5-7.	0.4	5
4013	Morphological and molecular characterizations of <i>Africanema multipapillatum</i> sp. nov. (Nematoda). <i>Tj ETQq1 1 0.784314 rgBT /Overl</i>	0.3	4
4014	The complete chloroplast genome of endangered <i>Manglietia insignis</i> , a rare landscaping tree with red lotus-like flowers. <i>Conservation Genetics Resources</i> , 2018, 10, 27-30.	0.4	6
4015	The complete description of larval stages of the lobster shrimp <i>Leonardsaxius amurensis</i> (Kobjakova). <i>Tj ETQq1 1 0.784314 rgBT /Overl</i> Association of the United Kingdom, 2018, 98, 1435-1453.	0.4	3
4016	Resolving Rapid Radiations within Angiosperm Families Using Anchored Phylogenomics. <i>Systematic Biology</i> , 2018, 67, 94-112.	2.7	102
4017	Species trees, temporal divergence and historical biogeography of coastal rove beetles (Coleoptera): the early Pliocene along the Pacific coasts. <i>Cladistics</i> , 2018, 34, 313-332.	1.5	18
4018	Taxonomy and phylogeny of <i>Lineus torquatus</i> and allies (Nemertea, Lineidae) with descriptions of a new genus and a new cryptic species. <i>Systematics and Biodiversity</i> , 2018, 16, 55-68.	0.5	20
4019	Lineage Diversity and Size Disparity in Musteloidea: Testing Patterns of Adaptive Radiation Using Molecular and Fossil-Based Methods. <i>Systematic Biology</i> , 2018, 67, 127-144.	2.7	75
4020	Myrothecium-like (Ascomycota, Hypocreales) species from tropical areas: <i>Digitiseta</i> gen. nov. and additions to <i>Inaequalispora</i> and <i>Parvothecium</i> . <i>Mycological Progress</i> , 2018, 17, 179-190.	0.5	1
4021	Communities of arbuscular mycorrhizal fungi under <i>Picconia azorica</i> in native forests of Azores. <i>Symbiosis</i> , 2018, 74, 43-54.	1.2	10
4022	Host specificity versus plasticity: testing the morphology-based taxonomy of the endoparasitic copepod family Splanchnotrophidae with COI barcoding. <i>Journal of the Marine Biological Association of the United Kingdom</i> , 2018, 98, 231-243.	0.4	2
4023	Optimal data partitioning, multispecies coalescent and Bayesian concordance analyses resolve early divergences of the grape family (Vitaceae). <i>Cladistics</i> , 2018, 34, 57-77.	1.5	44
4024	Host community similarity and geography shape the diversity and distribution of haemosporidian parasites in Amazonian birds. <i>Ecography</i> , 2018, 41, 505-515.	2.1	57
4025	Efficient Quartet Representations of Trees and Applications to Supertree and Summary Methods. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 1010-1015.	1.9	5

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4026	Hepatitis E in southern Vietnam: Seroepidemiology in humans and molecular epidemiology in pigs. <i>Zoonoses and Public Health</i> , 2018, 65, 43-50.	0.9	20
4027	Resurrection and emendation of the Hypoxylaceae, recognised from a multigene phylogeny of the Xylariales. <i>Mycological Progress</i> , 2018, 17, 115-154.	0.5	144
4028	Generic names in the Orbiliaceae (Orbiliomycetes) and recommendations on which names should be protected or suppressed. <i>Mycological Progress</i> , 2018, 17, 5-31.	0.5	34
4029	Phylogeny and historical biogeography of silky lacewings (<sc>N</sc>europtera:) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 62	1.7	5
4030	Fish Parasite Dinoflagellates <i>Haidadinium ichthyophilum</i> and <i>Piscinoodinium</i> Share a Recent Common Ancestor. <i>Journal of Eukaryotic Microbiology</i> , 2018, 65, 127-131.	0.8	1
4031	Complete mitochondrial genome and phylogenetic analysis of <i>Anabarilius grahami</i> (Teleostei,) Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.4	1
4032	The origin of king crabs: hermit crab ancestry under the magnifying glass. <i>Zoological Journal of the Linnean Society</i> , 2018, 182, 300-318.	1.0	17
4033	Molecular adaptation to high pressure in cytochrome P450 1A and aryl hydrocarbon receptor systems of the deep-sea fish <i>Coryphaenoides armatus</i> . <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2018, 1866, 155-165.	1.1	9
4034	Resolving Recent Plant Radiations: Power and Robustness of Genotyping-by-Sequencing. <i>Systematic Biology</i> , 2018, 67, 250-268.	2.7	78
4035	The complete chloroplast genome sequence of <i>Sophora japonica</i> var. <i>violacea</i> : gene organization and genomic resources. <i>Conservation Genetics Resources</i> , 2018, 10, 1-4.	0.4	5
4036	Identification of <i>Xanthomonas</i> species associated with bacterial leaf spot of tomato, capsicum and chilli crops in eastern Australia. <i>European Journal of Plant Pathology</i> , 2018, 150, 595-608.	0.8	37
4037	Genetic population structure of the round whitefish (<i>Prosopium cylindraceum</i>) in North America: multiple markers reveal glacial refugia and regional subdivision. <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 2018, 75, 836-849.	0.7	12
4038	Review of <i>Schismatogobius</i> (Gobiidae) from Japan, with the description of a new species. <i>Ichthyological Research</i> , 2018, 65, 56-77.	0.5	1
4039	Genetic diversity and phylogenetic relationships of seven <i>Amorphophallus</i> species in southwestern China revealed by chloroplast DNA sequences. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2018, 29, 679-686.	0.7	12
4040	Deep-sea amphipod genus <i>Eurythenes</i> from Japan, with a description of a new <i>Eurythenes</i> species from off Hokkaido (Crustacea: Amphipoda: Lysianassoidea). <i>Marine Biodiversity</i> , 2018, 48, 603-620.	0.3	10
4041	New Species of <i>Spirotrichonympha</i> from <i>Reticulitermes</i> and the Relationships Among Genera in Spirotrichonymphea (Parabasalia). <i>Journal of Eukaryotic Microbiology</i> , 2018, 65, 159-169.	0.8	12
4042	Pythiopina, an enigmatic subtribe of darkling beetles (<sc>C</sc>oleoptera:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 107 Td (<sc>T</sc>/s niche models and phylogenetic position. <i>Systematic Entomology</i> , 2018, 43, 147-165.	1.7	16
4043	Spatiotemporal evolutionary epidemiology of H5N1 highly pathogenic avian influenza in West Africa and Nigeria, 2006-2015. <i>Transboundary and Emerging Diseases</i> , 2018, 65, e70-e82.	1.3	15

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4044	Ethanol metabolism varies with hypoxia tolerance in ten cyprinid species. <i>Journal of Comparative Physiology B: Biochemical, Systemic, and Environmental Physiology</i> , 2018, 188, 283-293.	0.7	15
4045	The complete chloroplast genome sequence of <i>Actinidia arguta</i> : gene structure and genomic resources. <i>Conservation Genetics Resources</i> , 2018, 10, 423-425.	0.4	1
4046	Signal, Uncertainty, and Conflict in Phylogenomic Data for a Diverse Lineage of Microbial Eukaryotes (Diatoms, Bacillariophyta). <i>Molecular Biology and Evolution</i> , 2018, 35, 80-93.	3.5	43
4047	Analysis of Phylogenomic Tree Space Resolves Relationships Among Marsupial Families. <i>Systematic Biology</i> , 2018, 67, 400-412.	2.7	85
4048	Diversification in tropics and subtropics following the mid-Miocene climate change: A case study of the spider genus <i>Nesticella</i> . <i>Global Change Biology</i> , 2018, 24, e577-e591.	4.2	28
4049	Phylogeography of the sandy beach amphipod <i>Haustorioides japonicus</i> along the Sea of Japan: Paleogeographical signatures of cryptic regional divergences. <i>Estuarine, Coastal and Shelf Science</i> , 2018, 200, 19-30.	0.9	17
4050	Comprehensive phylogeny of acariform mites (Acariformes) provides insights on the origin of the four-legged mites (Eriophyoidea), a long branch. <i>Molecular Phylogenetics and Evolution</i> , 2018, 119, 105-117.	1.2	80
4051	Molecular and morphological data reveal non-monophyly and speciation in imperiled freshwater mussels (<i>Anodontoides</i> and <i>Strophitus</i>). <i>Molecular Phylogenetics and Evolution</i> , 2018, 119, 50-62.	1.2	37
4052	An Analysis of the Epidemic of <i>Klebsiella pneumoniae</i> Carbapenemase-Producing <i>K. pneumoniae</i> : Convergence of Two Evolutionary Mechanisms Creates the "Perfect Storm". <i>Journal of Infectious Diseases</i> , 2018, 217, 82-92.	1.9	70
4053	Targeted Enrichment of Large Gene Families for Phylogenetic Inference: Phylogeny and Molecular Evolution of Photosynthesis Genes in the <i>Portullugo</i> Clade (Caryophyllales). <i>Systematic Biology</i> , 2018, 67, 367-383.	2.7	46
4054	Dissemination and Characteristics of a Novel Plasmid-Encoded Carbapenem-Hydrolyzing Class D β -Lactamase, OXA-436, Found in Isolates from Four Patients at Six Different Hospitals in Denmark. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	1.4	24
4055	The hatching process and mechanisms of adaptive hatching acceleration in hourglass treefrogs, <i>Dendropsophus ebraccatus</i> . <i>Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology</i> , 2018, 217, 63-74.	0.8	5
4056	Influence of the geography of speciation on current patterns of coral reef fish biodiversity across the Indo-Pacific. <i>Ecography</i> , 2018, 41, 1295-1306.	2.1	20
4057	Phylogenetic Diversity and Taxonomic Problems of the <i>Dictyosphaerium</i> Morphotype within the <i>Parachlorella</i> Clade (Chlorellaceae, Trebouxiophyceae). <i>Journal of Eukaryotic Microbiology</i> , 2018, 65, 382-391.	0.8	10
4058	Successive evolutionary steps drove Pooideae grasses from tropical to temperate regions. <i>New Phytologist</i> , 2018, 217, 925-938.	3.5	27
4059	Trends in Antibiotic Susceptibility in <i>Staphylococcus aureus</i> in Boston, Massachusetts, from 2000 to 2014. <i>Journal of Clinical Microbiology</i> , 2018, 56, .	1.8	37
4060	Antibiotic pretreatment minimizes dietary effects on reconstruction of rumen fluid and mucosal microbiota in goats. <i>MicrobiologyOpen</i> , 2018, 7, e00537.	1.2	6
4061	Resolving a phylogenetic hypothesis for parrots: implications from systematics to conservation. <i>Emu</i> , 2018, 118, 7-21.	0.2	45

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4062	Facultative root-colonizing fungi dominate endophytic assemblages in roots of nonmycorrhizal <i>Microthlaspi</i> species. <i>New Phytologist</i> , 2018, 217, 1190-1202.	3.5	70
4063	Targeted sequencing of clade-specific markers from skin microbiomes for forensic human identification. <i>Forensic Science International: Genetics</i> , 2018, 32, 50-61.	1.6	69
4064	A phylogenetic and morphological overview of sections <i>Bohusia</i> , <i>Sanguinolenti</i> , and allied sections within <i>Agaricus</i> subg. <i>Pseudochitonina</i> with three new species from France, Iran, and Portugal. <i>Fungal Biology</i> , 2018, 122, 34-51.	1.1	8
4065	Complete mitochondrial genome of the yellowfin tuna (<i>Thunnus albacares</i>) and the blackfin tuna (<i>Thunnus atlanticus</i>): notes on mtDNA introgression and paraphyly on tunas. <i>Conservation Genetics Resources</i> , 2018, 10, 697-699.	0.4	3
4066	Molecular phylogenetics of dinophytes harboring diatoms as endosymbionts (<i>Kryptoperidiniaceae</i>). <i>Trends in Microbiology</i> , 2018, 26, 107-115.	1.2	26
4067	Out of Southern East Asia of the Brown Rat Revealed by Large-Scale Genome Sequencing. <i>Molecular Biology and Evolution</i> , 2018, 35, 149-158.	3.5	36
4068	Cryptic lineage diversity, body size divergence, and sympatry in a species complex of Australian lizards (<i>Gehyra</i>). <i>Evolution; International Journal of Organic Evolution</i> , 2018, 72, 54-66.	1.1	39
4069	Emergence and Adaptation of a Novel Highly Pathogenic H7N9 Influenza Virus in Birds and Humans from a 2013 Human-Infecting Low-Pathogenic Ancestor. <i>Journal of Virology</i> , 2018, 92, .	1.5	99
4070	Novel subfamilies of actin-regulating proteins. <i>Marine Genomics</i> , 2018, 37, 128-134.	0.4	5
4071	Evaluating methods for phylogenomic analyses, and a new phylogeny for a major frog clade (<i>Hyla</i>) based on 2214 loci. <i>Molecular Phylogenetics and Evolution</i> , 2018, 119, 128-143.	1.2	63
4072	A Gene Family Coding for Salivary Proteins (<i>SHOT</i>) of the Polyphagous Spider Mite <i>Tetranychus urticae</i> Exhibits Fast Host-Dependent Transcriptional Plasticity. <i>Molecular Plant-Microbe Interactions</i> , 2018, 31, 112-124.	1.4	29
4073	Organization of plastid genomes in the freshwater red algal order <i>Batrachospermales</i> (Rhodophyta). <i>Journal of Phycology</i> , 2018, 54, 25-33.	1.0	8
4074	Phylogenomics and evolution of floral traits in the Neotropical tribe <i>Malmeeae</i> (<i>Annonaceae</i>). <i>Molecular Phylogenetics and Evolution</i> , 2018, 118, 379-391.	1.2	17
4075	Molecular phylogeny of <i>Candidula</i> (<i>Geomitridae</i>) land snails inferred from mitochondrial and nuclear markers reveals the polyphyly of the genus. <i>Molecular Phylogenetics and Evolution</i> , 2018, 118, 357-368.	1.2	13
4076	To Include or Not to Include: The Impact of Gene Filtering on Species Tree Estimation Methods. <i>Systematic Biology</i> , 2018, 67, 285-303.	2.7	189
4077	Abundance and Multilocus Sequence Analysis of <i>Vibrio</i> Bacteria Associated with Diseased Elkhorn Coral (<i>Acropora palmata</i>) of the Florida Keys. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	23
4078	New barcoded primers for efficient retrieval of cercozoan sequences in high-throughput environmental diversity surveys, with emphasis on worldwide biological soil crusts. <i>Molecular Ecology Resources</i> , 2018, 18, 229-239.	2.2	71
4079	Molecular, morphological and acoustic identification of <i>Eumops maurus</i> and <i>Eumops hansae</i> (<i>Chiroptera: Molossidae</i>) with new reports from Central Amazonia. <i>Tropical Zoology</i> , 2018, 31, 1-20.	0.6	7

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4080	panX: pan-genome analysis and exploration. <i>Nucleic Acids Research</i> , 2018, 46, e5-e5.	6.5	241
4081	Probabilistic methods surpass parsimony when assessing clade support in phylogenetic analyses of discrete morphological data. <i>Palaeontology</i> , 2018, 61, 105-118.	1.0	61
4082	Phylogeny, biogeography and character evolution in the tribe Desmodieae (Fabaceae: Papilionoideae), with special emphasis on the New Caledonian endemic genera. <i>Molecular Phylogenetics and Evolution</i> , 2018, 118, 108-121.	1.2	19
4083	Reticulate Pleistocene evolution of Ethiopian rodent genus along remarkable altitudinal gradient. <i>Molecular Phylogenetics and Evolution</i> , 2018, 118, 75-87.	1.2	48
4084	Phylogenomic support for evolutionary relationships of New World direct-developing frogs (Anura: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 467 Td (Ros	1.2	74
4085	Independent pseudogenization of CYP2J19 in penguins, owls and kiwis implicates gene in red carotenoid synthesis. <i>Molecular Phylogenetics and Evolution</i> , 2018, 118, 47-53.	1.2	22
4086	Complete mitochondrial genome sequence of the tiny dragonfly, <i>Nannophya pygmaea</i> (Odonata: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 467 Td (Ros	0.4	8
4087	Towards resolving the evolutionary history of Caucasian pears (<i>Pyrus</i>), <i>Systematics and Evolution</i> , 2018, 56, 35-47.	1.6	21
4088	Focusing the diversity of <i>Gardnerella vaginalis</i> through the lens of ecotypes. <i>Evolutionary Applications</i> , 2018, 11, 312-324.	1.5	34
4089	Exon-based phylogenomics strengthens the phylogeny of Neotropical cichlids and identifies remaining conflicting clades (Cichliformes: Cichlidae: Cichlinae). <i>Molecular Phylogenetics and Evolution</i> , 2018, 118, 232-243.	1.2	44
4090	Phylogeography of a widespread sub-Saharan murid rodent <i>Aethomys chrysophilus</i> : the role of geographic barriers and paleoclimate in the Zambezi bioregion. <i>Mammalia</i> , 2018, 82, 373-387.	0.3	20
4091	On the origins and industrial applications of <i>Saccharomyces cerevisiae</i> – <i>Saccharomyces kudriavzevii</i> hybrids. <i>Yeast</i> , 2018, 35, 51-69.	0.8	75
4092	Reconsideration of the systematics of Peniculida (Protista, Ciliophora) based on SSU rRNA gene sequences and new morphological features of <i>Marituja</i> and <i>Disematostoma</i> . <i>Hydrobiologia</i> , 2018, 806, 313-331.	1.0	15
4093	The complete maternal mitochondrial genome sequence of <i>Cuneopsis heudei</i> (Bivalvia: Unionoida: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 467 Td (Ros	0.4	2
4094	A Trichosporonales genome tree based on 27 haploid and three evolutionarily conserved "natural" hybrid genomes. <i>Yeast</i> , 2018, 35, 99-111.	0.8	21
4095	The complete chloroplast genome of threatened <i>Magnolia laevifolia</i> , a rare ornamental shrub with strong aromatic flowers. <i>Conservation Genetics Resources</i> , 2018, 10, 339-342.	0.4	4
4096	Geobiological feedbacks and the evolution of thermoacidophiles. <i>ISME Journal</i> , 2018, 12, 225-236.	4.4	70
4097	Genetics and evolution of MIXTA genes regulating cotton lint fiber development. <i>New Phytologist</i> , 2018, 217, 883-895.	3.5	112

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4098	Nemerteans from deep-sea expedition SokhoBio with description of <i>Uniporus alisae</i> sp. nov. (Hoploneurata: Reptantia s.l.) from the Sea of Okhotsk. <i>Deep-Sea Research Part II: Topical Studies in Oceanography</i> , 2018, 154, 121-139.	0.6	19
4099	Tropical soils are a reservoir for fluorescent <i>Pseudomonas</i> spp. biodiversity. <i>Environmental Microbiology</i> , 2018, 20, 62-74.	1.8	28
4100	Cryptic speciation in the <i>Merodon luteomaculatus</i> complex (Diptera: Syrphidae) from the eastern Mediterranean. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2018, 56, 170-191.	0.6	25
4101	Unravelling the systematics of <i>Nodularia</i> (Bivalvia, Unionidae) species from eastern Russia. <i>Systematics and Biodiversity</i> , 2018, 16, 287-301.	0.5	21
4102	Pleistocene climatic fluctuations drive isolation and secondary contact in the red diamond rattlesnake (<i>Crotalus ruber</i>) in Baja California. <i>Journal of Biogeography</i> , 2018, 45, 64-75.	1.4	21
4103	A New Subspecies of <i>Oxytricha granulifera</i> (Hypotrichia: Oxytrichidae) from Mexico, with Notes on its Morphogenesis and Phylogenetic Position. <i>Journal of Eukaryotic Microbiology</i> , 2018, 65, 357-371.	0.8	16
4104	The molecular phylogeny of Omaliidae (Coleoptera) defines the family limits and demonstrates low dispersal propensity and ancient vicariance patterns. <i>Systematic Entomology</i> , 2018, 43, 250-261.	1.7	18
4105	Diversity and evolution of leaf anatomical characters in <i>Taxaceae</i> s.l. – fluorescence microscopy reveals new delimitating characters. <i>Journal of Plant Research</i> , 2018, 131, 125-141.	1.2	14
4106	Phenotypic evolution in marmoset and tamarin monkeys (Cebidae, Callitrichinae) and a revised genus-level classification. <i>Molecular Phylogenetics and Evolution</i> , 2018, 118, 156-171.	1.2	26
4107	Assessing the utility of transcriptome data for inferring phylogenetic relationships among coleoid cephalopods. <i>Molecular Phylogenetics and Evolution</i> , 2018, 118, 330-342.	1.2	29
4108	The completed chloroplast genome of <i>Ostrya trichocarpa</i> . <i>Conservation Genetics Resources</i> , 2018, 10, 579-581.	0.4	8
4109	Improved transcriptome sampling pinpoints 26 ancient and more recent polyploidy events in Caryophyllales, including two allopolyploidy events. <i>New Phytologist</i> , 2018, 217, 855-870.	3.5	85
4110	The complete chloroplast genome of the threatened <i>Prunus cerasoides</i> , a rare winter blooming cherry in the Himalayan region. <i>Conservation Genetics Resources</i> , 2018, 10, 499-502.	0.4	9
4111	The complete chloroplast genome of the threatened <i>Pistacia weinmannifolia</i> , an economically and horticulturally important evergreen plant. <i>Conservation Genetics Resources</i> , 2018, 10, 535-538.	0.4	3
4112	<i>Kondoa gutianensis</i> f.a. sp. nov., a novel ballistoconidium-forming yeast species isolated from plant leaves. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 155-160.	0.7	5
4113	Characterization of the complete chloroplast genome sequence of <i>Tigridiopalma magnifica</i> (Melastomataceae). <i>Conservation Genetics Resources</i> , 2018, 10, 571-573.	0.4	16
4114	A short-range endemic species from south-eastern Atlantic Rain Forest shows deep signature of historical events: phylogeography of harvestmen <i>Acutisoma longipes</i> (Arachnida: Opiliones). <i>Systematics and Biodiversity</i> , 2018, 16, 171-187.	0.5	35
4115	Characterization of the complete chloroplast genome sequence of <i>Littledalea racemosa</i> Keng (Poaceae: Bromeae). <i>Conservation Genetics Resources</i> , 2018, 10, 343-346.	0.4	5

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4116	Molecular Phylogenetic Positions of Two New Marine Gregarines (Apicomplexa) <i>Paralecudina ananke</i> n. sp. and <i>Lecudina caspera</i> n. sp. from the Intestine of <i>Lumbrineris inflata</i> (Polychaeta) Show Patterns of Coevolution. <i>Journal of Eukaryotic Microbiology</i> , 2018, 65, 211-219.	0.8	4
4117	Phylogenetic Relationships, Breeding Implications, and Cultivation History of Hawaiian Taro (<i>Colocasia Esculenta</i>) Through Genome-Wide SNP Genotyping. <i>Journal of Heredity</i> , 2018, 109, 272-282.	1.0	19
4118	Revisiting the taxonomy of the genus <i>Elizabethkingia</i> using whole-genome sequencing, optical mapping, and MALDI-TOF, along with proposal of three novel <i>Elizabethkingia</i> species: <i>Elizabethkingia bruuniana</i> sp. nov., <i>Elizabethkingia ursingii</i> sp. nov., and <i>Elizabethkingia occulta</i> sp. nov.. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 55-72.	0.7	91
4119	Mitochondrial genomes of the Pacific sierra mackerel <i>Scomberomorus sierra</i> and the Monterey Spanish mackerel <i>Scomberomorus concolor</i> (Perciformes, Scombridae). <i>Conservation Genetics Resources</i> , 2018, 10, 471-474.	0.4	1
4120	Cryptic genetic divergence in <i>Scolopsis taenioptera</i> (Perciformes: Nemipteridae) in the western Pacific Ocean. <i>Ichthyological Research</i> , 2018, 65, 92-100.	0.5	8
4121	Taxonomy and molecular systematic position of freshwater genus <i>Racekiela</i> (Porifera: Tj ETQq1 1 0.784314 rgBT /Overlock 10 T). <i>Biodiversity</i> , 2018, 16, 160-170.	0.5	9
4122	Divergence time, historical biogeography and evolutionary rate estimation of the order Bangiales (Rhodophyta) inferred from multilocus data. <i>Journal of Oceanology and Limnology</i> , 2018, 36, 870-881.	0.6	13
4123	The first complete organellar genomes of an Antarctic red alga, <i>Pyropia endiviifolia</i> : insights into its genome architecture and phylogenetic position within genus <i>Pyropia</i> (Bangiales, Rhodophyta). <i>Journal of Oceanology and Limnology</i> , 2018, 36, 1315-1328.	0.6	12
4124	Anchored hybrid enrichment provides new insights into the phylogeny and evolution of longhorned beetles (Coleoptera: Cerambycidae). <i>Systematic Entomology</i> , 2018, 43, 68-89.	1.7	73
4125	Photosynthetic Picoeukaryotes in the Land-Fast Ice of the White Sea, Russia. <i>Microbial Ecology</i> , 2018, 75, 582-597.	1.4	22
4126	The role of climatic cycles and trans-Saharan migration corridors in species diversification: Biogeography of <i>Psammophis schokari</i> group in North Africa. <i>Molecular Phylogenetics and Evolution</i> , 2018, 118, 64-74.	1.2	34
4127	A multilocus phylogeny of the genus <i>Sarcohylla</i> (Anura: Hylidae), and an investigation of species boundaries using statistical species delimitation. <i>Molecular Phylogenetics and Evolution</i> , 2018, 118, 184-193.	1.2	14
4128	<i>Tremblaya phenacola</i> PPER: an evolutionary beta-gammaproteobacterium collage. <i>ISME Journal</i> , 2018, 12, 124-135.	4.4	14
4129	Characterization of the complete mitochondrial genome of <i>Gymnocypris scleracanthus</i> (Teleostei: Tj ETQq1 1 0.784314 rgBT /Overlock 10 T). <i>Biodiversity</i> , 2018, 16, 160-170.	0.4	9
4130	Sympatric parallel diversification of major oak clades in the Americas and the origins of Mexican species diversity. <i>New Phytologist</i> , 2018, 217, 439-452.	3.5	216
4131	Metaproteomics of marine viral concentrates reveals key viral populations and abundant periplasmic proteins in the oligotrophic deep chlorophyll maximum of the South China Sea. <i>Environmental Microbiology</i> , 2018, 20, 477-491.	1.8	3
4132	Exploring deep-water coral communities using environmental DNA. <i>Deep-Sea Research Part II: Topical Studies in Oceanography</i> , 2018, 150, 229-241.	0.6	39
4133	Characterization of the complete chloroplast genome of the seagrass <i>Zostera marina</i> using Illumina sequencing technology. <i>Conservation Genetics Resources</i> , 2018, 10, 419-422.	0.4	4

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4134	A Contribution to the Morphology and Phylogeny of <i>Chlamydodon</i> , with Three New Species from China (Ciliophora, Cytrophoria). <i>Journal of Eukaryotic Microbiology</i> , 2018, 65, 236-249.	0.8	4
4135	Next generation sequencing for the investigation of an outbreak of <i>Salmonella</i> Schwarzengrund in Nanjing, China. <i>International Journal of Biological Macromolecules</i> , 2018, 107, 393-396.	3.6	7
4136	Genetic analysis of H7N9 highly pathogenic avian influenza virus in Guangdong, China, 2016–2017. <i>Journal of Infection</i> , 2018, 76, 93-96.	1.7	12
4137	Disparity, diversity, and duplications in the Caryophyllales. <i>New Phytologist</i> , 2018, 217, 836-854.	3.5	51
4138	Revisiting the phylogeny of Zoanthidea (Cnidaria: Anthozoa): Staggered alignment of hypervariable sequences improves species tree inference. <i>Molecular Phylogenetics and Evolution</i> , 2018, 118, 1-12.	1.2	18
4139	Mitochondrial recovery from shotgun metagenome sequencing enabling phylogenetic analysis of the common thresher shark (<i>Alopias vulpinus</i>). <i>Meta Gene</i> , 2018, 15, 10-15.	0.3	11
4140	Paleobiogeography of an Iberian endemic species, <i>Luciobarbus sclateri</i> (Günther, 1868) (Actinopterygii, Cyprinidae), inferred from mitochondrial and nuclear markers. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2018, 56, 127-147.	0.6	10
4141	Multi-approach analysis of the diversity in <i>Colletotrichum cliviae</i> sensu lato. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 423-435.	0.7	10
4142	Discovering the silk road: Nuclear and mitochondrial sequence data resolve the phylogenetic relationships among theraphosid spider subfamilies. <i>Molecular Phylogenetics and Evolution</i> , 2018, 119, 63-70.	1.2	35
4143	The complete chloroplast genome sequence of <i>Dodonaea viscosa</i> : comparative and phylogenetic analyses. <i>Genetica</i> , 2018, 146, 101-113.	0.5	54
4144	Discovery of an old, archipelago-wide, endemic radiation of Philippine snakes. <i>Molecular Phylogenetics and Evolution</i> , 2018, 119, 144-150.	1.2	14
4145	Evolution of lacewings and allied orders using anchored phylogenomics (Neuroptera). <i>Trends in Ecology and Evolution</i> , 2018, 33, 17-23.	1.7	133
4146	Authentication of Iceland Moss (<i>Cetraria islandica</i>) by UPLC-QToF-MS chemical profiling and DNA barcoding. <i>Food Chemistry</i> , 2018, 245, 989-996.	4.2	29
4147	How many pygmy marmoset (<i>Cebuella</i> Gray, 1870) species are there? A taxonomic re-appraisal based on new molecular evidence. <i>Molecular Phylogenetics and Evolution</i> , 2018, 120, 170-182.	1.2	23
4148	Prospects on the evolutionary mitogenomics of plants: A case study on the olive family (Oleaceae). <i>Molecular Ecology Resources</i> , 2018, 18, 407-423.	2.2	49
4149	Pleistocene climatic changes drive diversification across a tropical savanna. <i>Molecular Ecology</i> , 2018, 27, 520-532.	2.0	31
4150	Cryptic and non-cryptic diversity in New Guinea ground snakes of the genus <i>Stegonotus</i> Duméril, Bibron and Duméril, 1854: a description of four new species (Squamata: Colubridae). <i>Journal of Natural History</i> , 2018, 52, 917-944.	0.2	4
4151	<i>Dothiorella omnivora</i> isolated from grapevine with trunk disease symptoms in Hungary. <i>European Journal of Plant Pathology</i> , 2018, 150, 817-824.	0.8	14

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4152	A phylogeny of kingfishers reveals an Indomalayan origin and elevated rates of diversification on oceanic islands. <i>Journal of Biogeography</i> , 2018, 45, 269-281.	1.4	49
4153	Complete genome sequence of <i>Granulosicoccus antarcticus</i> type strain IMCC3135T, a marine gammaproteobacterium with a putative dimethylsulfoniopropionate demethylase gene. <i>Marine Genomics</i> , 2018, 37, 176-181.	0.4	45
4154	Using a new RAD-sequencing approach to study the evolution of <i>Micromeria</i> in the Canary islands. <i>Molecular Phylogenetics and Evolution</i> , 2018, 119, 160-169.	1.2	15
4155	Multi-gene phylogeny of jacks and pompanos (<i>Carangidae</i>), including placement of monotypic <i>Madidius</i> <i>campogramma</i> . <i>Journal of Fish Biology</i> , 2018, 92, 190-202.	0.7	12
4156	Nutrient-Colimited <i>Trichodesmium</i> as a Nitrogen Source or Sink in a Future Ocean. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	28
4157	Three new species within the genus <i>Entoloma</i> (Basidiomycota, Agaricales) with clamped basidia and a serrulatum-type lamellae edge, and their phylogenetic position. <i>Mycological Progress</i> , 2018, 17, 381-392.	0.5	10
4158	Intraspecific genetic structure, divergence and high rates of clonality in an amphiatlantic starfish. <i>Molecular Ecology</i> , 2018, 27, 752-772.	2.0	12
4159	A New Niche for Anoxygenic Phototrophs as Endoliths. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	8
4160	Rapid song divergence leads to discordance between genetic distance and phenotypic characters important in reproductive isolation. <i>Ecology and Evolution</i> , 2018, 8, 716-731.	0.8	23
4161	Two new <i>Sporothrix</i> species from Protea flower heads in South African Grassland and Savanna. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 965-979.	0.7	9
4162	Systematics and phylogeography of the widely distributed African skink <i>Trachylepis varia</i> species complex. <i>Molecular Phylogenetics and Evolution</i> , 2018, 120, 103-117.	1.2	11
4163	A preliminary molecular phylogeny of shield-bearer moths (Lepidoptera: Adeloidea: Heliozelidae) highlights rich undescribed diversity. <i>Molecular Phylogenetics and Evolution</i> , 2018, 120, 129-143.	1.2	13
4164	Metabolic versatility of small archaea <i>Micrarchaeota</i> and <i>Parvarchaeota</i> . <i>ISME Journal</i> , 2018, 12, 756-775.	4.4	91
4165	Phylogeny and the colourful history of jewel bugs (Insecta: Hemiptera: Scutelleridae). <i>Cladistics</i> , 2018, 34, 502-516.	1.5	15
4166	Phylogeny of <i>Campyloneurum</i> (Polypodiaceae). <i>International Journal of Plant Sciences</i> , 2018, 179, 36-49.	0.6	10
4167	Discordance between genomic divergence and phenotypic variation in a rapidly evolving avian genus (<i>Motacilla</i>). <i>Molecular Phylogenetics and Evolution</i> , 2018, 120, 183-195.	1.2	50
4168	Diversity and biogeography of frogs in the genus <i>Amnirana</i> (Anura: Ranidae) across sub-Saharan Africa. <i>Molecular Phylogenetics and Evolution</i> , 2018, 120, 274-285.	1.2	29
4169	Molecular evolution and expression of oxygen transport genes in livebearing fishes (<i>Poeciliidae</i>) from hydrogen sulfide rich springs. <i>Genome</i> , 2018, 61, 273-286.	0.9	18

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4170	Rapid allopolyploid radiation of moonwort ferns (<i>Botrychium</i> ; Ophioglossaceae) revealed by PacBio sequencing of homologous and homeologous nuclear regions. <i>Molecular Phylogenetics and Evolution</i> , 2018, 120, 342-353.	1.2	60
4171	Mitogenomics supports an unexpected taxonomic relationship for the extinct diving duck <i>Chendytes lawi</i> and definitively places the extinct Labrador Duck. <i>Molecular Phylogenetics and Evolution</i> , 2018, 122, 102-109.	1.2	14
4172	Convergent evolution of bilaterian nerve cords. <i>Nature</i> , 2018, 553, 45-50.	13.7	140
4173	First insights into the solenogaster diversity of the Sea of Okhotsk with the description of a new species of <i>Kruppomenia</i> (Simrothiellidae, Cavibelonia). <i>Deep-Sea Research Part II: Topical Studies in Oceanography</i> , 2018, 154, 214-229.	0.6	7
4174	Phylogenetic characterization of transporter proteins in the cnidarian-dinoflagellate symbiosis. <i>Molecular Phylogenetics and Evolution</i> , 2018, 120, 307-320.	1.2	30
4175	Detection and genetic characterization of diverse <i>Bartonella</i> genotypes in the small mammals of Singapore. <i>Zoonoses and Public Health</i> , 2018, 65, e207-e215.	0.9	18
4176	A new species of antbird (Passeriformes: <i>Thamnophilidae</i>) from the Cordillera Azul, San Martín, Peru. <i>Auk</i> , 2018, 135, 114-126.	0.7	8
4177	Vectors of diversity: Genome wide diversity across the geographic range of the Chagas disease vector <i>Triatoma dimidiata</i> sensu lato (Hemiptera: Reduviidae). <i>Molecular Phylogenetics and Evolution</i> , 2018, 120, 144-150.	1.2	22
4178	Frankia Diversity in Host Plant Root Nodules Is Independent of Abundance or Relative Diversity of Frankia Populations in Corresponding Rhizosphere Soils. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	13
4179	Associations between infant fungal and bacterial dysbiosis and childhood atopic wheeze in a nonindustrialized setting. <i>Journal of Allergy and Clinical Immunology</i> , 2018, 142, 424-434.e10.	1.5	181
4180	A Destructive Leaf Spot and Blight Caused by <i>Alternaria kareliniae</i> sp. nov. on a Sand-Stabilizing Plant, Caspian Sea Karelinia. <i>Plant Disease</i> , 2018, 102, 172-178.	0.7	8
4181	Rice Paddy Nitrospirae Carry and Express Genes Related to Sulfate Respiration: Proposal of the New Genus "Candidate <i>Sulfobium</i> ". <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	83
4182	Genetic Characterization of <i>Clavibacter michiganensis</i> subsp. <i>michiganensis</i> Population in Turkey. <i>Plant Disease</i> , 2018, 102, 300-308.	0.7	7
4183	Conservation phylogenetics and computational species delimitation of Neotropical primates. <i>Biological Conservation</i> , 2018, 217, 397-406.	1.9	11
4184	Reconstruction of mitogenomes by NGS and phylogenetic implications for leaf beetles. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2018, 29, 1041-1050.	0.7	17
4185	Molecular phylogeny of the Laboulbeniomycetes (Ascomycota). <i>Fungal Biology</i> , 2018, 122, 87-100.	1.1	26
4186	Cryptic diversity in <i>Rhampholeon boulengeri</i> (Sauria: Chamaeleonidae), a pygmy chameleon from the Albertine Rift biodiversity hotspot. <i>Molecular Phylogenetics and Evolution</i> , 2018, 122, 125-141.	1.2	17
4187	Recovering the evolutionary history of crowned pigeons (Columbidae: <i>Goura</i>): Implications for the biogeography and conservation of New Guinean lowland birds. <i>Molecular Phylogenetics and Evolution</i> , 2018, 120, 248-258.	1.2	27

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4188	Monophyly of the species of <i>Hepatozoon</i> (Adeleorina: Hepatozoidae) parasitizing (African) anurans, with the description of three new species from hyperoliid frogs in South Africa. <i>Parasitology</i> , 2018, 145, 1039-1050.	0.7	24
4189	The complete genome sequence of a third distinct baculovirus isolated from the true armyworm, <i>Mythimna unipuncta</i> , contains two copies of the <i>lef-7</i> gene. <i>Virus Genes</i> , 2018, 54, 297-310.	0.7	14
4190	Simplified and efficient DNA extraction protocol for Meliolaceae specimens. <i>Mycological Progress</i> , 2018, 17, 403-415.	0.5	10
4191	The complete chloroplast genome sequence of endangered camellias (<i>Camellia pubifurcata</i>). <i>Conservation Genetics Resources</i> , 2018, 10, 843-845.	0.4	3
4192	Rolling into the deep of the land planarian genus <i>Choeradoplana</i> (Tricladida, Continenticola). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Jf 50 582</i>	0.7	9
4193	Nemertean and phoronid genomes reveal lophotrochozoan evolution and the origin of bilaterian heads. <i>Nature Ecology and Evolution</i> , 2018, 2, 141-151.	3.4	98
4194	HIV-1 and hepatitis C virus selection bottleneck in Chinese people who inject drugs. <i>Aids</i> , 2018, 32, 309-320.	1.0	0
4195	Coexistence of poribacterial phylotypes among geographically widespread and phylogenetically divergent sponge hosts. <i>Environmental Microbiology Reports</i> , 2018, 10, 80-91.	1.0	5
4196	Challenges of <i>Francisella</i> classification exemplified by an atypical clinical isolate. <i>Diagnostic Microbiology and Infectious Disease</i> , 2018, 90, 241-247.	0.8	3
4197	Comparative analyses of species delimitation methods with molecular data in snappers (Perciformes). <i>Tj ETQq1 1 0,784314 rgBT /Overlock 20</i>	0.7	20
4198	Biogeographic implications of small mammals from Northern Highlands in Tanzania with first data from the volcanic Mount Kitumbeine. <i>Mammalia</i> , 2018, 82, 360-372.	0.3	23
4199	Diel behavior in moths and butterflies: a synthesis of data illuminates the evolution of temporal activity. <i>Organisms Diversity and Evolution</i> , 2018, 18, 13-27.	0.7	37
4200	<i>Pendulichytrium sphaericum</i> gen. et sp. nov. (Chytridiales, Chytriomycetaceae), a new chytrid parasitic on the diatom, <i>Aulacoseira granulata</i> . <i>Mycoscience</i> , 2018, 59, 59-66.	0.3	17
4201	Coelomycetous <i>Dothideomycetes</i> with emphasis on the families <i>Cucurbitariaceae</i> and <i>Didymellaceae</i> . <i>Studies in Mycology</i> , 2018, 90, 1-69.	4.5	129
4202	Acquisition of the Phosphate Transporter <i>NptA</i> Enhances <i>Staphylococcus aureus</i> Pathogenesis by Improving Phosphate Uptake in Divergent Environments. <i>Infection and Immunity</i> , 2018, 86, .	1.0	20
4203	<i>Streptomyces sediminis</i> sp. nov. isolated from crater lake sediment. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 493-500.	0.7	23
4204	The complete chloroplast genome of <i>Littledalea alaica</i> (Korsh.) Petr. ex Nevski (Poaceae), an endemic species from the Qinghai-Tibetan Plateau. <i>Conservation Genetics Resources</i> , 2018, 10, 639-642.	0.4	0
4205	Characterization of the complete chloroplast genome of the relict Chinese false tupelo, <i>Camptotheca acuminata</i> . <i>Conservation Genetics Resources</i> , 2018, 10, 659-662.	0.4	2

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4206	Species and hybrids in the genus <i>Diaphanosoma</i> Fischer, 1850 (Crustacea: Branchiopoda: Cladocera). <i>Molecular Phylogenetics and Evolution</i> , 2018, 118, 369-378.	1.2	24
4207	Porcine reproductive and respiratory disease virus: Evolution and recombination yields distinct ORF5 RFLP 1-7-4 viruses with individual pathogenicity. <i>Virology</i> , 2018, 513, 168-179.	1.1	75
4208	Phylogeny, new generic-level classification, and historical biogeography of the <i>Eucera</i> complex (Hymenoptera: Apidae). <i>Molecular Phylogenetics and Evolution</i> , 2018, 119, 81-92.	1.2	55
4209	Is subterranean lifestyle reversible? Independent and recent large-scale dispersal into surface waters by two species of the groundwater amphipod genus <i>Niphargus</i> . <i>Molecular Phylogenetics and Evolution</i> , 2018, 119, 37-49.	1.2	43
4210	Why are there so many sedges? Sumatrosclirpeae, a missing piece in the evolutionary puzzle of the giant genus <i>Carex</i> (Cyperaceae). <i>Molecular Phylogenetics and Evolution</i> , 2018, 119, 93-104.	1.2	28
4211	Isolation and identification of indigenous marine diatoms (Bacillariophyta) for biomass production in open raceway ponds. <i>Aquaculture Research</i> , 2018, 49, 928-938.	0.9	8
4212	Large-scale migrations of brown bears in Eurasia and to North America during the Late Pleistocene. <i>Journal of Biogeography</i> , 2018, 45, 394-405.	1.4	59
4213	Taxon sampling to address an ancient rapid radiation: a supermatrix phylogeny of early brachyceran flies (Diptera). <i>Systematic Entomology</i> , 2018, 43, 277-289.	1.7	28
4214	Phylogenetic relationships and molecular delimitation of <i>Culicoides</i> <i>latreille</i> (Diptera: Ceratopogonidae) species in the Afrotropical region: interest for the subgenus <i>Avaritia</i> . <i>Systematic Entomology</i> , 2018, 43, 355-371.	1.7	13
4215	A new aerobic chemolithoautotrophic arsenic oxidizing microorganism isolated from a high Andean watershed. <i>Biodegradation</i> , 2018, 29, 59-69.	1.5	20
4216	Contribution to the phylogeny and a new species of <i>Coccodiella</i> (Phyllachorales). <i>Mycological Progress</i> , 2018, 17, 205-213.	0.5	7
4217	Complete mitochondrial genome of bovine species Gayal (<i>Bos frontalis</i>). <i>Conservation Genetics Resources</i> , 2018, 10, 889-891.	0.4	9
4218	Phylogenomics of <i>Bartheletia paradoxa</i> reveals its basal position in Agaricomycotina and that the early evolutionary history of basidiomycetes was rapid and probably not strictly bifurcating. <i>Mycological Progress</i> , 2018, 17, 333-341.	0.5	11
4219	The complete chloroplast genome of <i>Bretschneidera sinensis</i> (Bretschneideraceae). <i>Conservation Genetics Resources</i> , 2018, 10, 751-753.	0.4	1
4220	Absence of co-phylogeny indicates repeated diatom capture in dinophytes hosting a tertiary endosymbiont. <i>Organisms Diversity and Evolution</i> , 2018, 18, 29-38.	0.7	12
4221	Multilocus sequence analysis of homologous recombination and diversity in <i>Arthrobacter</i> sensu lato named species and glacier-inhabiting strains. <i>Systematic and Applied Microbiology</i> , 2018, 41, 23-29.	1.2	19
4222	Resolving taxonomic turbulence and uncovering cryptic diversity in the musk turtles (<i>Sternotherus</i>) using robust demographic modeling. <i>Molecular Phylogenetics and Evolution</i> , 2018, 120, 1-15.	1.2	23
4223	<i>Tziminema unachin</i> , n. sp. (Nematoda: Strongylidae: Strongylinae) parasite of Baird's tapir <i>Tapirus bairdii</i> from Mexico. <i>Journal of Helminthology</i> , 2018, 92, 752-759.	0.4	2

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4224	Reconstructing Species Relationships within the Recently Diversified Genus <i>Odontites</i> (Orobanchaceae): Evidence for Extensive Reticulate Evolution. <i>International Journal of Plant Sciences</i> , 2018, 179, 1-20.	0.6	12
4225	Phylogeny and species diversity of the genus <i>Herichthys</i> (Teleostei: Cichlidae). <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2018, 56, 223-247.	0.6	12
4226	Phylogeny and biogeography of East Asian evergreen oaks (<i>Quercus</i> section <i>Cyclobalanopsis</i>). <i>Molecular Phylogenetics and Evolution</i> , 2018, 119, 170-181.	1.2	99
4227	Genetic Structure of the Bacterial Endosymbiont <i>Buchnera aphidicola</i> from Its Host Aphid <i>Schlechtendalia chinensis</i> and Evolutionary Implications. <i>Current Microbiology</i> , 2018, 75, 309-315.	1.0	7
4228	<i>Dartintinnus alderae</i> n. g., n. sp., a Brackish Water Tintinnid (Ciliophora, Spirotrichea) with Dual-ended Lorica Collapsibility. <i>Journal of Eukaryotic Microbiology</i> , 2018, 65, 400-411.	0.8	15
4229	Molecular identification of tick-borne pathogens infecting cattle in Mymensingh district of Bangladesh reveals emerging species of <i>Anaplasma</i> and <i>Babesia</i> . <i>Transboundary and Emerging Diseases</i> , 2018, 65, e231-e242.	1.3	33
4230	Invasive Disease Caused Simultaneously by Dual Serotypes of <i>Streptococcus pneumoniae</i> . <i>Journal of Clinical Microbiology</i> , 2018, 56, .	1.8	13
4231	SHORTROOT-Mediated Increase in Stomatal Density Has No Impact on Photosynthetic Efficiency. <i>Plant Physiology</i> , 2018, 176, 757-772.	2.3	56
4232	Exposure to predicted precipitation patterns decreases population size and alters community structure of cyanobacteria in biological soil crusts from the Chihuahuan Desert. <i>Environmental Microbiology</i> , 2018, 20, 259-269.	1.8	83
4233	Phylogenetic analyses of DENV-3 isolated from field-caught mosquitoes in Thailand. <i>Virus Research</i> , 2018, 244, 27-35.	1.1	4
4234	Phylogenetic analyses of transcriptome data resolve familial assignments for genera of the red-algal Acrochaetiales-Palmariales Complex (Nemaliophycidae). <i>Molecular Phylogenetics and Evolution</i> , 2018, 119, 151-159.	1.2	31
4235	Phylogenetic relationships of <i>Deprea</i> : New insights into the evolutionary history of physaloid groups. <i>Molecular Phylogenetics and Evolution</i> , 2018, 119, 71-80.	1.2	10
4236	Sequencing of the plastome in the leafless green mycoheterotroph <i>Cymbidium macrorhizon</i> helps us to understand an early stage of fully mycoheterotrophic plastome structure. <i>Plant Systematics and Evolution</i> , 2018, 304, 245-258.	0.3	21
4237	Mutualism between <i>Klebsiella</i> SGM 81 and <i>Dianthus caryophyllus</i> in modulating root plasticity and rhizospheric bacterial density. <i>Plant and Soil</i> , 2018, 424, 273-288.	1.8	22
4238	Biogeography and genetic diversity of the atlantid heteropods. <i>Progress in Oceanography</i> , 2018, 160, 1-25.	1.5	21
4239	Universal target-enrichment baits for anthozoan (Cnidaria) phylogenomics: New approaches to long-standing problems. <i>Molecular Ecology Resources</i> , 2018, 18, 281-295.	2.2	114
4240	Cryptic genetic diversity of <i>Neverita didyma</i> in the coast of China revealed by phylogeographic analysis: implications for management and conservation. <i>Conservation Genetics</i> , 2018, 19, 275-282.	0.8	10
4241	Hybridization and emergence of virulence in opportunistic human yeast pathogens. <i>Yeast</i> , 2018, 35, 5-20.	0.8	104

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4242	Development and evaluation of specific PCR primers targeting the ribosomal DNA-internal transcribed spacer (ITS) region of peritrich ciliates in environmental samples. <i>Journal of Oceanology and Limnology</i> , 2018, 36, 818-826.	0.6	13
4243	Plastid capture and resultant fitness costs of hybridization in the Hirta clade of southern African <i>Oxalis</i> . <i>South African Journal of Botany</i> , 2018, 118, 329-341.	1.2	4
4244	The abrogation of condensin function provides independent evidence for defining the self-renewing population of pluripotent stem cells. <i>Developmental Biology</i> , 2018, 433, 218-226.	0.9	13
4245	Modeling Site Heterogeneity with Posterior Mean Site Frequency Profiles Accelerates Accurate Phylogenomic Estimation. <i>Systematic Biology</i> , 2018, 67, 216-235.	2.7	328
4246	Historical and cospeciating associations between Cerataphidini aphids (Hemiptera: Aphididae: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 58). <i>Linnean Society</i> , 2018, 182, 604-613.	1.0	8
4247	Molecular phylogeny of trigonostomine turbellarians (Platyhelminthes: Rhabdozoa: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 58) of the Linnean Society, 2018, 182, 237-257.	1.0	4
4248	Chemical Biology Approaches for Investigating the Functions of Lysine Acetyltransferases. <i>Angewandte Chemie - International Edition</i> , 2018, 57, 1162-1184.	7.2	28
4249	A review of cross-backed grasshoppers of the genus <i>Dociostaurus</i> (Orthoptera: Acrididae) from the western Mediterranean: insights from phylogenetic analyses and DNA-based species delimitation. <i>Systematic Entomology</i> , 2018, 43, 136-146.	1.7	7
4250	Untersuchung der epigenetischen Funktionen von Lysin-Acetyltransferasen mit Methoden der chemischen Biologie. <i>Angewandte Chemie</i> , 2018, 130, 1176-1199.	1.6	3
4251	<i>Gordionus maori</i> (Nematomorpha: Gordiida), a new species of horsehair worm from New Zealand. <i>New Zealand Journal of Zoology</i> , 2018, 45, 29-42.	0.6	7
4252	Investigation of the diversity of effector genes in the banana pathogen, <i>Fusarium oxysporum</i> f. sp. <i>cubense</i> , reveals evidence of horizontal gene transfer. <i>Molecular Plant Pathology</i> , 2018, 19, 1155-1171.	2.0	102
4253	<i>Streptococcus agalactiae</i> Multilocus sequence type 261 is associated with mortalities in the emerging Ghanaian tilapia industry. <i>Journal of Fish Diseases</i> , 2018, 41, 175-179.	0.9	31
4254	HomBlocks: A multiple-alignment construction pipeline for organelle phylogenomics based on locally collinear block searching. <i>Genomics</i> , 2018, 110, 18-22.	1.3	183
4255	Genetic diversity and connectivity of the megamouth shark (<i>Megachasma pelagios</i>). <i>PeerJ</i> , 2018, 6, e4432.	0.9	8
4256	Phylogeography indicates incomplete genetic divergence among phenotypically differentiated montane forest populations of <i>Atlapetes albinucha</i> (Aves, Passerellidae). <i>ZooKeys</i> , 2018, 809, 125-148.	0.5	5
4257	Mycorrhizal fungi associated with <i>Codonorchis lessonii</i> (Brongn.) Lindl., a terrestrial orchid from Chile. <i>Gayana - Botanica</i> , 2018, 75, 447-458.	0.3	10
4258	Farm-to-fork investigation of an outbreak of Shiga toxin-producing <i>Escherichia coli</i> O157. <i>Microbial Genomics</i> , 2018, 4, .	1.0	27
4259	Characterization of the complete plastome of <i>Dysphania botrys</i> , a candidate plant for cancer treatment. <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 1214-1215.	0.2	5

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4260	The complete mitochondrial genome of a transitional form in secondary endosymbiotic Cryptophyte algae <i>Guillardia theta</i> strain CCMP2712. Mitochondrial DNA Part B: Resources, 2018, 3, 1304-1305.	0.2	4
4261	Untangling nets: elucidating the diversity and phylogeny of the clathrate brown algal genus <i>Hydroclathrus</i> , with the description of a new genus <i>Tronoella</i> (Scytosiphonaceae, Tj ETQq1 1 0.784314 rgBT /Overlock	1.4	0
4262	Hidden Diversity of African Yellow House Bats (Vespertilionidae, Scotophilus): Insights From Multilocus Phylogenetics and Lineage Delimitation. Frontiers in Ecology and Evolution, 2018, 6, .	1.1	19
4263	Cover Image, Volume 93, Issue 9. Journal of Chemical Technology and Biotechnology, 2018, 93, i-i.	1.6	0
4264	Concordance between DNA-based species boundaries and reproductive isolating barriers in the <i>Scytosiphon lomentaria</i> species complex (Ectocarpales, Phaeophyceae). Phycologia, 2018, 57, 232-242.	0.6	13
4265	The complete chloroplast genome of <i>Mimosa pudica</i> and the phylogenetic analysis of mimosoid species. Mitochondrial DNA Part B: Resources, 2018, 3, 1265-1266.	0.2	4
4266	Two novel species of Neoaquastroma (Parabambusicolaceae, Pleosporales) with their phoma-like asexual morphs. MycoKeys, 2018, 34, 47-62.	0.8	9
4267	Novel Diversity of Deeply Branching Holomycota and Unicellular Holozoans Revealed by Metabarcoding in Middle Paran River, Argentina. Frontiers in Ecology and Evolution, 2018, 6, .	1.1	20
4268	Characterization of the complete mitochondrial genome of the lung fluke, Paragonimus kellicotti. Mitochondrial DNA Part B: Resources, 2018, 3, 715-716.	0.2	4
4269	The complete chloroplast genome of Bambusa ventricosa (Bambusoideae: Bambuseae). Mitochondrial DNA Part B: Resources, 2018, 3, 986-987.	0.2	1
4270	The complete chloroplast genome of <i>Atraphaxis jrtyschensis</i> (polygonaceae), an endemic and endangered desert shrub to Xinjiang, China. Mitochondrial DNA Part B: Resources, 2018, 3, 1104-1105.	0.2	0
4271	Systematics of Phyllocnistis leaf-mining moths (Lepidoptera, Gracillariidae) feeding on dogwood (Cornus spp.) in Northeast Asia, with the description of three new species. ZooKeys, 2018, 736, 79-118.	0.5	12
4272	Plant Litter Type Dictates Microbial Communities Responsible for Greenhouse Gas Production in Amended Lake Sediments. Frontiers in Microbiology, 2018, 9, 2662.	1.5	14
4273	Genomic epidemiology of the commercially important pathogen Renibacterium salmoninarum within the Chilean salmon industry. Microbial Genomics, 2018, 4, .	1.0	12
4274	Cryptic Diversity Hidden within the Leafminer Genus Liriomyza (Diptera: Agromyzidae). Genes, 2018, 9, 554.	1.0	8
4275	The Phylogenomic Diversity of Herbivore-Associated <i>Fibrobacter</i> spp. Is Correlated to Lignocellulose-Degrading Potential. MSphere, 2018, 3, .	1.3	38
4276	Genomic epidemiology of meticillin-resistant Staphylococcus aureus ST22 widespread in communities of the Gaza Strip, 2009. Eurosurveillance, 2018, 23, .	3.9	25
4277	Symbiont Chloroplasts Remain Active During Bleaching-Like Response Induced by Thermal Stress in Collozoum pelagicum (Collodaria, Retaria). Frontiers in Marine Science, 2018, 5, .	1.2	21

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4278	First complete genome sequence in Arborophila and comparative genomics reveals the evolutionary adaptation of Hainan Partridge (<i>Arborophila ardens</i>). <i>Avian Research</i> , 2018, 9, .	0.5	2
4279	Molecular and morphological evidence reveal a new genus and species in Auriculariales from tropical China. <i>MycKeys</i> , 2018, 35, 27-39.	0.8	11
4280	Maintenance and reappearance of extremely divergent intra-host HIV-1 variants. <i>Virus Evolution</i> , 2018, 4, vey030.	2.2	5
4281	Recovery of the Peptidoglycan Turnover Product Released by the Autolysin Atl in <i>Staphylococcus aureus</i> Involves the Phosphotransferase System Transporter MurP and the Novel 6-phospho-N-acetylmuramidase MupG. <i>Frontiers in Microbiology</i> , 2018, 9, 2725.	1.5	22
4282	Microbial biodegradation of biuret: defining biuret hydrolases within the isochorismatase superfamily. <i>Environmental Microbiology</i> , 2018, 20, 2099-2111.	1.8	9
4283	The <i>Synechocystis</i> sp. PCC 6803 Genome Encodes Up to Four 2-Phosphoglycolate Phosphatases. <i>Frontiers in Plant Science</i> , 2018, 9, 1718.	1.7	7
4284	Ants in Australiaâ€™s Monsoonal Tropics: CO1 Barcoding Reveals Extensive Unrecognised Diversity. <i>Diversity</i> , 2018, 10, 36.	0.7	12
4285	<i>Malassezia vespertilionis</i> sp. nov.: a new cold-tolerant species of yeast isolated from bats. <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2018, 41, 56-70.	1.6	73
4286	Two new mitogenomes of Pellorneidae (Aves : Passeriformes) and a phylogeny of the superfamily Sylvioidea. <i>Australian Journal of Zoology</i> , 2018, 66, 167.	0.6	2
4287	GLUE: a flexible software system for virus sequence data. <i>BMC Bioinformatics</i> , 2018, 19, 532.	1.2	84
4288	Classification, substrate specificity and structural features of D-2-hydroxyacid dehydrogenases: 2HADH knowledgebase. <i>BMC Evolutionary Biology</i> , 2018, 18, 199.	3.2	21
4289	The complete chloroplast genome of <i>Melilotus albus</i> : an important source of forage species. <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 584-585.	0.2	0
4290	Characterization of complete chloroplast genome of endemic species of Korea Peninsular, <i>Salvia chanryoenica</i> (Lamiaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 992-993.	0.2	5
4291	Proteogenomic Analysis of <i>Epibacterium Mobile</i> BBCC367, a Relevant Marine Bacterium Isolated From the South Pacific Ocean. <i>Frontiers in Microbiology</i> , 2018, 9, 3125.	1.5	4
4292	Description of a new species of <i>Dacus</i> from Sri Lanka, and new country distribution records (Diptera.) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf</i>	0.5	9
4293	Draft Genome Sequences of Nine <i>Vibrio</i> sp. Isolates from across the United States Closely Related to <i>Vibrio cholerae</i> . <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	8
4294	The complete chloroplast genome of <i>Pterospermum kingtungense</i> , a Critically Endangered species. <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 1167-1168.	0.2	2
4295	Draft Genome Sequence of <i>Candidatus Bathyarchaeota</i> Archaeon BE326-BA-RLH, an Uncultured Denitrifier and Putative Anaerobic Methanotroph from South Africaâ€™s Deep Continental Biosphere. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	11

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4296	The <i>achaete</i> “scute” complex contains a single gene that controls bristle development in the semi-aquatic bugs. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018, 285, .	1.2	15
4297	Basal position of two new complete mitochondrial genomes of parasitic Cymothoidea (Crustacea: Tj ETQq1 1 0.784314 rgBT /Overl... Vectors, 2018, 11, 628.	1.0	18
4298	Heterogeneity of Microbial Communities on Deep-Sea Ferromanganese Crusts in the Takuyo-Daigo Seamount. <i>Microbes and Environments</i> , 2018, 33, 366-377.	0.7	18
4299	Evolution of Geosiris (Iridaceae): historical biogeography and plastid-genome evolution in a genus of non-photosynthetic tropical rainforest herbs disjunct across the Indian Ocean. <i>Australian Systematic Botany</i> , 2018, , .	0.3	8
4300	Expansion and Functional Divergence of the <i>SHORT VEGETATIVE PHASE</i> (<i>SVP</i>) Genes in Eudicots. <i>Genome Biology and Evolution</i> , 2018, 10, 3026-3037.	1.1	32
4301	The chloroplast genome of an Endangered orchid species, <i>Gastrochilus calceolaris</i> (Orchidaceae: Aeridinae). <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 988-989.	0.2	1
4302	A phylogenomic resolution of the sea urchin tree of life. <i>BMC Evolutionary Biology</i> , 2018, 18, 189.	3.2	42
4303	Genome wide characterization of enterotoxigenic <i>Escherichia coli</i> serogroup O6 isolates from multiple outbreaks and sporadic infections from 1975-2016. <i>PLoS ONE</i> , 2018, 13, e0208735.	1.1	8
4304	Multi-locus phylogeny and taxonomy of <i>Exserohilum</i> . <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2018, 41, 71-108.	1.6	54
4305	Removing chaos from confusion: assigning names to common human and animal pathogens in <i>Neocosmospora</i> . <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2018, 41, 109-129.	1.6	70
4306	Evolutionary dynamics of origin and loss in the deep history of phospholipase D toxin genes. <i>BMC Evolutionary Biology</i> , 2018, 18, 194.	3.2	9
4307	New species of <i>Hohenbuehelia</i> , with comments on the <i>Hohenbuehelia atrocoerulea</i> “ <i>Nematoctonus robustus</i> ” species complex. <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2018, 41, 202-212.	1.6	5
4308	Data for praying mantis mitochondrial genomes and phylogenetic constructions within Mantodea. <i>Data in Brief</i> , 2018, 21, 1277-1285.	0.5	5
4309	Genome Sequence of Chiqui Virus, a Novel Reovirus Isolated from Mosquitoes Collected in Colombia. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	2
4310	Patients with Chronic Obstructive Pulmonary Disease harbour a variation of <i>Haemophilus</i> species. <i>Scientific Reports</i> , 2018, 8, 14734.	1.6	14
4311	Contrasting phylogeographic structures between freshwater lycopods and angiosperms in the British Isles. <i>Botany Letters</i> , 2018, 165, 476-486.	0.7	7
4312	Topological assessment of metabolic networks reveals evolutionary information. <i>Scientific Reports</i> , 2018, 8, 15918.	1.6	10
4313	Evolution of six novel ORFs in the plastome of <i>Mankyua chejuense</i> and phylogeny of eusporangiate ferns. <i>Scientific Reports</i> , 2018, 8, 16466.	1.6	10

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4314	Polyphyly of the genus <i>Zanclaea</i> and family Zanclaeidae (Hydrozoa, Capitata) revealed by the integrative analysis of two bryozoan-associated species. <i>Contributions To Zoology</i> , 2018, 87, 87-104.	0.2	15
4315	Monogenean parasites of sardines in Lake Tanganyika: diversity, origin and intraspecific variability. <i>Contributions To Zoology</i> , 2018, 87, 105-132.	0.2	23
4316	Molecular and anatomical analyses reveal that <i>Peronia verruculata</i> (Gastropoda: Onchidiidae) is a cryptic species complex. <i>Contributions To Zoology</i> , 2018, 87, 149-165.	0.2	10
4317	Molecular phylogeny of Parabathynellidae (Crustacea, Bathynellacea), and three new species from Thai caves. <i>Contributions To Zoology</i> , 2018, 87, 227-260.	0.2	9
4318	<i>Candelaria asiatica</i> , an Ignored New Species from South Korea. <i>Mycobiology</i> , 2018, 46, 305-310.	0.6	3
4319	Characterization of the complete chloroplast genome of <i>Pinus wangii</i> (Pinaceae), an endangered and endemic species in China. <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 1195-1197.	0.2	3
4320	Participation, Reparation, and Redress. <i>Journal of International Criminal Justice</i> , 2018, 16, 813-834.	0.4	0
4321	Challenges and changes in the parenting experiences of Korean immigrants in New Zealand. <i>Asian and Pacific Migration Journal</i> , 2018, 27, 431-450.	0.5	4
4322	A revision of <i>Salispina</i> , its placement in a new family, Salispinaceae (Rhipidiales), and description of a fourth species, <i>S. hoi</i> sp. nov. <i>IMA Fungus</i> , 2018, 9, 259-269.	1.7	7
4323	Diversity of <i>Chroogomphus</i> (Gomphidiaceae, Boletales) in Europe, and typification of <i>C. rutilus</i> . <i>IMA Fungus</i> , 2018, 9, 271-290.	1.7	7
4324	Characterization of five complete <i>Cyrtodactylus</i> mitogenome structures reveals low structural diversity and conservation of repeated sequences in the lineage. <i>PeerJ</i> , 2018, 6, e6121.	0.9	5
4325	Tzeananiaceae, a new pleosporalean family associated with <i>Ophiocordyceps macroacicularis</i> fruiting bodies in Taiwan. <i>MycoKeys</i> , 2018, 37, 1-17.	0.8	11
4326	The complete chloroplast genome sequence of <i>Cremastra appendiculata</i> (Orchidaceae) revealed by next-generation sequencing and phylogenetic implication. <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 1108-1109.	0.2	2
4327	Marine <i>Macrotrichia</i> (Gastrotricha) from Hokkaido, Northern Japan. <i>Species Diversity</i> , 2018, 23, 183-192.	0.1	5
4328	Three new species of the fairy shrimp <i>Eubranchipus</i> Verill, 1870 (Branchiopoda: Anostraca) from northern Japan and far Eastern Russia. <i>BMC Zoology</i> , 2018, 3, .	0.3	4
4329	A Genetic Algorithm Formulation for Rogue Taxa Problem. , 2018, , .		1
4330	Phylogenetic and morphological characterization of <i>Byssosphaeria macarangae</i> sp. nov., and <i>B. taiwanense</i> sp. nov. from <i>Macaranga tanarius</i> . <i>Phytotaxa</i> , 2018, 364, 211.	0.1	6
4331	<i>Singerocomus atlanticus</i> sp. nov., and a first record of <i>Singerocomus rubriflavus</i> (Boletaceae,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T	0.8	10

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4332	A Survey of Phylogenetic Databases. , 2018, , .		0
4333	<i>Akanthomyces araneogenum</i> , a new <i>Isaria</i> -like araneogenous species. <i>Phytotaxa</i> , 2018, 379, 66.	0.1	14
4334	Fifteen <i>Cortinarius</i> species associated with <i>Helianthemum</i> in Great Britain: results of a DNA-based analysis. <i>Field Mycology</i> , 2018, 19, 119-135.	0.0	2
4335	A molecular phylogeny of Porcellionidae (Isopoda, Oniscidea) reveals inconsistencies with present taxonomy. <i>ZooKeys</i> , 2018, 801, 163-176.	0.5	12
4336	The complete mitochondrial genome of <i>Schisandra sphenanthera</i> (Schisandraceae). <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 1246-1247.	0.2	3
4337	The complete chloroplast genome of <i>Tetradoxa omeiensis</i> (Adoxaceae) provides insights into the phylogenetic relationship of Adoxaceae. <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 1149-1151.	0.2	0
4338	A level set method for shape reconstruction in seismic full waveform inversion using a linear elastic model in 2D. <i>Journal of Physics: Conference Series</i> , 2018, 1131, 012001.	0.3	2
4339	Phylogenetic Reconstructions Using an Indicator-Based Bat Algorithm for Multicore Processors. , 2018, , .		0
4340	<i>Crossospora</i> , a new tropical genus of rust fungi. <i>Phytotaxa</i> , 2018, 375, 189.	0.1	5
4341	The complete chloroplast genome of <i>Macrothelypteris torresiana</i> , a reputed medicinal fern (Thelypteridaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 949-950.	0.2	0
4342	Characterization of the complete chloroplast genome sequence of <i>Sphagneticola calendulacea</i> (Asteraceae). <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 1029-1030.	0.2	0
4343	The complete chloroplast genome sequence of <i>Campylandra chinensis</i> (Liliaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 780-781.	0.2	4
4344	The complete chloroplast genome of <i>Antiaris toxicaria</i> , a medicinal and extremely toxic species. <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 1100-1101.	0.2	2
4345	Early human dispersals within the Americas. <i>Science</i> , 2018, 362, .	6.0	230
4346	Molecular insights into the phylogenetic placement of the poorly known genus <i>Niceforonia</i> Goin & Cochran, 1963 (Anura: Brachycephaloidea). <i>Zootaxa</i> , 2018, 4514, 487.	0.2	3
4347	<i>Cortinarius</i> sect. <i>Riederi</i> : taxonomy and phylogeny of the new section with European and North American distribution. <i>Mycological Progress</i> , 2018, 17, 1323-1354.	0.5	10
4348	Members of the Genus <i>Methylobacter</i> Are Inferred To Account for the Majority of Aerobic Methane Oxidation in Oxidic Soils from a Freshwater Wetland. <i>MBio</i> , 2018, 9, .	1.8	64
4349	Novel Divergent Polar Bear-Associated Mastadenovirus Recovered from a Deceased Juvenile Polar Bear. <i>MSphere</i> , 2018, 3, .	1.3	8

#	ARTICLE	IF	CITATIONS
4350	Equine Methicillin-Resistant Sequence Type 398 <i>Staphylococcus aureus</i> (MRSA) Harbor Mobile Genetic Elements Promoting Host Adaptation. <i>Frontiers in Microbiology</i> , 2018, 9, 2516.	1.5	31
4351	The first set of universal nuclear protein-coding loci markers for avian phylogenetic and population genetic studies. <i>Scientific Reports</i> , 2018, 8, 15723.	1.6	16
4352	The genomic basis of adaptation to calcareous and siliceous soils in <i>Arabidopsis lyrata</i> . <i>Molecular Ecology</i> , 2018, 27, 5088-5103.	2.0	20
4353	Duplications and losses of genes encoding known elements of the stress defence system of the <i>Aspergilli</i> contribute to the evolution of these filamentous fungi but do not directly influence their environmental stress tolerance. <i>Studies in Mycology</i> , 2018, 91, 23-36.	4.5	21
4354	Ancient DNA of the extinct Jamaican monkey <i>Xenothrix</i> reveals extreme insular change within a morphologically conservative radiation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 12769-12774.	3.3	39
4355	Systematics of the Australian spiny trapdoor spiders of the genus <i>Blakistonia</i> Hogg (Araneae: Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.2	8
4356	Visualization-assisted binning of metagenome assemblies reveals potential new pathogenic profiles in idiopathic travelers' diarrhea. <i>Microbiome</i> , 2018, 6, 201.	4.9	20
4357	Characterization of <i>Campylobacter</i> spp. isolated from wild birds in the Antarctic and Sub-Antarctic. <i>PLoS ONE</i> , 2018, 13, e0206502.	1.1	6
4358	Phylogenetic Analysis Reveals that the "Radial Centric" Diatom <i>Orthoseira Thwaites</i> (Orthoseiraceae,) Tj ETQq0 0 0 rgBT /Overlock 11	0.6	11
4359	The complete chloroplast genome of <i>Narcissus poeticus</i> L. (Amaryllidaceae: Amaryllidoideae). <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 1137-1138.	0.2	11
4360	Contrasting phylogeographic patterns and demographic history in closely related species of <i>Daphnia longispina</i> group (Crustacea: Cladocera) with focus on North-Eastern Eurasia. <i>PLoS ONE</i> , 2018, 13, e0207347.	1.1	15
4361	Genome-wide analysis of the soybean CRK-family and transcriptional regulation by biotic stress signals triggering plant immunity. <i>PLoS ONE</i> , 2018, 13, e0207438.	1.1	36
4362	First Report of a Helminth Parasite, <i>Clinostomum marginatum</i> (Digenea: Clinostomidae) from the Federally Threatened Jollyville Plateau Salamander, <i>Eurycea tonkawae</i> (Caudata:) Tj ETQq0 0 0 rgBT /Overlock 10 1 50 257 T	0.0	1
4363	Fungal adaptation to plant defences through convergent assembly of metabolic modules. <i>Molecular Ecology</i> , 2018, 27, 5120-5136.	2.0	17
4364	Evolutionary dynamics of the Wnt gene family: implications for lophotrochozoans. <i>Journal of Oceanology and Limnology</i> , 2018, 36, 1720-1730.	0.6	4
4365	Molecular Investigation of the Ciliate <i>Spirostomum semivirescens</i> , with First Transcriptome and New Geographical Records. <i>Protist</i> , 2018, 169, 875-886.	0.6	22
4366	The global origins of resistance-associated variants in the non-structural proteins 5A and 5B of the hepatitis C virus. <i>Virus Evolution</i> , 2018, 4, vex041.	2.2	7
4367	<i>Salmonella enterica</i> Serovar Typhi in Bangladesh: Exploration of Genomic Diversity and Antimicrobial Resistance. <i>MBio</i> , 2018, 9, .	1.8	54

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4368	Systematics of Clupeiformes and testing for ecological limits on species richness in a trans-marine/freshwater clade. <i>Neotropical Ichthyology</i> , 2018, 16, .	0.5	23
4369	Benchmarking Tree and Ancestral Sequence Inference for B Cell Receptor Sequences. <i>Frontiers in Immunology</i> , 2018, 9, 2451.	2.2	26
4370	The genome of an underwater architect, the caddisfly <i>Stenopsyche tienmushanensis</i> Hwang (Insecta: Trichoptera). <i>GigaScience</i> , 2018, 7, .	3.3	41
4371	Phylogenomic history of enigmatic pygmy perches: implications for biogeography, taxonomy and conservation. <i>Royal Society Open Science</i> , 2018, 5, 172125.	1.1	17
4372	Assembly of a Complete Mitogenome of <i>Chrysanthemum nankingense</i> Using Oxford Nanopore Long Reads and the Diversity and Evolution of Asteraceae Mitogenomes. <i>Genes</i> , 2018, 9, 547.	1.0	34
4373	The <i>Chrysanthemum nankingense</i> Genome Provides Insights into the Evolution and Diversification of <i>Chrysanthemum</i> Flowers and Medicinal Traits. <i>Molecular Plant</i> , 2018, 11, 1482-1491.	3.9	148
4374	Expansive microbial metabolic versatility and biodiversity in dynamic Guaymas Basin hydrothermal sediments. <i>Nature Communications</i> , 2018, 9, 4999.	5.8	205
4375	Revision of pyrophilous taxa of <i>Pholiota</i> described from North America reveals four species— <i>P. brunnescens</i> , <i>P. castanea</i> , <i>P. highlandensis</i> , and <i>P. molesta</i> . <i>Mycologia</i> , 2018, 110, 997-1016.	0.8	16
4376	The complete mitogenome of <i>Metopograpsus quadridentatus</i> and phylogenetic analysis. <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 1169-1171.	0.2	1
4377	Highlights on the Application of Genomics and Bioinformatics in the Fight Against Infectious Diseases: Challenges and Opportunities in Africa. <i>Frontiers in Genetics</i> , 2018, 9, 575.	1.1	23
4378	<i>Cucumis omissus</i> sp. nov. (Cucurbitaceae) from southern Arabia and Ethiopia and its phylogenetic position. <i>Nordic Journal of Botany</i> , 2018, 36, e02056.	0.2	1
4379	Comparative Characterization of the Complete Mitochondrial Genomes of the Three Apple Snails (Gastropoda: Ampullariidae) and the Phylogenetic Analyses. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3646.	1.8	14
4380	<i>Ramalina sarahae</i> (Ramalinaceae), a new species from the Channel Islands of California, U.S.A.. <i>Bryologist</i> , 2018, 121, 513-519.	0.1	2
4381	Evolution of the Natural Transformation Protein, ComEC, in Bacteria. <i>Frontiers in Microbiology</i> , 2018, 9, 2980.	1.5	42
4382	Pseudogenization and Resurrection of a Speciation Gene. <i>Current Biology</i> , 2018, 28, 3776-3786.e7.	1.8	57
4383	The evolution of selector gene function: Expression dynamics and regulatory interactions of <i>tip/top/teashirt</i> across Arthropoda. <i>Evolution & Development</i> , 2018, 20, 219-232.	1.1	4
4384	Flanders hapavirus in western North America. <i>Archives of Virology</i> , 2018, 163, 3351-3356.	0.9	0
4385	Cryptic diversity within the <i>Megophrys</i> major species group (Amphibia: Megophryidae) of the Asian Horned Frogs: Phylogenetic perspectives and a taxonomic revision of South Asian taxa, with descriptions of four new species. <i>Zootaxa</i> , 2018, 4523, 1.	0.2	33

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4386	Base-By-Base Version 3: New Comparative Tools for Large Virus Genomes. <i>Viruses</i> , 2018, 10, 637.	1.5	24
4387	Characterization of the whole chloroplast genome <i>Caulerpa lentillifera</i> J. Agardh (Bryopsidales,) Tj ETQq1 1 0.784314,rgBT /Oyerlock 10 0.2	0.2	2
4388	Phylogeny, Evidence for a Cryptic Plastid, and Distribution of <i>Chytriodinium</i> Parasites (Dinophyceae) Infecting Copepods. <i>Journal of Eukaryotic Microbiology</i> , 2019, 66, 574-581.	0.8	2
4389	Identification of Lake Baikal Plankton Dinoflagellates from the Genera <i>Gyrodinium</i> and <i>Gymnodinium</i> Using Single-Cell PCR. <i>Russian Journal of Genetics</i> , 2018, 54, 1302-1313.	0.2	1
4390	Bark Beetle-Associated Blue-Stain Fungi Increase Antioxidant Enzyme Activities and Monoterpene Concentrations in <i>Pinus yunnanensis</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 1731.	1.7	11
4391	<i>Cystotheca kusanoi</i> comb. nov.: a redescription with new morphological observations. <i>Mycotaxon</i> , 2018, 133, 401-414.	0.1	2
4392	<i>Teuvoa saxicola</i> and <i>T. alpina</i> spp. nov. and the genus in China. <i>Mycotaxon</i> , 2018, 133, 79-87.	0.1	1
4393	Population Genomics and Biogeography of the Northern Acorn Barnacle (<i>Semibalanus balanoides</i>) Using Pooled Sequencing Approaches. <i>Population Genomics</i> , 2018, , 139-168.	0.2	9
4394	The first record of <i>Ophioleila elegans</i> (Echinodermata: Ophiuroidea) from a deep-sea seamount in the Northwest Pacific Ocean. <i>Acta Oceanologica Sinica</i> , 2018, 37, 180-184.	0.4	6
4395	<i>Allobodo chlorophagus</i> n. gen. n. sp., a Kinetoplastid that Infiltrates and Feeds on the Invasive Alga <i>Codium fragile</i> . <i>Protist</i> , 2018, 169, 911-925.	0.6	4
4396	Genome-wide analysis of <i>Streptococcus pneumoniae</i> serogroup 19 in the decade after the introduction of pneumococcal conjugate vaccines in Australia. <i>Scientific Reports</i> , 2018, 8, 16969.	1.6	14
4397	Evolution of host support for two ancient bacterial symbionts with differentially degraded genomes in a leafhopper host. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E11691-E11700.	3.3	49
4398	Taxonomic revision of the Western Palaearctic bees of the subgenus <i>Pseudomegachile</i> (Hymenoptera,) Tj ETQq0 0 0,rgBT /Oyerlock 10 0.2	0.2	7
4399	Complete mitochondrial genomes of six species of the freshwater red algal order <i>Batrachospermales</i> (Rhodophyta). <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 607-610.	0.2	4
4400	Complete chloroplast genome sequence of an endangered tree species, <i>Magnolia sieboldii</i> (Magnoliaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 1261-1262.	0.2	2
4401	Reevaluating the Salty Divide: Phylogenetic Specificity of Transitions between Marine and Freshwater Systems. <i>MSystems</i> , 2018, 3, .	1.7	37
4402	Hemimastigophora is a novel supra-kingdom-level lineage of eukaryotes. <i>Nature</i> , 2018, 564, 410-414.	13.7	101
4403	Computational enhancement of single-cell sequences for inferring tumor evolution. <i>Bioinformatics</i> , 2018, 34, i917-i926.	1.8	32

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4404	Comparative morphology and evolution of the cnidosac in Cladobronchia (Gastropoda: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50,742 Td (H	0.9	33
4405	Whole genome screen reveals a novel relationship between Wolbachia levels and Drosophila host translation. PLoS Pathogens, 2018, 14, e1007445.	2.1	42
4406	Delineation of the Genera Haemoproteus and Plasmodium Using RNA-Seq and Multi-gene Phylogenetics. Journal of Molecular Evolution, 2018, 86, 646-654.	0.8	18
4407	Morphological Data Sets Fit a Common Mechanism Much More Poorly than DNA Sequences and Call Into Question the Mkv Model. Systematic Biology, 2019, 68, 494-504.	2.7	47
4408	Whole-genome epidemiology, characterisation, and phylogenetic reconstruction of Staphylococcus aureus strains in a paediatric hospital. Genome Medicine, 2018, 10, 82.	3.6	54
4409	The gill-associated microbiome is the main source of wood plant polysaccharide hydrolases and secondary metabolite gene clusters in the mangrove shipworm Neoteredo reynei. PLoS ONE, 2018, 13, e0200437.	1.1	18
4410	Whole Genome Sequencing for Determining the Source of Mycobacterium bovis Infections in Livestock Herds and Wildlife in New Zealand. Frontiers in Veterinary Science, 2018, 5, 272.	0.9	44
4411	Whole-genome sequencing of 175 Mongolians uncovers population-specific genetic architecture and gene flow throughout North and East Asia. Nature Genetics, 2018, 50, 1696-1704.	9.4	38
4412	Multiple transmissions of de novo mutations in families. Nature Genetics, 2018, 50, 1674-1680.	9.4	89
4413	Integrative taxonomy resolves taxonomic uncertainty for freshwater mussels being considered for protection under the U.S. Endangered Species Act. Scientific Reports, 2018, 8, 15892.	1.6	51
4414	The complete chloroplast genome of Menispermum dauricum (Menispermaceae, Ranunculales). Mitochondrial DNA Part B: Resources, 2018, 3, 913-914.	0.2	6
4415	Computational Tools for Population Genomics. Population Genomics, 2018, , 127-160.	0.2	2
4416	The complete chloroplast genome of Zelkova schneideriana (Rosales: Ulmaceae), an Endangered species endemic to China. Mitochondrial DNA Part B: Resources, 2018, 3, 734-735.	0.2	0
4417	The first complete chloroplast genome of Pteris vittata (Pteridaceae), an arsenic hyperaccumulating fern. Mitochondrial DNA Part B: Resources, 2018, 3, 947-948.	0.2	2
4418	The genome of the oyster <i>Saccostrea</i> offers insight into the environmental resilience of bivalves. DNA Research, 2018, 25, 655-665.	1.5	92
4419	Halonatospora gen. nov. with H. pansihalos comb. nov. and Glomus bareae sp. nov. (Glomeromycota: Tj ETQq1 1 0,784314 rgBT /Overlock 10 Tf 15	0.5	15
4420	Spatial phylogenetics reveals evolutionary constraints on the assembly of a large regional flora. American Journal of Botany, 2018, 105, 1938-1950.	0.8	21
4421	Tempo and Mode of Genome Evolution in the Budding Yeast Subphylum. Cell, 2018, 175, 1533-1545.e20.	13.5	445

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4422	Resolving distribution and population fragmentation in two leaf-tailed gecko species of north-east Australia: key steps in the conservation of microendemic species. <i>Australian Journal of Zoology</i> , 2018, 66, 152.	0.6	4
4423	Fungal diversity notes 840–928: micro-fungi associated with Pandanaceae. <i>Fungal Diversity</i> , 2018, 93, 1-160.	4.7	125
4424	Contribution of Eat1 and Other Alcohol Acyltransferases to Ester Production in <i>Saccharomyces cerevisiae</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 3202.	1.5	25
4425	The first world swimming championships of roseobacters—Phylogenomic insights into an exceptional motility phenotype. <i>Systematic and Applied Microbiology</i> , 2018, 41, 544-554.	1.2	23
4426	Rapid Expansion of a Highly Germline-Expressed <i>Mariner</i> Element Acquired by Horizontal Transfer in the Fire Ant Genome. <i>Genome Biology and Evolution</i> , 2018, 10, 3262-3278.	1.1	6
4427	Molecular phylogeny, morphological diversity, and systematic revision of a species complex of common wild rat species in China (Rodentia, Murinae). <i>Journal of Mammalogy</i> , 2018, 99, 1350-1374.	0.6	15
4428	<i>Exostoma tibetana</i> , a new glyptosternine catfish from the lower Yarlung Tsangpo River drainage in southeastern Tibet, China (Siluriformes: Sisoridae). <i>Zootaxa</i> , 2018, 4527, 392.	0.2	7
4429	Cleaning a taxonomic dustbin: placing the European <i>Hypnum</i> species in a phylogenetic context!. <i>Bryophyte Diversity and Evolution</i> , 2018, 40, 37.	1.0	24
4430	Taxonomic revision of <i>Carpesium linearibracteatum</i> (Asteraceae: Inulinae) from China. <i>Phytotaxa</i> , 2018, 371, 111.	0.1	0
4431	<i>Ochrolechia incarnata</i> comb. nov. (Lecanoromycetes, Ascomycota), a distinct species of the <i>O. parella</i> group from Europe and Macaronesia. <i>Phytotaxa</i> , 2018, 371, 119.	0.1	2
4432	<i>Betaphycus gelatinus</i> and <i>B. philippinensis</i> (Gigartinales, Rhodophyta) are conspecific. <i>Phytotaxa</i> , 2018, 372, 22.	0.1	5
4433	Morphological and molecular characterization of <i>Lobophora declerckii</i> and <i>L. variegata</i> (Dictyotales, Tj ETQq1 1 0.784314 rgBT / Overbo	0.1	5
4434	The genus <i>Mycena</i> (Basidiomycota, Agaricales, Mycenaceae) and allied genera from Republic of São Tomé and Príncipe, West Africa. <i>Phytotaxa</i> , 2018, 383, 1.	0.1	6
4435	Evaluation of diagnostic chemical and morphological characters in five <i>Parmelia</i> species (Parmeliaceae, lichenized Ascomycota) with special emphasis on the thallus pruinosity. <i>Phytotaxa</i> , 2018, 383, 165.	0.1	11
4436	New dictyostelid cellular slime molds from South Africa. <i>Phytotaxa</i> , 2018, 383, 233.	0.1	3
4437	A new species of <i>Hygrocybe</i> from Kerala State, India. <i>Phytotaxa</i> , 2018, 385, 13.	0.1	5
4438	Genome rearrangements and selection in multi-chromosome bacteria <i>Burkholderia</i> spp.. <i>BMC Genomics</i> , 2018, 19, 965.	1.2	30
4439	Whole genome sequencing of <i>Moraxella bovoculi</i> reveals high genetic diversity and evidence for interspecies recombination at multiple loci. <i>PLoS ONE</i> , 2018, 13, e0209113.	1.1	19

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4440	A New Species of <i>Enyalius</i> (Squamata, Leiosauridae) Endemic to the Brazilian Cerrado. <i>Herpetologica</i> , 2018, 74, 355-369.	0.2	6
4441	Assessing the Efficiency of Molecular Markers for the Species Identification of Gregarines Isolated from the Mealworm and Super Worm Midgut. <i>Microorganisms</i> , 2018, 6, 119.	1.6	4
4442	Giant flagellins form thick flagellar filaments in two species of marine β -proteobacteria. <i>PLoS ONE</i> , 2018, 13, e0206544.	1.1	10
4443	<i>Bacidia albogranulosa</i> (Ramalinaceae, lichenized Ascomycota), a new sorediate lichen from European old-growth forests. <i>MycKeys</i> , 2018, 44, 51-62.	0.8	12
4444	Gene characteristics of the complete mitochondrial genomes of <i>Paratoxodera polyacantha</i> and <i>Toxodera hauseri</i> (Mantodea: Toxoderidae). <i>PeerJ</i> , 2018, 6, e4595.	0.9	45
4445	A new species of <i>Gyroporus</i> (Gyroporaceae, Boletales) from Atlantic Forest in Southern Brazil. <i>Nova Hedwigia</i> , 2018, 107, 291-301.	0.2	6
4446	A re-evaluation of Neotropical <i>Junghuhnia</i> s.lat. (<i>Polyporales</i> , <i>Basidiomycota</i>) based on morphological and multigene analyses. <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2018, 41, 130-141.	1.6	21
4447	Molecular phylogenetic data and seed coat anatomy resolve the generic position of some critical <i>Chenopodioidae</i> (<i>Chenopodiaceae</i> $\hat{=}$ <i>Amaranthaceae</i>) with reduced perianth segments. <i>PhytoKeys</i> , 2018, 109, 103-128.	0.4	15
4448	First records of the fall armyworm, <i>Spodoptera frugiperda</i> (Lepidoptera: Noctuidae), in Senegal. <i>Entomologia Generalis</i> , 2018, 37, 129-142.	1.1	24
4449	Improving Our Understanding of <i>Salmonella enterica</i> Serovar Paratyphi B through the Engineering and Testing of a Live Attenuated Vaccine Strain. <i>MSphere</i> , 2018, 3, .	1.3	7
4450	Two new species of <i>Barssia</i> from China <i>Phytotaxa</i> , 2018, 374, 129.	0.1	2
4451	A new species of <i>Agaricus</i> sect. <i>Brunneopicti</i> from Eastern India. <i>Phytotaxa</i> , 2018, 374, 139.	0.1	5
4452	Species delimitation of <i>Stemona</i> (<i>Stemonaceae</i>) based on sequences of five plastid DNA regions. <i>Phytotaxa</i> , 2018, 374, 291.	0.1	1
4453	Bacterial Associates of a Gregarious Riparian Beetle With Explosive Defensive Chemistry. <i>Frontiers in Microbiology</i> , 2018, 9, 2361.	1.5	19
4454	Phylogenomic Analysis of the Gammaproteobacterial Methanotrophs (Order <i>Methylococcales</i>) Calls for the Reclassification of Members at the Genus and Species Levels. <i>Frontiers in Microbiology</i> , 2018, 9, 3162.	1.5	156
4455	Genome Sequences and Comparative Analysis of Two Extended-Spectrum Extensively-Drug Resistant <i>Mycobacterium tuberculosis</i> Strains. <i>Frontiers in Pharmacology</i> , 2018, 9, 1492.	1.6	2
4456	Intact cell MALDI-TOF mass spectrometric analysis of <i>Chroococcidiopsis</i> cyanobacteria for classification purposes and identification of possible marker proteins. <i>PLoS ONE</i> , 2018, 13, e0208275.	1.1	9
4457	Formal description of sequence-based voucherless Fungi: promises and pitfalls, and how to resolve them. <i>IMA Fungus</i> , 2018, 9, 143-165.	1.7	42

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4458	The Microbial Diversity of Caves. <i>Ecological Studies</i> , 2018, , 69-90.	0.4	31
4459	A sulfotransferase dosage-dependently regulates mouthpart polyphenism in the nematode <i>Pristionchus pacificus</i> . <i>Nature Communications</i> , 2018, 9, 4119.	5.8	28
4460	First evidence of the presence and activity of archaeal C3 group members in an Atlantic intertidal mudflat. <i>Scientific Reports</i> , 2018, 8, 11790.	1.6	5
4461	The complete mitochondrial genome of <i>Tylosotriton anhuiensis</i> and implications for its taxonomy. <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 1300-1301.	0.2	0
4462	Carbapenem-resistant Isolates of the <i>Klebsiella pneumoniae</i> Complex in Western China: The Common ST11 and the Surprising Hospital-specific Types. <i>Clinical Infectious Diseases</i> , 2018, 67, S263-S265.	2.9	36
4463	Species Delineation Within the <i>Euwallacea fornicatus</i> (Coleoptera: Curculionidae) Complex Revealed by Morphometric and Phylogenetic Analyses. <i>Insect Systematics and Diversity</i> , 2018, 2, .	0.7	46
4464	Transcriptional response of the obligate anaerobe <i>Desulfuribacillus stibiiarsenatis</i> MLFWâ€² ^T to growth on antimonate and other terminal electron acceptors. <i>Environmental Microbiology</i> , 2019, 21, 618-630.	1.8	19
4465	Genome Sequences of Two Novel Papillomaviruses Isolated from Healthy Skin of Pudu puda and Cervus elaphus Deer. <i>Genome Announcements</i> , 2018, 6, .	0.8	2
4466	Two Novel, Distantly Related Papillomaviruses Isolated from Healthy Skin of the Timor Deer (<i>Rusa</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.8	2
4467	<i>Enterococcus faecium</i> TIR-Domain Genes Are Part of a Gene Cluster Which Promotes Bacterial Survival in Blood. <i>International Journal of Microbiology</i> , 2018, 2018, 1-17.	0.9	7
4468	Combining Phylogenetic and Network Approaches to Identify HIV-1 Transmission Links in San Mateo County, California. <i>Frontiers in Microbiology</i> , 2018, 9, 2799.	1.5	9
4469	Split-inducing indels in phylogenomic analysis. <i>Algorithms for Molecular Biology</i> , 2018, 13, 12.	0.3	11
4470	Comparative analysis of <i>Faecalibacterium prausnitzii</i> genomes shows a high level of genome plasticity and warrants separation into new species-level taxa. <i>BMC Genomics</i> , 2018, 19, 931.	1.2	78
4471	A multigene typing system for human adenoviruses reveals a new genotype in a collection of Swedish clinical isolates. <i>PLoS ONE</i> , 2018, 13, e0209038.	1.1	13
4472	Powdery Mildews Are Characterized by Contracted Carbohydrate Metabolism and Diverse Effectors to Adapt to Obligate Biotrophic Lifestyle. <i>Frontiers in Microbiology</i> , 2018, 9, 3160.	1.5	45
4473	Complete Genome Sequence of <i>Streptomyces</i> sp. Strain SHP22-7, a New Species Isolated from Mangrove of Enggano Island, Indonesia. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	7
4474	Description of the larva of <i>Holocentropus insignis</i> Martynov 1924 (Trichoptera: Polycentropodidae) with notes on biology and distribution. <i>Zootaxa</i> , 2018, 4532, 231-247.	0.2	1
4475	Comparative genomics of downy mildews reveals potential adaptations to biotrophy. <i>BMC Genomics</i> , 2018, 19, 851.	1.2	59

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4476	Homologous recombination changes the context of Cytochrome b transcription in the mitochondrial genome of <i>Silene vulgaris</i> KRA. <i>BMC Genomics</i> , 2018, 19, 874.	1.2	16
4477	Integrated evidence reveals a new species in the ancient blue coral genus <i>Heliopora</i> (Octocorallia). <i>Scientific Reports</i> , 2018, 8, 15875.	1.6	27
4478	The complete mitochondrial genome of the Caribbean spiny lobster <i>Panulirus argus</i> . <i>Scientific Reports</i> , 2018, 8, 17690.	1.6	31
4479	Australasian orchid diversification in time and space: molecular phylogenetic insights from the beard orchids (<i>Calochilus</i> , Diurideae). <i>Australian Systematic Botany</i> , 2018, , .	0.3	3
4480	The shadow of the past: Convergence of young and old South American desert lizards as measured by head shape traits. <i>Ecology and Evolution</i> , 2018, 8, 11399-11409.	0.8	13
4481	Molecular epidemiology of a primarily MSM acute HIV-1 cohort in Bangkok, Thailand and connections within networks of transmission in Asia. <i>Journal of the International AIDS Society</i> , 2018, 21, e25204.	1.2	14
4482	A taxonomic reassessment of Tubeufiales based on multi-locus phylogeny and morphology. <i>Fungal Diversity</i> , 2018, 92, 131-344.	4.7	49
4483	Towards an accurate and efficient heuristic for species/gene tree co-estimation. <i>Bioinformatics</i> , 2018, 34, i697-i705.	1.8	10
4484	First insights on the genetic diversity of MDR <i>Mycobacterium tuberculosis</i> in Lebanon. <i>BMC Infectious Diseases</i> , 2018, 18, 710.	1.3	7
4485	Discovery of novel geranylgeranyl reductases and characterization of their substrate promiscuity. <i>Biotechnology for Biofuels</i> , 2018, 11, 340.	6.2	17
4486	Enrichment and Genomic Characterization of a N ₂ O-Reducing Chemolithoautotroph From a Deep-Sea Hydrothermal Vent. <i>Frontiers in Bioengineering and Biotechnology</i> , 2018, 6, 184.	2.0	6
4487	Complement Susceptibility in Relation to Genome Sequence of Recent <i>Klebsiella pneumoniae</i> Isolates from Thai Hospitals. <i>MSphere</i> , 2018, 3, .	1.3	25
4488	Two new species of <i>Garra</i> (Cypriniformes: Cyprinidae) from the lower Yarlung Tsangpo River drainage in southeastern Tibet, China. <i>Zootaxa</i> , 2018, 4532, 367-384.	0.2	8
4489	Phylogeography of <i>Bulinus truncatus</i> (Audouin, 1827) (Gastropoda: Planorbidae) in Selected African Countries. <i>Tropical Medicine and Infectious Disease</i> , 2018, 3, 127.	0.9	10
4490	Uncovering secondary metabolite evolution and biosynthesis using gene cluster networks and genetic dereplication. <i>Scientific Reports</i> , 2018, 8, 17957.	1.6	33
4491	Description of a New <i>Rhagoletis</i> (Diptera: Tephritidae) Species in the <i>tabellaria</i> Species Group. <i>Insect Systematics and Diversity</i> , 2018, 2, .	0.7	4
4492	Monophyly of the subfamily Neobisiinae (Pseudoscorpiones: Neobisiidae). <i>Journal of Arachnology</i> , 2018, 46, 481-487.	0.3	3
4493	Expansion and Divergence of Argonaute Genes in the Oomycete Genus <i>Phytophthora</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 2841.	1.5	14

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4494	Relation between mitochondrial DNA hyperdiversity, mutation rate and mitochondrial genome evolution in <i>Melarhaphe neritoides</i> (Gastropoda: Littorinidae) and other Caenogastropoda. <i>Scientific Reports</i> , 2018, 8, 17964.	1.6	21
4495	Photoecology of the Antarctic cyanobacterium <i>Leptolyngbya</i> sp. BC1307 brought to light through community analysis, comparative genomics and in vitro photophysiology. <i>Molecular Ecology</i> , 2018, 27, 5279-5293.	2.0	14
4496	Genome sequence of walking catfish (<i>Clarias batrachus</i>) provides insights into terrestrial adaptation. <i>BMC Genomics</i> , 2018, 19, 952.	1.2	36
4497	Morphology and molecular phylogeny of <i>Pleurosira nanjiensis</i> sp. nov., a new marine benthic diatom from the Nanji Islands, China. <i>Acta Oceanologica Sinica</i> , 2018, 37, 33-39.	0.4	6
4498	<i>Ototyphlonemertes longissima</i> sp. nov. (Hoplonemertea: Monostilifera: Ototyphlonemertidae), a new interstitial nemertean from the South China Sea. <i>Zootaxa</i> , 2018, 4527, 581-587.	0.2	1
4499	Genome of the small hive beetle (<i>Aethina tumida</i> , Coleoptera: Nitidulidae), a worldwide parasite of social bee colonies, provides insights into detoxification and herbivory. <i>GigaScience</i> , 2018, 7, .	3.3	49
4500	Transmission of <i>mcr-1</i> -Producing Multidrug-resistant Enterobacteriaceae in Public Transportation in Guangzhou, China. <i>Clinical Infectious Diseases</i> , 2018, 67, S217-S224.	2.9	33
4501	Molecular characterization of eukaryotic algal communities in the tropical phyllosphere based on real-time sequencing of the 18S rDNA gene. <i>BMC Plant Biology</i> , 2018, 18, 365.	1.6	40
4502	Contrasting Symbiotic Patterns in Two Closely Related Lineages of Trimembered Lichens of the Genus <i>Peltigera</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 2770.	1.5	25
4503	A genome-wide association analysis reveals a potential role for recombination in the evolution of antimicrobial resistance in <i>Burkholderia multivorans</i> . <i>PLoS Pathogens</i> , 2018, 14, e1007453.	2.1	28
4504	Colouration, chaetotaxy and molecular data provide species-level resolution in a species complex of <i>Dicranocentrus</i> (Collembola : Entomobryidae). <i>Invertebrate Systematics</i> , 2018, 32, 1298.	0.5	9
4505	Molecular phylogeny and systematics of the centipede genus <i>Ethmostigmus</i> Pocock (Chilopoda : Tj ETQq1 1 0.784314 rgBT /Overlooked	0.5	10
4506	Integrative taxonomy helps separate four species of freshwater shrimps commonly overlooked as <i>Caridina longirostris</i> (Crustacea : Decapoda : Atyidae) on Indo-West Pacific islands. <i>Invertebrate Systematics</i> , 2018, 32, 1422.	0.5	8
4507	Systematics of the genus <i>Halgerda</i> Bergh, 1880 (Heterobranchia : Nudibranchia) of Mozambique with descriptions of six new species. <i>Invertebrate Systematics</i> , 2018, 32, 1388.	0.5	10
4508	Cryptic Diversity in Colombian Edible Leaf-Cutting Ants (Hymenoptera: Formicidae). <i>Insects</i> , 2018, 9, 191.	1.0	3
4509	The genomic landscape of molecular responses to natural drought stress in <i>Panicum hallii</i> . <i>Nature Communications</i> , 2018, 9, 5213.	5.8	101
4510	Antimicrobial resistance prediction and phylogenetic analysis of <i>Neisseria gonorrhoeae</i> isolates using the Oxford Nanopore MinION sequencer. <i>Scientific Reports</i> , 2018, 8, 17596.	1.6	59
4511	Identification and partial characterization of a novel serpin from <i>Eudiplozoon nipponicum</i> (Monogenea, Polyopisthocotylea). <i>Parasite</i> , 2018, 25, 61.	0.8	12

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4512	Evolution of mitochondrial TAT translocases illustrates the loss of bacterial protein transport machines in mitochondria. <i>BMC Biology</i> , 2018, 16, 141.	1.7	21
4513	Mitochondrial genomes of two diplectanids (Platyhelminthes: Monogenea) expose paraphyly of the order Dactylogyridea and extensive tRNA gene rearrangements. <i>Parasites and Vectors</i> , 2018, 11, 601.	1.0	37
4514	High genetic diversity and distinct ancient lineage of Asiatic black bears revealed by non-invasive surveys in the Annapurna Conservation Area, Nepal. <i>PLoS ONE</i> , 2018, 13, e0207662.	1.1	45
4515	An expanded molecular phylogeny of Plumbaginaceae, with emphasis on <i>Limonium</i> (sea) Tj ETQq1 1 0.784314 rgBT /Overlock 10 12397-12424.	0.8	37
4516	Metatranscriptomic and Thermodynamic Insights into Medium-Chain Fatty Acid Production Using an Anaerobic Microbiome. <i>MSystems</i> , 2018, 3, .	1.7	69
4517	Phylogenetic study and taxonomic revision of the <i>Xanthoparmelia mexicana</i> group, including the description of a new species (Parmeliaceae, Ascomycota). <i>MycKeys</i> , 2018, 40, 13-28.	0.8	4
4518	Four new species of <i>Bacidia</i> s.s. (<i>Ramalinaceae</i> , <i>Lecanorales</i>) in the Russian Far East. <i>Lichenologist</i> , 2018, 50, 603-625.	0.5	6
4519	The phylogeography and incidence of multi-drug resistant typhoid fever in sub-Saharan Africa. <i>Nature Communications</i> , 2018, 9, 5094.	5.8	98
4520	Characterization of the complete chloroplast genome of <i>Camellia granthamiana</i> (Theaceae), a Vulnerable species endemic to China. <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 1139-1140.	0.2	4
4521	A new species of <i>Lecidea</i> (Lecanorales, Ascomycota) from Pakistan. <i>MycKeys</i> , 2018, 38, 25-34.	0.8	35
4522	Pre-Pleistocene origin of phylogeographical breaks in African rain forest trees: New insights from <i>Greenwayodendron</i> (Annonaceae) phylogenomics. <i>Journal of Biogeography</i> , 2019, 46, 212-223.	1.4	30
4523	Genomic insights into virulence mechanisms of <i>Leishmania donovani</i> : evidence from an atypical strain. <i>BMC Genomics</i> , 2018, 19, 843.	1.2	33
4524	Prevalence and Intra-Family Phylogenetic Divergence of <i>Burkholderiaceae</i> -Related Endobacteria Associated with Species of <i>Mortierella</i> . <i>Microbes and Environments</i> , 2018, 33, 417-427.	0.7	30
4525	Isolation and Characterization of Anaepheneas "C, Alkylphenols from a Filamentous Cyanobacterium (<i>Hormoscilla</i> sp., Oscillatoriales). <i>Journal of Natural Products</i> , 2018, 81, 2716-2721.	1.5	21
4526	Genetic characterization and molecular epidemiological analysis of novel enterovirus EV-B80 in China. <i>Emerging Microbes and Infections</i> , 2018, 7, 1-12.	3.0	23
4527	New species of <i>Cortinarius</i> sect. <i>Austroamericani</i> , sect. nov., from South American Nothofagaceae forests. <i>Mycologia</i> , 2018, 110, 1127-1144.	0.8	8
4528	The complete chloroplast genome of the Chinese <i>Abelia Lineae chinensis</i> (R.Br.) A.Braun & Vatke (Caprifoliaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 1081-1082.	0.2	0
4529	Characterization of the complete mitochondrial genomes and phylogenetic analysis of the two <i>Luciogobius</i> species (Perciformes, Gobionellinae) from Korea. <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 1154-1155.	0.2	0

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4530	Population genomics and climate adaptation of a C4 perennial grass, <i>Panicum hallii</i> (Poaceae). <i>BMC Genomics</i> , 2018, 19, 792.	1.2	9
4531	Selective constraint and adaptive potential of West Nile virus within and among naturally infected avian hosts and mosquito vectors. <i>Virus Evolution</i> , 2018, 4, vey013.	2.2	13
4532	Redescription and phylogenetic placement of <i>Cirrhilabrus sanguineus</i> Cornic (Teleostei: Labridae), with first documentation of the female form. <i>Zootaxa</i> , 2018, 4526, 358.	0.2	6
4533	The complete chloroplast genome of <i>Aquilaria malaccensis</i> Lam. (Thymelaeaceae), an important and threatened agarwood-producing tree species. <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 1120-1121.	0.2	10
4534	<i>Salmonella enterica</i> Phylogeny Based on Whole-Genome Sequencing Reveals Two New Clades and Novel Patterns of Horizontally Acquired Genetic Elements. <i>MBio</i> , 2018, 9, .	1.8	71
4535	Comparative Analysis of the Nodule Transcriptomes of <i>Ceanothus thyrsiflorus</i> (Rhamnaceae, Rosales) and <i>Datisca glomerata</i> (Datiscaceae, Cucurbitales). <i>Frontiers in Plant Science</i> , 2018, 9, 1629.	1.7	12
4536	Introduction to Bioinformatics in Microbiology. <i>Learning Materials in Biosciences</i> , 2018, , .	0.2	5
4537	Short Introduction to Phylogenetic Analysis of Molecular Sequence Data. <i>Learning Materials in Biosciences</i> , 2018, , 103-120.	0.2	0
4538	Daily changes in phytoplankton lipidomes reveal mechanisms of energy storage in the open ocean. <i>Nature Communications</i> , 2018, 9, 5179.	5.8	63
4539	Opposite macroevolutionary responses to environmental changes in grasses and insects during the Neogene grassland expansion. <i>Nature Communications</i> , 2018, 9, 5089.	5.8	32
4540	The complete chloroplast genome of <i>Sarcandra glabra</i> (Chloranthaceae): a perianthless basal angiosperm. <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 661-662.	0.2	3
4541	Where is the enigmatic <i>Telmatobius halli</i> Noble 1938? Rediscovery and clarification of a frog species not seen for 80 years. <i>Zootaxa</i> , 2018, 4527, 61.	0.2	5
4542	A new species of <i>Brasilotyphlus</i> (Gymnophiona: Siphonopidae) and a contribution to the knowledge of the relationship between <i>Microcaecilia</i> and <i>Brasilotyphlus</i> . <i>Zootaxa</i> , 2018, 4527, 186-196.	0.2	4
4543	Phylogenomics of a putatively convergent novelty: did hypertrophied lips evolve once or repeatedly in Lake Malawi cichlid fishes?. <i>BMC Evolutionary Biology</i> , 2018, 18, 179.	3.2	14
4544	Egg Case Silk Gene Sequences from <i>Argiope</i> Spiders: Evidence for Multiple Loci and a Loss of Function Between Paralogs. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 231-238.	0.8	18
4545	A Taxonomic and Biogeographic Reappraisal of the Genus <i>Dicksonia</i> (Dicksoniaceae) in the Neotropics. <i>Systematic Botany</i> , 2018, 43, 839-857.	0.2	5
4546	Genomic and Genetic Insights Into a Cosmopolitan Fungus, <i>Paecilomyces variotii</i> (Eurotiales). <i>Frontiers in Microbiology</i> , 2018, 9, 3058.	1.5	35
4547	Intergeneric Relationships within the Early-Diverging Angiosperm Family Nymphaeaceae Based on Chloroplast Phylogenomics. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3780.	1.8	11

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4548	Co-culture of a Novel Fermentative Bacterium, <i>Lucifera butyrica</i> gen. nov. sp. nov., With the Sulfur Reducer <i>Desulfurella amilsii</i> for Enhanced Sulfidogenesis. <i>Frontiers in Microbiology</i> , 2018, 9, 3108.	1.5	22
4549	An Introduction to the Systematics of Small-Bodied <i>Neacomys</i> (Rodentia: Cricetidae) from Peru with Descriptions of Two New Species. <i>American Museum Novitates</i> , 2018, 3913, 1-38.	0.2	12
4550	Phylogeny and spatio-temporal diversification of <i>Prunus</i> subgenus <i>Laurocerasus</i> section <i>Mesopygeum</i> (Rosaceae) in the Malesian region. <i>Journal of Systematics and Evolution</i> , 2018, 56, 637-651.	1.6	22
4551	Cloning of the wheat Yr15 resistance gene sheds light on the plant tandem kinase-pseudokinase family. <i>Nature Communications</i> , 2018, 9, 3735.	5.8	204
4552	Genome-wide analysis of horizontally acquired genes in the genus <i>Mycobacterium</i> . <i>Scientific Reports</i> , 2018, 8, 14817.	1.6	21
4553	Environmentally-driven gene content convergence and the <i>Bacillus</i> phylogeny. <i>BMC Evolutionary Biology</i> , 2018, 18, 148.	3.2	23
4554	Shark genomes provide insights into elasmobranch evolution and the origin of vertebrates. <i>Nature Ecology and Evolution</i> , 2018, 2, 1761-1771.	3.4	197
4555	A phylogenetic study of two recently described endemic species of the <i>Saxifraga granulata</i> group from the central-north Mediterranean region (Italy) and their position in the context of the series <i>Saxifraga</i> (Saxifragaceae). <i>Systematics and Biodiversity</i> , 2018, 16, 784-790.	0.5	2
4556	The complete chloroplast genome sequence of <i>Abies beshanzuensis</i> , a highly endangered fir species from south China. <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 921-922.	0.2	10
4557	<i>Kindia</i> (Pavetteae, Rubiaceae), a new cliff-dwelling genus with chemically profiled colleter exudate from Mt Gangan, Republic of Guinea. <i>PeerJ</i> , 2018, 6, e4666.	0.9	19
4558	NJMerge: A Generic Technique for Scaling Phylogeny Estimation Methods and Its Application to Species Trees. <i>Lecture Notes in Computer Science</i> , 2018, , 260-276.	1.0	11
4559	The role of gene flow in rapid and repeated evolution of cave-related traits in Mexican tetra, <i>Astyanax mexicanus</i> . <i>Molecular Ecology</i> , 2018, 27, 4397-4416.	2.0	160
4560	Transpacific coalescent pathways of coconut rhinoceros beetle biotypes: Resistance to biological control catalyses resurgence of an old pest. <i>Molecular Ecology</i> , 2018, 27, 4459-4474.	2.0	26
4561	Delimiting species of marine gastropods (Turridae, Conoidea) using RAD sequencing in an integrative taxonomy framework. <i>Molecular Ecology</i> , 2018, 27, 4591-4611.	2.0	20
4562	Novel Class of Viral Ankyrin Proteins Targeting the Host E3 Ubiquitin Ligase Cullin-2. <i>Journal of Virology</i> , 2018, 92, .	1.5	25
4563	Molecular phylogeny and biogeographic history of the Neotropical tribe Glandulocaudini (Characiformes: Characidae: Stevardiinae). <i>Neotropical Ichthyology</i> , 2018, 16, .	0.5	7
4564	<i>Postia caesia</i> complex (<i>Polyporales</i> , <i>Basidiomycota</i>) in temperate Northern Hemisphere. <i>Fungal Systematics and Evolution</i> , 2018, 1, 101-129.	0.9	27
4565	Towards integrative taxonomy in Neotropical botany: disentangling the <i>Pagamea guianensis</i> species complex (Rubiaceae). <i>Botanical Journal of the Linnean Society</i> , 2018, 188, 213-231.	0.8	41

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4566	Molecular parallelism in fast-twitch muscle proteins in echolocating mammals. <i>Science Advances</i> , 2018, 4, eaat9660.	4.7	17
4567	Widespread Antibiotic, Biocide, and Metal Resistance in Microbial Communities Inhabiting a Municipal Waste Environment and Anthropogenically Impacted River. <i>MSphere</i> , 2018, 3, .	1.3	12
4568	Phylogenetic relationships of the Balkan Moitessieriidae (Caenogastropoda: Truncatelloidea). <i>Zootaxa</i> , 2018, 4486, 311-339.	0.2	18
4569	Silk genes and silk gene expression in the spider <i>Tengella perfuga</i> (Zoropsidae), including a potential cribellar spidroin (CrSp). <i>PLoS ONE</i> , 2018, 13, e0203563.	1.1	13
4570	Functional Analysis of Four Terpene Synthases in Rose-Scented Pelargonium Cultivars (<i>Pelargonium</i> Å—) Tj ETQq0 0.0 rgBT /Overlock 10	1.7	16
4571	RAD sequencing resolved phylogenetic relationships in European shrub willows (<i>Salix</i> L. subg.) Tj ETQq1 1 0.784314 rgBT /Overlock 39 and Evolution, 2018, 8, 8243-8255.	0.8	39
4572	An updated phylogeny of <i>Deprea</i> (Solanaceae) with a new species from Colombia: interspecific relationships, conservation assessment, and a key for Colombian species. <i>Systematics and Biodiversity</i> , 2018, 16, 680-691.	0.5	6
4573	Paleotropical Diversification Dominates the Evolution of the Hyperdiverse Ant Tribe Crematogastrini (Hymenoptera: Formicidae). <i>Insect Systematics and Diversity</i> , 2018, 2, .	0.7	27
4574	Opaque-2 Regulates a Complex Gene Network Associated with Cell Differentiation and Storage Functions of Maize Endosperm. <i>Plant Cell</i> , 2018, 30, 2425-2446.	3.1	83
4575	A review of the genus <i>Labeo</i> (Teleostei: Cyprinidae) in Sri Lanka. <i>Zootaxa</i> , 2018, 4486, 201-235.	0.2	20
4576	Comparative Analysis of Genetic and Chemical Differences between Four <i>Berberis</i> Herbs Based on Molecular Phylogenetic and HPLC Methods. <i>Biological and Pharmaceutical Bulletin</i> , 2018, 41, 1870-1873.	0.6	11
4577	<i>Seiridium</i> (<i>Sporocadaceae</i>): an important genus of plant pathogenic fungi. <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2018, 40, 96-118.	1.6	27
4578	Building (Viral) Phylogenetic Trees Using a Maximum Likelihood Approach. <i>Current Protocols in Microbiology</i> , 2018, 51, e63.	6.5	5
4579	Genome-wide analysis of <i>Borrelia turcica</i> and <i>Candidatus Borrelia tachyglossi</i> ™ shows relapsing fever-like genomes with unique genomic links to Lyme disease <i>Borrelia</i> . <i>Infection, Genetics and Evolution</i> , 2018, 66, 72-81.	1.0	28
4580	Punctuated plastome reduction and host-parasite horizontal gene transfer in the holoparasitic plant genus <i>Aphyllon</i> . <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018, 285, 20181535.	1.2	25
4581	Diversity and phylogeny of <i>Sargassum</i> (Fucales, Phaeophyceae) in Singapore. <i>Phytotaxa</i> , 2018, 369, 200.	0.1	23
4582	Single-Cell Genomics Reveals a Diverse Metabolic Potential of Uncultivated <i>Desulfatiglans</i> -Related Deltaproteobacteria Widely Distributed in Marine Sediment. <i>Frontiers in Microbiology</i> , 2018, 9, 2038.	1.5	69
4583	Repeated inversions within a pannier intron drive diversification of intraspecific colour patterns of ladybird beetles. <i>Nature Communications</i> , 2018, 9, 3843.	5.8	61

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4584	A systematic revision of the ectomycorrhizal genus <i>Laccaria</i> from Korea. <i>Mycologia</i> , 2018, 110, 948-961.	0.8	25
4585	Comparative description of mitochondrial genomes of the honey bee <i>Apis</i> (Hymenoptera: Apidae): four new genome sequences and <i>Apis</i> phylogeny using whole genomes and individual genes. <i>Journal of Apicultural Research</i> , 2018, 57, 484-503.	0.7	8
4586	Something special about CO ₂ -dependent CO ₂ fixation. <i>FEBS Journal</i> , 2018, 285, 4181-4195.	2.2	26
4587	The genome of common long-arm octopus <i>Octopus minor</i> . <i>GigaScience</i> , 2018, 7, .	3.3	43
4588	Technical Advances and Challenges in Genome-Scale Analysis of Ancient DNA. <i>Population Genomics</i> , 2018, , 3-29.	0.2	2
4589	Testing reticulate evolution of four <i>Vitis</i> species from East Asia using restriction-site associated DNA sequencing. <i>Journal of Systematics and Evolution</i> , 2018, 56, 331-339.	1.6	29
4590	Molecular phylogeny and morphological diversity of inland <i>Cladophora</i> (Cladophorales, Tj ETQq0 0 0 rBT /Overlock 10 Tf 50 50)	0.6	8
4591	Phylogenetic relationships of <i>Stenogramma</i> (Gigartinales, Rhodophyta) with a description of <i>S. coreanum</i> sp. nov. <i>Phycologia</i> , 2018, 57, 243-250.	0.6	1
4592	Molecular and morphological characterization of <i>Laurencia intricata</i> and <i>Laurenciella mayaimii</i> sp. nov. (Ceramiales, Rhodophyta) in South Florida, USA. <i>Phycologia</i> , 2018, 57, 287-297.	0.6	8
4593	<i>Neochondria</i> gen. nov. (Rhodomelaceae, Rhodophyta), a segregate of <i>Chondria</i> , including <i>N. ammophila</i> sp. nov. and <i>N. nidifica</i> comb. nov.. <i>Phycologia</i> , 2018, 57, 262-272.	0.6	3
4594	Microbial Community and Metabolic Activity in Thiocyanate Degrading Low Temperature Microbial Fuel Cells. <i>Frontiers in Microbiology</i> , 2018, 9, 2308.	1.5	7
4595	Patterns of chromosomal evolution in the florally diverse Andean clade <i>Lochrominae</i> (Solanaceae). <i>Perspectives in Plant Ecology, Evolution and Systematics</i> , 2018, 35, 31-43.	1.1	13
4596	The complete plastid genomes of <i>Ophrys iricolor</i> and <i>O. sphegodes</i> (Orchidaceae) and comparative analyses with other orchids. <i>PLoS ONE</i> , 2018, 13, e0204174.	1.1	34
4597	Changes in mRNA abundance of insulin-like growth factors in the brain and liver of a tropical damselfish, <i>Chrysiptera cyanea</i> , in relation to seasonal and food-manipulated reproduction. <i>General and Comparative Endocrinology</i> , 2018, 269, 112-121.	0.8	9
4598	Single Nucleotide Polymorphism Analysis Indicates Genetic Distinction and Reduced Diversity of Swine-Associated Methicillin Resistant <i>Staphylococcus aureus</i> (MRSA) ST5 Isolates Compared to Clinical MRSA ST5 Isolates. <i>Frontiers in Microbiology</i> , 2018, 9, 2078.	1.5	28
4599	Heterobucephalopsine and prosorhynchine trematodes (Digenea: Bucephalidae) from teleost fishes of Moreton Bay, Queensland, Australia, with the description of two new species. <i>Systematic Parasitology</i> , 2018, 95, 783-806.	0.5	6
4600	Conformational changes on substrate binding revealed by structures of <i>Methylobacterium extorquens</i> malate dehydrogenase. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018, 74, 610-616.	0.4	8
4601	Integrating coalescent species delimitation with analysis of host specificity reveals extensive cryptic diversity despite minimal mitochondrial divergence in the malaria parasite genus <i>Leucocytozoon</i> . <i>BMC Evolutionary Biology</i> , 2018, 18, 128.	3.2	49

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4602	Phylogenetic, comparative genomic and structural analyses of human <i>Streptococcus agalactiae</i> ST485 in China. <i>BMC Genomics</i> , 2018, 19, 716.	1.2	7
4603	Genetic Analysis of Floral Symmetry Transition in African Violet Suggests the Involvement of Trans-acting Factor for <i>CYCLOIDEA</i> Expression Shifts. <i>Frontiers in Plant Science</i> , 2018, 9, 1008.	1.7	13
4604	Pinopsin evolved as the ancestral dim-light visual opsin in vertebrates. <i>Communications Biology</i> , 2018, 1, 156.	2.0	23
4605	Ecological speciation in darkness? Spatial niche partitioning in sibling subterranean spiders (Araneae: Tj ETQq1 1 0.784314 rgBT /Overlock 10 T	0.5	25
4606	Phylogeny of Hesionidae (Aciculata, Annelida), with four new species from deep-sea eastern Pacific methane seeps, and resolution of the affinity of Hesiolyra. <i>Invertebrate Systematics</i> , 2018, 32, 1050.	0.5	15
4607	Waking sleeping beauties: a molecular phylogeny and nomenclator of <i>Halgania</i> (Ehretiaceae, Tj ETQq1 1 0.784314 rgBT /Overlock 10 T	0.5	1
4608	Unveiling the RNA virosphere associated with marine microorganisms. <i>Molecular Ecology Resources</i> , 2018, 18, 1444-1455.	2.2	59
4609	<i>Kaviengella jeffkinchi</i> , a new genus and species of symbiotic shrimp (Crustacea: Decapoda: Tj ETQq1 1 0.784314 rgBT /Overlock 10 T	0.2	2
4610	Morphological and molecular evidence reveal a new species of the earthworm genus <i>Pontodrilus</i> Perrier, 1874 (Clitellata, Megascolecidae) from Thailand and Peninsular Malaysia. <i>Zootaxa</i> , 2018, 4496, 218-237.	0.2	11
4611	The complete mitochondrial genome of <i>Cymothoa indica</i> has a highly rearranged gene order and clusters at the very base of the Isopoda clade. <i>PLoS ONE</i> , 2018, 13, e0203089.	1.1	14
4612	Whole Genome Sequencing of <i>Mycobacterium bovis</i> Isolated From Livestock in the United States, 1989–2018. <i>Frontiers in Veterinary Science</i> , 2018, 5, 253.	0.9	51
4613	Morphology and molecular phylogeny of two new species of <i>Spirostrombidium</i> (Ciliophora, Tj ETQq1 1 0.784314 rgBT /Overlock 10 T	0.5	14
4614	Reconciling species diversity in a tropical plant clade (Canarium, Burseraceae). <i>PLoS ONE</i> , 2018, 13, e0198882.	1.1	13
4615	Taxonomy and phylogeny of <i>Macrolepiota</i> : two new species from Brazil. <i>Mycologia</i> , 2018, 110, 930-940.	0.8	3
4616	Novel diversity in <i>Lactifluus</i> section <i>Gerardii</i> from Asia: five new species with pleurotoid or small agaricoid basidiocarps. <i>Mycologia</i> , 2018, 110, 962-984.	0.8	9
4617	Evolutionary trends in the columnar cactus genus <i>Eulychnia</i> (Cactaceae) based on molecular phylogenetics, morphology, distribution, and habitat. <i>Systematics and Biodiversity</i> , 2018, 16, 643-657.	0.5	4
4618	The genomic architecture and molecular evolution of ant odorant receptors. <i>Genome Research</i> , 2018, 28, 1757-1765.	2.4	59
4619	Methanogens and Iron-Reducing Bacteria: the Overlooked Members of Mercury-Methylating Microbial Communities in Boreal Lakes. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	46

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4620	Microhabitat change drives diversification in pholcid spiders. <i>BMC Evolutionary Biology</i> , 2018, 18, 141.	3.2	52
4621	Genome-wide markers reveal a complex evolutionary history involving divergence and introgression in the Abert's squirrel (<i>Sciurus aberti</i>) species group. <i>BMC Evolutionary Biology</i> , 2018, 18, 139.	3.2	3
4622	Recent advances in computational phylodynamics. <i>Current Opinion in Virology</i> , 2018, 31, 24-32.	2.6	45
4623	Phylotranscriptomics of <i>Pristionchus</i> Nematodes Reveals Parallel Gene Loss in Six Hermaphroditic Lineages. <i>Current Biology</i> , 2018, 28, 3123-3127.e5.	1.8	33
4624	Robust demarcation of fourteen different species groups within the genus <i>Streptococcus</i> based on genome-based phylogenies and molecular signatures. <i>Infection, Genetics and Evolution</i> , 2018, 66, 130-151.	1.0	34
4625	<i>Bifidobacterium primatium</i> sp. nov., <i>Bifidobacterium scaligerum</i> sp. nov., <i>Bifidobacterium felsineum</i> sp. nov. and <i>Bifidobacterium simiarum</i> sp. nov.: Four novel taxa isolated from the faeces of the cotton top tamarin (<i>Saguinus oedipus</i>) and the emperor tamarin (<i>Saguinus imperator</i>). <i>Systematic and Applied Microbiology</i> , 2018, 41, 593-603.	1.2	38
4626	Exploring the genome and transcriptome of the cave nectar bat <i>Eonycteris spelaea</i> with PacBio long-read sequencing. <i>GigaScience</i> , 2018, 7, .	3.3	33
4627	From Gondwana to <i>GAARlandia</i> : Evolutionary history and biogeography of <i>Deinopis</i> spiders (<i>Deinopis</i>). <i>Journal of Biogeography</i> , 2018, 45, 2442-2457.	1.4	39
4628	Taxonomic re-evaluation of the monotypic genus <i>Pararhabdophis</i> Bourret, 1934 (Squamata: Colubridae: Tj ETQq0 0.0 rgBT /Overlock 10	0.2	10
4629	Hidden diversity: Phylogeography of genus <i>Ototyphlonemertes</i> Diesing, 1863 (<i>Ototyphlonemertidae</i> : Tj ETQq1 1 0.784314 rgBT /Overl e0195833.	1.1	8
4630	So many genes, so little time: A practical approach to divergence-time estimation in the genomic era. <i>PLoS ONE</i> , 2018, 13, e0197433.	1.1	167
4631	Sequencing of complete mitochondrial genomes confirms synonymization of <i>Hyalomma asiaticum asiaticum</i> and <i>kozlovi</i> , and advances phylogenetic hypotheses for the Ixodidae. <i>PLoS ONE</i> , 2018, 13, e0197524.	1.1	22
4632	Combination therapy with anti-HIV-1 antibodies maintains viral suppression. <i>Nature</i> , 2018, 561, 479-484.	13.7	392
4633	Safety and antiviral activity of combination HIV-1 broadly neutralizing antibodies in viremic individuals. <i>Nature Medicine</i> , 2018, 24, 1701-1707.	15.2	195
4634	Community phylogeny of the globally critically imperiled pine rockland ecosystem. <i>American Journal of Botany</i> , 2018, 105, 1735-1747.	0.8	9
4635	An integrative approach in the assessment of species delimitation and structure of the <i>Merodon nanus</i> species group (Diptera: Syrphidae). <i>Organisms Diversity and Evolution</i> , 2018, 18, 479-497.	0.7	20
4636	Evidence of positive selection suggests possible role of aquaporins in the water-to-land transition of mudskippers. <i>Organisms Diversity and Evolution</i> , 2018, 18, 499-514.	0.7	8
4637	The complete chloroplast genome of the miracle tree <i>Neolamarckia cadamba</i> and its comparison in Rubiaceae family. <i>Biotechnology and Biotechnological Equipment</i> , 2018, 32, 1087-1097.	0.5	8

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4638	Ancient plants with ancient fungi: liverworts associate with early-diverging arbuscular mycorrhizal fungi. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018, 285, 20181600.	1.2	46
4639	Exclusivity offers a sound yet practical species criterion for bacteria despite abundant gene flow. <i>BMC Genomics</i> , 2018, 19, 724.	1.2	14
4640	Molecular Phylogeny of the Family Capitellidae (Annelida). <i>Zoological Science</i> , 2018, 35, 436-445.	0.3	4
4641	Reassessment of the Groundwater Amphipod <i>Paramoera relict</i> Synonymizes the Genus <i>Relictomoera</i> with <i>Paramoera</i> (Crustacea: Amphipoda: Pontogeneiidae). <i>Zoological Science</i> , 2018, 35, 459-467.	0.3	5
4642	Unicellular Origin of the Animal MicroRNA Machinery. <i>Current Biology</i> , 2018, 28, 3288-3295.e5.	1.8	42
4643	A Ycf2-FtsHi Heteromeric AAA-ATPase Complex Is Required for Chloroplast Protein Import. <i>Plant Cell</i> , 2018, 30, 2677-2703.	3.1	128
4644	Discovery of <i>mcr-1</i> -Mediated Colistin Resistance in a Highly Virulent <i>Escherichia coli</i> Lineage. <i>MSphere</i> , 2018, 3, .	1.3	48
4645	Exploring malaria vector diversity on the Amazon Frontier. <i>Malaria Journal</i> , 2018, 17, 342.	0.8	26
4646	<i>Coronacoccus hengyangensis</i> gen. et sp. nov., a new member of Chlorellaceae (Trebouxiophyceae, Chlorophyta) with radiococcacean morphology. <i>Phycologia</i> , 2018, 57, 363-373.	0.6	6
4647	Genomic characterization reveals significant divergence within <i>Chlorella sorokiniana</i> (Chlorellales.) Tj ETQq1 1 0.784314 rgBT / Overlook 2.4 27	0.784314	27
4648	Whole-genome analysis and description of an outbreak due to carbapenem-resistant <i>Ochrobactrum anthropi</i> causing pseudo-bacteraemias. <i>New Microbes and New Infections</i> , 2018, 26, 100-106.	0.8	3
4649	Genome-Wide Identification and Characterization of wALOG Family Genes Involved in Branch Meristem Development of Branching Head Wheat. <i>Genes</i> , 2018, 9, 510.	1.0	8
4650	Monocot plastid phylogenomics, timeline, net rates of species diversification, the power of multi-gene analyses, and a functional model for the origin of monocots. <i>American Journal of Botany</i> , 2018, 105, 1888-1910.	0.8	161
4651	Using insects to detect, monitor and predict the distribution of <i>Xylella fastidiosa</i> : a case study in Corsica. <i>Scientific Reports</i> , 2018, 8, 15628.	1.6	69
4652	Characterisation of the complete chloroplast genome of the common bean, <i>Phaseolus vulgaris</i> L.. <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 918-920.	0.2	0
4653	Molecules and morphology reveal a new aberrant harvestman genus of Ortholasmatinae (Opiliones.) Tj ETQq1 1 0.784314 rgBT / Overlook 0.5 30	0.784314	30
4654	The mitochondrial genome of the endemic Brazilian paradoxical frog <i>Pseudis tocantins</i> (Hylidae). <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 1106-1107.	0.2	1
4655	Stable isotope analyses reveal previously unknown trophic mode diversity in the Hymenochaetales. <i>American Journal of Botany</i> , 2018, 105, 1869-1887.	0.8	19

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4656	Species recognition in social amoebae. <i>Journal of Biosciences</i> , 2018, 43, 1025-1036.	0.5	2
4657	Sequencing HIV-neutralizing antibody exons and introns reveals detailed aspects of lineage maturation. <i>Nature Communications</i> , 2018, 9, 4136.	5.8	11
4658	Complete mitochondrial genome of a leaf-mining beetle, <i>Podagricomela nigricollis</i> (Coleoptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 262	0.2	1
4659	Evolution by duplication: paleopolyploidy events in plants reconstructed by deciphering the evolutionary history of VOZ transcription factors. <i>BMC Plant Biology</i> , 2018, 18, 256.	1.6	13
4660	Characterization of the Complete Mitochondrial Genome Sequences of Three Croakers (Perciformes,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 262	1.8	32
4661	Riverine barrier effects on population genetic structure of the Hanuman langur (<i>Semnopithecus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 262	3.2	10
4662	Genomic discovery of the hypsin gene and biosynthetic pathways for terpenoids in <i>Hypsizygus marmoreus</i> . <i>BMC Genomics</i> , 2018, 19, 789.	1.2	21
4663	Evidence of peripheral olfactory impairment in the domestic silkworms: insight from the comparative transcriptome and population genetics. <i>BMC Genomics</i> , 2018, 19, 788.	1.2	14
4664	Rapid Intraspecific Diversification of the Alpine Species <i>Saxifraga sinomontana</i> (Saxifragaceae) in the Qinghai-Tibetan Plateau and Himalayas. <i>Frontiers in Genetics</i> , 2018, 9, 381.	1.1	18
4665	Genome sequences of two diploid wild relatives of cultivated sweetpotato reveal targets for genetic improvement. <i>Nature Communications</i> , 2018, 9, 4580.	5.8	181
4666	Evaluation of phylogenetic reconstruction methods using bacterial whole genomes: a simulation based study. <i>Wellcome Open Research</i> , 2018, 3, 33.	0.9	42
4667	The complete mitochondrial genome of Melon thrips, <i>Thrips palmi</i> (Thripinae): Comparative analysis. <i>PLoS ONE</i> , 2018, 13, e0199404.	1.1	18
4668	Complete mitochondrial genome of the Salangid icefish <i>Neosalanx taihuensis</i> (Actinopterygii: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 262	0.2	3
4669	Molecular phylogeny, ecology and multispecies aggregation behaviour of bombardier beetles in Arizona. <i>PLoS ONE</i> , 2018, 13, e0205192.	1.1	10
4670	A mosaic of independent innovations involving eyes shut are critical for the evolutionary transition from fused to open rhabdoms. <i>Developmental Biology</i> , 2018, 443, 188-202.	0.9	6
4671	Capsular Switching and ICE Transformation Occurred in Human <i>Streptococcus agalactiae</i> ST19 With High Pathogenicity to Fish. <i>Frontiers in Veterinary Science</i> , 2018, 5, 281.	0.9	3
4672	Genetic diversity of Microsporidia in the circulatory system of endemic amphipods from different locations and depths of ancient Lake Baikal. <i>PeerJ</i> , 2018, 6, e5329.	0.9	11
4673	A striking new species of leaf warbler from the Lesser Sundas as uncovered through morphology and genomics. <i>Scientific Reports</i> , 2018, 8, 15646.	1.6	11

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4674	Characterization of the complete plastid genome of a Chinese endemic species <i>Carya kweichowensis</i> . Mitochondrial DNA Part B: Resources, 2018, 3, 492-493.	0.2	6
4675	A new species of <i>Chusquea</i> subg. <i>Chusquea</i> (Poaceae "Bambusoideae" Bambuseae) from Minas Gerais, Brazil: morphological evidence and phylogenetic placement within the <i>Euchusquea</i> clade. Phytotaxa, 2018, 365, 73.	0.1	8
4676	An unusual disjunction in Loasaceae: Central American <i>Chichicaste grandis</i> is nested in Brazilian <i>Aosa</i> . Phytotaxa, 2018, 365, 273.	0.1	4
4677	In silico characterization of a novel putative aerotaxis chemosensory system in the myxobacterium, <i>Corallococcus coralloides</i> . BMC Genomics, 2018, 19, 757.	1.2	3
4678	Carotenoid Presence Is Associated with the Or Gene in Domesticated Carrot. Genetics, 2018, 210, 1497-1508.	1.2	75
4679	Opistholobetines (Digenea: Opecoelidae) in Australian tetraodontiform fishes. Systematic Parasitology, 2018, 95, 743-781.	0.5	5
4680	Completeness of HIV-1 Envelope Glycan Shield at Transmission Determines Neutralization Breadth. Cell Reports, 2018, 25, 893-908.e7.	2.9	91
4681	Interspecies cross-feeding orchestrates carbon degradation in the rumen ecosystem. Nature Microbiology, 2018, 3, 1274-1284.	5.9	144
4682	The complete chloroplast genome sequences of <i>Barnardia japonica</i> (Thunb.) Schult. and Schult.f. Mitochondrial DNA Part B: Resources, 2018, 3, 697-698.	0.2	2
4683	Characterization of the complete chloroplast genome of Chinese privet <i>Ligustrum lucidum</i> (Oleaceae). Mitochondrial DNA Part B: Resources, 2018, 3, 862-863.	0.2	2
4684	Characterization of the complete chloroplast genome of summer snowflake (<i>Leucojum aestivum</i>). Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.2	3
4685	Population genomic analysis reveals that homoploid hybrid speciation can be a lengthy process. Molecular Ecology, 2018, 27, 4875-4887.	2.0	45
4686	Bacterial virulence against an oceanic bloom-forming phytoplankter is mediated by algal DMSP. Science Advances, 2018, 4, eaau5716.	4.7	78
4687	A new species of <i>Alvinocaris</i> (Crustacea: Decapoda: Caridea: Alvinocarididae) from Costa Rican methane seeps. Zootaxa, 2018, 4504, 418-430.	0.2	4
4688	A phylogenomic approach to reconstruct interrelationships of main clupecocephalan lineages with a critical discussion of morphological apomorphies. BMC Evolutionary Biology, 2018, 18, 158.	3.2	16
4689	Historical biogeography of the leopard (<i>Panthera pardus</i>) and its extinct Eurasian populations. BMC Evolutionary Biology, 2018, 18, 156.	3.2	16
4690	Pollen characters and DNA sequence data converge on a monophyletic genus <i>Iresine</i> (Amaranthaceae, Caryophyllales) and help to elucidate its species diversity. Taxon, 2018, 67, 944-976.	0.4	21
4691	<i>Ustilago</i> species causing leaf-stripe smut revisited. IMA Fungus, 2018, 9, 49-73.	1.7	24

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4692	A promiscuous beta-glucosidase is involved in benzoxazinoid deglycosylation in <i>Lamium galeobdolon</i> . <i>Phytochemistry</i> , 2018, 156, 224-233.	1.4	11
4693	Characterization of the complete chloroplast genome of Jilin ginseng (<i>Panax ginseng</i> C. A. Meyer) using next generation sequencing. <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 685-686.	0.2	3
4694	Characterization of the complete chloroplast genome of <i>Caulerpa cupressoides</i> (Bryopsidales), Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 66.	0.2	7
4695	Molecular phylogeny and taxonomy of the genus <i>Chaetophora</i> (Chlorophyceae, Chlorophyta), including descriptions of <i>Chaetophoropsis aershanensis</i> gen. et sp. nov.. <i>Journal of Phycology</i> , 2018, 55, 74-83.	1.0	9
4696	Redescription and geographic distribution of <i>Raorchestes shillongensis</i> (Anura: Rhacophoridae) from Meghalaya, Northeast India. <i>Phyllomedusa</i> , 2018, 17, 3.	0.2	2
4697	Molecular phylogeny and cryptic morphology reveal a new genus of West Indian woody bamboo (Poaceae: Bambusoideae: Bambuseae) hidden by convergent character evolution. <i>Taxon</i> , 2018, 67, 916-930.	0.4	18
4698	The complete chloroplast genome of monotypic fern, <i>Mesopteris tonkinensis</i> (Thelypteridaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 868-869.	0.2	0
4699	Comparative population genomics reveals key barriers to dispersal in Southern Ocean penguins. <i>Molecular Ecology</i> , 2018, 27, 4680-4697.	2.0	40
4700	<i>Russula vinosoflavescens</i> sp. nov., from deciduous forests of Northern Alsace, France. <i>Mycotaxon</i> , 2018, 132, 707-721.	0.1	2
4701	Effects of glaciation and whole genome duplication on the distribution of the <i>Campanula rotundifolia</i> polyploid complex. <i>American Journal of Botany</i> , 2018, 105, 1760-1770.	0.8	13
4702	Convergent evolution of complex genomic rearrangements in two fungal meiotic drive elements. <i>Nature Communications</i> , 2018, 9, 4242.	5.8	40
4703	EukRef: Phylogenetic curation of ribosomal RNA to enhance understanding of eukaryotic diversity and distribution. <i>PLoS Biology</i> , 2018, 16, e2005849.	2.6	101
4704	Genome Structure of the Opportunistic Pathogen <i>Paracoccus yeei</i> (Alphaproteobacteria) and Identification of Putative Virulence Factors. <i>Frontiers in Microbiology</i> , 2018, 9, 2553.	1.5	37
4705	Rediscovery after Almost 120 Years: Morphological and Genetic Evidence Supporting the Validity of <i>Daphnia mitsukurini</i> (Crustacea: Cladocera). <i>Zoological Science</i> , 2018, 35, 468.	0.3	8
4706	Chinese black truffles: <i>Tuber yigongense</i> sp. nov., taxonomic reassessment of <i>T. indicum</i> s.l., and re-examination of the <i>T. sinense</i> isotype. <i>Mycotaxon</i> , 2018, 133, 183-196.	0.1	1
4707	The flounder next door: Closer evolutionary relationship between allopatric than sympatric <i>Bothus</i> (<i>Rafinesque</i> , 1810) species (Pleuronectiformes, Bothidae). <i>Zoologischer Anzeiger</i> , 2018, 277, 131-142.	0.4	3
4708	The distribution of bacterial doubling times in the wild. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018, 285, 20180789.	1.2	182
4709	Terrestrial species adapted to sea dispersal: Differences in propagule dispersal of two Caribbean mangroves. <i>Molecular Ecology</i> , 2018, 27, 4612-4626.	2.0	25

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4710	Early Diverging Insect-Pathogenic Fungi of the Order Entomophthorales Possess Diverse and Unique Subtilisin-Like Serine Proteases. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3311-3319.	0.8	20
4711	Cytological and genome size data analyzed in a phylogenetic frame: Evolutionary implications concerning <i>Sisyrrinchium</i> taxa (Iridaceae: Iridoideae). <i>Genetics and Molecular Biology</i> , 2018, 41, 288-307.	0.6	5
4712	Two new species of <i>Padina</i> (Dictyotales, Phaeophyceae) from southern Japan, <i>P. ogasawaraensis</i> sp. nov. and <i>P. reniformis</i> sp. nov., based on morphology and molecular markers. <i>Phycologia</i> , 2018, 57, 20-31.	0.6	3
4713	The Occurrence of Colistin-Resistant Hypervirulent <i>Klebsiella pneumoniae</i> in China. <i>Frontiers in Microbiology</i> , 2018, 9, 2568.	1.5	36
4714	Genetic Diversity of Aphid (Hemiptera: Aphididae) Species Attacking Amaranth and Nightshades in Different Agro-Ecological Zones of Kenya and Tanzania. <i>African Entomology</i> , 2018, 26, 407-421.	0.6	1
4715	Repeated domestication of melon (<i>Cucumis melo</i>) in Africa and Asia and a new close relative from India. <i>American Journal of Botany</i> , 2018, 105, 1662-1671.	0.8	59
4716	Assessing genomic admixture between cryptic <i>Plutella</i> moth species following secondary contact. <i>Genome Biology and Evolution</i> , 2018, 10, 2973-2985.	1.1	5
4717	PQ, a new program for phylogeny reconstruction. <i>BMC Bioinformatics</i> , 2018, 19, 374.	1.2	0
4718	A New Species of <i>Sulcospira</i> (Gastropoda: Pachychilidae) from Hunan, China. <i>Zoological Science</i> , 2018, 35, 476-482.	0.3	2
4719	Out of the Canals: A Draft Genome Assembly, Liver Transcriptome, and Nutrigenomics of the European Sardine, <i>Sardina pilchardus</i> . <i>Genes</i> , 2018, 9, 485.	1.0	30
4720	Comparative Genome-Wide Survey of Single Nucleotide Variation Uncovers the Genetic Diversity and Potential Biomedical Applications among Six <i>Macaca</i> Species. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3123.	1.8	3
4721	Heavy Metal Pumps in Plants: Structure, Function and Origin. <i>Advances in Botanical Research</i> , 2018, , 57-89.	0.5	11
4722	On the affinities and systematic position of <i>Pachytychius</i> Jekel, a genus currently incertae sedis in Coleoptera, Curculionidae: Evidence from immature stages and the COI gene support its placement in Smicronychini. <i>Zoologischer Anzeiger</i> , 2018, 277, 218-230.	0.4	2
4723	A revision of eastern Australian land snails placed in Nitor Gude (Helicarionidae, Stylommatophora). <i>Invertebrate Systematics</i> , 2018, 32, 1171.	0.5	6
4724	Mobile-Genetic-Element-Encoded Hypertolerance to Copper Protects <i>Staphylococcus aureus</i> from Killing by Host Phagocytes. <i>MBio</i> , 2018, 9, .	1.8	33
4725	Genome-Wide Analysis of the NAC Transcription Factor Gene Family Reveals Differential Expression Patterns and Cold-Stress Responses in the Woody Plant <i>Prunus mume</i> . <i>Genes</i> , 2018, 9, 494.	1.0	47
4726	<i>Gomphoneis tegelensis</i> sp. nov. (Bacillariophyceae): a morphological and molecular investigation based on selected single cells. <i>Diatom Research</i> , 2018, 33, 251-262.	0.5	9
4727	The complete chloroplast genome of <i>Cycas Szechuanensis</i> , an extremely endangered species. <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 974-975.	0.2	3

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4728	Programmed DNA destruction by miniature CRISPR-Cas14 enzymes. <i>Science</i> , 2018, 362, 839-842.	6.0	757
4729	Genome sequencing and assessment of plant growth-promoting properties of a <i>Serratia marcescens</i> strain isolated from vermicompost. <i>BMC Genomics</i> , 2018, 19, 750.	1.2	58
4730	Genome Sequence of Peacock Reveals the Peculiar Case of a Glittering Bird. <i>Frontiers in Genetics</i> , 2018, 9, 392.	1.1	32
4731	Antennal Transcriptome Analysis of the Chemosensory Gene Families From Trichoptera and Basal Lepidoptera. <i>Frontiers in Physiology</i> , 2018, 9, 1365.	1.3	26
4732	New molecular sequences for two genera of marine planarians facilitate determination of their position in the phylogenetic tree, with new records for two species (Platyhelminthes, Tricladida), <i>Tj ETQq0 0 0 rgBTQ0 0 0 rTf 50 5</i>		
4733	An integrated morpho-molecular approach to delineate species boundaries of <i>Millepora</i> from the Red Sea. <i>Coral Reefs</i> , 2018, 37, 967-984.	0.9	26
4734	Interspecific Gene Flow Shaped the Evolution of the Genus <i>Canis</i> . <i>Current Biology</i> , 2018, 28, 3441-3449.e5.	1.8	110
4735	The Roles of Introgression and Climate Change in the Rise to Dominance of <i>Acropora</i> Corals. <i>Current Biology</i> , 2018, 28, 3373-3382.e5.	1.8	65
4736	Positive Selection in the Evolution of Mammalian CRISPs. <i>Journal of Molecular Evolution</i> , 2018, 86, 635-645.	0.8	6
4737	Complete genome sequencing of sixteen <i>Francisella noatunensis</i> subsp. <i>orientalis</i> isolates: A genomic approach for molecular characterization and spread dynamics of this clonal population. <i>Genomics</i> , 2018, 110, 442-449.	1.3	2
4738	Subfunctionalization of the Ruby2â€“Ruby1 gene cluster during the domestication of citrus. <i>Nature Plants</i> , 2018, 4, 930-941.	4.7	121
4739	The complete chloroplast genome of <i>Carpinus hebestroma</i> , a critically endangered species endemic to Taiwan. <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 693-694.	0.2	0
4740	The complete chloroplast genome sequence of <i>Histiopteris incisa</i> (Dennstaedtiaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 772-773.	0.2	1
4741	The obligate alkalophilic sodaâ€“lake fungus <i>Sodiomyces alkalinus</i> has shifted to a protein diet. <i>Molecular Ecology</i> , 2018, 27, 4808-4819.	2.0	20
4742	Metapopulation Structure of CRISPR-Cas Immunity in <i>Pseudomonas aeruginosa</i> and Its Viruses. <i>MSystems</i> , 2018, 3, .	1.7	24
4743	Comparative analysis of swallowtail transcriptomes suggests molecular determinants for speciation and adaptation. <i>Genome</i> , 2018, 61, 843-855.	0.9	2
4744	Sub-Class Differences of PH-Dependent HIV GP120-CD4 Interactions. , 2018, , .		3
4745	A genomic infection control study for <i>Staphylococcus aureus</i> in two Ghanaian hospitals. <i>Infection and Drug Resistance</i> , 2018, Volume 11, 1757-1765.	1.1	24

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4746	Phylogeny Construction. Computational Biology, 2018, , 395-466.	0.1	0
4747	The Diverged Trypanosome MICOS Complex as a Hub for Mitochondrial Cristae Shaping and Protein Import. Current Biology, 2018, 28, 3393-3407.e5.	1.8	47
4748	Intermediate host switches drive diversification among the largest trematode family: evidence from the Polypipapiliotrematinae n. subf. (Opecoelidae), parasites transmitted to butterflyfishes via predation of coral polyps. International Journal for Parasitology, 2018, 48, 1107-1126.	1.3	24
4749	Development of reverse genetics systems and investigation of host response antagonism and reassortment potential for Cache Valley and Kairi viruses, two emerging orthobunyaviruses of the Americas. PLoS Neglected Tropical Diseases, 2018, 12, e0006884.	1.3	12
4750	Metal-free ribonucleotide reduction powered by a DOPA radical in Mycoplasma pathogens. Nature, 2018, 563, 416-420.	13.7	50
4751	Genome sequence of the cauliflower mushroom Sparassis crispa (Hanabiratake) and its association with beneficial usage. Scientific Reports, 2018, 8, 16053.	1.6	32
4752	The complete chloroplast genome sequence of medicinal fern <i>Polypodiodes niponica</i> (Polypodiaceae). Mitochondrial DNA Part B: Resources, 2018, 3, 770-771.	0.2	1
4753	Bacillus wiedmannii biovar thuringiensis: a specialized mosquitocidal pathogen with plasmids from diverse origins. Genome Biology and Evolution, 2018, 10, 2823-2833.	1.1	28
4754	Potential of Herbariomics for Studying Repetitive DNA in Angiosperms. Frontiers in Ecology and Evolution, 2018, 6, .	1.1	7
4755	Diversity and taxonomy of <i>Tricholoma</i> species from Yunnan, China, and notes on species from Europe and North America. Mycologia, 2018, 110, 1081-1109.	0.8	18
4756	Machine learning and structural analysis of Mycobacterium tuberculosis pan-genome identifies genetic signatures of antibiotic resistance. Nature Communications, 2018, 9, 4306.	5.8	126
4757	Antagonistic Pleiotropy in the Bifunctional Surface Protein FadL (OmpP1) during Adaptation of Haemophilus influenzae to Chronic Lung Infection Associated with Chronic Obstructive Pulmonary Disease. MBio, 2018, 9, .	1.8	39
4758	Phylogenetics of tick-borne encephalitis virus in endemic foci in the upper Rhine region in France and Germany. PLoS ONE, 2018, 13, e0204790.	1.1	31
4759	Validity of the Diplostomoidea and Diplostomida (Digenea, Platyhelminthes) upheld in phylogenomic analysis. International Journal for Parasitology, 2018, 48, 1043-1059.	1.3	69
4760	Study of Genetic Diversity and Population Structure of the Yak (Bos grunniens) in the Sayan-Altai Region. Russian Journal of Genetics, 2018, 54, 1210-1220.	0.2	3
4761	Compositional and Functional Shifts in the Epibiotic Bacterial Community of <i>Shinkaia crosnieri</i> & Baba & Williams (a Squat Lobster from Hydrothermal Vents) during Methane-Fed Rearing. Microbes and Environments, 2018, 33, 348-356.	0.7	9
4762	FtsZ of Filamentous, Heterocyst-Forming Cyanobacteria Has a Conserved N-Terminal Peptide Required for Normal FtsZ Polymerization and Cell Division. Frontiers in Microbiology, 2018, 9, 2260.	1.5	24
4763	The colorful mantle of the giant clam, Tridacna squamosa, expresses a light-dependent manganese superoxide dismutase to ameliorate oxidative stresses due to its symbiotic association with zooxanthellae. Coral Reefs, 2018, 37, 1039-1051.	0.9	8

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4764	Comparative venom-gland transcriptomics and venom proteomics of four Sidewinder Rattlesnake (<i>Crotalus cerastes</i>) lineages reveal little differential expression despite individual variation. <i>Scientific Reports</i> , 2018, 8, 15534.	1.6	41
4765	Incomplete lineage sorting rather than hybridization explains the inconsistent phylogeny of the wisent. <i>Communications Biology</i> , 2018, 1, 169.	2.0	84
4766	rDNA analysis of the Red Sea seagrass, <i>Halophila</i> , reveals vicariant evolutionary diversification. <i>Systematics and Biodiversity</i> , 2018, 16, 668-679.	0.5	5
4767	A new species and a new record of <i>Parasola</i> from Kerala State, India. <i>Phytotaxa</i> , 2018, 369, 260.	0.1	3
4768	Transcriptomic Plasticity in the Arthropod Generalist <i>Tetranychus urticae</i> Upon Long-Term Acclimation to Different Host Plants. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3865-3879.	0.8	36
4769	The Complete Plastome Sequences of Eleven Capsicum Genotypes: Insights into DNA Variation and Molecular Evolution. <i>Genes</i> , 2018, 9, 503.	1.0	25
4770	Clade-specific diversification dynamics of marine diatoms since the Jurassic. <i>Nature Ecology and Evolution</i> , 2018, 2, 1715-1723.	3.4	40
4771	Investigation of inter- and intraspecies variation through genome sequencing of <i>Aspergillus</i> section <i>Nigri</i> . <i>Nature Genetics</i> , 2018, 50, 1688-1695.	9.4	160
4772	Species groups distributed across elevational gradients reveal convergent and continuous genetic adaptation to high elevations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E10634-E10641.	3.3	57
4773	Characterization of the complete mitochondrial genome of <i>Inara alboguttata</i> (Hemiptera: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 18)	0.2	1
4774	Divergent subgenome evolution after allopolyploidization in African clawed frogs (<i>Xenopus</i>). <i>Journal of Evolutionary Biology</i> , 2018, 31, 1945-1958.	0.8	13
4775	Rediscovery of <i>Dacrymyces pezizoides</i> (Dacrymycetes, Basidiomycota) 80 years after its original description. <i>Phytotaxa</i> , 2018, 371, 293.	0.1	1
4776	A new <i>Lamellibrachia</i> species and confirmed range extension for <i>Lamellibrachia barhami</i> (Siboglinidae.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 18	0.2	10
4777	Genetic characterization of norovirus GII.4 variants circulating in Canada using a metagenomic technique. <i>BMC Infectious Diseases</i> , 2018, 18, 521.	1.3	23
4778	Molecular systematics and character evolution in the lichen family Ramalinaceae (Ascomycota: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 18)	0.4	57
4779	Guinea yam (<i>Dioscorea</i> spp., Dioscoreaceae) wild relatives identified using whole plastome phylogenetic analyses. <i>Taxon</i> , 2018, 67, 905-915.	0.4	15
4780	Genome-wide identification of evolutionarily conserved Small Heat-Shock and eight other proteins bearing β -crystallin domain-like in kinetoplastid protists. <i>PLoS ONE</i> , 2018, 13, e0206012.	1.1	13
4781	<i>Lecanora caperatica</i> (Lecanoraceae, lichenized ascomycetes) a new sorediate species widespread in eastern North America. <i>Bryologist</i> , 2018, 121, 306.	0.1	2

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4782	Flexibility and constraint: Evolutionary remodeling of the sporulation initiation pathway in Firmicutes. <i>PLoS Genetics</i> , 2018, 14, e1007470.	1.5	13
4783	Resolving deep-sea pelagic saccopharyngiform eel mysteries: Identification of <i>Neocyema</i> and <i>Monognathidae leptocephali</i> and establishment of a new fish family "Neocyematidae" based on larvae, adults and mitogenomic gene orders. <i>PLoS ONE</i> , 2018, 13, e0199982.	1.1	15
4784	Viruses of Eukaryotic Algae: Diversity, Methods for Detection, and Future Directions. <i>Viruses</i> , 2018, 10, 487.	1.5	56
4785	Influenza Virus. <i>Methods in Molecular Biology</i> , 2018, , .	0.4	10
4786	DM-PhyClus: a Bayesian phylogenetic algorithm for infectious disease transmission cluster inference. <i>BMC Bioinformatics</i> , 2018, 19, 324.	1.2	6
4787	Phylogeny of the spider mite sub-family Tetranychinae (Acari: Tetranychidae) inferred from RNA-Seq data. <i>PLoS ONE</i> , 2018, 13, e0203136.	1.1	15
4789	Clinical Mass Spectrometry in the Bioinformatics Era: A Hitchhiker's Guide. <i>Computational and Structural Biotechnology Journal</i> , 2018, 16, 316-334.	1.9	24
4790	Thriving populations with low genetic diversity in giant clam species, <i>Tridacna maxima</i> and <i>Tridacna noae</i> , at Dongsha Atoll, South China Sea. <i>Regional Studies in Marine Science</i> , 2018, 24, 278-287.	0.4	14
4791	Evolutionary pathway for the 2017 emergence of a novel highly pathogenic avian influenza A(H7N9) virus among domestic poultry in Tennessee, United States. <i>Virology</i> , 2018, 525, 32-39.	1.1	6
4792	<i>Mycobacterium tuberculosis</i> carrying a rifampicin drug resistance mutation reprograms macrophage metabolism through cell wall lipid changes. <i>Nature Microbiology</i> , 2018, 3, 1099-1108.	5.9	90
4793	<i>Spongispora temasekensis</i> , a new boletoid genus and species from Singapore. <i>Mycologia</i> , 2018, 110, 919-929.	0.8	15
4794	RADseq data reveal ancient, but not pervasive, introgression between Californian tree and scrub oak species (<i>Quercus</i> sect. <i>Quercus</i> : Fagaceae). <i>Molecular Ecology</i> , 2018, 27, 4556-4571.	2.0	33
4795	The genome of <i>Naegleria lovaniensis</i> , the basis for a comparative approach to unravel pathogenicity factors of the human pathogenic amoeba <i>N. fowleri</i> . <i>BMC Genomics</i> , 2018, 19, 654.	1.2	23
4796	Bipolar dispersal of red-snow algae. <i>Nature Communications</i> , 2018, 9, 3094.	5.8	75
4797	Complete plastome sequence of <i>Lilium pardalinum</i> Kellogg (Liliaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 478-479.	0.2	2
4798	The mitochondrial genomes of five frog species of the Neotropical genus <i>Ischnocnema</i> (Anura): Tj ETQq1 1 0,784314 rgBT /Over 0,2 4	0.2	4
4799	Complete chloroplast genome sequences of two <i>Boehmeria</i> species (Urticaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 937-938.	0.2	3
4800	The genome of a novel isolate of <i>Prochlorococcus</i> from the Red Sea contains transcribed genes for compatible solute biosynthesis. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	5

#	ARTICLE	IF	CITATIONS
4801	Lanlabeo duanensis, a new genus and species of labeonin fish (Teleostei: Cyprinidae) from southern China. Zootaxa, 2018, 4471, 556-568.	0.2	4
4802	Living with marginal coral communities: Diversity and host-specificity in coral-associated barnacles in the northern coral distribution limit of the East China Sea. PLoS ONE, 2018, 13, e0196309.	1.1	15
4803	A Gene-Based Positive Selection Detection Approach to Identify Vaccine Candidates Using Toxoplasma gondii as a Test Case Protozoan Pathogen. Frontiers in Genetics, 2018, 9, 332.	1.1	17
4804	Cyclins in aspergilli: Phylogenetic and functional analyses of group I cyclins. Studies in Mycology, 2018, 91, 1-22.	4.5	9
4805	Phylogenomics, biogeography, and adaptive radiation of grapes. Molecular Phylogenetics and Evolution, 2018, 129, 258-267.	1.2	56
4806	Bayesian inference of ancestral dates on bacterial phylogenetic trees. Nucleic Acids Research, 2018, 46, e134-e134.	6.5	174
4807	Joint Genomic and Proteomic Analysis Identifies Meta-Trait Characteristics of Virulent and Non-virulent Staphylococcus aureus Strains. Frontiers in Cellular and Infection Microbiology, 2018, 8, 313.	1.8	10
4808	Genome-Based Taxonomic Classification of the Phylum Actinobacteria. Frontiers in Microbiology, 2018, 9, 2007.	1.5	2,599
4809	First detection of Anopheles stephensi Liston, 1901 (Diptera: culicidae) in Ethiopia using molecular and morphological approaches. Acta Tropica, 2018, 188, 180-186.	0.9	112
4810	A simple strategy for recovering ultraconserved elements, exons, and introns from low coverage shotgun sequencing of museum specimens: Placement of the partridge genus Tropicoperdix within the galliformes. Molecular Phylogenetics and Evolution, 2018, 129, 304-314.	1.2	13
4811	The changing landscape of vancomycin-resistant Enterococcus faecium in Australia: a population-level genomic study. Journal of Antimicrobial Chemotherapy, 2018, 73, 3268-3278.	1.3	27
4812	Blame It on the Metabolite: 3,5-Dichloroaniline Rather than the Parent Compound Is Responsible for the Decreasing Diversity and Function of Soil Microorganisms. Applied and Environmental Microbiology, 2018, 84, .	1.4	41
4813	Positive and balancing selection on <i>SLC18A1</i> gene associated with psychiatric disorders and human-unique personality traits. Evolution Letters, 2018, 2, 499-510.	1.6	16
4814	Four new choanoflagellate species from extreme saline environments: Indication for isolation-driven speciation exemplified by highly adapted Craspedida from salt flats in the Atacama Desert (Northern) Tj ETQq1 1 0.084314 rgBT /Ove	0.2	0
4815	Population and Evolutionary Genetic Inferences in the Whole-Genome Era: Software Challenges. Population Genomics, 2018, , 161-175.	0.2	0
4816	Whole Genome Sequencing of the Pirarucu (Arapaima gigas) Supports Independent Emergence of Major Teleost Clades. Genome Biology and Evolution, 2018, 10, 2366-2379.	1.1	33
4817	Rapid Divergence of Genome Architectures Following the Origin of an Ectomycorrhizal Symbiosis in the Genus Amanita. Molecular Biology and Evolution, 2018, 35, 2786-2804.	3.5	28
4818	Branchinotogluma bipapillata n. sp., a new branchiate scale worm (Annelida: Polynoidae) from two hydrothermal fields on the Southwest Indian Ridge. Zootaxa, 2018, 4482, 527-540.	0.2	9

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4819	The subspecies concept in Geocorinae: an integrated taxonomic case study on <i>Geocoris</i> (<i>Piocoris</i>) <i>erythrocephalus</i> (Lepelletier & Serville, 1825) (Hemiptera: Heteroptera: Geocoridae). <i>Zootaxa</i> , 2018, 4482, 541-550.	0.2	0
4820	Whole genome sequencing reveals the emergence of a <i>Pseudomonas aeruginosa</i> shared strain sub-lineage among patients treated within a single cystic fibrosis centre. <i>BMC Genomics</i> , 2018, 19, 644.	1.2	16
4821	Transmission Dynamics of Highly Pathogenic Avian Influenza Virus A(H5Nx) Clade 2.3.4.4, North America, 2014–2015. <i>Emerging Infectious Diseases</i> , 2018, 24, 1840-1848.	2.0	41
4822	A case of behavioural diversification in male floral function – the evolution of thigmonastic pollen presentation. <i>Scientific Reports</i> , 2018, 8, 14018.	1.6	13
4823	Evolution of Spore Morphology in the Blechnaceae. <i>International Journal of Plant Sciences</i> , 2018, 179, 712-729.	0.6	12
4824	Factors Influencing Gene Family Size Variation Among Related Species in a Plant Family, Solanaceae. <i>Genome Biology and Evolution</i> , 2018, 10, 2596-2613.	1.1	54
4825	Origin and phylogenetic relationships of [4Fe–4S]–containing O ₂ sensors of bacteria. <i>Environmental Microbiology</i> , 2018, 20, 4567-4586.	1.8	13
4826	Population structure and phylogenetic relationships of a new shallow-water Antarctic phyllozoan annelid. <i>Zoologica Scripta</i> , 2018, 47, 714-726.	0.7	9
4827	<i>Chroakolemma</i> gen. nov. (Leptolyngbyaceae, Cyanobacteria) from soil biocrusts in the semi-desert Central Region of Mexico. <i>Phytotaxa</i> , 2018, 367, 201.	0.1	33
4828	Diversity of miniaturized frogs of the genus <i>Adelophryne</i> (Anura: Eleutherodactylidae): A new species from the Atlantic Forest of northeast Brazil. <i>PLoS ONE</i> , 2018, 13, e0201781.	1.1	12
4829	Noise and biases in genomic data may underlie radically different hypotheses for the position of <i>Iguania</i> within Squamata. <i>PLoS ONE</i> , 2018, 13, e0202729.	1.1	25
4830	A Conserved Role for Serotonergic Neurotransmission in Mediating Social Behavior in Octopus. <i>Current Biology</i> , 2018, 28, 3136-3142.e4.	1.8	58
4831	Basidiomycota isolated from the Mediterranean Sea – Phylogeny and putative ecological roles. <i>Fungal Ecology</i> , 2018, 36, 51-62.	0.7	20
4832	Conserved collateral antibiotic susceptibility networks in diverse clinical strains of <i>Escherichia coli</i> . <i>Nature Communications</i> , 2018, 9, 3673.	5.8	76
4833	Two new species of <i>Scapheremaeus</i> from Southern Japan (Acari: Oribatida: Cymbaeremaeidae), with genetic information. <i>Systematic and Applied Acarology</i> , 2018, 23, 1545.	0.5	2
4834	A genome wide survey reveals multiple nematocyst-specific genes in Myxozoa. <i>BMC Evolutionary Biology</i> , 2018, 18, 138.	3.2	8
4835	Hybridization between two bitterling fish species in their sympatric range and a river where one species is native and the other is introduced. <i>PLoS ONE</i> , 2018, 13, e0203423.	1.1	11
4836	<i>Soella</i> (Marchantiophyta: Lejeuneaceae) a new genus from China and Japan. <i>Bryologist</i> , 2018, 121, 324-339.	0.1	10

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4837	Diverse Bacteria Utilize Alginate Within the Microbiome of the Giant Kelp <i>Macrocystis pyrifera</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 1914.	1.5	38
4838	Diversity of gall-forming rusts (<i>Uromycladium</i> , <i>Pucciniales</i>) on <i>Acacia</i> in Australia. <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2018, 40, 221-238.	1.6	18
4839	Genome Evolution of Bartonellaceae Symbionts of Ants at the Opposite Ends of the Trophic Scale. <i>Genome Biology and Evolution</i> , 2018, 10, 1687-1704.	1.1	26
4840	Ecological specialization is associated with genetic structure in the ant-associated butterfly family Lycaenidae. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018, 285, 20181158.	1.2	9
4841	Distribution, Diversity, and Evolution of Endogenous Retroviruses in Perissodactyl Genomes. <i>Journal of Virology</i> , 2018, 92, .	1.5	6
4842	Insights into the Evolution of Multicellularity from the Sea Lettuce Genome. <i>Current Biology</i> , 2018, 28, 2921-2933.e5.	1.8	134
4843	Evidence of introgressive hybridization between <i>Stenella coeruleoalba</i> and <i>Delphinus delphis</i> in the Greek Seas. <i>Molecular Phylogenetics and Evolution</i> , 2018, 129, 325-337.	1.2	23
4844	Transcriptomic analyses of cacao cell suspensions in light and dark provide target genes for controlled flavonoid production. <i>Scientific Reports</i> , 2018, 8, 13575.	1.6	14
4845	Four new <i>Tuber</i> species added to the <i>Rufum</i> group from China based on morphological and molecular evidence. <i>Mycologia</i> , 2018, 110, 771-779.	0.8	4
4846	Emergence of soil bacterial ecotypes along a climate gradient. <i>Environmental Microbiology</i> , 2018, 20, 4112-4126.	1.8	32
4847	Bovine <i>Staphylococcus aureus</i> Superantigens Stimulate the Entire T Cell Repertoire of Cattle. <i>Infection and Immunity</i> , 2018, 86, .	1.0	42
4848	A new species of sinistral flatfish of the genus <i>Chascanopsetta</i> (Teleostei: Bothidae) from off Papua New Guinea, western Pacific Ocean. <i>Zootaxa</i> , 2018, 4476, 168.	0.2	2
4849	Shell-Less Egg Syndrome (SES) Widespread in Western Canadian Layer Operations Is Linked to a Massachusetts (Mass) Type Infectious Bronchitis Virus (IBV) Isolate. <i>Viruses</i> , 2018, 10, 437.	1.5	16
4850	Evolution of Human Respiratory Syncytial Virus (RSV) over Multiple Seasons in New South Wales, Australia. <i>Viruses</i> , 2018, 10, 476.	1.5	28
4851	Community composition and distribution of <i>Phytophthora</i> species across adjacent native and non-native forests of South Africa. <i>Fungal Ecology</i> , 2018, 36, 17-25.	0.7	31
4852	New neotropical species of Phyllachorales based on molecular, morphological, and ecological data. <i>Mycologia</i> , 2018, 110, 835-859.	0.8	4
4853	Genome-Wide Sequence Analysis of Kaposi Sarcoma-Associated Herpesvirus Shows Diversification Driven by Recombination. <i>Journal of Infectious Diseases</i> , 2018, 218, 1700-1710.	1.9	25
4854	Recent northward range extension of <i>Nerita yoldii</i> (Gastropoda: Neritidae) on artificial rocky shores in China. <i>Journal of Molluscan Studies</i> , 2018, , .	0.4	0

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4855	Phylogenetic relationships among Capuchin (Cebidae, Platyrrhini) lineages: An old event of sympatry explains the current distribution of <i>Cebus</i> and <i>Sapajus</i> . <i>Genetics and Molecular Biology</i> , 2018, 41, 699-712.	0.6	10
4856	Phylogenetic approach to recover integration dates of latent HIV sequences within-host. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E8958-E8967.	3.3	50
4857	Species distinctions among closely related strains of Eustigmatophyceae (Stramenopiles) emphasizing ITS2 sequence-structure data: <i>Eustigmatos</i> and <i>Vischeria</i> . <i>European Journal of Phycology</i> , 2018, 53, 471-491.	0.9	26
4858	The complete mitochondrial genome of a freshwater mussel <i>Nodularia douglasiae</i> (Bivalvia). <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 T</i>	0.2	6
4859	A revised classification of orders and families in the two major subclasses of Lecanoromycetes (Ascomycota) based on a temporal approach. <i>Botanical Journal of the Linnean Society</i> , 0, , .	0.8	17
4860	A New Species of the Genus <i>Calamaria</i> (Squamata: Colubridae) from Yunnan Province, China. <i>Copeia</i> , 2018, 106, 485-491.	1.4	5
4861	Pleistocene diversification in an ancient lineage: a role for glacial cycles in the evolutionary history of <i>Dioon</i> Lindl. (Zamiaceae). <i>American Journal of Botany</i> , 2018, 105, 1512-1530.	0.8	18
4862	Tracing HIV-1 strains that imprint broadly neutralizing antibody responses. <i>Nature</i> , 2018, 561, 406-410.	13.7	47
4863	Polyphyly and morphological convergence in Atlantic Forest species of <i>Aechmea</i> subgenus <i>Chevaliera</i> (Bromeliaceae). <i>Botanical Journal of the Linnean Society</i> , 2018, , .	0.8	2
4864	Molecular evidence for the paraphyly of Scolecophidia and its evolutionary implications. <i>Journal of Evolutionary Biology</i> , 2018, 31, 1782-1793.	0.8	52
4865	Revision of the genus <i>Eumorphobotys</i> with descriptions of two new species (Lepidoptera, Crambidae). <i>Tj ETQq0 0 0 rgBT /Overlock 10 T</i>	0.2	5
4866	The Incidence and Genetic Diversity of Apple Mosaic Virus (ApMV) and Prune Dwarf Virus (PDV) in <i>Prunus</i> Species in Australia. <i>Viruses</i> , 2018, 10, 136.	1.5	8
4867	A Novel Squirrel Respirivirus with Putative Zoonotic Potential. <i>Viruses</i> , 2018, 10, 373.	1.5	11
4868	Restricted Localization of Photosynthetic Intracytoplasmic Membranes (ICMs) in Multiple Genera of Purple Nonsulfur Bacteria. <i>MBio</i> , 2018, 9, .	1.8	18
4869	New <i>Ceratocystis</i> species associated with rapid death of <i>Metrosideros polymorpha</i> in Hawai'i. <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2018, 40, 154-181.	1.6	106
4870	Hidden diversity within the depauperate genera of the snake tribe Lampropeltini (Serpentes). <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 T</i>	1.2	7
4871	Global spread of three multidrug-resistant lineages of <i>Staphylococcus epidermidis</i> . <i>Nature Microbiology</i> , 2018, 3, 1175-1185.	5.9	206
4872	<i>Gatesina colombiana</i> n. gen. & n. sp. (Hymenoptera: Chalcidoidea, Eurytomidae), new Rileyinae associated with <i>Myrcianthes</i> (Myrtaceae) from Colombia. <i>Zootaxa</i> , 2018, 4471, 111.	0.2	0

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4873	A new subspecies of <i>Zamenis hohenackeri</i> (Strauch, 1873) (Serpentes: Colubridae) based on morphological and molecular data. <i>Zootaxa</i> , 2018, 4471, 137.	0.2	6
4874	Zika Virus MB16-23 in Mosquitoes, Miami-Dade County, Florida, USA, 2016. <i>Emerging Infectious Diseases</i> , 2018, 24, 808-810.	2.0	15
4875	Opposite Polarity Monospore Genome De Novo Sequencing and Comparative Analysis Reveal the Possible Heterothallic Life Cycle of <i>Morchella importuna</i> . <i>International Journal of Molecular Sciences</i> , 2018, 19, 2525.	1.8	31
4876	Integrating embryonic development and evolutionary history to characterize tentacle-specific cell types in a ctenophore. <i>Molecular Biology and Evolution</i> , 2018, 35, 2940-2956.	3.5	29
4877	Three new Diplozoidae mitogenomes expose unusual compositional biases within the Monogenea class: implications for phylogenetic studies. <i>BMC Evolutionary Biology</i> , 2018, 18, 133.	3.2	28
4878	Evolutionarily conserved partial gene duplication in the Triticeae tribe of grasses confers pathogen resistance. <i>Genome Biology</i> , 2018, 19, 116.	3.8	9
4879	A Dynamic Co-expression Map of Early Inflorescence Development in <i>Setaria viridis</i> Provides a Resource for Gene Discovery and Comparative Genomics. <i>Frontiers in Plant Science</i> , 2018, 9, 1309.	1.7	19
4880	Molecular phylogeny of marine mites (Acariformes: Halacaridae), the oldest radiation of extant secondarily marine animals. <i>Molecular Phylogenetics and Evolution</i> , 2018, 129, 182-188.	1.2	18
4881	The phylogenetic relationships and species richness of host-specific <i>Dactylogyrus</i> parasites shaped by the biogeography of Balkan cyprinids. <i>Scientific Reports</i> , 2018, 8, 13006.	1.6	28
4882	Origin and macroevolution of micro-moths on sunken Hawaiian Islands. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018, 285, 20181047.	1.2	24
4883	Trade and conservation implications of new beak and feather disease virus detection in native and introduced parrots. <i>Conservation Biology</i> , 2018, 32, 1325-1335.	2.4	39
4884	Origins and structural properties of novel and <i>de novo</i> protein domains during insect evolution. <i>FEBS Journal</i> , 2018, 285, 2605-2625.	2.2	30
4885	A comparison of methods for estimating substitution rates from ancient DNA sequence data. <i>BMC Evolutionary Biology</i> , 2018, 18, 70.	3.2	23
4886	Expression of NK cluster genes in the onychophoran <i>Euperipatoides rowelli</i> : implications for the evolution of NK family genes in nephrozoans. <i>EvoDevo</i> , 2018, 9, 17.	1.3	29
4887	Short term colour vision plasticity on the reef: Changes in opsin expression under varying light conditions differ between ecologically distinct reef fish species. <i>Journal of Experimental Biology</i> , 2018, 221, .	0.8	26
4888	Intra-host and intra-household diversity of influenza A viruses during household transmissions in the 2013 season in 2 peri-urban communities of South Africa. <i>PLoS ONE</i> , 2018, 13, e0198101.	1.1	4
4889	Molecular epidemiology of cattle tuberculosis in Mexico through whole-genome sequencing and spoligotyping. <i>PLoS ONE</i> , 2018, 13, e0201981.	1.1	24
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4891	Software for Characterizing the Antigenic and Genetic Evolution of Human Influenza Viruses. <i>Methods in Molecular Biology</i> , 2018, 1836, 551-565.	0.4	1
4892	<i>Thalictrum nainitalense</i> (Ranunculaceae), a new species from the Uttarakhand Himalaya, India. <i>Folia Geobotanica</i> , 2018, 53, 449-455.	0.4	4
4893	Comparative analysis of mitochondrial genomes of the superfamily Grylloidea (Insecta, Orthoptera) reveals phylogenetic distribution of gene rearrangements. <i>International Journal of Biological Macromolecules</i> , 2018, 120, 1048-1054.	3.6	11
4894	Hidden diversity in mushrooms explored: A new nematode species, <i>Neodiplogaster unguispiculata</i> sp. n. (Rhabditida, Diplogastridae), with a key to the species of <i>Neodiplogaster</i> . <i>Zoologischer Anzeiger</i> , 2018, 276, 71-85.	0.4	4
4895	Differentiation underground: Range-wide multilocus genetic structure of the silvery mole-rat does not support current taxonomy based on mitochondrial sequences. <i>Mammalian Biology</i> , 2018, 93, 82-92.	0.8	20
4896	Integrative species delimitation in practice: Revealing cryptic lineages within the short-nosed skink <i>Plestiodon brevirostris</i> (Squamata: Scincidae). <i>Molecular Phylogenetics and Evolution</i> , 2018, 129, 242-257.	1.2	17
4897	The Structure of a Conserved Telomeric Region Associated with Variant Antigen Loci in the Blood Parasite <i>Trypanosoma congolense</i> . <i>Genome Biology and Evolution</i> , 2018, 10, 2458-2473.	1.1	19
4898	Dual Gene Repertoires for Larval and Adult Shells Reveal Molecules Essential for Molluscan Shell Formation. <i>Molecular Biology and Evolution</i> , 2018, 35, 2751-2761.	3.5	43
4899	Whole-Genome Sequencing and Bioinformatic Analysis of Isolates from Foodborne Illness Outbreaks of <i>Campylobacter jejuni</i> and <i>Salmonella enterica</i> . <i>Journal of Clinical Microbiology</i> , 2018, 56, .	1.8	29
4900	Genomic Characterization and Copy Number Variation of <i>Bacillus anthracis</i> Plasmids pXO1 and pXO2 in a Historical Collection of 412 Strains. <i>MSystems</i> , 2018, 3, .	1.7	32
4901	Evolution of the U.S. Biological Select Agent <i>Rathayibacter toxicus</i> . <i>MBio</i> , 2018, 9, .	1.8	10
4902	Phacidiaceae endophytes of <i>Picea rubens</i> in Eastern Canada. <i>Botany</i> , 2018, 96, 555-588.	0.5	11
4903	From marine caves to the deep sea, a new look at <i>Caminella</i> (Demospongiae, Geodiidae) in the Atlanto-Mediterranean region. <i>Zootaxa</i> , 2018, 4466, 174-196.	0.2	13
4904	A new species of <i>Hymeraphia</i> Bowerbank, 1864 (Axinellida: Raspailiidae) from a deep-water canyon southwest off Ireland. <i>Zootaxa</i> , 2018, 4466, 61.	0.2	2
4905	Phylogenetic relationships in Malesian Pacific <i>Piper</i> (Piperaceae) and their implications for systematics. <i>Taxon</i> , 2018, 67, 693-724.	0.4	15
4906	Comparative phylogeography of amphibians and reptiles in Algeria suggests common causes for the east-west phylogeographic breaks in the Maghreb. <i>PLoS ONE</i> , 2018, 13, e0201218.	1.1	31
4907	Hotspot mutations and ColE1 plasmids contribute to the fitness of <i>Salmonella</i> Heidelberg in poultry litter. <i>PLoS ONE</i> , 2018, 13, e0202286.	1.1	34
4908	A family of silicon transporter structural genes in a pennate diatom <i>Synedra ulna</i> subsp. <i>danica</i> (Kŷ4tz.) Skabitsch. <i>PLoS ONE</i> , 2018, 13, e0203161.	1.1	11

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4909	Complete Genome Sequence of a Novel RNA Virus Identified from a Deep-Sea Animal, <i>Osedax japonicus</i>. <i>Microbes and Environments</i> , 2018, 33, 446-449.	0.7	9
4910	Molecular phylogeny, morphology and pathogenicity of <i>Pseudopestalotiopsis</i> species on <i>Ixora</i> in Taiwan. <i>Mycological Progress</i> , 2018, 17, 941-952.	0.5	17
4911	Whole-genome sequencing enabling the detection of a colistin-resistant hypermutating <i>Citrobacter werkmanii</i> strain harbouring a novel metallo- β -lactamase VIM-48. <i>International Journal of Antimicrobial Agents</i> , 2018, 51, 867-874.	1.1	12
4912	<i>Balantidium grimi</i> n. sp. (Ciliophora, Litostomatea), a new species inhabiting the rectum of the frog <i>Quasipaa spinosa</i> from Lishui, China. <i>Parasite</i> , 2018, 25, 29.	0.8	4
4913	Molecular evolution methods to study HIV-1 epidemics. <i>Future Virology</i> , 2018, 13, 399-404.	0.9	1
4914	New contributions to <i>Gruberia lanceolata</i> (Gruber, 1884) Kahl, 1932 based on analyses of multiple populations and genes (Ciliophora, Heterotrichea, Gruberiidae). <i>European Journal of Protistology</i> , 2018, 65, 16-30.	0.5	10
4915	<i>Ophiostoma quercus</i> : An unusually diverse and globally widespread tree-infecting fungus. <i>Fungal Biology</i> , 2018, 122, 900-910.	1.1	6
4916	Undersampling Genomes has Biased Time and Rate Estimates Throughout the Tree of Life. <i>Molecular Biology and Evolution</i> , 2018, 35, 2077-2084.	3.5	26
4917	Bloom of a denitrifying methanotroph, <i>Candidatus</i> <i>Methylomirabilis limnetica</i> TM , in a deep stratified lake. <i>Environmental Microbiology</i> , 2018, 20, 2598-2614.	1.8	87
4918	Genomic footprint of evolution of eusociality in bees: floral food use and CYPome <i>blooms</i> . <i>Insectes Sociaux</i> , 2018, 65, 445-454.	0.7	29
4919	Atypical virulence in a type III <i>Toxoplasma gondii</i> strain isolated in Japan. <i>Parasitology International</i> , 2018, 67, 587-592.	0.6	20
4920	A new microcystin producing <i>Nostoc</i> strain discovered in broad toxicological screening of non-planktic <i>Nostocaceae</i> (cyanobacteria). <i>Toxicon</i> , 2018, 150, 66-73.	0.8	6
4921	Horizontal operon transfer, plasmids, and the evolution of photosynthesis in <i>Rhodobacteraceae</i> . <i>ISME Journal</i> , 2018, 12, 1994-2010.	4.4	75
4922	Introggression and gene family contraction drive the evolution of lifestyle and host shifts of hypocrealean fungi. <i>Mycology</i> , 2018, 9, 176-188.	2.0	35
4923	The complete chloroplast genome of the endangered species <i>Triaenophora shennongjiaensis</i> (Orobanchaceae s.l.). <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 506-507.	0.2	4
4924	Assessing the role of aridity-induced vicariance and ecological divergence in species diversification in North-West Africa using <i>Agama</i> lizards. <i>Biological Journal of the Linnean Society</i> , 2018, 124, 363-380.	0.7	17
4925	PHYLOSCANNER: Inferring Transmission from Within- and Between-Host Pathogen Genetic Diversity. <i>Molecular Biology and Evolution</i> , 2018, 35, 719-733.	3.5	122
4926	Resilience to fire of phylogenetic diversity across biological domains. <i>Molecular Ecology</i> , 2018, 27, 2896-2908.	2.0	49

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4927	Fungal Isocyanide Synthases and Xanthocillin Biosynthesis in <i>Aspergillus fumigatus</i> . <i>MBio</i> , 2018, 9, .	1.8	44
4928	Resolving the phylogenetic position of Darwin's extinct ground sloth (<i>Mylodon darwini</i>) using mitogenomic and nuclear exon data. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018, 285, 20180214.	1.2	16
4929	How small an island? Speciation by endemic mammals (<i>Apomys</i> , Muridae) on an oceanic Philippine island. <i>Journal of Biogeography</i> , 2018, 45, 1675-1687.	1.4	13
4930	Multiple origins of green blood in New Guinea lizards. <i>Science Advances</i> , 2018, 4, eaao5017.	4.7	19
4931	Chitinase genes (<i>CHIA</i> s) provide genomic footprints of a post-Cretaceous dietary radiation in placental mammals. <i>Science Advances</i> , 2018, 4, eaar6478.	4.7	55
4932	Molecular Epidemiology of Shiga Toxin-Producing <i>Escherichia coli</i> (STEC) on New Zealand Dairy Farms: Application of a Culture-Independent Assay and Whole-Genome Sequencing. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	31
4933	Host-Symbiont Cospeciation of Termite-Gut Cellulolytic Protists of the Genera <i>Teranympha</i> and <i>Eucomonympha</i> and their <i>Treponema</i> Endosymbionts. <i>Microbes and Environments</i> , 2018, 33, 26-33.	0.7	47
4934	Worms that suck: Phylogenetic analysis of Hirudinea solidifies the position of Acanthobdellida and necessitates the dissolution of Rhynchobdellida. <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 129-134.	1.2	61
4935	Rapid diversification and hybridization have shaped the dynamic history of the genus <i>Elaenia</i> . <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 522-533.	1.2	9
4936	A tangle of forms and phylogeny: Extensive morphological homoplasy and molecular clock heterogeneity in <i>Bonnetina</i> and related tarantulas. <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 55-73.	1.2	25
4937	Genomic basis of recombination suppression in the hybrid between <i>Caenorhabditis briggsae</i> and <i>C. nigoni</i> . <i>Nucleic Acids Research</i> , 2018, 46, 1295-1307.	6.5	31
4938	Paleocene–Eocene and Pleistocene sea-level changes as <i>species pumps</i> in Southeast Asia: Evidence from <i>Altheopus</i> spiders. <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 545-555.	1.2	33
4939	Phylogenomics resolves evolutionary relationships and provides insights into floral evolution in the tribe Shoreaeae (Dipterocarpaceae). <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 1-13.	1.2	29
4940	Pervasive introgression facilitated domestication and adaptation in the <i>Bos</i> species complex. <i>Nature Ecology and Evolution</i> , 2018, 2, 1139-1145.	3.4	157
4941	Genomes of all known members of a <i>Plasmodium</i> subgenus reveal paths to virulent human malaria. <i>Nature Microbiology</i> , 2018, 3, 687-697.	5.9	129
4942	Frequent transmission of the <i>Mycobacterium tuberculosis</i> Beijing lineage and positive selection for the <i>EsxW</i> Beijing variant in Vietnam. <i>Nature Genetics</i> , 2018, 50, 849-856.	9.4	167
4943	Unexpected species diversity within Japanese <i>Mundochthonius</i> pseudoscorpions (<i>Pseudoscorpiones</i>): morphological examination. <i>Invertebrate Systematics</i> , 2018, 32, 259.	0.5	14
4944	Integrative systematic revision of a Mediterranean earthworm family: Hormogastridae (Annelida). <i>Tj ETQq1 1 0.784314 rgBT /Overlock 17</i>	0.5	17

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4945	Bathyarchaeota: globally distributed metabolic generalists in anoxic environments. FEMS Microbiology Reviews, 2018, 42, 639-655.	3.9	206
4946	Evolution of Gustatory Receptor Gene Family Provides Insights into Adaptation to Diverse Host Plants in Nymphalid Butterflies. Genome Biology and Evolution, 2018, 10, 1351-1362.	1.1	28
4947	Revised Phylogeny of the <i>Cellulose Synthase</i> Gene Superfamily: Insights into Cell Wall Evolution. Plant Physiology, 2018, 177, 1124-1141.	2.3	118
4948	Stochastic and deterministic effects on interactions between canopy and recruiting species in forest communities. Functional Ecology, 2018, 32, 2264-2274.	1.7	13
4949	RADseq approaches and applications for forest tree genetics. Tree Genetics and Genomes, 2018, 14, 1.	0.6	58
4950	Identification of <i>Mycobacterium chimaera</i> in heater-cooler units in China. Scientific Reports, 2018, 8, 7843.	1.6	10
4951	Reconciling comparative anatomy and mitochondrial phylogenetics in revising species limits in the Australian semislug <i>Helicarion fâ©russac</i> , 1821 (Gastropoda: Stylommatophora). Zoological Journal of the Linnean Society, 0, , .	1.0	7
4952	ORDER within the chaos: Insights into phylogenetic relationships within the Anomura (Crustacea: Tj ETQq1 1 0.784314 rgBT /Overlock and Evolution, 2018, 127, 320-331.	1.2	83
4953	Evolutionary instability of CUG-Leu in the genetic code of budding yeasts. Nature Communications, 2018, 9, 1887.	5.8	70
4954	Two new subterranean species of <i>Pseudocrangonyx</i> Akatsuka & Komai, 1922 (Amphipoda: Tj ETQq1 1 0.784314 rgBT /Overlock 10 T 5 western Japan. Journal of Crustacean Biology, 2018, 38, 460-474.	0.3	15
4955	Repeated Cis-Regulatory Tuning of a Metabolic Bottleneck Gene during Evolution. Molecular Biology and Evolution, 2018, 35, 1968-1981.	3.5	30
4956	Simultaneous radiation of bird and mammal lice following the K-Pg boundary. Biology Letters, 2018, 14, 20180141.	1.0	33
4957	The polyphyly of <i>Plasmodium</i> : comprehensive phylogenetic analyses of the malaria parasites (order Haemosporida) reveal widespread taxonomic conflict. Royal Society Open Science, 2018, 5, 171780.	1.1	123
4958	Genome skimming provides new insight into the relationships in <i>Ludwigia</i> section <i>Macrocarpon</i> , a polyploid complex. American Journal of Botany, 2018, 105, 875-887.	0.8	7
4959	Genetic diversity and identification of putative recombination events in grapevine rupestris stem pitting-associated virus. Archives of Virology, 2018, 163, 2491-2496.	0.9	7
4960	Environmental transition zone and rivers shape intraspecific population structure and genetic diversity of an Amazonian rain forest tree frog. Evolutionary Ecology, 2018, 32, 359-378.	0.5	28
4961	Pan-genomic approach shows insight of genetic divergence and pathogenic-adaptation of <i>Pasteurella multocida</i> . Gene, 2018, 670, 193-206.	1.0	31
4962	Early Cretaceous greenhouse pumped higher taxa diversification in spiders. Molecular Phylogenetics and Evolution, 2018, 127, 146-155.	1.2	38

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4963	Morphological and molecular identification of three new species of <i>Tomentella</i> from Finland. <i>Mycologia</i> , 2018, 110, 677-691.	0.8	7
4964	Identifying and naming the currently known diversity of the genus <i>Hydnum</i> , with an emphasis on European and North American taxa. <i>Mycologia</i> , 2018, 110, 890-918.	0.8	18
4965	Phylogenomics reveals multiple losses of nitrogen-fixing root nodule symbiosis. <i>Science</i> , 2018, 361, .	6.0	339
4966	Two new species of <i>Oobius</i> (Hymenoptera: Encyrtidae) and their phylogenetic relationship with other congeners from northeastern Asia. <i>Canadian Entomologist</i> , 2018, 150, 303-316.	0.4	3
4967	Phylogenetic analysis of the tree-kangaroos (<i>Dendrolagus</i>) reveals multiple divergent lineages within New Guinea. <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 589-599.	1.2	28
4968	The Cefazolin Inoculum Effect Is Associated With Increased Mortality in Methicillin-Susceptible <i>Staphylococcus aureus</i> Bacteremia. <i>Open Forum Infectious Diseases</i> , 2018, 5, ofy123.	0.4	72
4969	Revision of the Genus <i>Chroomonas</i> HANSGIRG: The Benefits of DNA-containing Specimens. <i>Protist</i> , 2018, 169, 662-681.	0.6	12
4970	New insights on the phylogenetic relationships among the traditional <i>Philodendron</i> subgenera and the other groups of the <i>Homalomena</i> clade (Araceae). <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 168-178.	1.2	9
4971	The complete mitochondrial genome of yellow crazy ant, <i>Anoplolepis gracilipes</i> (Hymenoptera: Tj ETQq0 0 0 rgBT /Overlock 10 T	0.2	13
4972	Phototransduction Gene Expression and Evolution in Cave and Surface Crayfishes. <i>Integrative and Comparative Biology</i> , 2018, 58, 398-410.	0.9	17
4973	A new species of <i>Scrophularia</i> (Scrophulariaceae) from Hubei, China. <i>Phytotaxa</i> , 2018, 350, 1.	0.1	2
4974	<i>Neohygrocybe griseonigra</i> (Hygrophoraceae, Agaricales), a new species from subtropical China. <i>Phytotaxa</i> , 2018, 350, 64.	0.1	1
4975	First record of two ectoparasitic ciliates of the genus <i>Trichodina</i> (Ciliophora: Trichodinidae) parasitizing gills of an invasive freshwater fish, <i>Micropercops swinhonis</i> , in Tibet. <i>Parasitology Research</i> , 2018, 117, 2233-2242.	0.6	5
4976	Recovery of genomes from metagenomes via a dereplication, aggregation and scoring strategy. <i>Nature Microbiology</i> , 2018, 3, 836-843.	5.9	906
4977	<i>Raphidocelis subcapitata</i> (= <i>Pseudokirchneriella subcapitata</i>) provides an insight into genome evolution and environmental adaptations in the Sphaeropleales. <i>Scientific Reports</i> , 2018, 8, 8058.	1.6	52
4978	Network-guided genomic and metagenomic analysis of the faecal microbiota of the critically endangered kakapo. <i>Scientific Reports</i> , 2018, 8, 8128.	1.6	11
4979	Distribution of Eurasian minnows (<i>Phoxinus</i> : Cypriniformes) in the Western Balkans. <i>Knowledge and Management of Aquatic Ecosystems</i> , 2018, , 11.	0.5	23
4980	LEA Proteins and the Evolution of the WHY Domain. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	48

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4981	Lepocreadiidae Odhner, 1905 and Aephnidiogenidae Yamaguti, 1934 (Digenea: Lepocreadiidae) of fishes from Moreton Bay, Queensland, Australia, with the erection of a new family and genus. <i>Systematic Parasitology</i> , 2018, 95, 479-498.	0.5	29
4982	Tick-Bacteria Mutualism Depends on B Vitamin Synthesis Pathways. <i>Current Biology</i> , 2018, 28, 1896-1902.e5.	1.8	246
4983	Molecular phylogeny of the genus <i>Fissidens</i> (Fissidentaceae, Bryophyta) and a refinement of the infrageneric classification. <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 190-202.	1.2	15
4984	Phylogenomics clarifies repeated evolutionary origins of inbreeding and fungus farming in bark beetles (Curculionidae, Scolytinae). <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 229-238.	1.2	49
4985	Comparative Genomics Reveals a Burst of Homoplasmy-Free Numt Insertions. <i>Molecular Biology and Evolution</i> , 2018, 35, 2060-2064.	3.5	32
4986	Tropidoatractidae fam. nov., a Deep Branching Lineage of Metopida (Armophorea, Ciliophora) Found in Diverse Habitats and Possessing Prokaryotic Symbionts. <i>Protist</i> , 2018, 169, 362-405.	0.6	27
4987	Consistent patterns of high alpha and low beta diversity in tropical parasitic and free-living protists. <i>Molecular Ecology</i> , 2018, 27, 2846-2857.	2.0	43
4988	Molecular and plumage analyses indicate the incomplete separation of two woodpeckers (Aves). <i>Trends in Ecology and Evolution</i> , 2018, 33, 1074-1084.	0.7	4
4989	Direct Whole-Genome Sequencing of Sputum Accurately Identifies Drug-Resistant <i>Mycobacterium tuberculosis</i> Faster than MGIT Culture Sequencing. <i>Journal of Clinical Microbiology</i> , 2018, 56, .	1.8	131
4990	Phylogenetic and morphological investigation of the <i>Mochlus afer-sundevallii</i> species complex (Squamata: Scincidae) across the arid corridor of sub-Saharan Africa. <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 280-287.	1.2	13
4991	A mitochondrial phylogeny of the family Onychoteuthidae (Cephalopoda: Oegopsida). <i>Molecular Phylogenetics and Evolution</i> , 2018, 128, 88-97.	1.2	18
4992	Prokaryotic assemblages in suspended and subglacial sediments within a glacierized catchment on Qeqertarsuaq (Disko Island), west Greenland. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	12
4993	Evolutionary Origin of OwlRep, a Megasatellite DNA Associated with Adaptation of Owl Monkeys to Nocturnal Lifestyle. <i>Genome Biology and Evolution</i> , 2018, 10, 157-165.	1.1	5
4994	Targeted Long-Read Sequencing of a Locus Under Long-Term Balancing Selection in <i>Capsella</i> . <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 1327-1333.	0.8	9
4995	Conservation genomics reveals possible illegal trade routes and admixture across pangolin lineages in Southeast Asia. <i>Conservation Genetics</i> , 2018, 19, 1083-1095.	0.8	29
4996	Modelling alpha-diversities of coastal lagoon fish assemblages from the Mediterranean Sea. <i>Progress in Oceanography</i> , 2018, 165, 100-109.	1.5	7
4997	Selection and environmental adaptation along a path to speciation in the Tibetan frog <i>Nanorana parkeri</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E5056-E5065.	3.3	49
4998	Chemokine C-C motif ligand 33 is a key regulator of teleost fish barbel development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E5018-E5027.	3.3	29

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4999	Comprehensive phylogeny of ray-finned fishes (Actinopterygii) based on transcriptomic and genomic data. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 6249-6254.	3.3	445
5000	Long-Term, Low-Frequency Cluster of a German-Imipenemase-1-Producing <i>Enterobacter hormaechei</i> ssp. <i>steigerwaltii</i> ST89 in a Tertiary Care Hospital in Germany. Microbial Drug Resistance, 2018, 24, 1305-1315.	0.9	13
5001	Seed characters in Molluginaceae (Caryophyllales): implications for taxonomy and evolution. Botanical Journal of the Linnean Society, 2018, 187, 167-208.	0.8	8
5002	De novo genome assembly of the red silk cotton tree (<i>Bombax ceiba</i>). GigaScience, 2018, 7, .	3.3	27
5003	Genotyping and Whole-Genome Sequencing to Identify Tuberculosis Transmission to Pediatric Patients in British Columbia, Canada, 2005–2014. Journal of Infectious Diseases, 2018, 218, 1155-1163.	1.9	23
5004	The genome of an endosymbiotic methanogen is very similar to those of its free-living relatives. Environmental Microbiology, 2018, 20, 2538-2551.	1.8	21
5005	Nucleotide-binding resistance gene signatures in sugar beet, insights from a new reference genome. Plant Journal, 2018, 95, 659-671.	2.8	48
5006	Complete mitochondrial genome of <i>Periplaneta brunnea</i> (Blattodea: Blattidae) and phylogenetic analyses within Blattodea. Journal of Asia-Pacific Entomology, 2018, 21, 885-895.	0.4	7
5007	Supergene Evolution Triggered by the Introgression of a Chromosomal Inversion. Current Biology, 2018, 28, 1839-1845.e3.	1.8	130
5008	Convergent evolution of tertiary structure in rhodopsin visual proteins from vertebrates and box jellyfish. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 6201-6206.	3.3	19
5009	Review of the <i>Merodon albifasciatus</i> Macquart species complex (Diptera: Syrphidae): the nomenclatural type located and its provenance discussed. Zootaxa, 2018, 4374, 25-48.	0.2	14
5010	A new leaf-litter harvestman species of the genus <i>Karos</i> (Opiliones: Stygnopsidae: Karosinae), with a reanalysis of the morphological phylogeny of the genus. Zootaxa, 2018, 4378, 533.	0.2	3
5011	The South American spider genera <i>Mesabolivar</i> and <i>Carapoia</i> (Araneae, &Pholcidae): new species and a framework for redrawing generic limits. Zootaxa, 2018, 4395, 1-178.	0.2	10
5012	Molecular systematics of <i>Caryopteris</i> (Lamiaceae) and its allies with reference to the molecular phylogeny of subfamily Ajugoideae. Taxon, 2018, 67, 376-394.	0.4	17
5013	DNA barcoding suggested the existence of cryptic species and high biodiversity of South Korean pseudoscorpions (Arachnida, Pseudoscorpiones). Journal of Asia-Pacific Biodiversity, 2018, 11, 399-407.	0.2	9
5014	The Little-known Freshwater Metopid Ciliate, <i>Idiometopus turbo</i> (Dragesco and Dragesco-KernÃ©is,) Tj ETQq1 1 0.784314 rgBT /Ove Protist, 2018, 169, 494-506.	0.6	15
5015	The complete chloroplast genome sequence of <i>Sphagneticola trilobata</i> (Asteraceae). Mitochondrial DNA Part B: Resources, 2018, 3, 740-741.	0.2	0
5016	Ancient DNA provides evidence of 27,000-year-old papillomavirus infection and long-term codivergence with rodents. Virus Evolution, 2018, 4, vey014.	2.2	12

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5017	Speciation in sympatry with ongoing secondary gene flow and a potential olfactory trigger in a radiation of Cameroon cichlids. <i>Molecular Ecology</i> , 2018, 27, 4270-4288.	2.0	45
5018	Ancient Evolutionary Origin and Positive Selection of the Retroviral Restriction Factor <i>Fv1</i> in Muroid Rodents. <i>Journal of Virology</i> , 2018, 92, .	1.5	23
5019	A new genus and species of primary freshwater crab and a new species of <i>Artopotamon</i> Dai & Chen, 1985 (Crustacea, Brachyura, Potamidae) from western Yunnan, China. <i>Zootaxa</i> , 2018, 4422, 115.	0.2	13
5020	Genetic profiling of <i>Mycobacterium bovis</i> strains from slaughtered cattle in Eritrea. <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006406.	1.3	34
5021	HIV-1 diversity among young women in rural South Africa: HPTN 068. <i>PLoS ONE</i> , 2018, 13, e0198999.	1.1	12
5022	The kinetoplastid-infecting <i>Bodo saltans</i> virus (BsV), a window into the most abundant giant viruses in the sea. <i>ELife</i> , 2018, 7, .	2.8	71
5023	Multi-view light-sheet imaging and tracking with the MaMuT software reveals the cell lineage of a direct developing arthropod limb. <i>ELife</i> , 2018, 7, .	2.8	134
5024	A new species and phylogenetic insights in <i>Hesiospina</i> (Annelida, Hesionidae). <i>Zootaxa</i> , 2018, 4441, 59-75.	0.2	4
5025	Characterization of four new mitogenomes from <i>Ocypodoidea</i> & <i>Grapsodoidea</i> , and phylomitogenomic insights into thoracotreme evolution. <i>Gene</i> , 2018, 675, 27-35.	1.0	26
5026	Next-generation museum genomics: Phylogenetic relationships among palpimanoid spiders using sequence capture techniques (Araneae: Palpimanoidea). <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 907-918.	1.2	65
5027	Molecular phylogeny of <i>Ischnocnema</i> (Anura: Brachycephalidae) with the redefinition of its series and the description of two new species. <i>Molecular Phylogenetics and Evolution</i> , 2018, 128, 123-146.	1.2	18
5028	Structure of the Lassa virus glycan shield provides a model for immunological resistance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 7320-7325.	3.3	95
5029	Phylogeny and staminal evolution of <i>Salvia</i> (Lamiaceae, Nepetoideae) in East Asia. <i>Annals of Botany</i> , 2018, 122, 649-668.	1.4	65
5030	Isolation by marine barriers and climate explain areas of endemism in an island rodent. <i>Journal of Biogeography</i> , 2018, 45, 2053-2066.	1.4	12
5031	Taxonomic revision of Israeli snakes belonging to the <i>Platyceps rhodorachis</i> species complex (Reptilia: Tj ETQq0 0 0 rgBT /Overlock 10 T	0.2	4
5032	A new species of <i>Leptolalax</i> (Anura: Megophryidae) from Son Tra Peninsula, central Vietnam. <i>Zootaxa</i> , 2018, 4388, 1-21.	0.2	25
5033	A new species of Caribbean toad (Bufonidae, Peltophryne) from southern Hispaniola. <i>Zootaxa</i> , 2018, 4403, 523-539.	0.2	4
5034	An extinct hummingbird species that never was: a cautionary tale about sampling issues in molecular phylogenetics. <i>Zootaxa</i> , 2018, 4442, 491-497.	0.2	8

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5035	A New Megophrys Kuhl and Van Hasselt (Amphibia: Megophryidae) from southwestern Sumatra, Indonesia. <i>Zootaxa</i> , 2018, 4442, 389.	0.2	18
5036	Izenamides A and B, Statine-Containing Depsipeptides, and an Analogue from a Marine Cyanobacterium. <i>Journal of Natural Products</i> , 2018, 81, 1673-1681.	1.5	10
5037	The complete mitochondrial genome of <i>Isonychia kiangsinensis</i> (Ephemeroptera: Isonychiidae). <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 541-542.	0.2	13
5038	A new miniature Melanesian Forest Frog (Ceratobatrachidae: Cornufer) from New Britain Island, constituting the first record of the subgenus <i>Batrachylodes</i> from outside of the Solomon Archipelago. <i>Zootaxa</i> , 2018, 4370, 23.	0.2	2
5039	A new Reed Frog (Hyperoliidae: Hyperolius) from coastal northeastern Mozambique. <i>Zootaxa</i> , 2018, 4379, 177-198.	0.2	8
5040	The curious case of <i>Hemidactylus gujaratensis</i> (Squamata: Gekkonidae). <i>Zootaxa</i> , 2018, 4388, 137-142.	0.2	8
5041	A new species of cascade frog (Amphibia: Ranidae) in the <i>Amolops monticola</i> group from China. <i>Zootaxa</i> , 2018, 4415, 498-512.	0.2	20
5042	A new cryptic species of <i>Oreobates</i> (Anura: Craugastoridae) from the seasonally dry tropical forest of central Brazil. <i>Zootaxa</i> , 2018, 4441, 89.	0.2	4
5043	<i>Morosphaeria muthupetensis</i> sp. nov. (Morosphaeriaceae) from India: morphological characterization and multigene phylogenetic inference. <i>Botanica Marina</i> , 2018, 61, 395-405.	0.6	10
5044	Improving the standards for gut microbiome analysis of fecal samples: insights from the field biology of Japanese macaques on Yakushima Island. <i>Primates</i> , 2018, 59, 423-436.	0.7	18
5045	National outbreak of <i>Salmonella</i> Give linked to a local food manufacturer in Malta, October 2016. <i>Epidemiology and Infection</i> , 2018, 146, 1425-1432.	1.0	13
5046	Phylogeography of the Northern Alligator Lizard (Squamata, Anguinae): Hidden diversity in a western endemic. <i>Zoologica Scripta</i> , 2018, 47, 462-476.	0.7	8
5047	Phylogenetics of New World <i>Justicioids</i> ™ (Justicieae: Acanthaceae): Major Lineages, Morphological Patterns, and Widespread Incongruence with Classification. <i>Systematic Botany</i> , 2018, 43, 459-484.	0.2	27
5048	Expansion and diversification of the gibberellin receptor GIBBERELLIN INSENSITIVE DWARF1 (GID1) family in land plants. <i>Plant Molecular Biology</i> , 2018, 97, 435-449.	2.0	22
5049	Do Holarctic ant species exist? Trans-Beringian dispersal and homoplasy in the Formicidae. <i>Journal of Biogeography</i> , 2018, 45, 1917-1928.	1.4	33
5050	New 1,3-benzodioxin-4-ones from <i>Synnemapestaloides ericacearum</i> sp. nov., a biosynthetic link to remarkable compounds within the Xylariales. <i>PLoS ONE</i> , 2018, 13, e0198321.	1.1	10
5051	<i>Miconia clasei</i> , a New Species of <i>Miconia</i> sect. <i>Calycodomatia</i> (Miconieae: Melastomataceae) from the Sierra de Bahoruco, Dominican Republic and a Closer Look at Species Relationships in the Sandpaper Clade. <i>Systematic Botany</i> , 2018, 43, 430-438.	0.2	4
5052	Mapping mutational effects along the evolutionary landscape of HIV envelope. <i>ELife</i> , 2018, 7, .	2.8	96

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5053	Origin and evolution of the nuclear auxin response system. <i>ELife</i> , 2018, 7, .	2.8	195
5054	Characterization of the mitochondrial genomes of three species in the ectomycorrhizal genus <i>Cantharellus</i> and phylogeny of Agaricomycetes. <i>International Journal of Biological Macromolecules</i> , 2018, 118, 756-769.	3.6	43
5055	Evolution of floral traits and impact of reproductive mode on diversification in the phlox family (Polemoniaceae). <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 878-890.	1.2	40
5056	Darwinian Positive Selection on the Pleiotropic Effects of <i>KITLG</i> Explain Skin Pigmentation and Winter Temperature Adaptation in Eurasians. <i>Molecular Biology and Evolution</i> , 2018, 35, 2272-2283.	3.5	27
5057	Evaluation of global HIV/SIV envelope gp120 RNA structure and evolution within and among infected hosts. <i>Virus Evolution</i> , 2018, 4, vey018.	2.2	2
5058	Hotspots of Independent and Multiple Rounds of LTR-retrotransposon Bursts in Brassica Species. <i>Horticultural Plant Journal</i> , 2018, 4, 165-174.	2.3	13
5059	Genetic and phenotypic features defining industrial relevant <i>Lactococcus lactis</i> , <i>L. cremoris</i> and <i>L. lactis</i> biovar. <i>diacetylactis</i> strains. <i>Journal of Biotechnology</i> , 2018, 282, 25-31.	1.9	9
5060	Cloning and characterization of a second lamprey pituitary glycoprotein hormone, thyrostimulin (GpA2/GpB5). <i>General and Comparative Endocrinology</i> , 2018, 264, 16-27.	0.8	10
5061	The effect of dictionary omissions on phylogenies computationally inferred from lexical data. <i>Language Dynamics and Change</i> , 2018, 8, 78-107.	0.4	1
5062	An inordinate fondness for <i>Osedax</i> (Siboglinidae: Annelida): Fourteen new species of bone worms from California. <i>Zootaxa</i> , 2018, 4377, 451-489.	0.2	37
5063	A new phytotelm-breeding treefrog of the genus <i>Nasutixalus</i> (Rhacophoridae) from western Yunnan of China. <i>Zootaxa</i> , 2018, 4388, 191.	0.2	7
5064	Machine learning identifies signatures of host adaptation in the bacterial pathogen <i>Salmonella enterica</i> . <i>PLoS Genetics</i> , 2018, 14, e1007333.	1.5	73
5065	Long-read whole genome sequencing and comparative analysis of six strains of the human pathogen <i>Orientia tsutsugamushi</i> . <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006566.	1.3	50
5066	Opening the file drawer: Unexpected insights from a chytrid infection experiment. <i>PLoS ONE</i> , 2018, 13, e0196851.	1.1	8
5067	Macroevolution of gastric <i>Helicobacter</i> species unveils interspecies admixture and time of divergence. <i>ISME Journal</i> , 2018, 12, 2518-2531.	4.4	35
5068	Specialized proteomic responses and an ancient photoprotection mechanism sustain marine green algal growth during phosphate limitation. <i>Nature Microbiology</i> , 2018, 3, 781-790.	5.9	26
5069	Defining endemic cholera at three levels of spatiotemporal resolution within Bangladesh. <i>Nature Genetics</i> , 2018, 50, 951-955.	9.4	37
5070	Characterization and phylogenetic analysis of the complete mitochondrial genome of the medicinal fungus <i>Laetiporus sulphureus</i> . <i>Scientific Reports</i> , 2018, 8, 9104.	1.6	51

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5071	A novel adenovirus isolated from the Egyptian fruit bat in South Africa is closely related to recent isolates from China. <i>Scientific Reports</i> , 2018, 8, 9584.	1.6	13
5072	Whole-genome analysis of <i>Mustela erminea</i> finds that pulsed hybridization impacts evolution at high latitudes. <i>Communications Biology</i> , 2018, 1, 51.	2.0	24
5073	A gonad-expressed opsin mediates light-induced spawning in the jellyfish <i>Clytia</i> . <i>ELife</i> , 2018, 7, .	2.8	69
5074	The last common ancestor of animals lacked the HIF pathway and respired in low-oxygen environments. <i>ELife</i> , 2018, 7, .	2.8	88
5075	Population genomic data reveal extreme geographic subdivision and novel conservation actions for the declining foothill yellow-legged frog. <i>Heredity</i> , 2018, 121, 112-125.	1.2	27
5076	Molecular Phylogenetic Analysis and Species Delimitation in the Pine Needle-feeding Aphid Genus <i>Essigella</i> (Hemiptera, Sternorrhyncha, Aphididae). <i>Insect Systematics and Diversity</i> , 2018, 2, .	0.7	3
5077	Phylogeny of Maleae (Rosaceae) Based on Multiple Chloroplast Regions: Implications to Genera Circumscription. <i>BioMed Research International</i> , 2018, 2018, 1-10.	0.9	23
5078	A new pygmy squid, <i>Idiosepius hallami</i> n. sp. (Cephalopoda: Idiosepiidae) from eastern Australia and elevation of the southern endemic "notoides" clade to a new genus, <i>Xipholeptos</i> n. gen.. <i>Zootaxa</i> , 2018, 4369, 451.	0.2	2
5079	Vitellogenin-like A-associated shifts in social cue responsiveness regulate behavioral task specialization in an ant. <i>PLoS Biology</i> , 2018, 16, e2005747.	2.6	62
5080	<i>Kupeantha</i> (Coffeeae, Rubiaceae), a new genus from Cameroon and Equatorial Guinea. <i>PLoS ONE</i> , 2018, 13, e0199324.	1.1	25
5081	Annotation, classification, genomic organization and expression of the <i>Vitis vinifera</i> CYPome. <i>PLoS ONE</i> , 2018, 13, e0199902.	1.1	11
5082	Gene family innovation, conservation and loss on the animal stem lineage. <i>ELife</i> , 2018, 7, .	2.8	149
5083	Two new species of <i>Bacciger</i> Nicoll, 1914 (Trematoda: Faustulidae) in species of <i>Herklotsichthys</i> Whitley (Clupeidae) from Queensland waters. <i>Systematic Parasitology</i> , 2018, 95, 645-654.	0.5	6
5084	An inverse latitudinal gradient in speciation rate for marine fishes. <i>Nature</i> , 2018, 559, 392-395.	13.7	579
5085	Diversification across biomes in a continental lizard radiation. <i>Evolution; International Journal of Organic Evolution</i> , 2018, 72, 1553-1569.	1.1	21
5086	Molecular systematics and phylogeography of the endemic <i>Osgoodia</i> 's deer mouse <i>Osgoodomys banderanus</i> (Rodentia: Cricetidae) in the lowlands of western Mexico. <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 867-877.	1.2	1
5087	Complete Genome Sequence of <i>Streptomyces</i> sp. Strain BSE7F, a Bali Mangrove Sediment Actinobacterium with Antimicrobial Activities. <i>Genome Announcements</i> , 2018, 6, .	0.8	4
5088	Characterization and Comparative Analysis of the Complete Chloroplast Genome of the Critically Endangered Species <i>Streptocarpus teitensis</i> (Gesneriaceae). <i>BioMed Research International</i> , 2018, 2018, 1-11.	0.9	6

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5089	Inverted formin 2 regulates intracellular trafficking, placentation, and pregnancy outcome. <i>ELife</i> , 2018, 7, .	2.8	11
5090	The CLAVATA receptor FASCIATED EAR2 responds to distinct CLE peptides by signaling through two downstream effectors. <i>ELife</i> , 2018, 7, .	2.8	69
5091	The first complete mitochondrial genome sequence of <i>Nanorana parkeri</i> and <i>Nanorana ventripunctata</i> (Amphibia: Anura: Dicroglossidae), with related phylogenetic analyses. <i>Ecology and Evolution</i> , 2018, 8, 6972-6987.	0.8	11
5092	Dimensions of Host Specificity in Foliar Fungal Endophytes. <i>Forestry Sciences</i> , 2018, , 15-42.	0.4	9
5093	Comparative Transcriptomics in Two Extreme Neopterans Reveals General Trends in the Evolution of Modern Insects. <i>IScience</i> , 2018, 4, 164-179.	1.9	32
5094	<i>Lactifluus kigomaensis</i> and <i>L. subkigomaensis</i> : Two look-alikes in Tanzania. <i>Mycoscience</i> , 2018, 59, 371-378.	0.3	5
5095	Topological support and data quality can only be assessed through multiple tests in reviewing Blattodea phylogeny. <i>Molecular Phylogenetics and Evolution</i> , 2018, 128, 112-122.	1.2	16
5096	Nanopore sequencing as a revolutionary diagnostic tool for porcine viral enteric disease complexes identifies porcine kobuvirus as an important enteric virus. <i>Scientific Reports</i> , 2018, 8, 9830.	1.6	59
5097	Morphological, genomic and transcriptomic responses of <i>Klebsiella pneumoniae</i> to the last-line antibiotic colistin. <i>Scientific Reports</i> , 2018, 8, 9868.	1.6	20
5098	De Novo Sequencing of a <i>Sparassis latifolia</i> Genome and Its Associated Comparative Analyses. <i>Canadian Journal of Infectious Diseases and Medical Microbiology</i> , 2018, 2018, 1-12.	0.7	9
5099	Double-digest RADseq loci using standard Illumina indexes improve deep and shallow phylogenetic resolution of <i>Lophodermium</i> , a widespread fungal endophyte of pine needles. <i>Ecology and Evolution</i> , 2018, 8, 6638-6651.	0.8	14
5100	Novel palmicolous taxa within Pleosporales: multigene phylogeny and taxonomic circumscription. <i>Mycological Progress</i> , 2018, 17, 571-590.	0.5	19
5101	Fungal diversity notes 709–839: taxonomic and phylogenetic contributions to fungal taxa with an emphasis on fungi on Rosaceae. <i>Fungal Diversity</i> , 2018, 89, 1-236.	4.7	169
5102	Comparative Plastid Genomics of Glaucophytes. <i>Advances in Botanical Research</i> , 2018, 85, 95-127.	0.5	6
5103	Multilocus phylogeny, species age and biogeography of the Lesser Antillean anoles. <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 682-695.	1.2	7
5104	Exploring the Udoteaceae diversity (Bryopsidales, Chlorophyta) in the Caribbean region based on molecular and morphological data. <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 758-769.	1.2	8
5105	Phylogenetics of <i>Camelina</i> Crantz. (Brassicaceae) and insights on the origin of gold-of-pleasure (<i>Camelina sativa</i>). <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 834-842.	1.2	55
5106	<i>Collapsimycopappus</i> : A new leaf pathogen with mycopappus-like propagules in Mycosphaerellaceae. <i>Forest Pathology</i> , 2018, 48, e12452.	0.5	0

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5107	<i>Leightoniella zeylanensis</i> belongs to the Pannariaceae. Nordic Journal of Botany, 2018, 36, e01880.	0.2	3
5108	Historic <i>Treponema pallidum</i> genomes from Colonial Mexico retrieved from archaeological remains. PLoS Neglected Tropical Diseases, 2018, 12, e0006447.	1.3	58
5109	Molecular and morphological data of the freshwater fish <i>Glandulocauda melanopleura</i> (Characiformes: Characidae) provide evidences of river captures and local differentiation in the Brazilian Atlantic Forest. PLoS ONE, 2018, 13, e0194247.	1.1	19
5110	Chloroplast variation is incongruent with classification of the Australian bloodwood eucalypts (genus <i>Corymbia</i> , family Myrtaceae). PLoS ONE, 2018, 13, e0195034.	1.1	46
5111	Resolving the rapid plant radiation of early diverging lineages in the tropical Zingiberales: Pushing the limits of genomic data. Molecular Phylogenetics and Evolution, 2018, 128, 55-68.	1.2	53
5112	Experimental signal dissection and method sensitivity analyses reaffirm the potential of fossils and morphology in the resolution of the relationship of angiosperms and Gnetales. Paleobiology, 2018, 44, 490-510.	1.3	26
5113	Bacterial diversification through geological time. Nature Ecology and Evolution, 2018, 2, 1458-1467.	3.4	81
5114	First Report of Two <i>Colletotrichum</i> Species Associated with Bitter Rot on Apple Fruit in Korea – <i>C. fructicola</i> and <i>C. siamense</i> . Mycobiology, 2018, 46, 154-158.	0.6	23
5115	The complete mitochondrial genome of the <i>Cyclemys fusca</i> (Chelonia: Geoemydidae). Mitochondrial DNA Part B: Resources, 2018, 3, 805-806.	0.2	0
5116	Cameroonian fruit bats harbor divergent viruses, including rotavirus H, bastroviruses, and picobirnaviruses using an alternative genetic code. Virus Evolution, 2018, 4, vey008.	2.2	90
5117	Two new species of <i>Phyllonema</i> (Rivulariaceae, Cyanobacteria) with an emendation of the genus. Journal of Phycology, 2018, 54, 638-652.	1.0	17
5118	Molecular Phylogeny of the <i>Ficus auriculata</i> Complex (Moraceae). Phytotaxa, 2018, 362, 39.	0.1	11
5119	A new species of the genus <i>Dysommia</i> (Teleostei: Anguilliformes: Synphobranchidae: Ilyophinae) from the Western Pacific. Zootaxa, 2018, 4454, 43-51.	0.2	6
5120	TERribly Difficult: Searching for Telomerase RNAs in Saccharomycetes. Genes, 2018, 9, 372.	1.0	12
5121	Ediacarans, Protolichens, and Lichen-Derived Penicillium. , 2018, , 551-590.		29
5122	Molecular systematics of the digenean community parasitising the cerithiid gastropod <i>Clypeomorus batillariaeformis</i> Habe & Kusage on the Great Barrier Reef. Parasitology International, 2018, 67, 722-735.	0.6	16
5123	<i>Trigonocephalotrema</i> (Digenea : Haplospalchnidae), a new genus for trematodes parasitising fishes of two Indo-West Pacific acanthurid genera. Invertebrate Systematics, 2018, 32, 759.	0.5	8
5124	Molecular Adaptations for Sensing and Securing Prey and Insight into Amniote Genome Diversity from the Garter Snake Genome. Genome Biology and Evolution, 2018, 10, 2110-2129.	1.1	72

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5125	A Tangled Web: Origins of Reproductive Parasitism. <i>Genome Biology and Evolution</i> , 2018, 10, 2292-2309.	1.1	47
5126	Closed Genome and Comparative Phylogenetic Analysis of the Clinical Multidrug Resistant <i>Shigella sonnei</i> Strain 866. <i>Genome Biology and Evolution</i> , 2018, 10, 2241-2247.	1.1	10
5127	Multispecies coalescent analysis confirms standing phylogenetic instability in Hexapoda. <i>Journal of Evolutionary Biology</i> , 2018, 31, 1623-1631.	0.8	7
5128	Increasing tolerance of hospital <i>Enterococcus faecium</i> to handwash alcohols. <i>Science Translational Medicine</i> , 2018, 10, .	5.8	165
5129	<i>Flabelloporina</i> , a new genus in the Porinaceae (Ascomycota, Ostropales), with the first record of <i>F. squamulifera</i> from Brazil. <i>Phytotaxa</i> , 2018, 358, 67.	0.1	7
5130	<i>Verrucaria tenebrosa</i> (Verrucariaceae), a new lichen species from Finland and Norway, and notes on the taxonomy of epiphytic taxa belonging to the <i>V. hydrophila</i> complex. <i>Phytotaxa</i> , 2018, 361, 211.	0.1	6
5131	Checklist of decapods (Crustacea) from the coast of the SÃ£o Paulo state (Brazil) supported by integrative molecular and morphological data: I. Infraorder Caridea: families Hippolytidae, Lysmatidae, Ogyrididae, Processidae and Thoridae. <i>Zootaxa</i> , 2018, 4370, 76.	0.2	18
5132	Genome sequence and effectorome of <i>Moniliophthora perniciosa</i> and <i>Moniliophthora roreri</i> subpopulations. <i>BMC Genomics</i> , 2018, 19, 509.	1.2	18
5133	New diagnostic SNP molecular markers for the <i>Mytilus</i> species complex. <i>PLoS ONE</i> , 2018, 13, e0200654.	1.1	32
5134	A new and cryptic species of <i>Trentepohlia</i> (Ulvophyceae, Chlorophyta) from Brazilian mixed forests. <i>Phycologia</i> , 2018, 57, 385-393.	0.6	3
5135	Pyrosequencing and culturing of Hawaiian corticolous biofilms demonstrate high diversity and confirm phylogenetic placement of the green alga <i>Spongiochrysis hawaiiensis</i> in Cladophorales (Ulvophyceae). <i>Phycologia</i> , 2018, 57, 572-580.	0.6	7
5136	A mitochondrial genome of Micronectidae and implications for its phylogenetic position. <i>International Journal of Biological Macromolecules</i> , 2018, 119, 747-757.	3.6	11
5137	Influenza A(H5N1) viruses with A(H9N2) single gene (matrix or PB1) reassortment isolated from Cambodian live bird markets. <i>Virology</i> , 2018, 523, 22-26.	1.1	13
5138	Investigation of recombination-intense viral groups and their genes in the Earth's virome. <i>Scientific Reports</i> , 2018, 8, 11496.	1.6	14
5139	A taxonomic revision of the genus <i>Puccinia</i> on Lyceae, a tribe of Solanaceae. <i>Mycologia</i> , 2018, 110, 692-709.	0.8	3
5140	Within-Gene Shine-Dalgarno Sequences Are Not Selected for Function. <i>Molecular Biology and Evolution</i> , 2018, 35, 2487-2498.	3.5	16
5141	Genome Plasticity of <i>agr</i> -Defective <i>Staphylococcus aureus</i> during Clinical Infection. <i>Infection and Immunity</i> , 2018, 86, .	1.0	50
5142	Unrealized diversity in an urban rainforest: A new species of <i>Lygosoma</i> (Squamata: Scincidae) from western Sarawak, Malaysia (Borneo). <i>Zootaxa</i> , 2018, 4370, 345-362.	0.2	15

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5143	Distinctive characters of Nostoc genomes in cyanolichens. BMC Genomics, 2018, 19, 434.	1.2	30
5144	Restriction associated DNA-genotyping at multiple spatial scales in Arabidopsis lyrata reveals signatures of pathogen-mediated selection. BMC Genomics, 2018, 19, 496.	1.2	12
5145	Morphological plasticity in Myxobolus BÃ¼ttschli, 1882: a taxonomic dilemma case and renaming of a parasite species of the common carp. Parasites and Vectors, 2018, 11, 399.	1.0	13
5146	A new cryptic species of Pseudopestalotiopsis from Taiwan. Phytotaxa, 2018, 357, 133.	0.1	3
5147	First report of Agaricus sect. Brunneopicti from Pakistan with descriptions of two new species. Phytotaxa, 2018, 357, 167.	0.1	8
5148	Live neighbor-joining. BMC Bioinformatics, 2018, 19, 172.	1.2	11
5149	Inferring demographic parameters in bacterial genomic data using Bayesian and hybrid phylogenetic methods. BMC Evolutionary Biology, 2018, 18, 95.	3.2	16
5150	Mixed evolutionary origins of endogenous biomass-depolymerizing enzymes in animals. BMC Genomics, 2018, 19, 483.	1.2	8
5151	Horizontal transfer and proliferation of Tsu4 in Saccharomyces paradoxus. Mobile DNA, 2018, 9, 18.	1.3	18
5152	Titan cells formation in Cryptococcus neoformans is finely tuned by environmental conditions and modulated by positive and negative genetic regulators. PLoS Pathogens, 2018, 14, e1006982.	2.1	119
5153	<i>Gonyaulax hyalina</i> and <i>Gonyaulax fragilis</i> (Dinoflagellata), two names associated with â€mare sporcoâ€, indicate the same species. Phycologia, 2018, 57, 453-464.	0.6	12
5154	Identification of Wild Boarâ€™ Habitat Epidemiologic Cycle in African Swine Fever Epizootic. Emerging Infectious Diseases, 2018, 24, 810-812.	2.0	110
5155	The Complete Chloroplast Genomes of Six Ipomoea Species and Indel Marker Development for the Discrimination of Authentic Pharbitidis Semen (Seeds of I. nil or I. purpurea). Frontiers in Plant Science, 2018, 9, 965.	1.7	61
5156	A High-Quality, Long-Read De Novo Genome Assembly to Aid Conservation of Hawaiiâ€™s Last Remaining Crow Species. Genes, 2018, 9, 393.	1.0	22
5157	Laboulbeniales hyperparasites (Fungi, Ascomycota) of bat flies: Independent origins and host associations. Ecology and Evolution, 2018, 8, 8396-8418.	0.8	16
5158	Growth of Carnobacterium spp. isolated from chilled vacuum-packaged meat under relevant acidic conditions. International Journal of Food Microbiology, 2018, 286, 120-127.	2.1	20
5159	Individual components of paired typical NLR immune receptors are regulated by distinct E3 ligases. Nature Plants, 2018, 4, 699-710.	4.7	43
5160	Clinically prevalent mutations in Mycobacterium tuberculosis alter propionate metabolism and mediate multidrug tolerance. Nature Microbiology, 2018, 3, 1032-1042.	5.9	132

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5161	Characterization of Bathyarchaeota genomes assembled from metagenomes of biofilms residing in mesophilic and thermophilic biogas reactors. <i>Biotechnology for Biofuels</i> , 2018, 11, 167.	6.2	38
5162	Reassortant Clade 2.3.4.4 of Highly Pathogenic Avian Influenza A(H5N6) Virus, Taiwan, 2017. <i>Emerging Infectious Diseases</i> , 2018, 24, 1147-1149.	2.0	6
5163	Speciation patterns in complex subterranean environments: a case study using short-tailed whipscorpions (Schizomida: Hubbardiidae). <i>Biological Journal of the Linnean Society</i> , 2018, 125, 355-367.	0.7	16
5164	The endemic Cladophorales (Ulvophyceae) of ancient Lake Baikal represent a monophyletic group of very closely related but morphologically diverse species. <i>Journal of Phycology</i> , 2018, 54, 616-629.	1.0	12
5165	Molecular and morphological variation in <i>Terniopsis</i> (Podostemaceae) show contrasting patterns. <i>Nordic Journal of Botany</i> , 2018, 36, e01872.	0.2	3
5166	Phylogeny and taxonomic reassessment of jerboa, <i>Dipus</i> (Rodentia, Dipodinae), in inland Asia. <i>Zoologica Scripta</i> , 2018, 47, 630-644.	0.7	4
5167	Two new species of <i>Gerronema</i> (Agaricales, Basidiomycota) from Kerala State, India. <i>Phytotaxa</i> , 2018, 364, 81.	0.1	5
5168	A new species of <i>Marasmius</i> section <i>Globulares</i> from Kerala State, India. <i>Phytotaxa</i> , 2018, 364, 92.	0.1	3
5169	Multiple independent structural dynamic events in the evolution of snake mitochondrial genomes. <i>BMC Genomics</i> , 2018, 19, 354.	1.2	16
5170	Parallel evolution of storage roots in morning glories (Convolvulaceae). <i>BMC Plant Biology</i> , 2018, 18, 95.	1.6	17
5171	1-Aminocyclopropane-1-carboxylate deaminase producers associated to maize and other Poaceae species. <i>Microbiome</i> , 2018, 6, 114.	4.9	55
5172	The changing views on the evolutionary relationships of extant Salamandridae (Amphibia: Urodela). <i>PLoS ONE</i> , 2018, 13, e0198237.	1.1	13
5173	Functional Studies of Sex Pheromone Receptors in Asian Corn Borer <i>Ostrinia furnacalis</i> . <i>Frontiers in Physiology</i> , 2018, 9, 591.	1.3	32
5174	Genomic Sequencing of Japanese Plum (<i>Prunus salicina</i> Lindl.) Mutants Provides a New Model for Rosaceae Fruit Ripening Studies. <i>Frontiers in Plant Science</i> , 2018, 9, 21.	1.7	55
5175	Non-parent of Origin Expression of Numerous Effector Genes Indicates a Role of Gene Regulation in Host Adaption of the Hybrid Triticale Powdery Mildew Pathogen. <i>Frontiers in Plant Science</i> , 2018, 9, 49.	1.7	33
5176	Evolutionary Origin, Gradual Accumulation and Functional Divergence of Heat Shock Factor Gene Family with Plant Evolution. <i>Frontiers in Plant Science</i> , 2018, 9, 71.	1.7	41
5177	Molecular Phylogeny and Dating of Forsythieae (Oleaceae) Provide Insight into the Miocene History of Eurasian Temperate Shrubs. <i>Frontiers in Plant Science</i> , 2018, 9, 99.	1.7	32
5178	Plastid Genome Evolution in the Early-Diverging Legume Subfamily Cercidoideae (Fabaceae). <i>Frontiers in Plant Science</i> , 2018, 9, 138.	1.7	97

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5179	Geometry, Allometry and Biomechanics of Fern Leaf Petioles: Their Significance for the Evolution of Functional and Ecological Diversity Within the Pteridaceae. <i>Frontiers in Plant Science</i> , 2018, 9, 197.	1.7	18
5180	Patterning the Asteraceae Capitulum: Duplications and Differential Expression of the Flower Symmetry CYC2-Like Genes. <i>Frontiers in Plant Science</i> , 2018, 9, 551.	1.7	39
5181	Which Plants Used in Ethnomedicine Are Characterized? Phylogenetic Patterns in Traditional Use Related to Research Effort. <i>Frontiers in Plant Science</i> , 2018, 9, 834.	1.7	33
5182	Dramatic evolution of body length due to postembryonic changes in cell size in a newly discovered close relative of <i>Caenorhabditis elegans</i> . <i>Evolution Letters</i> , 2018, 2, 427-441.	1.6	13
5183	<i>Caloplaca sol</i> (<i>Teloschistaceae</i>), a new coastal lichen from Great Britain. <i>Lichenologist</i> , 2018, 50, 411-424.	0.5	2
5184	Gene exchange drives the ecological success of a multi-host bacterial pathogen. <i>Nature Ecology and Evolution</i> , 2018, 2, 1468-1478.	3.4	156
5185	Complete chloroplast genome of an endangered tree species, <i>Toona ciliata</i> (Sapindales). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 50</i>	0.2	4
5186	Stream flow alone does not predict population structure of diving beetles across complex tropical landscapes. <i>Molecular Ecology</i> , 2018, 27, 3541-3554.	2.0	8
5187	Genetic Evidence Supports Sporadic and Independent Introductions of Subtype H5 Low-Pathogenic Avian Influenza A Viruses from Wild Birds to Domestic Poultry in North America. <i>Journal of Virology</i> , 2018, 92, .	1.5	23
5188	Specific and promiscuous ophiostomatalean fungi associated with Platypodinae ambrosia beetles in the southeastern United States. <i>Fungal Ecology</i> , 2018, 35, 42-50.	0.7	23
5189	Isolation of a divergent strain of <i>Rickettsia japonica</i> from Dew's Australian bat Argasid ticks (<i>Argas</i>). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 50</i>	1.1	7
5190	Comparative genomics of <i>Mycobacterium africanum</i> Lineage 5 and Lineage 6 from Ghana suggests distinct ecological niches. <i>Scientific Reports</i> , 2018, 8, 11269.	1.6	34
5191	A rare case of stygophily in the Hydrobiidae (Gastropoda: Sadleriana). <i>Journal of Molluscan Studies</i> , 0, , .	0.4	4
5192	Bacterial interactions during sequential degradation of cyanobacterial necromass in a sulfidic arctic marine sediment. <i>Environmental Microbiology</i> , 2018, 20, 2927-2940.	1.8	50
5193	Multiple origins of sexual dichromatism and aposematism within large carpenter bees. <i>Evolution; International Journal of Organic Evolution</i> , 2018, 72, 1874-1889.	1.1	16
5194	A genome scan of diversifying selection in <i>Ophiocordyceps zombiae</i> fungi suggests a role for enterotoxins in co-evolution and host specificity. <i>Molecular Ecology</i> , 2018, 27, 3582-3598.	2.0	22
5195	Consensus assessment of the contamination level of publicly available cyanobacterial genomes. <i>PLoS ONE</i> , 2018, 13, e0200323.	1.1	41
5196	Complete Genome Sequence of Industrial Biocontrol Strain <i>Paenibacillus polymyxa</i> HY96-2 and Further Analysis of Its Biocontrol Mechanism. <i>Frontiers in Microbiology</i> , 2018, 9, 1520.	1.5	49

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5197	Systematics of the broad-nosed bats, <i>Platyrrhinus umbratus</i> (Lyon, 1902) and <i>P. nigellus</i> (Gardner and Carter, 1972) (Chiroptera: Phyllostomidae), based on genetic, morphometric, and ecological niche analyses. <i>Neotropical Biodiversity</i> , 2018, 4, 119-133.	0.2	6
5198	Contributions to the taxonomy of Rhyncholacis (Podostemaceae): Evidence of monophyly, description of a new species, and transfer of the monotypic Macarenia. <i>Phytotaxa</i> , 2018, 357, 107.	0.1	3
5199	Origin, Genetic Diversity, and Evolutionary Dynamics of Novel Porcine Circovirus 3. <i>Advanced Science</i> , 2018, 5, 1800275.	5.6	92
5200	<i>Fuscidea lightfootii</i> and <i>F. pusilla</i> (Fuscideaceae, Umbilicariomycetidae.) <i>Tj ETQq1 1 0.784314 rgBT /Overloc</i>	0.5	4
5201	<i>Sporastatia crassulata</i> , a new species from the Altai Mountains with a key to <i>Sporastatia</i> and remarks on some additional species. <i>Lichenologist</i> , 2018, 50, 439-450.	0.5	3
5202	Low-Level Antimicrobials in the Medicinal Leech Select for Resistant Pathogens That Spread to Patients. <i>MBio</i> , 2018, 9, .	1.8	25
5203	A new species of small, long-snouted Hypogeophis Peters, 1880 (Amphibia: Gymnophiona: Indotyphlidae) from the highest elevations of the Seychelles island of MahÃ©. <i>Zootaxa</i> , 2018, 4450, 359-375.	0.2	8
5204	Matrix-assisted laser desorption/ionization time-of-flight mass spectrometry identification of <i>Moraxella bovoculi</i> and <i>Moraxella bovis</i> isolates from cattle. <i>Journal of Veterinary Diagnostic Investigation</i> , 2018, 30, 739-742.	0.5	13
5205	Whole genome analysis reveals the diversity and evolutionary relationships between necrotic enteritis-causing strains of <i>Clostridium perfringens</i> . <i>BMC Genomics</i> , 2018, 19, 379.	1.2	46
5206	Integrative visual omics of the white-rot fungus <i>Polyporus brumalis</i> exposes the biotechnological potential of its oxidative enzymes for delignifying raw plant biomass. <i>Biotechnology for Biofuels</i> , 2018, 11, 201.	6.2	45
5207	Unexpected invasion of miniature inverted-repeat transposable elements in viral genomes. <i>Mobile DNA</i> , 2018, 9, 19.	1.3	20
5209	<i>Superficieibacter electus</i> gen. nov., sp. nov., an Extended-Spectrum β -Lactamase Possessing Member of the Enterobacteriaceae Family, Isolated From Intensive Care Unit Surfaces. <i>Frontiers in Microbiology</i> , 2018, 9, 1629.	1.5	14
5210	Molecular characterization of emerging avian reovirus variants isolated from viral arthritis cases in Western Canada 2012–2017 based on partial sigma (σ) C gene. <i>Virology</i> , 2018, 522, 138-146.	1.1	37
5211	The contribution of mitochondrial metagenomics to large-scale data mining and phylogenetic analysis of Coleoptera. <i>Molecular Phylogenetics and Evolution</i> , 2018, 128, 1-11.	1.2	41
5212	Updating <i>Plakobranchnus cf. ianthobapsus</i> (Gastropoda, Sacoglossa) host use: Diverse algal-animal interactions revealed by NGS with implications for invasive species management. <i>Molecular Phylogenetics and Evolution</i> , 2018, 128, 172-181.	1.2	16
5213	Endosymbiont genomes yield clues of tubeworm success. <i>ISME Journal</i> , 2018, 12, 2785-2795.	4.4	33
5214	The complete chloroplast genome of <i>Gymnospermium kiangnanense</i> (Berberidaceae): an endangered species endemic to Eastern China. <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 713-714.	0.2	4
5215	The complete chloroplast genome of <i>Leptochilus hemionitideus</i> , a traditional Chinese medical fern. <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 784-785.	0.2	3

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5216	Rapid Viral Symbiogenesis via Changes in Parasitoid Wasp Genome Architecture. <i>Molecular Biology and Evolution</i> , 2018, 35, 2463-2474.	3.5	44
5217	Detection of Cryptic taxa in the genus <i>Leptophryne</i> (Fitzinger, 1843) (Amphibia; Bufonidae) and the description of a new species from Java, Indonesia. <i>Zootaxa</i> , 2018, 4450, 427-444.	0.2	7
5218	Comparative transcriptomics reveals shared gene expression changes during independent evolutionary origins of stem and hypocotyl/root tubers in Brassica (Brassicaceae). <i>PLoS ONE</i> , 2018, 13, e0197166.	1.1	16
5219	Identifying the ‘Mushroom of Immortality’ Assessing the Ganoderma Species Composition in Commercial Reishi Products. <i>Frontiers in Microbiology</i> , 2018, 9, 1557.	1.5	35
5220	Capturing variation in <i>Lens</i> (Fabaceae): Development and utility of an exome capture array for lentil. <i>Applications in Plant Sciences</i> , 2018, 6, e01165.	0.8	54
5221	Morphology and phylogeny of <i>Apertospathula oktemae</i> n. sp. (Ciliophora, Haptoria, Spathidiida) from Lake Van, Turkey. <i>European Journal of Protistology</i> , 2018, 66, 1-8.	0.5	6
5222	GrapeTree: visualization of core genomic relationships among 100,000 bacterial pathogens. <i>Genome Research</i> , 2018, 28, 1395-1404.	2.4	553
5223	Comparative genomics of a quadripartite symbiosis in a planthopper host reveals the origins and rearranged nutritional responsibilities of anciently diverged bacterial lineages. <i>Environmental Microbiology</i> , 2018, 20, 4461-4472.	1.8	34
5224	Biogeography and early emergence of the genus <i>Didelphis</i> (Didelphimorphia, Mammalia). <i>Zoologica Scripta</i> , 2018, 47, 645-654.	0.7	21
5225	Social regulation of insulin signaling and the evolution of eusociality in ants. <i>Science</i> , 2018, 361, 398-402.	6.0	125
5226	A new fistulose demosponge species from the Persian Gulf. <i>Zootaxa</i> , 2018, 4450, 565.	0.2	4
5227	Genome-Wide Characterization and Expression Analyses of <i>Pleurotus ostreatus</i> MYB Transcription Factors during Developmental Stages and under Heat Stress Based on de novo Sequenced Genome. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2052.	1.8	36
5228	Comparative genomics and the nature of placozoan species. <i>PLoS Biology</i> , 2018, 16, e2005359.	2.6	73
5229	Plastome phylogenomics of the early-diverging eudicot family Berberidaceae. <i>Molecular Phylogenetics and Evolution</i> , 2018, 128, 203-211.	1.2	29
5230	Horse Y chromosome assembly displays unique evolutionary features and putative stallion fertility genes. <i>Nature Communications</i> , 2018, 9, 2945.	5.8	56
5231	Full-length transcriptome of <i>Misgurnus anguillicaudatus</i> provides insights into evolution of genus <i>Misgurnus</i> . <i>Scientific Reports</i> , 2018, 8, 11699.	1.6	44
5232	Conotoxin Diversity in <i>Chelyconus ermineus</i> (Born, 1778) and the Convergent Origin of Piscivory in the Atlantic and Indo-Pacific Cones. <i>Genome Biology and Evolution</i> , 2018, 10, 2643-2662.	1.1	28
5233	Systematic revision of the Antarctic gastropod family Newnesiidae (Heterobranchia: Cephalaspidea) with the description of a new genus and a new abyssal species. <i>Zoological Journal of the Linnean Society</i> , 2018, 183, 763-775.	1.0	10

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5234	Transfer of <i>Senecio karelinioides</i> (Asteraceae~Senecioneae) to <i>Synotis</i> based on evidence from morphology, karyology and ITS/ETS sequence data. <i>Nordic Journal of Botany</i> , 2018, 36, e01838.	0.2	2
5235	Of teeth and trees: A fossil tip-dating approach to infer divergence times of extinct and extant squaliform sharks. <i>Zoologica Scripta</i> , 2018, 47, 539-557.	0.7	12
5236	<i>cytb</i> as a New Genetic Marker for Differentiation of <i>Prototheca</i> Species. <i>Journal of Clinical Microbiology</i> , 2018, 56, .	1.8	36
5237	A new moss salamander, genus <i>Nototriton</i> (Caudata: Plethodontidae), from the Cordillera de Talamanca, in the Costa Rica-Panama border region. <i>Zootaxa</i> , 2018, 4369, 487-500.	0.2	4
5238	Phylogenetic relationships, stage-specific expression and localisation of a unique family of inactive cysteine proteases in <i>Sarcoptes scabiei</i> . <i>Parasites and Vectors</i> , 2018, 11, 301.	1.0	9
5239	Exploring the biological roles of Dothideomycetes ABC proteins: Leads from their phylogenetic relationships with functionally-characterized Ascomycetes homologs. <i>PLoS ONE</i> , 2018, 13, e0197447.	1.1	9
5240	Whole Genome Analyses Suggests that <i>Burkholderia sensu lato</i> Contains Two Additional Novel Genera (<i>Mycetohabitans</i> gen. nov., and <i>Trinickia</i> gen. nov.): Implications for the Evolution of Diazotrophy and Nodulation in the Burkholderiaceae. <i>Genes</i> , 2018, 9, 389.	1.0	252
5241	Investigating the NAD-ME biochemical pathway within C4 grasses using transcript and amino acid variation in C4 photosynthetic genes. <i>Photosynthesis Research</i> , 2018, 138, 233-248.	1.6	13
5242	Novel insights on colonization routes and evolutionary potential of <i>Colletotrichum kahawae</i> , a severe pathogen of <i>Coffea arabica</i> . <i>Molecular Plant Pathology</i> , 2018, 19, 2488-2501.	2.0	22
5243	First records of <i>Knufia marmoricola</i> from limestone outcrops in the WyÅynaÅKrakowsko-CzÅstochowska Upland, Poland. <i>Phytotaxa</i> , 2018, 357, 94.	0.1	7
5244	<i>Isoperla vjosae</i> sp. n., a new species of the <i>Isoperla tripartita</i> group from Albania (Plecoptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 342	0.2	3
5245	Three new species of <i>Parapercis</i> (Perciformes: Pinguipedidae) and first records of <i>P. muronis</i> (Tanaka.) Tj ETQq1 1 0,784314 rgBT /Overlock 10 Tf 50 342	0.2	1
5246	The effects of repeated whole genome duplication events on the evolution of cytokinin signaling pathway. <i>BMC Evolutionary Biology</i> , 2018, 18, 76.	3.2	23
5247	<i>Aedes aegypti</i> in the Black Sea: recent introduction or ancient remnant?. <i>Parasites and Vectors</i> , 2018, 11, 396.	1.0	39
5248	Environmental adaptation of <i>Acanthamoeba castellanii</i> and <i>Entamoeba histolytica</i> at genome level as seen by comparative genomic analysis. <i>International Journal of Biological Sciences</i> , 2018, 14, 306-320.	2.6	17
5249	DNA analysis reveals rich diversity of <i>Hydnotrya</i> with emphasis on the species found in China. <i>Mycological Progress</i> , 2018, 17, 1123-1137.	0.5	2
5250	Genetic Separation of <i>Listeria monocytogenes</i> Causing Central Nervous System Infections in Animals. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 20.	1.8	22
5251	Tachykinin-3 Genes and Peptides Characterized in a Basal Teleost, the European Eel: Evolutionary Perspective and Pituitary Role. <i>Frontiers in Endocrinology</i> , 2018, 9, 304.	1.5	18

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5252	Silencing of Iron and Heme-Related Genes Revealed a Paramount Role of Iron in the Physiology of the Hematophagous Vector <i>Rhodnius prolixus</i> . <i>Frontiers in Genetics</i> , 2018, 9, 19.	1.1	18
5253	Molecular Identification of Shark Meat From Local Markets in Southern Brazil Based on DNA Barcoding: Evidence for Mislabeling and Trade of Endangered Species. <i>Frontiers in Genetics</i> , 2018, 9, 138.	1.1	50
5254	Computational Strategies for Dissecting the High-Dimensional Complexity of Adaptive Immune Repertoires. <i>Frontiers in Immunology</i> , 2018, 9, 224.	2.2	164
5255	Comparative Genomics of Completely Sequenced <i>Lactobacillus helveticus</i> Genomes Provides Insights into Strain-Specific Genes and Resolves Metagenomics Data Down to the Strain Level. <i>Frontiers in Microbiology</i> , 2018, 9, 63.	1.5	73
5256	Phylogenomics and Comparative Genomic Studies Robustly Support Division of the Genus <i>Mycobacterium</i> into an Emended Genus <i>Mycobacterium</i> and Four Novel Genera. <i>Frontiers in Microbiology</i> , 2018, 9, 67.	1.5	878
5257	Morphology and Phylogeny of a New Species of Anaerobic Ciliate, <i>Trimyema finlayi</i> n. sp., with Endosymbiotic Methanogens. <i>Frontiers in Microbiology</i> , 2018, 9, 140.	1.5	23
5258	<i>Pseudomonas orientalis</i> F9: A Potent Antagonist against Phytopathogens with Phytotoxic Effect in the Apple Flower. <i>Frontiers in Microbiology</i> , 2018, 9, 145.	1.5	34
5259	Plant Rhizosphere Selection of Plasmodiophorid Lineages from Bulk Soil: The Importance of "Hidden" Diversity. <i>Frontiers in Microbiology</i> , 2018, 9, 168.	1.5	7
5260	Characterization of Asymptomatic Bacteriuria <i>Escherichia coli</i> Isolates in Search of Alternative Strains for Efficient Bacterial Interference against Uropathogens. <i>Frontiers in Microbiology</i> , 2018, 9, 214.	1.5	24
5261	Evolution of Phototrophy in the Chloroflexi Phylum Driven by Horizontal Gene Transfer. <i>Frontiers in Microbiology</i> , 2018, 9, 260.	1.5	143
5262	Genome-Wide Analysis of <i>Corynespora cassicola</i> Leaf Fall Disease Putative Effectors. <i>Frontiers in Microbiology</i> , 2018, 9, 276.	1.5	58
5263	Genomic and Genotypic Characterization of <i>Cylindrospermopsis raciborskii</i> : Toward an Intraspecific Phylogenetic Evaluation by Comparative Genomics. <i>Frontiers in Microbiology</i> , 2018, 9, 306.	1.5	26
5264	Sulfate Transporters in Dissimilatory Sulfate Reducing Microorganisms: A Comparative Genomics Analysis. <i>Frontiers in Microbiology</i> , 2018, 9, 309.	1.5	63
5265	Whole Genome Sequence Analysis of CTX-M-15 Producing <i>Klebsiella</i> Isolates Allowed Dissecting a Polyclonal Outbreak Scenario. <i>Frontiers in Microbiology</i> , 2018, 9, 322.	1.5	40
5266	Revisiting <i>Francisella tularensis</i> subsp. <i>holarctica</i> , Causative Agent of Tularemia in Germany With Bioinformatics: New Insights in Genome Structure, DNA Methylation and Comparative Phylogenetic Analysis. <i>Frontiers in Microbiology</i> , 2018, 9, 344.	1.5	27
5267	A Retrospective Review of Microbiological Methods Applied in Studies Following the Deepwater Horizon Oil Spill. <i>Frontiers in Microbiology</i> , 2018, 9, 520.	1.5	8
5268	Comparative Genomics of Smut Pathogens: Insights From Orphans and Positively Selected Genes Into Host Specialization. <i>Frontiers in Microbiology</i> , 2018, 9, 660.	1.5	33
5269	Metabolic and Evolutionary Insights in the Transformation of Diphenylamine by a <i>Pseudomonas putida</i> Strain Unravelling by Genomic, Proteomic, and Transcription Analysis. <i>Frontiers in Microbiology</i> , 2018, 9, 676.	1.5	4

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5270	Evaluation of Primers Targeting the Diazotroph Functional Gene and Development of NifMAP – A Bioinformatics Pipeline for Analyzing nifH Amplicon Data. <i>Frontiers in Microbiology</i> , 2018, 9, 703.	1.5	50
5271	A Polyphasic and Taxogenomic Evaluation Uncovers <i>Arcobacter cryaerophilus</i> as a Species Complex That Embraces Four Genomovars. <i>Frontiers in Microbiology</i> , 2018, 9, 805.	1.5	22
5272	Phylogeny Trumps Chemotaxonomy: A Case Study Involving <i>Turicella otitidis</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 834.	1.5	44
5273	Polyphyletic Nature of <i>Salmonella enterica</i> Serotype Derby and Lineage-Specific Host-Association Revealed by Genome-Wide Analysis. <i>Frontiers in Microbiology</i> , 2018, 9, 891.	1.5	47
5274	A Novel Strategy for Detecting Recent Horizontal Gene Transfer and Its Application to <i>Rhizobium</i> Strains. <i>Frontiers in Microbiology</i> , 2018, 9, 973.	1.5	36
5275	In Silico Analysis of Putative Sugar Transporter Genes in <i>Aspergillus niger</i> Using Phylogeny and Comparative Transcriptomics. <i>Frontiers in Microbiology</i> , 2018, 9, 1045.	1.5	47
5276	Distinct Microbial Assemblage Structure and Archaeal Diversity in Sediments of Arctic Thermokarst Lakes Differing in Methane Sources. <i>Frontiers in Microbiology</i> , 2018, 9, 1192.	1.5	25
5277	Comparative Genomic and Phenotypic Analysis of the Vaginal Probiotic <i>Lactobacillus rhamnosus</i> GR-1. <i>Frontiers in Microbiology</i> , 2018, 9, 1278.	1.5	42
5278	Microbial Community Structure – Function Relationships in Yaquina Bay Estuary Reveal Spatially Distinct Carbon and Nitrogen Cycling Capacities. <i>Frontiers in Microbiology</i> , 2018, 9, 1282.	1.5	48
5279	Identification of Novel Biomarkers for Priority Serotypes of Shiga Toxin-Producing <i>Escherichia coli</i> and the Development of Multiplex PCR for Their Detection. <i>Frontiers in Microbiology</i> , 2018, 9, 1321.	1.5	7
5280	Origin of Cave Fungi. <i>Frontiers in Microbiology</i> , 2018, 9, 1407.	1.5	30
5281	Independent Evolution of Strychnine Recognition by Bitter Taste Receptor Subtypes. <i>Frontiers in Molecular Biosciences</i> , 2018, 5, 9.	1.6	12
5282	Ligand-Induced Variations in Structural and Dynamical Properties Within an Enzyme Superfamily. <i>Frontiers in Molecular Biosciences</i> , 2018, 5, 54.	1.6	30
5283	Epidemiological significance of dengue virus genetic variation in mosquito infection dynamics. <i>PLoS Pathogens</i> , 2018, 14, e1007187.	2.1	41
5284	Genome size estimation of brackishwater fishes and penaeid shrimps by flow cytometry. <i>Molecular Biology Reports</i> , 2018, 45, 951-960.	1.0	13
5285	Refining a steroidogenic model: an analysis of RNA-seq datasets from insect prothoracic glands. <i>BMC Genomics</i> , 2018, 19, 537.	1.2	8
5286	Insights into the ecology, evolution, and metabolism of the widespread Woese archaeotal lineages. <i>Microbiome</i> , 2018, 6, 102.	4.9	181
5287	Disentangling the infrageneric classification of megadiverse taxa from Mata Atlantica: Phylogeny of <i>Miconia</i> section <i>Chaenantha</i> (Melastomataceae: Miconieae). <i>Taxon</i> , 2018, 67, 537-551.	0.4	10

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5288	<i>Karlodinium zhouanum</i> , a new dinoflagellate species from China, and molecular phylogeny of <i>Karenia digitata</i> and <i>Karenia longicanalis</i> (Gymnodiniales, Dinophyceae). <i>Phycologia</i> , 2018, 57, 401-412.	0.6	36
5289	Isolation, Characterization, and Antibacterial Activity of Hard-to-Culture Actinobacteria from Cave Moonmilk Deposits. <i>Antibiotics</i> , 2018, 7, 28.	1.5	68
5290	Genotyping by Sequencing Reasserts the Close Relationship between Tef and Its Putative Wild Eragrostis Progenitors. <i>Diversity</i> , 2018, 10, 17.	0.7	19
5291	Molecular and Morphological Phylogenetic Analyses of New World Cycad Beetles: What They Reveal about Cycad Evolution in the New World. <i>Diversity</i> , 2018, 10, 38.	0.7	19
5292	Differential Preference of Burkholderia and Mesorhizobium to pH and Soil Types in the Core Cape Subregion, South Africa. <i>Genes</i> , 2018, 9, 2.	1.0	16
5293	Evolutionary Mechanisms of Varying Chromosome Numbers in the Radiation of Erebia Butterflies. <i>Genes</i> , 2018, 9, 166.	1.0	18
5294	Assembly of the Boechera retrofracta Genome and Evolutionary Analysis of Apomixis-Associated Genes. <i>Genes</i> , 2018, 9, 185.	1.0	24
5295	Genome Sequence of the Freshwater Yangtze Finless Porpoise. <i>Genes</i> , 2018, 9, 213.	1.0	16
5296	A Comparison of Selective Pressures in Plant X-Linked and Autosomal Genes. <i>Genes</i> , 2018, 9, 234.	1.0	5
5297	The Complete Mitochondrial Genome of Glyptothorax macromaculatus Provides a Well-Resolved Molecular Phylogeny of the Chinese Sisorid Catfishes. <i>Genes</i> , 2018, 9, 282.	1.0	12
5298	Understanding plastome evolution in Hemiparasitic Santalales: Complete chloroplast genomes of three species, Dendrotrophe varians, Helixanthera parasitica, and Macrosolen cochinchinensis. <i>PLoS ONE</i> , 2018, 13, e0200293.	1.1	32
5300	Aquimarina sediminis sp. nov., isolated from coastal sediment. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 2257-2265.	0.7	13
5301	Plastome organization, genome-based phylogeny and evolution of plastid genes in Podophylloideae (Berberidaceae). <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 978-987.	1.2	44
5302	<i>Bredia repens</i> (Melastomataceae), a New Species from Hunan, China. <i>Systematic Botany</i> , 2018, 43, 544-551.	0.2	18
5303	Hidden diversity in forest soils: Characterization and comparison of terrestrial flatworm communities in two national parks in Spain. <i>Ecology and Evolution</i> , 2018, 8, 7386-7400.	0.8	2
5304	Influence of macroclimate and local conservation measures on taxonomic, functional, and phylogenetic diversities of saproxylic beetles and wood-inhabiting fungi. <i>Biodiversity and Conservation</i> , 2018, 27, 3119-3135.	1.2	27
5305	Horizontal gene transfer of Chlamydia: Novel insights from tree reconciliation. <i>PLoS ONE</i> , 2018, 13, e0195139.	1.1	6
5306	Detection of a root-associated group of Hyaloscyphaceae (Helotiales) species that commonly colonizes Fagaceae roots and description of three new species in genus Glutinomyces. <i>Mycoscience</i> , 2018, 59, 397-408.	0.3	8

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5307	Genomic signatures of mitonuclear coevolution across populations of <i>Tigriopus californicus</i> . <i>Nature Ecology and Evolution</i> , 2018, 2, 1250-1257.	3.4	154
5308	Hypothesis on monochromatic vision in scorpionflies questioned by new transcriptomic data. <i>Scientific Reports</i> , 2018, 8, 9872.	1.6	7
5309	Using MOEA with Redistribution and Consensus Branches to Infer Phylogenies. <i>International Journal of Molecular Sciences</i> , 2018, 19, 62.	1.8	5
5310	Comparative Genomics of the Balsaminaceae Sister Genera <i>Hydrocera triflora</i> and <i>Impatiens pinfanensis</i> . <i>International Journal of Molecular Sciences</i> , 2018, 19, 319.	1.8	19
5311	Whole-Genome Comparison Reveals Heterogeneous Divergence and Mutation Hotspots in Chloroplast Genome of <i>Eucommia ulmoides</i> Oliver. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1037.	1.8	30
5312	Complete Chloroplast Genome of <i>Cercis chuniana</i> (Fabaceae) with Structural and Genetic Comparison to Six Species in Caesalpinioideae. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1286.	1.8	28
5313	Sequencing, Characterization, and Comparative Analyses of the Plastome of <i>Caragana rosea</i> var. <i>rosea</i> . <i>International Journal of Molecular Sciences</i> , 2018, 19, 1419.	1.8	30
5314	The Diverging Routes of BORIS and CTCF: An Interactomic and Phylogenomic Analysis. <i>Life</i> , 2018, 8, 4.	1.1	9
5315	Whole-Genome Comparison Reveals Divergent IR Borders and Mutation Hotspots in Chloroplast Genomes of Herbaceous Bamboos (Bambusoideae: Olyreae). <i>Molecules</i> , 2018, 23, 1537.	1.7	29
5316	Molecular and Antigenic Characterization of Piscine orthoreovirus (PRV) from Rainbow Trout (<i>Oncorhynchus mykiss</i>). <i>Viruses</i> , 2018, 10, 170.	1.5	38
5317	Structural Variants in Ancient Genomes. <i>Population Genomics</i> , 2018, , 375-391.	0.2	1
5318	Phylogenomics of montane frogs of the Brazilian Atlantic Forest is consistent with isolation in sky islands followed by climatic stability. <i>Biological Journal of the Linnean Society</i> , 0, , .	0.7	7
5319	Variant antigen repertoires in <i>Trypanosoma congolense</i> populations and experimental infections can be profiled from deep sequence data using universal protein motifs. <i>Genome Research</i> , 2018, 28, 1383-1394.	2.4	15
5320	OneTwoTree: An online tool for phylogeny reconstruction. <i>Molecular Ecology Resources</i> , 2018, 18, 1492-1499.	2.2	29
5321	Genome of Wild Mandarin and Domestication History of Mandarin. <i>Molecular Plant</i> , 2018, 11, 1024-1037.	3.9	130
5322	Evidence for mtDNA capture in the jacamar <i>Galbula leucogastra</i> /chaltothorax species-complex and insights on the evolution of white-sand ecosystems in the Amazon basin. <i>Molecular Phylogenetics and Evolution</i> , 2018, 129, 149-157.	1.2	24
5323	Detecting introgression despite phylogenetic uncertainty: The case of the South American siskins. <i>Molecular Ecology</i> , 2018, 27, 4350-4367.	2.0	18
5324	Phylogeography and population genomics of a lotic water beetle across a complex tropical landscape. <i>Molecular Ecology</i> , 2018, 27, 3346-3356.	2.0	12

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5325	TPP riboswitch-dependent regulation of an ancient thiamin transporter in <i>Candida</i> . <i>PLoS Genetics</i> , 2018, 14, e1007429.	1.5	29
5326	Plastome phylogeny and lineage diversification of Salicaceae with focus on poplars and willows. <i>Ecology and Evolution</i> , 2018, 8, 7817-7823.	0.8	47
5327	Fossils know it best: Using a new set of fossil calibrations to improve the temporal phylogenetic framework of murid rodents (Rodentia: Muridae). <i>Molecular Phylogenetics and Evolution</i> , 2018, 128, 98-111.	1.2	61
5328	Utilization of urea and cyanate in waters overlying and within the eastern tropical north Pacific oxygen deficient zone. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	28
5329	Fern and lycophyte diversity in the Pacific Northwest: Patterns and predictors. <i>Journal of Systematics and Evolution</i> , 2018, 56, 498-522.	1.6	14
5330	Chloroplast phylogenomics of the New World grape species (<i>Vitis</i> , Vitaceae). <i>Journal of Systematics and Evolution</i> , 2018, 56, 297-308.	1.6	89
5331	Bridging the micro- and macroevolutionary levels in phylogenomics: Hyb-Seq solves relationships from populations to species and above. <i>New Phytologist</i> , 2018, 220, 636-650.	3.5	152
5332	Elucidating "lucidum": Distinguishing the diverse laccate <i>Ganoderma</i> species of the United States. <i>PLoS ONE</i> , 2018, 13, e0199738.	1.1	42
5333	The genus <i>Rosenvingea</i> (Phaeophyceae: Scytosiphonaceae) in south-west Australia, with the description of <i>Rosenvingea australis</i> sp. nov.. <i>Botanica Marina</i> , 2018, 61, 373-382.	0.6	2
5334	Sequences of Circadian Clock Proteins in the Nudibranch Molluscs <i>Hermisenda crassicornis</i> , <i>Melibe leonina</i> , and <i>Tritonia diomedea</i> . <i>Biological Bulletin</i> , 2018, 234, 207-218.	0.7	20
5335	Molecular marker sequences of cattle <i>Cooperia</i> species identify <i>Cooperia spatulata</i> as a morphotype of <i>Cooperia punctata</i> . <i>PLoS ONE</i> , 2018, 13, e0200390.	1.1	21
5336	Phylogeny, evolution, and biogeographic history of <i>Calandrinia</i> (Montiaceae). <i>American Journal of Botany</i> , 2018, 105, 1021-1034.	0.8	12
5337	Mother-to-Infant Microbial Transmission from Different Body Sites Shapes the Developing Infant Gut Microbiome. <i>Cell Host and Microbe</i> , 2018, 24, 133-145.e5.	5.1	822
5338	Evolutionary and ecological drivers of plant flavonoids across a large latitudinal gradient. <i>Molecular Phylogenetics and Evolution</i> , 2018, 128, 147-161.	1.2	25
5339	Molecular systematics of swifts of the genus <i>Chaetura</i> (Aves: Apodiformes: Apodidae). <i>Molecular Phylogenetics and Evolution</i> , 2018, 128, 162-171.	1.2	2
5340	Authentication of <i>Garcinia</i> fruits and food supplements using DNA barcoding and NMR spectroscopy. <i>Scientific Reports</i> , 2018, 8, 10561.	1.6	36
5341	Sympatric Parasites Have Similar Host-Associated, but Asynchronous, Patterns of Diversification. <i>American Naturalist</i> , 2018, 192, E106-E119.	1.0	10
5342	Choice between phylogram and chronogram can have a dramatic impact on the location of phylogenetic diversity hotspots. <i>Journal of Biogeography</i> , 2018, 45, 2190-2201.	1.4	14

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5343	Multidrug-resistant <i>Citrobacter freundii</i> ST139 co-producing NDM-1 and CMY-152 from China. <i>Scientific Reports</i> , 2018, 8, 10653.	1.6	26
5344	Characterization of the First <i>Candidatus</i> Nitrotoga Isolate Reveals Metabolic Versatility and Separate Evolution of Widespread Nitrite-Oxidizing Bacteria. <i>MBio</i> , 2018, 9, .	1.8	112
5345	The origin and adaptive evolution of domesticated populations of yeast from Far East Asia. <i>Nature Communications</i> , 2018, 9, 2690.	5.8	176
5346	Unexpected Genomic and Phenotypic Diversity of <i>Mycobacterium africanum</i> Lineage 5 Affects Drug Resistance, Protein Secretion, and Immunogenicity. <i>Genome Biology and Evolution</i> , 2018, 10, 1858-1874.	1.1	47
5347	Phylogeography of the critically endangered neotropical annual fish, <i>Austrolebias wolterstorffi</i> (Cyprinodontiformes: Aplocheilidae): genetic and morphometric evidence of a new species complex. <i>Environmental Biology of Fishes</i> , 2018, 101, 1503-1515.	0.4	6
5348	Pan-genome Analysis of Ancient and Modern <i>Salmonella enterica</i> Demonstrates Genomic Stability of the Invasive Para C Lineage for Millennia. <i>Current Biology</i> , 2018, 28, 2420-2428.e10.	1.8	65
5349	Molecular footprints of selective pressure in the neuraminidase gene of currently circulating human influenza subtypes and lineages. <i>Virology</i> , 2018, 522, 122-130.	1.1	7
5350	Two different <i>Xylella fastidiosa</i> strains circulating in Italy: phylogenetic and evolutionary analyses. <i>Journal of Plant Interactions</i> , 2018, 13, 428-432.	1.0	6
5351	Silica bodies in leaves of neotropical Podostemaceae: taxonomic and phylogenetic perspectives. <i>Annals of Botany</i> , 2018, 122, 1187-1201.	1.4	6
5352	Exon-Capture-Based Phylogeny and Diversification of the Venomous Gastropods (Neogastropoda). <i>Tj ETQq1 1 0.784314 rgBT /Overlook</i>	3.5	46
5353	Identification of candidate chemosensory genes in <i>Mythimna separata</i> by transcriptomic analysis. <i>BMC Genomics</i> , 2018, 19, 518.	1.2	34
5354	Morphological and Molecular Perspectives on the Phylogeny, Evolution, and Classification of Weevils (Coleoptera: Curculionoidea): Proceedings from the 2016 International Weevil Meeting. <i>Diversity</i> , 2018, 10, 64.	0.7	10
5355	Comparative Chloroplast Genome Analyses of Species in <i>Gentiana</i> section <i>Cruciata</i> (Gentianaceae) and the Development of Authentication Markers. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1962.	1.8	60
5356	Population structure of a vector of human diseases: <i>Aedes aegypti</i> in its ancestral range, Africa. <i>Ecology and Evolution</i> , 2018, 8, 7835-7848.	0.8	57
5357	Prolific Origination of Eyes in Cnidaria with Co-option of Non-visual Opsins. <i>Current Biology</i> , 2018, 28, 2413-2419.e4.	1.8	48
5358	Multilocus phylogeny of the zebra mussel family Dreissenidae (Mollusca: Bivalvia) reveals a fourth Neotropical genus sister to all other genera. <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 1020-1033.	1.2	13
5359	Combining complete chloroplast genome sequences with target loci data and morphology to resolve species limits in <i>Triplostegia</i> (Caprifoliaceae). <i>Molecular Phylogenetics and Evolution</i> , 2018, 129, 15-26.	1.2	40
5360	Genome-wide expert annotation of the epigenetic machinery of the plant-parasitic nematodes <i>Meloidogyne</i> spp., with a focus on the asexually reproducing species. <i>BMC Genomics</i> , 2018, 19, 321.	1.2	18

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5361	Comparative analysis reveals unexpected genome features of newly isolated Thraustochytrids strains: on ecological function and PUFAs biosynthesis. <i>BMC Genomics</i> , 2018, 19, 541.	1.2	30
5362	Molecular characterization of invasive meningococcal isolates in Burkina Faso as the relative importance of serogroups X and W increases, 2008–2012. <i>BMC Infectious Diseases</i> , 2018, 18, 337.	1.3	8
5363	Phylogeny of Map Tree Frogs, <i>Boana semilineata</i> Species Group, with a New Amazonian Species (Anura: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 50)	0.5	18
5364	Epizootic and Apochlorotic <i>Tursiocola</i> species (Bacillariophyta) from the Skin of Florida Manatees (<i>Trichechus manatus latirostris</i>). <i>Protist</i> , 2018, 169, 539-568.	0.6	26
5365	Exploring data processing strategies in NGS target enrichment to disentangle radiations in the tribe Cardueae (Compositae). <i>Molecular Phylogenetics and Evolution</i> , 2018, 128, 69-87.	1.2	38
5366	Diversity of yeast species from Dutch garden soil and the description of six novel Ascomycetes. <i>FEMS Yeast Research</i> , 2018, 18, .	1.1	25
5367	<i>Madangella altirostris</i> , a new genus and species of palaemonid shrimps (Crustacea: Decapoda: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 50)	0.2	1
5368	<i>Ceratocystis cacaofunesta</i> genome analysis reveals a large expansion of extracellular phosphatidylinositol-specific phospholipase-C genes (PI-PLC). <i>BMC Genomics</i> , 2018, 19, 58.	1.2	19
5369	Analysis of the canid Y-chromosome phylogeny using short-read sequencing data reveals the presence of distinct haplogroups among Neolithic European dogs. <i>BMC Genomics</i> , 2018, 19, 350.	1.2	24
5370	Comparative genomics of the miniature wasp and pest control agent <i>Trichogramma pretiosum</i> . <i>BMC Biology</i> , 2018, 16, 54.	1.7	57
5371	Increasing the economic value of lignocellulosic stillage through medium-chain fatty acid production. <i>Biotechnology for Biofuels</i> , 2018, 11, 200.	6.2	99
5372	<i>Lachesiodendron</i> , a new monospecific genus segregated from <i>Piptadenia</i> (Leguminosae: Tj ETQq1 1 0,784314 rgBT /Overlock 13 13)	0.4	13
5373	<i>Yanoella</i> (Marchantiophyta: Lejeuneaceae), a new genus from the Brazilian Atlantic Forest. <i>Bryologist</i> , 2018, 121, 264.	0.1	6
5374	Selective constraints in cold-region wild boars may defuse the effects of small effective population size on molecular evolution of mitogenomes. <i>Ecology and Evolution</i> , 2018, 8, 8102-8114.	0.8	19
5375	Anchored hybrid enrichment generated nuclear, plastid and mitochondrial markers resolve the <i>Lepanthes horrida</i> (Orchidaceae: Pleurothallidinae) species complex. <i>Molecular Phylogenetics and Evolution</i> , 2018, 129, 27-47.	1.2	42
5376	Genome variations between rhizosphere and bulk soil ecotypes of a <i>Pseudomonas koreensis</i> population. <i>Environmental Microbiology</i> , 2018, 20, 4401-4414.	1.8	16
5377	Divergence times in demosponges (Porifera): first insights from new mitogenomes and the inclusion of fossils in a birth-death clock model. <i>BMC Evolutionary Biology</i> , 2018, 18, 114.	3.2	49
5378	Exploration of <i>Plasmodium vivax</i> transmission dynamics and recurrent infections in the Peruvian Amazon using whole genome sequencing. <i>Genome Medicine</i> , 2018, 10, 52.	3.6	27

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5379	Phylogenetic convolutional neural networks in metagenomics. <i>BMC Bioinformatics</i> , 2018, 19, 49.	1.2	75
5380	Evolving in the highlands: the case of the Neotropical Lerma live-bearing <i>Poeciliopsis infans</i> (Woolman, 1894) (Cyprinodontiformes: Poeciliidae) in Central Mexico. <i>BMC Evolutionary Biology</i> , 2018, 18, 56.	3.2	12
5381	Comparative mitochondrial genomics of cryptophyte algae: gene shuffling and dynamic mobile genetic elements. <i>BMC Genomics</i> , 2018, 19, 275.	1.2	23
5382	A sophisticated, differentiated Golgi in the ancestor of eukaryotes. <i>BMC Biology</i> , 2018, 16, 27.	1.7	35
5383	Occurrence of <i>Hepatozoon canis</i> (Adeleorina: Hepatozoidae) and <i>Anaplasma</i> spp. (Rickettsiales) in <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 5</i> . <i>BMC Evolutionary Biology</i> , 2018, 18, 158.	1.0	20
5384	The role of retinoic acid signaling in starfish metamorphosis. <i>EvoDevo</i> , 2018, 9, 10.	1.3	15
5385	Whole Genome Sequence and Comparative Genomics Analysis of Multi-drug Resistant Environmental <i>Staphylococcus epidermidis</i> ST59. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2225-2230.	0.8	21
5386	A Tandem Amino Acid Residue Motif in Guard Cell SLAC1 Anion Channel of Grasses Allows for the Control of Stomatal Aperture by Nitrate. <i>Current Biology</i> , 2018, 28, 1370-1379.e5.	1.8	46
5387	Discovery of the First Germline-Restricted Gene by Subtractive Transcriptomic Analysis in the Zebra Finch, <i>Taeniopygia guttata</i> . <i>Current Biology</i> , 2018, 28, 1620-1627.e5.	1.8	51
5388	The complete plastome sequence of <i>Lilium Bulbiferum</i> (Liliaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 30-31.	0.2	0
5389	The complete chloroplast genome sequence of <i>Viburnum Japonicum</i> (Adoxaceae), an evergreen broad-leaved shrub. <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 458-459.	0.2	8
5390	Complete mitochondrial genome sequence of the mountain nyala (<i>Tragelaphus buxtoni</i>). <i>Conservation Genetics Resources</i> , 2018, 10, 547-550.	0.4	0
5391	Historical biogeography of the lichenized fungal genus <i>Hypotrachyna</i> (Parmeliaceae, Ascomycota): insights into the evolutionary history of a pantropical clade. <i>Lichenologist</i> , 2018, 50, 283-298.	0.5	5
5392	Molecular and morphological data from Thoosidae in favour of the creation of a new suborder of Tetractinellida. <i>Systematics and Biodiversity</i> , 2018, 16, 512-521.	0.5	6
5393	New imine-reducing enzymes from α^2 -hydroxyacid dehydrogenases by single amino acid substitutions. <i>Protein Engineering, Design and Selection</i> , 2018, 31, 109-120.	1.0	33
5394	SIESTA: enhancing searches for optimal supertrees and species trees. <i>BMC Genomics</i> , 2018, 19, 252.	1.2	4
5395	Comparison of the Chinese bamboo partridge and red Junglefowl genome sequences highlights the importance of demography in genome evolution. <i>BMC Genomics</i> , 2018, 19, 336.	1.2	17
5396	Mobilization of retrotransposons as a cause of chromosomal diversification and rapid speciation: the case for the Antarctic teleost genus <i>Trematomus</i> . <i>BMC Genomics</i> , 2018, 19, 339.	1.2	45

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5397	Allele phasing has minimal impact on phylogenetic reconstruction from targeted nuclear gene sequences in a case study of <i>Artocarpus</i> . <i>American Journal of Botany</i> , 2018, 105, 404-416.	0.8	74
5398	A new <i>Bunodophoron</i> species (<i>Sphaerophoraceae</i> , <i>Lecanorales</i>) from the Neotropics. <i>Lichenologist</i> , 2018, 50, 255-266.	0.5	6
5399	Genomic expansion of magnetotactic bacteria reveals an early common origin of magnetotaxis with lineage-specific evolution. <i>ISME Journal</i> , 2018, 12, 1508-1519.	4.4	103
5400	Predator size divergence depends on community context. <i>Ecology Letters</i> , 2018, 21, 1097-1107.	3.0	9
5401	Phylogenetic patterns of ant-fungus associations indicate that farming strategies, not only a superior fungal cultivar, explain the ecological success of leafcutter ants. <i>Molecular Ecology</i> , 2018, 27, 2414-2434.	2.0	68
5402	Population size may shape the accumulation of functional mutations following domestication. <i>BMC Evolutionary Biology</i> , 2018, 18, 4.	3.2	15
5403	Widespread signatures of selection for secreted peptidases in a fungal plant pathogen. <i>BMC Evolutionary Biology</i> , 2018, 18, 7.	3.2	27
5404	Phylogenomics of a rapid radiation: the Australian rainbow skinks. <i>BMC Evolutionary Biology</i> , 2018, 18, 15.	3.2	26
5405	Phylogenomics provides a robust topology of the major cnidarian lineages and insights on the origins of key organismal traits. <i>BMC Evolutionary Biology</i> , 2018, 18, .	3.2	182
5406	A phylogenetic analysis of the Primnoidae (Anthozoa: Octocorallia: Calcaxonia) with analyses of character evolution and a key to the genera and subgenera. <i>BMC Evolutionary Biology</i> , 2018, 18, 66.	3.2	15
5407	Reconstruction of a replication-competent ancestral murine endogenous retrovirus-L. <i>Retrovirology</i> , 2018, 15, 34.	0.9	11
5408	SACCHARIS: an automated pipeline to streamline discovery of carbohydrate active enzyme activities within polyspecific families and de novo sequence datasets. <i>Biotechnology for Biofuels</i> , 2018, 11, 27.	6.2	52
5409	Mouse Obox and Crxos modulate preimplantation transcriptional profiles revealing similarity between paralogous mouse and human homeobox genes. <i>EvoDevo</i> , 2018, 9, 2.	1.3	13
5410	Genome-based analysis of Carbapenemase-producing <i>Klebsiella pneumoniae</i> isolates from German hospital patients, 2008-2014. <i>Antimicrobial Resistance and Infection Control</i> , 2018, 7, 62.	1.5	100
5411	Comparative genomic analysis reveals the evolution and environmental adaptation strategies of vibrios. <i>BMC Genomics</i> , 2018, 19, 135.	1.2	71
5412	A software tool â€”CroCoâ™ detects pervasive cross-species contamination in next generation sequencing data. <i>BMC Biology</i> , 2018, 16, 28.	1.7	82
5413	Genomic comparison of <i>Clostridium</i> species with the potential of utilizing red algal biomass for biobutanol production. <i>Biotechnology for Biofuels</i> , 2018, 11, 42.	6.2	41
5414	Identification of wild-caught phlebotomine sand flies from Crete and Cyprus using DNA barcoding. <i>Parasites and Vectors</i> , 2018, 11, 94.	1.0	14

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5415	A reservoir of "historical" antibiotic resistance genes in remote pristine Antarctic soils. <i>Microbiome</i> , 2018, 6, 40.	4.9	244
5416	The complete chloroplast genome of <i>Littledealea przewalskii</i> Tzvelev (Poaceae: Bromaceae), an endemic of the Qinghai-Tibetan Plateau. <i>Conservation Genetics Resources</i> , 2018, 10, 647-650.	0.4	0
5417	Two new complete mitochondrial genomes of <i>Dorcus</i> stag beetles (Coleoptera, Lucanidae). <i>Genes and Genomics</i> , 2018, 40, 873-880.	0.5	11
5418	Complete mitochondrial genome of the darkling beetle <i>Gonocephalum outreyi</i> (Coleoptera: Tj ETQq1 1 0.784314 rgBT / Overlock 10 0.24	0.4	0
5419	Recent Asian origin of chytrid fungi causing global amphibian declines. <i>Science</i> , 2018, 360, 621-627.	6.0	389
5420	Insight into Energy Conservation via Alternative Carbon Monoxide Metabolism in <i>Carboxythermus pertinax</i> Revealed by Comparative Genome Analysis. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	9
5421	Generation of a novel next-generation sequencing-based method for the isolation of new human papillomavirus types. <i>Virology</i> , 2018, 520, 1-10.	1.1	25
5422	A genomic evaluation of taxonomic trends through time in coast horned lizards (genus <i>Phrynosoma</i>) Tj ETQq1 1 0.784314 rgBT / Overlock 10 2.0 14	2.0	14
5423	Divergent trait and environment relationships among parallel radiations in <i>Pelargonium</i> (Geraniaceae): a role for evolutionary legacy?. <i>New Phytologist</i> , 2018, 219, 794-807.	3.5	8
5424	Identification and characterization of chemosensory genes in the antennal transcriptome of <i>Spodoptera exigua</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2018, 27, 54-65.	0.4	39
5425	Comparative transcriptomics gives insights into the evolution of parasitism in <i>Strongyloides</i> nematodes at the genus, subclade and species level. <i>Scientific Reports</i> , 2018, 8, 5192.	1.6	24
5426	Anaerobic carbon monoxide metabolism by <i>Pleomorphomonas carboxyditropha</i> sp. nov., a new mesophilic hydrogenogenic carboxydotroph. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	18
5427	Adaptation of <i>S. cerevisiae</i> to Fermented Food Environments Reveals Remarkable Genome Plasticity and the Footprints of Domestication. <i>Molecular Biology and Evolution</i> , 2018, 35, 1712-1727.	3.5	214
5428	ASTRAL-III: polynomial time species tree reconstruction from partially resolved gene trees. <i>BMC Bioinformatics</i> , 2018, 19, 153.	1.2	1,451
5429	Profiling microbial strains in urban environments using metagenomic sequencing data. <i>Biology Direct</i> , 2018, 13, 9.	1.9	29
5430	Phylogenomic inference in extremis: A case study with mycoheterotroph plastomes. <i>American Journal of Botany</i> , 2018, 105, 480-494.	0.8	40
5431	The complete plastome sequence of <i>Lilium wahingtonianum</i> Kellogg (Liliaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 120-121.	0.2	1
5432	Characterization of the complete chloroplast genome of toad lily <i>Tricyrtis Macropoda</i> (Liliaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 145-146.	0.2	1

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5433	Complete chloroplast genome sequence of <i>Rosa roxburghii</i> and its phylogenetic analysis. Mitochondrial DNA Part B: Resources, 2018, 3, 149-150.	0.2	10
5434	Complete mitochondrial genome of the dark mealworm <i>Tenebrio obscurus</i> Fabricius (Insecta: Tj ETQq1 1 0.784314 rgBT /Overlock 107	0.2	20
5435	The complete mitochondrial genome of <i>Cyclocheilichthys enoplos</i> (Teleostei, Cyprinidae). Mitochondrial DNA Part B: Resources, 2018, 3, 220-221.	0.2	1
5436	The complete chloroplast genome sequence of <i>Cyrtomium fortunei</i> (Dryopteridaceae), an important medical fern. Mitochondrial DNA Part B: Resources, 2018, 3, 288-289.	0.2	0
5437	The complete chloroplast genome sequence of <i>Camellia ptilophylla</i> (Theaceae): a natural caffeine-free tea plant endemic to China. Mitochondrial DNA Part B: Resources, 2018, 3, 426-427.	0.2	5
5438	The complete chloroplast genome sequence of <i>Echinocodon Lobophyllus</i> (Campanulaceae) revealed by next-generation sequencing and phylogenetic implication. Mitochondrial DNA Part B: Resources, 2018, 3, 450-451.	0.2	0
5439	A nuclear Xdh phylogenetic analysis of yams (Dioscorea: Dioscoreaceae) congruent with plastid trees reveals a new Neotropical lineage. Botanical Journal of the Linnean Society, 2018, 187, 232-246.	0.8	38
5440	Whole-genome de novo sequencing reveals unique genes that contributed to the adaptive evolution of the Mikado pheasant. GigaScience, 2018, 7, .	3.3	21
5441	Co-circulation of Flanders Virus and West Nile Virus in <i>Culex</i> Mosquitoes (Diptera: Culicidae) from Chicago, Illinois. Journal of Medical Entomology, 2018, 55, 1062-1066.	0.9	3
5442	Multiobjective Frog-Leaping Optimization for the Study of Ancestral Relationships in Protein Data. IEEE Transactions on Evolutionary Computation, 2018, 22, 879-893.	7.5	8
5443	Comparative genomics of <i>Pseudomonas syringae</i> reveals convergent gene gain and loss associated with specialization onto cherry (<i>Prunus avium</i>). New Phytologist, 2018, 219, 672-696.	3.5	52
5444	Molecular and morphometric analyses reveal cryptic diversity within freshwater mussels (Bivalvia: Tj ETQq1 1 0.784314 rgBT /Overlock 107 Society, 2018, 124, 261-277.	0.7	30
5445	IMPUTOR: Phylogenetically Aware Software for Imputation of Errors in Next-Generation Sequencing. Genome Biology and Evolution, 2018, 10, 1248-1254.	1.1	7
5446	A new genus and species of shrew (Mammalia: Soricidae) from Palawan Island, Philippines. Journal of Mammalogy, 2018, 99, 518-536.	0.6	12
5447	EukRefâ€Ciliophora: a manually curated, phylogenyâ€Cbased database of small subunit rRNA gene sequences of ciliates. Environmental Microbiology, 2018, 20, 2218-2230.	1.8	27
5448	From cacti to carnivores: Improved phylotranscriptomic sampling and hierarchical homology inference provide further insight into the evolution of Caryophyllales. American Journal of Botany, 2018, 105, 446-462.	0.8	87
5449	The mitochondrial genomes of the barklice, <i>Lepinotus reticulatus</i> and <i>Dorypteryx domestica</i> (Psocodea: Trogiomorpha): Insight into phylogeny of the order Psocodea. International Journal of Biological Macromolecules, 2018, 116, 247-254.	3.6	8
5450	Morphological and mitochondrial DNA data reshuffle the taxonomy of the genera <i>Atopochetus</i> Attems, <i>Litostrophus</i> Chamberlin and <i>Tonkinbolus</i> Verhoeff (Diplopoda: Spirobolida: Pachybolidae), with descriptions of nine new species. Invertebrate Systematics, 2018, 32, 159.	0.5	12

#	ARTICLE	IF	CITATIONS
5451	The first horse herders and the impact of early Bronze Age steppe expansions into Asia. <i>Science</i> , 2018, 360, .	6.0	262
5452	Biodiversity estimates and ecological interpretations of meiofaunal communities are biased by the taxonomic approach. <i>Communications Biology</i> , 2018, 1, 112.	2.0	28
5453	Phylogeny and Systematics of <i>Kewia</i> (Kewaceae). <i>Systematic Botany</i> , 2018, 43, 689-700.	0.2	2
5454	Genomic Epidemiology of Global Carbapenemase-Producing <i>Enterobacter</i> spp., 2008–2014. <i>Emerging Infectious Diseases</i> , 2018, 24, 1010-1019.	2.0	107
5455	Whole-Genome Analysis of Three Yeast Strains Used for Production of Sherry-Like Wines Revealed Genetic Traits Specific to Flor Yeasts. <i>Frontiers in Microbiology</i> , 2018, 9, 965.	1.5	30
5456	Full Genome Sequencing Reveals New Southern African Territories Genotypes Bringing Us Closer to Understanding True Variability of Foot-and-Mouth Disease Virus in Africa. <i>Viruses</i> , 2018, 10, 192.	1.5	24
5457	Fungal Planet description sheets: 716–784. <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2018, 40, 239-392.	1.6	142
5458	Iterative taxonomy based on morphological and molecular evidence to estimate species boundaries: a case study in <i>Cypella</i> (Iridaceae: Iridoideae). <i>Plant Systematics and Evolution</i> , 2018, 304, 1117-1140.	0.3	7
5459	Biogeographic analyses support an Australian origin for the Indomalayan-Australasian wet forest-adapted tropical tree and shrub genus <i>Alphitonia</i> and its close allies (Rhamnaceae). <i>Botanical Journal of the Linnean Society</i> , 2018, 188, 1-20.	0.8	13
5460	Genome Analyses of the Microalga <i>Picochlorum</i> Provide Insights into the Evolution of Thermotolerance in the Green Lineage. <i>Genome Biology and Evolution</i> , 2018, 10, 2347-2365.	1.1	36
5461	Comparison of metaheuristics to measure gene effects on phylogenetic supports and topologies. <i>BMC Bioinformatics</i> , 2018, 19, 218.	1.2	1
5462	Fungi Indirectly Affect Plant Root Architecture by Modulating Soil Volatile Organic Compounds. <i>Frontiers in Microbiology</i> , 2018, 9, 1847.	1.5	36
5463	Revision of Tasmanian viviparous velvet worms (Onychophora : Peripatopsidae) with descriptions of two new species. <i>Invertebrate Systematics</i> , 2018, 32, 909.	0.5	6
5464	A novel glycosyltransferase catalyses the transfer of glucose to glucosylated anthocyanins in purple sweet potato. <i>Journal of Experimental Botany</i> , 2018, 69, 5444-5459.	2.4	26
5465	Genetic Variation of the Pathogen Causing Impatiens Downy Mildew Predating and Including Twenty-first Century Epidemics on <i>Impatiens walleriana</i> . <i>Plant Disease</i> , 2018, 102, 2411-2420.	0.7	17
5466	A new species of <i>Clitocybula</i> (Marasmiaceae) from West Bengal, India. <i>Nova Hedwigia</i> , 2018, 107, 195-203.	0.2	4
5467	<i>Escalonius</i> , a new subgenus of <i>Calochromus</i> Guérin-Méneville, 1833 identified by the molecular phylogeny of Calochromini (Coleoptera: Lycidae). <i>Zootaxa</i> , 2018, 4461, 77.	0.2	0
5468	PdumBase: a transcriptome database and research tool for <i>Platynereis dumerilii</i> and early development of other metazoans. <i>BMC Genomics</i> , 2018, 19, 618.	1.2	18

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5469	Related Endogenous Retrovirus-K Elements Harbor Distinct Protease Active Site Motifs. <i>Frontiers in Microbiology</i> , 2018, 9, 1577.	1.5	6
5470	Iterative <scp>l</scp>â€”tryptophan Methylation in <i>Psilocybe</i> Evolved by Subdomain Duplication. <i>ChemBioChem</i> , 2018, 19, 2160-2166.	1.3	16
5471	Whole genome analyses of CMY-2-producing <i>Escherichia coli</i> isolates from humans, animals and food in Germany. <i>BMC Genomics</i> , 2018, 19, 601.	1.2	128
5472	Characterization of the Complete Chloroplast Genomes of <i>Buddleja colvilei</i> and <i>B. sessilifolia</i> : Implications for the Taxonomy of <i>Buddleja</i> L.. <i>Molecules</i> , 2018, 23, 1248.	1.7	17
5473	Do Antarctic populations represent local or widespread phylogenetic and ecological lineages? Complicated fate of bipolar moss concepts with <i>Drepanocladus longifolius</i> as a case study. <i>Organisms Diversity and Evolution</i> , 2018, 18, 263-278.	0.7	20
5474	Anchored phylogenomics unravels the evolution of spider flies (Diptera, Acroceridae) and reveals discordance between nucleotides and amino acids. <i>Molecular Phylogenetics and Evolution</i> , 2018, 128, 233-245.	1.2	35
5475	Phylogenetic analysis of symbiont transmission mechanisms reveal evolutionary patterns in thermotolerance and host specificity that enhance bleaching resistance among vertically transmitted <i>Symbiodinium</i>. <i>European Journal of Phycology</i> , 2018, 53, 443-459.	0.9	12
5476	Coalescent Analysis of Phylogenomic Data Confidently Resolves the Species Relationships in the <i>Anopheles gambiae</i> Species Complex. <i>Molecular Biology and Evolution</i> , 2018, 35, 2512-2527.	3.5	76
5477	Detection and phylogenetic characterization of atypical porcine pestivirus strains in Hungary. <i>Transboundary and Emerging Diseases</i> , 2018, 65, 2039-2042.	1.3	26
5478	Hybridizationâ€”facilitated genome merger and repeated chromosome fusion after 8Â”million years. <i>Plant Journal</i> , 2018, 96, 748-760.	2.8	21
5479	Chemoreception of Mouthparts: Sensilla Morphology and Discovery of Chemosensory Genes in Proboscis and Labial Palps of Adult <i>Helicoverpa armigera</i> (Lepidoptera: Noctuidae). <i>Frontiers in Physiology</i> , 2018, 9, 970.	1.3	24
5480	A paralog of a bacteriochlorophyll biosynthesis enzyme catalyzes the formation of 1,2-dihydrocarotenoids in green sulfur bacteria. <i>Journal of Biological Chemistry</i> , 2018, 293, 15233-15242.	1.6	9
5481	Ten fish mitogenomes of the tribe Gobionini (Cypriniformes: Cyprinidae: Gobioninae). <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 803-804.	0.2	15
5482	Genetic Characterization of Some <i>Neoponera</i> (Hymenoptera: Formicidae) Populations Within the foetida Species Complex. <i>Journal of Insect Science</i> , 2018, 18, .	0.6	3
5483	Genomic and epidemiological monitoring of yellow fever virus transmission potential. <i>Science</i> , 2018, 361, 894-899.	6.0	279
5484	The unusual flagellar targeting mechanism and functions of the trypanosome orthologue of the ciliary GTPase Arl13b. <i>Journal of Cell Science</i> , 2018, 131, .	1.2	5
5485	Molecular analyses resolve the phylogenetic position of <i>Polysiphonia adamsiae</i> (Rhodomelaceae,) Tj ETQq0 0 0 rgBT /Overlock 10	0.6	9
5486	The Endophytic Strain <i>Klebsiella michiganensis</i> Kd70 Lacks Pathogenic Island-Like Regions in Its Genome and Is Incapable of Infecting the Urinary Tract in Mice. <i>Frontiers in Microbiology</i> , 2018, 9, 1548.	1.5	12

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5487	A novel marine genus, <i>Halobyssothecium</i> (Lentitheciaceae) and epitypification of <i>Halobyssothecium obiones</i> comb. nov.. <i>Mycological Progress</i> , 2018, 17, 1161-1171.	0.5	15
5488	Employing hypothesis testing and data from multiple genomic compartments to resolve recalcitrant backbone nodes in <i>Goodenia</i> s.l. (Goodeniaceae). <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 502-512.	1.2	2
5489	Deciphering the biology of <i>Cryptophyllachora eurasiatica</i> gen. et sp. nov., an often cryptic pathogen of an allergenic weed, <i>Ambrosia artemisiifolia</i> . <i>Scientific Reports</i> , 2018, 8, 10806.	1.6	3
5490	Molecular and morphological evidence for a new subspecies of <i>Fazila</i> ™s Lycian Salamander <i>Lyciasalamandra fazilae</i> in South-west Anatolia. <i>Zoology in the Middle East</i> , 2018, 64, 304-314.	0.2	2
5491	Xenacoelomorph Neuropeptidomes Reveal a Major Expansion of Neuropeptide Systems during Early Bilaterian Evolution. <i>Molecular Biology and Evolution</i> , 2018, 35, 2528-2543.	3.5	35
5492	Widely distributed red algae often represent hidden introductions, complexes of cryptic species or species with strong phylogeographic structure. <i>Journal of Phycology</i> , 2018, 54, 829-839.	1.0	49
5493	Evaluation of Whole-Genome Sequencing for Identification and Typing of <i>Vibrio cholerae</i> . <i>Journal of Clinical Microbiology</i> , 2018, 56, .	1.8	25
5494	Phenotypic and Genotypic Characterization of <i>Enterobacteriaceae</i> Producing Oxacillinase-48â€“Like Carbapenemases, United States. <i>Emerging Infectious Diseases</i> , 2018, 24, 700-709.	2.0	58
5495	Comparative Genomics and Description of Putative Virulence Factors of <i>Melissococcus plutonius</i> , the Causative Agent of European Foulbrood Disease in Honey Bees. <i>Genes</i> , 2018, 9, 419.	1.0	28
5496	Phylogeny and evolutionary history of Pinaceae updated by transcriptomic analysis. <i>Molecular Phylogenetics and Evolution</i> , 2018, 129, 106-116.	1.2	70
5497	En garde! Redefinition of <i>Nebela militaris</i> (Arcellinida, Hyalospheniidae) and erection of <i>Alabasta</i> gen. nov.. <i>European Journal of Protistology</i> , 2018, 66, 156-165.	0.5	17
5498	Towards solving the taxonomic impasse of the biocontrol plant bug subgenus <i>Dicyphus</i> (<i>Dicyphus</i>) (Insecta: Heteroptera: Miridae) using molecular, morphometric and morphological partitions. <i>Zoological Journal of the Linnean Society</i> , 2018, 184, 330-406.	1.0	18
5499	Molecular Detection of Eukaryotic Diets and Gut Mycobiomes in Two Marine Sediment-Dwelling Worms, <i>Sipunculus nudus</i> and <i>Urechis unicinctus</i> . <i>Microbes and Environments</i> , 2018, 33, 290-300.	0.7	6
5500	<i>Plasmodium vivax</i> -like genome sequences shed new insights into <i>Plasmodium vivax</i> biology and evolution. <i>PLoS Biology</i> , 2018, 16, e2006035.	2.6	32
5501	Morphology, morphogenesis and molecular phylogeny of a new brackish water subspecies, <i>Neurostylopsis flava paraflava</i> nov. subsp. (Ciliophora, Hypotrichia, Urostylidae), with redefinition of the genus <i>Neurostylopsis</i> . <i>European Journal of Protistology</i> , 2018, 66, 48-62.	0.5	24
5502	A standardized bacterial taxonomy based on genome phylogeny substantially revises the tree of life. <i>Nature Biotechnology</i> , 2018, 36, 996-1004.	9.4	2,615
5503	Partial genomic survival of cave bears in living brown bears. <i>Nature Ecology and Evolution</i> , 2018, 2, 1563-1570.	3.4	132
5504	Floral evolution by simplification in <i>Monanthotaxis</i> (Annonaceae) and hypotheses for pollination system shifts. <i>Scientific Reports</i> , 2018, 8, 12066.	1.6	2

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5505	Taxonomy of the traditional medicinal plant genus <i>Ferula</i> (Apiaceae) is confounded by incongruence between nuclear rDNA and plastid DNA. <i>Botanical Journal of the Linnean Society</i> , 2018, 188, 173-189.	0.8	23
5506	Mobile Elements Shape Plastome Evolution in Ferns. <i>Genome Biology and Evolution</i> , 2018, 10, 2558-2571.	1.1	25
5507	Two New Species of <i>Ischnocnema</i> (Anura: Brachycephalidae) from Southeastern Brazil and their Phylogenetic Position within the <i>l. guentheri</i> Series. <i>Herpetological Monographs</i> , 2018, 32, 1-21.	1.1	9
5508	Northern Hemisphere disjunctions in <i>Lactuca</i> (Cichorieae, Asteraceae): independent Eurasia to North America migrations and allopolyploidization. <i>Willdenowia</i> , 2018, 48, 259.	0.5	7
5509	Horizontal gene transfer of three co-inherited methane monooxygenase systems gave rise to methanotrophy in the Proteobacteria. <i>Molecular Phylogenetics and Evolution</i> , 2018, 129, 171-181.	1.2	16
5510	Plastomes of nine hornbeams and phylogenetic implications. <i>Ecology and Evolution</i> , 2018, 8, 8770-8778.	0.8	15
5511	Evolutionary history of the podoplanin gene. <i>Gene Reports</i> , 2018, 13, 28-37.	0.4	3
5512	Microevolution of epidemiological highly relevant non-O157 enterohemorrhagic <i>Escherichia coli</i> of serogroups O26 and O111. <i>International Journal of Medical Microbiology</i> , 2018, 308, 1085-1095.	1.5	7
5513	The complete chloroplast genome of <i>Pyrrosia bonii</i> (Polypodiaceae), an important ornamental and medical fern. <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 801-802.	0.2	4
5514	Does Population Structure Predict the Rate of Speciation? A Comparative Test across Australia's Most Diverse Vertebrate Radiation. <i>American Naturalist</i> , 2018, 192, 432-447.	1.0	35
5515	The role of history and ecology as drivers of song divergence in Bell's and Sagebrush sparrows (<i>Artemisospiza</i> , Aves: Passerellidae). <i>Biological Journal of the Linnean Society</i> , 2018, 125, 421-440.	0.7	12
5516	The chromosome-level genome assemblies of two rattans (<i>Calamus simplicifolius</i> and <i>Daemonorops</i>) Tj ETQq1 1 0.784314 rgBT /Overlo 3.3 28		
5517	Phylogenomics of colistin-susceptible and resistant XDR <i>Acinetobacter baumannii</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2018, 73, 2952-2959.	1.3	41
5518	Bayesian Phylogeography and Pathogenic Characterization of Smallpox Based on <i>HA</i> , <i>ATI</i> , and <i>CrmB</i> Genes. <i>Molecular Biology and Evolution</i> , 2018, 35, 2607-2617.	3.5	6
5519	The onset of ecological diversification 50 years after colonization of a crater lake by haplochromine cichlid fishes. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018, 285, 20180171.	1.2	21
5520	Taxon cycle predictions supported by model-based inference in Indo-Pacific trapjaw ants (Hymenoptera:) Tj ETQq1 1 0.784314 rgBT /Overlo 2.0 28		
5521	Genome-wide systematic characterization and its regulatory expression reprogramming process of the bZIP transcription factors during trauma response in <i>Camellia sinensis</i> . <i>Canadian Journal of Forest Research</i> , 2018, 48, 1279-1291.	0.8	2
5522	ezTree: an automated pipeline for identifying phylogenetic marker genes and inferring evolutionary relationships among uncultivated prokaryotic draft genomes. <i>BMC Genomics</i> , 2018, 19, 921.	1.2	50

#	ARTICLE	IF	CITATIONS
5523	Diversity and evolution of anuran trypanosomes: insights from the study of European species. <i>Parasites and Vectors</i> , 2018, 11, 447.	1.0	36
5524	Improved <i>Brassica rapa</i> reference genome by single-molecule sequencing and chromosome conformation capture technologies. <i>Horticulture Research</i> , 2018, 5, 50.	2.9	224
5525	A pipeline for metabarcoding and diet analysis from fecal samples developed for a small semi-aquatic mammal. <i>PLoS ONE</i> , 2018, 13, e0201763.	1.1	22
5526	Diatoms do radiate: evidence for a freshwater species flock. <i>Journal of Evolutionary Biology</i> , 2018, 31, 1969-1975.	0.8	18
5527	Evolution of Sequence Type 4821 Clonal Complex Meningococcal Strains in China from Prequinolone to Quinolone Era, 1972–2013. <i>Emerging Infectious Diseases</i> , 2018, 24, 683-690.	2.0	11
5528	Remarkable Geographic Structuring of Rheophilic Fishes of the Lower Araguaia River. <i>Frontiers in Genetics</i> , 2018, 9, 295.	1.1	13
5529	Genetic Diversity, Population Structure, and Genetic Correlation with Climatic Variation in Chickpea (<i>Cicer arietinum</i>) Landraces from Pakistan. <i>Plant Genome</i> , 2018, 11, 170067.	1.6	14
5530	Monoclonal antibodies from a patient with anti-NMDA receptor encephalitis. <i>Annals of Clinical and Translational Neurology</i> , 2018, 5, 935-951.	1.7	24
5531	The Evolutionary Conserved β -Core Motif Influences the Anti-Candida Activity of the <i>Penicillium chrysogenum</i> Antifungal Protein PAF. <i>Frontiers in Microbiology</i> , 2018, 9, 1655.	1.5	29
5532	phylotaR: An Automated Pipeline for Retrieving Orthologous DNA Sequences from GenBank in R. <i>Life</i> , 2018, 8, 20.	1.1	26
5533	Comparative mitochondrial genomics reveals a possible role of a recent duplication of NADH dehydrogenase subunit 5 in gene regulation. <i>DNA Research</i> , 2018, 25, 577-586.	1.5	7
5534	Azithromycin Resistance through Interspecific Acquisition of an Epistasis-Dependent Efflux Pump Component and Transcriptional Regulator in <i>Neisseria gonorrhoeae</i> . <i>MBio</i> , 2018, 9, .	1.8	133
5535	Phylogenomic analysis of Apoidea sheds new light on the sister group of bees. <i>BMC Evolutionary Biology</i> , 2018, 18, 71.	3.2	131
5536	Cryptic <i>Plutella</i> species show deep divergence despite the capacity to hybridize. <i>BMC Evolutionary Biology</i> , 2018, 18, 77.	3.2	26
5537	Genome-Wide Comparative Analysis of <i>Aspergillus fumigatus</i> Strains: The Reference Genome as a Matter of Concern. <i>Genes</i> , 2018, 9, 363.	1.0	51
5538	Characterization of MyD88 in Japanese eel, <i>Anguilla japonica</i> . <i>Fish and Shellfish Immunology</i> , 2018, 81, 374-382.	1.6	17
5539	Clarifying the phylogenetic relationships and taxonomy of <i>Stenonema</i> , <i>Stenacron</i> and <i>Maccaffertium</i> , three common eastern North American mayfly genera. <i>Molecular Phylogenetics and Evolution</i> , 2018, 128, 212-220.	1.2	4
5540	Evolutionary cell biology traces the rise of the exomer complex in Fungi from an ancient eukaryotic component. <i>Scientific Reports</i> , 2018, 8, 11154.	1.6	7

#	ARTICLE	IF	CITATIONS
5541	Whole genome sequencing of the monomorphic pathogen <i>Mycobacterium bovis</i> reveals local differentiation of cattle clinical isolates. <i>BMC Genomics</i> , 2018, 19, 2.	1.2	36
5542	Investigation of mitochondrial-derived plastome sequences in the <i>Paspalum</i> lineage (Panicoideae; Tj ETQq1 1 0.784314 rgBT /Overlock 12	1.6	12
5543	Viral and metabolic controls on high rates of microbial sulfur and carbon cycling in wetland ecosystems. <i>Microbiome</i> , 2018, 6, 138.	4.9	63
5544	Testing the utility of DNA barcodes and a preliminary phylogenetic framework for Chinese freshwater mussels (<i>Bivalvia</i> : Unionidae) from the middle and lower Yangtze River. <i>PLoS ONE</i> , 2018, 13, e0200956.	1.1	20
5545	Epistatic Interactions in NS5A of Hepatitis C Virus Suggest Drug Resistance Mechanisms. <i>Genes</i> , 2018, 9, 343.	1.0	12
5546	Shedding new light on the origin and spread of the brinjal eggplant (<i>Solanum melongena</i> L.) and its wild relatives. <i>American Journal of Botany</i> , 2018, 105, 1175-1187.	0.8	42
5547	Phylogenetic analysis of the mitochondrial genomes in bees (Hymenoptera: Apoidea: Anthophila). <i>PLoS ONE</i> , 2018, 13, e0202187.	1.1	11
5548	Molecular and Morphological Diversity of the Oxymonad Genera <i>Monocercomonoides</i> and <i>Blattamonas</i> gen. nov.. <i>Protist</i> , 2018, 169, 744-783.	0.6	19
5549	Genomic analysis of <i>Sparus aurata</i> reveals the evolutionary dynamics of sex-biased genes in a sequential hermaphrodite fish. <i>Communications Biology</i> , 2018, 1, 119.	2.0	84
5550	The first complete chloroplast genome of <i>Coptis chinensis</i> var. <i>brevisepala</i> , with implication for the phylogeny of Ranunculaceae. <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 951-952.	0.2	1
5551	Proceeding From in vivo Functions of Pheromone Receptors: Peripheral-Coding Perception of Pheromones From Three Closely Related Species, <i>Helicoverpa armigera</i> , <i>H. assulta</i> , and <i>Heliothis virescens</i> . <i>Frontiers in Physiology</i> , 2018, 9, 1188.	1.3	11
5552	SLING: a tool to search for linked genes in bacterial datasets. <i>Nucleic Acids Research</i> , 2018, 46, e128.	6.5	18
5553	Multilocus phylogeny, diagnosis and generic revision of the Guiana Shield endemic suckermouth armoured catfish tribe Lithoxini (Loricariidae: Hypostominae). <i>Zoological Journal of the Linnean Society</i> , 2018, , .	1.0	3
5554	Origin and Evolution of Flavin-Based Electron Bifurcating Enzymes. <i>Frontiers in Microbiology</i> , 2018, 9, 1762.	1.5	34
5555	More amoebae from the deep-sea: Two new marine species of <i>Vexillifera</i> (Amoebozoa, Dactylopodida) with notes on taxonomy of the genus. <i>European Journal of Protistology</i> , 2018, 66, 9-25.	0.5	8
5556	<i>Tuber brennemanii</i> and <i>Tuber floridanum</i> : Two new <i>Tuber</i> species are among the most commonly detected ectomycorrhizal taxa within commercial pecan (<i>Carya illinoensis</i>) orchards. <i>Mycologia</i> , 2018, 110, 780-790.	0.8	14
5557	Origin and hidden diversity within the poorly known Galápagos snake radiation (Serpentes: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 102	0.5	23
5558	Tetraconatan phylogeny with special focus on Malacostraca and Branchiopoda: highlighting the strength of taxon-specific matrices in phylogenomics. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018, 285, 20181524.	1.2	80

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5559	Phylogenetic analysis and a review of the history of the accidental phytoplankter, <i>Phaeodactylum tricornutum</i> Bohlin (Bacillariophyta). <i>PLoS ONE</i> , 2018, 13, e0196744.	1.1	17
5560	Functional and Genome Sequence-Driven Characterization of tal Effector Gene Repertoires Reveals Novel Variants With Altered Specificities in Closely Related Malian <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> Strains. <i>Frontiers in Microbiology</i> , 2018, 9, 1657.	1.5	40
5561	Genomic and Biotechnological Characterization of the Heavy-Metal Resistant, Arsenic-Oxidizing Bacterium <i>Ensifer</i> sp. M14. <i>Genes</i> , 2018, 9, 379.	1.0	25
5562	Australasian orchid biogeography at continental scale: Molecular phylogenetic insights from the Sun Orchids (<i>Thelymitra</i> , Orchidaceae). <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 304-319.	1.2	19
5563	Accurate authentication of <i>Dendrobium officinale</i> and its closely related species by comparative analysis of complete plastomes. <i>Acta Pharmaceutica Sinica B</i> , 2018, 8, 969-980.	5.7	52
5564	Parallel and Gradual Genome Erosion in the <i>Blattabacterium</i> Endosymbionts of <i>Mastotermes darwiniensis</i> and <i>Cryptocercus</i> Wood Roaches. <i>Genome Biology and Evolution</i> , 2018, 10, 1622-1630.	1.1	14
5565	Pleistocene glacial cycles drive isolation, gene flow and speciation in the high-elevation Andes. <i>New Phytologist</i> , 2018, 219, 779-793.	3.5	96
5566	Phylogeny, ecology and taxonomy of systemic pathogens and their relatives in Ajellomycetaceae (Onygenales): <i>Blastomyces</i> , <i>Emergomyces</i> , <i>Emmonsia</i> , <i>Emmonsiiellopsis</i> . <i>Fungal Diversity</i> , 2018, 90, 245-291.	4.7	71
5567	Use of Whole-Genome Sequencing in the Investigation of a Nosocomial Influenza Virus Outbreak. <i>Journal of Infectious Diseases</i> , 2018, 218, 1485-1489.	1.9	62
5568	The spatial structure of phylogenetic and functional diversity in the United States and Canada: An example using the sedge family (Cyperaceae). <i>Journal of Systematics and Evolution</i> , 2018, 56, 449-465.	1.6	31
5569	Evolution, systematics, and natural history of a new genus of cryptobiotic fungus growing ants. <i>Systematic Entomology</i> , 2018, 43, 549-567.	1.7	23
5570	Fungal Genomics. <i>Methods in Molecular Biology</i> , 2018, , .	0.4	3
5571	Origin and diversity of an underutilized fruit tree crop, cempedak (<i>Artocarpus integer</i> , Moraceae). <i>American Journal of Botany</i> , 2018, 105, 898-914.	0.8	9
5572	Molecular taxonomy of five species of microfungi on <i>Alnus</i> spp. from Italy. <i>Mycological Progress</i> , 2018, 17, 255-274.	0.5	14
5573	Whole-genome sequencing and antimicrobial resistance in <i>Brucella melitensis</i> from a Norwegian perspective. <i>Scientific Reports</i> , 2018, 8, 8538.	1.6	37
5574	The Messinian imprint on the evolution of freshwater fishes of the genus <i>Luciobarbus</i> Heckel, 1843 (Teleostei, Cyprinidae) in the western Mediterranean. <i>Journal of Biogeography</i> , 2018, 45, 1593-1603.	1.4	12
5575	Demographic expansion and genetic load of the halophyte model plant <i>Eutrema salsugineum</i> . <i>Molecular Ecology</i> , 2018, 27, 2943-2955.	2.0	11
5576	Recurrent diversification patterns and taxonomic complexity in morphologically conservative ancient lineages of <i>Pimelia</i> (Coleoptera: Tenebrionidae). <i>Systematic Entomology</i> , 2018, 43, 522-548.	1.7	16

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5577	Comprehensive phylogeny of the laughingthrushes and allies (Aves, Leiothrichidae) and a proposal for a revised taxonomy. <i>Zoologica Scripta</i> , 2018, 47, 428-440.	0.7	15
5578	A High Quality Genome for <i>Mus spicilegus</i> , a Close Relative of House Mice with Unique Social and Ecological Adaptations. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2145-2152.	0.8	8
5579	Phylogenetic Analysis of Protein Family. <i>Methods in Molecular Biology</i> , 2018, 1775, 267-275.	0.4	9
5580	Novel Cryphonectriaceae from La Réunion and South Africa, and their pathogenicity on Eucalyptus. <i>Mycological Progress</i> , 2018, 17, 953-966.	0.5	8
5581	Improved de novo genome assembly and analysis of the Chinese cucurbit <i>Siraitia grosvenorii</i> , also known as monk fruit or luo-han-guo. <i>GigaScience</i> , 2018, 7, .	3.3	32
5582	Functional characterization of CYP4G11, a highly conserved enzyme in the western honey bee <i>Apis mellifera</i> . <i>Insect Molecular Biology</i> , 2018, 27, 661-674.	1.0	33
5583	Untangling phylogenetic patterns and taxonomic confusion in tribe Caryophylleae (Caryophyllaceae) with special focus on generic boundaries. <i>Taxon</i> , 2018, 67, 83-112.	0.4	24
5584	<i>Microspongium alariae</i> in <i>Alaria esculenta</i> : a widely-distributed non-parasitic brown algal endophyte that shows cell modifications within its host. <i>Botanica Marina</i> , 2018, 61, 343-354.	0.6	8
5585	An expanded molecular phylogeny of metaine spiders (Araneae, Tetragnathidae) with description of new taxa from Taiwan and the Philippines. <i>Invertebrate Systematics</i> , 2018, 32, 400.	0.5	10
5586	On the Origin of Isoprenoid Biosynthesis. <i>Molecular Biology and Evolution</i> , 2018, 35, 2185-2197.	3.5	54
5587	Seed bank and seasonal patterns of the eukaryotic SAR (Stramenopila, Alveolata and Rhizaria) clade in a New England vernal pool. <i>Journal of Plankton Research</i> , 2018, 40, 376-390.	0.8	15
5588	Phylogenetic annotation and genomic architecture of opsin genes in Crustacea. <i>Hydrobiologia</i> , 2018, 825, 159-175.	1.0	13
5589	Evolutionary lineages of marine snails identified using molecular phylogenetics and geometric morphometric analysis of shells. <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 626-637.	1.2	16
5590	Renewed classification within <i>Goniurosaurus</i> (Squamata: Eublepharidae) uncovers the dual roles of a continental island (Hainan) in species evolution. <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 646-654.	1.2	19
5591	New <i>Meredithiella</i> species from mycangia of <i>Corthylus</i> ambrosia beetles suggest genus-level coadaptation but not species-level coevolution. <i>Mycologia</i> , 2018, 110, 63-78.	0.8	11
5592	Identification and validation of a novel panel of <i>Plasmodium knowlesi</i> biomarkers of serological exposure. <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006457.	1.3	26
5593	Parkinson disease related ATP13A2 evolved early in animal evolution. <i>PLoS ONE</i> , 2018, 13, e0193228.	1.1	47
5594	The chloroplast genome of <i>Cerasus humilis</i> : Genomic characterization and phylogenetic analysis. <i>PLoS ONE</i> , 2018, 13, e0196473.	1.1	15

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5595	Complete mitochondrial genome of <i>Parasesarma</i> affine (Brachyura: Sesarmidae): Gene rearrangements in Sesarmidae and phylogenetic analysis of the Brachyura. <i>International Journal of Biological Macromolecules</i> , 2018, 118, 31-40.	3.6	51
5596	Out of North Africa by different routes: phylogeography and species distribution model of the western Mediterranean <i>Lavatera maritima</i> (Malvaceae). <i>Botanical Journal of the Linnean Society</i> , 2018, 187, 441-455.	0.8	13
5597	A phylogenetic analysis of the genus <i>Aloe</i> (Asphodelaceae) in Madagascar and the Mascarene Islands. <i>Botanical Journal of the Linnean Society</i> , 2018, 187, 428-440.	0.8	11
5598	Metagenomic insights into diazotrophic communities across Arctic glacier forefields. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	36
5599	Viral Discovery in the Invasive Australian Cane Toad (<i>Rhinella marina</i>) Using Metatranscriptomic and Genomic Approaches. <i>Journal of Virology</i> , 2018, 92, .	1.5	13
5600	<i>Ipomoea kahloiae</i> (Convolvulaceae), a noteworthy new species endemic to Guerrero, Mexico. <i>Phytotaxa</i> , 2018, 356, 49.	0.1	1
5601	Mitoâ€nuclear discordance across a recent contact zone for California voles. <i>Ecology and Evolution</i> , 2018, 8, 6226-6241.	0.8	6
5602	<i>Marteilia refringens</i> and <i>Marteilia pararefringens</i> sp. nov. are distinct parasites of bivalves and have different European distributions. <i>Parasitology</i> , 2018, 145, 1483-1492.	0.7	16
5603	<i>Conoscyphus</i> belongs to Acrobolbaceae (Jungermanniineae) not Lophocoleaceae (Lophocoleineae). <i>Australian Systematic Botany</i> , 2018, 31, 209.	0.3	2
5604	Comparative genomic analysis of <i>Genlisea</i> (corkscrew plantsâ€™Lentibulariaceae) chloroplast genomes reveals an increasing loss of the <i>ndh</i> genes. <i>PLoS ONE</i> , 2018, 13, e0190321.	1.1	17
5605	Revisiting the phylogeography, demography and taxonomy of the frog genus <i>Ptychadena</i> in the Ethiopian highlands with the use of genome-wide SNP data. <i>PLoS ONE</i> , 2018, 13, e0190440.	1.1	19
5606	Molecular phylogeny of <i>Panicum</i> s. str. (Poaceae, Panicoideae, Paniceae) and insights into its biogeography and evolution. <i>PLoS ONE</i> , 2018, 13, e0191529.	1.1	23
5607	Extended-spectrum beta-lactamase (ESBL)-producing <i>Escherichia coli</i> and <i>Acinetobacter baumannii</i> among horses entering a veterinary teaching hospital: The contemporary "Trojan Horse". <i>PLoS ONE</i> , 2018, 13, e0191873.	1.1	43
5608	An integrative description of <i>Macrobotis shonaicus</i> sp. nov. (Tardigrada: Macrobiotidae) from Japan with notes on its phylogenetic position within the <i>hufelandi</i> group. <i>PLoS ONE</i> , 2018, 13, e0192210.	1.1	28
5609	The critically endangered forest owlet <i>Heteroglaux blewitti</i> is nested within the currently recognized <i>Athene</i> clade: A century-old debate addressed. <i>PLoS ONE</i> , 2018, 13, e0192359.	1.1	8
5610	Population genomics of <i>Fusarium graminearum</i> reveals signatures of divergent evolution within a major cereal pathogen. <i>PLoS ONE</i> , 2018, 13, e0194616.	1.1	75
5611	The first mitochondrial genomes for Pyralinae (Pyralidae) and Glaphyriinae (Crambidae), with phylogenetic implications of Pyraloidea. <i>PLoS ONE</i> , 2018, 13, e0194672.	1.1	13
5612	Continental synchronicity of human influenza virus epidemics despite climactic variation. <i>PLoS Pathogens</i> , 2018, 14, e1006780.	2.1	38

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5613	Discovery of a novel species, <i>Theileria haneyi</i> n. sp., infective to equids, highlights exceptional genomic diversity within the genus <i>Theileria</i> : implications for apicomplexan parasite surveillance. <i>International Journal for Parasitology</i> , 2018, 48, 679-690.	1.3	61
5614	Analysis of 3800-year-old <i>Yersinia pestis</i> genomes suggests Bronze Age origin for bubonic plague. <i>Nature Communications</i> , 2018, 9, 2234.	5.8	123
5615	Gene flow contributes to diversification of the major fungal pathogen <i>Candida albicans</i> . <i>Nature Communications</i> , 2018, 9, 2253.	5.8	131
5616	Analyzing Contentious Relationships and Outlier Genes in Phylogenomics. <i>Systematic Biology</i> , 2018, 67, 916-924.	2.7	69
5617	Systematics, phylogeny and biogeography of the Australasian leaf-curling orb-weaving spiders (Araneae: Araneidae: Zyiellinae), with a comparative analysis of retreat evolution. <i>Zoological Journal of the Linnean Society</i> , 0, , .	1.0	15
5618	Divergent Human-Origin Influenza Viruses Detected in Australian Swine Populations. <i>Journal of Virology</i> , 2018, 92, .	1.5	16
5619	Phylogeny of <i>Zehneria</i> (<i>Cucurbitaceae</i>) with special focus on Asia. <i>Taxon</i> , 2018, 67, 55-65.	0.4	10
5620	Molecular phylogeny and diversification of Malagasy bright-eyed tree frogs (Mantellidae: Boophis). <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 568-578.	1.2	9
5621	A gene transfer event suggests a long-term partnership between eustigmatophyte algae and a novel lineage of endosymbiotic bacteria. <i>ISME Journal</i> , 2018, 12, 2163-2175.	4.4	57
5622	Improving phylogenetic inference of core Chlorophyta using chloroplast sequences with strong phylogenetic signals and heterogeneous models. <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 248-255.	1.2	24
5623	Mutations in blind cavefish target the light-regulated circadian clock gene, period 2. <i>Scientific Reports</i> , 2018, 8, 8754.	1.6	29
5624	Molecular phylogeny of <i>Pedinini</i> (Coleoptera, Tenebrionidae) and its implications for higher-level classification. <i>Zoological Journal of the Linnean Society</i> , 0, , .	1.0	15
5625	Fungal Phylogenomics. <i>Methods in Molecular Biology</i> , 2018, 1775, 251-266.	0.4	4
5626	Characterization and phylogenetic analysis of the complete mitogenome of a rare cavefish, <i>Sinocyclocheilus multipunctatus</i> (Cypriniformes: Cyprinidae). <i>Genes and Genomics</i> , 2018, 40, 1033-1040.	0.5	9
5627	Reanalyzing the Palaeoptera problem – The origin of insect flight remains obscure. <i>Arthropod Structure and Development</i> , 2018, 47, 328-338.	0.8	51
5628	A Developmental Switch Generating Phenotypic Plasticity Is Part of a Conserved Multi-gene Locus. <i>Cell Reports</i> , 2018, 23, 2835-2843.e4.	2.9	50
5629	Connecting Amazonian, Cerrado, and Atlantic forest histories: Paraphyly, old divergences, and modern population dynamics in tyrant-manakins (Neopelma/Tyranneutes, Aves: Pipridae). <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 696-705.	1.2	26
5630	Phylogeny and systematics of <i>Chiroxiphia</i> and <i>Antilophia</i> manakins (Aves, Pipridae). <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 706-711.	1.2	12

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5631	Complete Plastome Sequencing Reveals an Extremely Diminished SSC Region in Hemiparasitic <i>Pedicularis ishidoyana</i> (Orobanchaceae). <i>Annales Botanici Fennici</i> , 2018, 55, 171-183.	0.0	27
5632	Complete plastome sequences from <i>Bertholletia excelsa</i> and 23 related species yield informative markers for Lecythidaceae. <i>Applications in Plant Sciences</i> , 2018, 6, e01151.	0.8	24
5633	Reconstructed evolution of insulin receptors in insects reveals duplications in early insects and cockroaches. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2018, 330, 305-311.	0.6	26
5634	Increased taxon sampling provides new insights into the phylogeny and evolution of the subclass Calcaronea (Porifera, Calcarea). <i>Organisms Diversity and Evolution</i> , 2018, 18, 279-290.	0.7	17
5635	Single nucleotide polymorphisms of Beijing lineage <i>Mycobacterium tuberculosis</i> toxin-antitoxin system genes: Their role in the changes of protein activity and evolution. <i>Tuberculosis</i> , 2018, 112, 11-19.	0.8	5
5636	Global evolution of glycosylated polyene macrolide antibiotic biosynthesis. <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 239-247.	1.2	4
5637	A new species of squirrel (Sciuridae: <i>Callosciurus</i>) from an isolated island off the Indochina Peninsula in southern Vietnam. <i>Journal of Mammalogy</i> , 2018, 99, 813-825.	0.6	11
5638	The evolutionary history of <i>Lygodactylus</i> lizards in the South American open diagonal. <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 638-645.	1.2	22
5639	A high-quality genome sequence of <i>Rosa chinensis</i> to elucidate ornamental traits. <i>Nature Plants</i> , 2018, 4, 473-484.	4.7	224
5640	Boosting <i>scp</i> DNA metabarcoding for biomonitoring with phylogenetic estimation of operational taxonomic units' ecological profiles. <i>Molecular Ecology Resources</i> , 2018, 18, 1299-1309.	2.2	45
5641	Microevolution of <i>Streptococcus agalactiae</i> ST-261 from Australia Indicates Dissemination via Imported Tilapia and Ongoing Adaptation to Marine Hosts or Environment. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	33
5642	Estimating TimeTrees with MEGA and the TimeTree Resource. <i>Molecular Biology and Evolution</i> , 2018, 35, 2334-2342.	3.5	92
5643	Adaptive introgression underlies polymorphic seasonal camouflage in snowshoe hares. <i>Science</i> , 2018, 360, 1355-1358.	6.0	234
5644	Molecular epidemiology of dengue viruses in three provinces of Lao PDR, 2006-2010. <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006203.	1.3	17
5645	<i>Tropicoporus drechsleri</i> (Hymenochaetales, Basidiomycota), a new species in the <i>Nonotus linteus</i> complex from northern Argentina. <i>Phytotaxa</i> , 2018, 338, 75.	0.1	11
5646	<i>Palicella lueckingii</i> (Lecanorales, Ascomycota), a new lichen species inhabiting <i>Araucaria</i> from the extratropical South America. <i>Phytotaxa</i> , 2018, 344, 24.	0.1	2
5647	<i>Marinophialophora garethjonesii</i> gen. et sp. nov.: a new hyphomycete associated with Halocyphina from marine habitats in Thailand. <i>Phytotaxa</i> , 2018, 345, 1.	0.1	9
5648	Powdery mildew caused by <i>Erysiphe lespedezae</i> (including <i>Pseudoidium caesalpinicearum</i> , syn. nov.) on <i>Bauhinia blakeana</i> and <i>B. purpurea</i> in China. <i>Phytotaxa</i> , 2018, 345, 35.	0.1	4

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5649	A new perennial species of <i>Portulaca</i> (Portulacaceae) from central Mexico. <i>Phytotaxa</i> , 2018, 347, 89.	0.1	1
5650	<i>Lecanicillium subprimulinum</i> (Cordycipitaceae, Hypocreales), a novel species from Baoshan, Yunnan. <i>Phytotaxa</i> , 2018, 348, 99.	0.1	13
5651	The morphology and molecular phylogenetics of some marine diatom taxa within the Fragilariaceae, including twenty undescribed species and their relationship to <i>Nanofrustulum</i> , <i>Opephora</i> and <i>Pseudostaurosira</i> . <i>Phytotaxa</i> , 2018, 355, 1.	0.1	35
5652	Evolutionary novelty in gravity sensing through horizontal gene transfer and high-order protein assembly. <i>PLoS Biology</i> , 2018, 16, e2004920.	2.6	14
5653	Two essential Thioredoxins mediate apicoplast biogenesis, protein import, and gene expression in <i>Toxoplasma gondii</i> . <i>PLoS Pathogens</i> , 2018, 14, e1006836.	2.1	40
5654	Biomonitoring for the 21st Century: Integrating Next-Generation Sequencing Into Ecological Network Analysis. <i>Advances in Ecological Research</i> , 2018, 58, 1-62.	1.4	68
5655	Endogenous Stochastic Decoding of the CUG Codon by Competing Ser- and Leu-tRNAs in <i>Ascoidea asiatica</i> . <i>Current Biology</i> , 2018, 28, 2046-2057.e5.	1.8	22
5656	Molecular phylogenetic analysis and generic delimitations in tribe Chiococceae (Cinchonoideae). <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 11 50 342 T</i>	0.8	12
5657	Phylogenetic Analysis of the Genus <i>Pohlia</i> (Bryophyta, Bryaceae) Using Chloroplast and Nuclear Ribosomal DNA. <i>Phytotaxa</i> , 2018, 351, 141.	0.1	4
5658	Phylogenetics and evolutionary epidemiology of African swine fever p72-CVR genes in Eurasia and Africa. <i>PLoS ONE</i> , 2018, 13, e0192565.	1.1	44
5659	Comprehensive evolutionary analysis of the Anthroherpon radiation (Coleoptera, Leiodidae). <i>Tj ETQq0 0 0 rgBT /Overlock 10 11 50 342 T</i>	1.1	11
5660	Morphology, morphogenesis, and phylogeny of an <i>Anteholosticha intermedia</i> (Ciliophora, Urostylida) population from the United States. <i>European Journal of Protistology</i> , 2018, 65, 1-15.	0.5	25
5661	Comparative chloroplast genomics and phylogenetics of nine <i>Lindera</i> species (Lauraceae). <i>Scientific Reports</i> , 2018, 8, 8844.	1.6	50
5662	Four new <i>Licmophora</i> species (Licmophorales), with a review of valve characters and exploration of cingulum characters, including a new septum type. <i>Diatom Research</i> , 2018, 33, 187-217.	0.5	8
5663	Characterization of the complete mitochondrial genome of the lung fluke, <i>Paragonimus heterotremus</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 560-561.	0.2	7
5664	Phylogenomic Evidence Overturns Current Conceptions of Social Evolution in Wasps (Vespidae). <i>Molecular Biology and Evolution</i> , 2018, 35, 2097-2109.	3.5	108
5665	Phylogenomics resolves the deep phylogeny of seed plants and indicates partial convergent or homoplastic evolution between Gnetales and angiosperms. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018, 285, 20181012.	1.2	149
5666	Cryptic species within <i>Ophiocordyceps myrmecophila</i> complex on formicine ants from Thailand. <i>Mycological Progress</i> , 2019, 18, 147-161.	0.5	22

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5667	Integrative transcriptomic and genomic analysis of odorant binding proteins and chemosensory proteins in aphids. <i>Insect Molecular Biology</i> , 2019, 28, 1-22.	1.0	45
5668	Genome-wide genotyping of a novel Mexican Chile Pepper collection illuminates the history of landrace differentiation after <i>Capsicum annuum</i> L. domestication. <i>Evolutionary Applications</i> , 2019, 12, 78-92.	1.5	21
5669	Mutations in voltage-gated sodium channels from pyrethroid resistant salmon lice (<i>Lepeophtheirus salmonis</i>). <i>Pest Management Science</i> , 2019, 75, 527-536.	1.7	10
5670	DNA barcodes uncover hidden taxonomic diversity behind the variable wing patterns in the Neotropical butterfly genus <i>Zaretis</i> (Lepidoptera: Nymphalidae: Charaxinae). <i>Zoological Journal of the Linnean Society</i> , 2019, 185, 132-192.	1.0	7
5671	Progress in glass sponge phylogenetics: a comment on Kersken et al. (2018). <i>Hydrobiologia</i> , 2019, 843, 51-59.	1.0	7
5672	The first draft genome of <i>Lophophorus</i> : A step forward for Phasianidae genomic diversity and conservation. <i>Genomics</i> , 2019, 111, 1209-1215.	1.3	9
5673	Semi-aquatic spider silks: transcripts, proteins, and silk fibres of the fishing spider, <i>Dolomedes triton</i> (Pisauridae). <i>Insect Molecular Biology</i> , 2019, 28, 35-51.	1.0	9
5674	The complete mitochondrial genome of <i>Eterusia aeda</i> (Lepidoptera, Zygaenidae) and comparison with other zygaenid moths. <i>Genomics</i> , 2019, 111, 1043-1052.	1.3	19
5675	What Can Environmental Sequences Tell Us About the Distribution of Low-Rank Taxa? The Case of <i>Euplotes</i> (Ciliophora, Spirotrichea), Including a Description of <i>Euplotes enigma</i> sp. nov.. <i>Journal of Eukaryotic Microbiology</i> , 2019, 66, 281-293.	0.8	17
5676	<i>Pileospora piceae</i> gen. et sp. nov. (Septorioideaceae, Botryosphaeriales) from <i>Picea rubens</i> . <i>Mycological Progress</i> , 2019, 18, 163-174.	0.5	3
5677	Phylogenetic relationships and convergent evolution of ocean-shore ground beetles (Coleoptera: Carabidae: Tenebrioninae: Bembidion and relatives). <i>Systematic Entomology</i> , 2019, 44, 39-60.	1.7	8
5678	Evolution and Design of Invertebrate Circadian Clocks. , 0, , 595-614.		5
5679	First molecular phylogeny of <i>Agrilus</i> (Coleoptera: Buprestidae), the largest genus on Earth, with DNA barcode database for forestry pest diagnostics. <i>Bulletin of Entomological Research</i> , 2019, 109, 200-211.	0.5	32
5680	<i>Dactylomonas</i> gen. nov., a Novel Lineage of Heterolobosean Flagellates with Unique Ultrastructure, Closely Related to the Amoeba <i>Selenia koniopes</i> Park, De Jonckheere & Simpson, 2012. <i>Journal of Eukaryotic Microbiology</i> , 2019, 66, 120-139.	0.8	12
5681	Multiple Sequence Alignment Averaging Improves Phylogeny Reconstruction. <i>Systematic Biology</i> , 2019, 68, 117-130.	2.7	24
5682	Characterization of the complete chloroplast genome of <i>Euryodendron excelsum</i> (Pentaphragmataceae), a critically endangered species endemic to China. <i>Conservation Genetics Resources</i> , 2019, 11, 275-278.	0.4	5
5683	Molecular diagnosis for a <i>Tamarix</i> species from two reclaimed lands along the Yellow Sea in Korea inferred from genome wide SNP markers. <i>Journal of Systematics and Evolution</i> , 2019, 57, 247-255.	1.6	7
5684	Repeated formation of correlated species in <i>Tranzschelia</i> (Pucciniales). <i>Mycological Progress</i> , 2019, 18, 295-303.	0.5	10

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5685	Tree Evaluation and Robustness Testing. , 2019, , 736-745.		0
5686	Minimal genetic divergence among South American samples of the water opossum <i>Chironectes minimus</i> : evidence for transcontinental gene flow?. <i>Mammalia</i> , 2019, 83, 190-192.	0.3	10
5687	Mitochondrial genome characteristics of <i>Somena scintillans</i> (Lepidoptera: Erebidiae) and comparison with other Noctuoidea insects. <i>Genomics</i> , 2019, 111, 1239-1248.	1.3	14
5688	Multiple evolutionary origins lead to diversity in the metabolic profiles of ambrosia fungi. <i>Fungal Ecology</i> , 2019, 38, 80-88.	0.7	18
5689	An evaluation of alternative explanations for widespread cytonuclear discordance in annual sunflowers (<i>Helianthus</i>). <i>New Phytologist</i> , 2019, 221, 515-526.	3.5	118
5690	A preliminary DNA barcode selection for the genus <i>Russula</i> (Russulales, Basidiomycota). <i>Mycology</i> , 2019, 10, 61-74.	2.0	17
5691	Next-generation DNA sequencing analysis of two <i>Streptococcus suis</i> ST28 isolates associated with human infective endocarditis and meningitis in Gunma, Japan: a case report. <i>Infectious Diseases</i> , 2019, 51, 62-66.	1.4	6
5692	A transcriptome-based resolution for a key taxonomic controversy in Cupressaceae. <i>Annals of Botany</i> , 2019, 123, 153-167.	1.4	18
5693	Redescription of a Hymenostome Ciliate, <i>Tetrahymana setosa</i> (Protozoa, Ciliophora) Notes on its Molecular Phylogeny. <i>Journal of Eukaryotic Microbiology</i> , 2019, 66, 413-423.	0.8	3
5694	Morphogenesis and Molecular Phylogeny of a Soil Ciliate <i>Uroleptoides longiseries</i> (Foissner), Tj ETQq1 1 0.784314 rgBT /Overl... 2019, 66, 334-342.	0.8	15
5695	Molecular phylogeny of neodalyellid flatworms (Rhabdocoela), including three new species from British Columbia. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2019, 57, 41-56.	0.6	6
5696	A Revised Taxonomy of Diplonemids Including the Eupelagonemidae n. fam. and a Type Species, <i>Eupelagonema oceanica</i> n. gen. & sp.. <i>Journal of Eukaryotic Microbiology</i> , 2019, 66, 519-524.	0.8	17
5697	Phylogeny and genetic diversity of the banana Fusarium wilt pathogen <i>Fusarium oxysporum</i> f. sp. <i>cubense</i> in the Indonesian centre of origin. <i>Studies in Mycology</i> , 2019, 92, 155-194.	4.5	184
5698	A quantitative map of protein sequence space for the cis-defensin superfamily. <i>Bioinformatics</i> , 2019, 35, 743-752.	1.8	27
5699	Systematics, phylogeny and biogeography of the Australasian leaf-curling orb-weaving spiders (Araneae: Araneidae: Zygiellinae), with a comparative analysis of retreat evolution. <i>Zoological Journal of the Linnean Society</i> , 2019, 185, 300-300.	1.0	0
5700	Cryptic Speciation in Western North America and Eastern Eurasia of the Pathogens Responsible for Laminated Root Rot. <i>Phytopathology</i> , 2019, 109, 456-468.	1.1	8
5701	Molecular phylogeny of the scorpionflies Panorpidae (Insecta: Mecoptera) and chromosomal evolution. <i>Cladistics</i> , 2019, 35, 385-400.	1.5	31
5702	Phylogenomics of pike cichlids (Cichlidae: Crenicichla) of the <i>C. mandelburgeri</i> species complex: rapid ecological speciation in the Iguaz� River and high endemism in the Middle Paran� basin. <i>Hydrobiologia</i> , 2019, 832, 355-375.	1.0	29

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5703	Picoeukaryotes of the <i>Micromonas</i> genus: sentinels of a warming ocean. ISME Journal, 2019, 13, 132-146.	4.4	35
5704	Elucidation of glutamine lipid biosynthesis in marine bacteria reveals its importance under phosphorus deplete growth in <i>Rhodobacteraceae</i> . ISME Journal, 2019, 13, 39-49.	4.4	27
5705	Widespread ancient whole-genome duplications in Malpighiales coincide with Eocene global climatic upheaval. New Phytologist, 2019, 221, 565-576.	3.5	86
5706	Phylogeny and biogeography of the endemic Hemidactylus geckos of the Indian subregion suggest multiple dispersals from Peninsular India to Sri Lanka. Zoological Journal of the Linnean Society, 2019, 186, 286-301.	1.0	19
5707	Molecular phylogeny of the fungus gnat subfamilies Gnoristinae and Mycomyinae, and their position within Mycetophilidae (Diptera). Systematic Entomology, 2019, 44, 128-138.	1.7	20
5708	CRISPR-Cas systems in multicellular cyanobacteria. RNA Biology, 2019, 16, 518-529.	1.5	31
5709	Congruent species delimitation of two controversial goldthread nanmu tree species based on morphological and restriction site-associated DNA sequencing data. Journal of Systematics and Evolution, 2019, 57, 234-246.	1.6	19
5710	Phylogeny and evolution of the cryptic fungus-farming ant genus Myrmicocrypta F. Smith (Hymenoptera: Formicidae) inferred from multilocus data. Systematic Entomology, 2019, 44, 139-162.	1.7	8
5711	Redescription of the bigeye chimaera, Hydrolagus macrophthalmus de Buen, 1959 (Chondrichthyes: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 1605-1614.	0.3	1
5712	<i>Milnesium tardigradum</i> Doyère, 1840: The first integrative study of interpopulation variability in a tardigrade species. Journal of Zoological Systematics and Evolutionary Research, 2019, 57, 1-23.	0.6	58
5713	Characterization of the complete chloroplast genome of the Qinghai-Tibet Plateau endemic Pomatosace filicula. Mitochondrial DNA Part B: Resources, 2019, 4, 1211-1212.	0.2	1
5714	Next-generation sequencing yields the complete chloroplast genome of Abies fargesii. Mitochondrial DNA Part B: Resources, 2019, 4, 1273-1274.	0.2	1
5715	The complete chloroplast genome sequence of <i>Crepidiastrum lanceolatum</i> (<i>Asteraceae</i>). Mitochondrial DNA Part B: Resources, 2019, 4, 1404-1405.	0.2	4
5716	Phylogenomics and genital morphology of cave raptor spiders (Araneae, Trogloraptoridae) reveal an independent origin of a flow-through female genital system. Journal of Zoological Systematics and Evolutionary Research, 2019, 57, 737-747.	0.6	14
5717	Further analyses on the evolutionary key protist <i>Halteria</i> (Protista, Ciliophora) based on transcriptomic data. Zoologica Scripta, 2019, 48, 813-825.	0.7	8
5718	Plastid Genomes of Five Species of Riverweeds (Podostemaceae): Structural Organization and Comparative Analysis in Malpighiales. Frontiers in Plant Science, 2019, 10, 1035.	1.7	43
5719	Structure on the Simple Canonical Nambu Rota-Baxter 3-Lie Algebra $SA_{\partial} A^{\wedge}$. Bulletin of the Iranian Mathematical Society, 2019, 45, 1659-1679.	0.4	0
5720	Multiple Independent Origins of Apicomplexan-Like Parasites. Current Biology, 2019, 29, 2936-2941.e5.	1.8	84

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5721	Ancestral biogeography and ecology of marine angelfishes (F: Pomacanthidae). <i>Molecular Phylogenetics and Evolution</i> , 2019, 140, 106596.	1.2	8
5722	The complete mitochondrial genome sequence of <i>Caryanda elegans</i> (Orthoptera: Acrididae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1580-1581.	0.2	3
5723	The complete chloroplast genome of the endangered tree <i>Parashorea chinensis</i> (Dipterocarpaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1163-1164.	0.2	4
5724	The complete chloroplast genome sequence of <i>Berchemia flavescens</i> (Rhamnaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1302-1303.	0.2	4
5725	Characterization of the complete chloroplast genome of black poplar (<i>Populus nigra</i> L.). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1261-1262.	0.2	1
5726	Complete chloroplast genome of a Mangrove Natural Hybrid, <i>Rhizophora lamarckii</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1465-1466.	0.2	5
5727	Characterization of the complete chloroplast genome of the Chinese sorghum, <i>Sorghum bicolor</i> from China. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1421-1423.	0.2	2
5728	Chloroplast phylogenomics of <i>Calocedrus</i> (Cupressaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1435-1436.	0.2	2
5729	Next-generation sequencing yields the complete chloroplast genome of <i>Abies balsamea</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1445-1446.	0.2	3
5730	The complete mitochondrial genome of the hymenopteran hunting robber fly <i>Dasygogon diadema</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1584-1585.	0.2	0
5731	The complete chloroplast genome sequence of <i>Acer takesimensense</i> (Sapindaceae), an endemic to Ulleung Island of Korea. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1531-1532.	0.2	3
5732	Complete mitochondrial genome of the silkworm strain, Hukpyobeom <i>Bombyx mori</i> (Lepidoptera: Tj ETQq1 1 0.784314 rgBT /Overlook). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1547-1548.	0.2	4
5733	The complete chloroplast genome of <i>Carpinus laxiflora</i> (Betulaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1643-1644.	0.2	1
5734	Genetic and phylogenetic analysis of the complete genome for the herbal medicine plant of <i>Scutellaria baicalensis</i> from China. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1683-1685.	0.2	4
5735	Complete chloroplast genome of <i>Fagus multinervis</i> , a beech species endemic to Ulleung Island in South Korea. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1698-1699.	0.2	7
5736	The complete chloroplast genome of <i>Siraitia grosvenorii</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1718-1719.	0.2	0
5737	The first complete chloroplast genome sequence of a medicinal goldthread species, <i>Coptis omeiensis</i> (Ranunculaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1754-1756.	0.2	0
5738	The complete chloroplast genome of <i>Rosa berberifolia</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1741-1742.	0.2	9

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5739	Evolution of the rodent Trim5 cluster is marked by divergent paralogous expansions and independent acquisitions of TrimCyp fusions. <i>Scientific Reports</i> , 2019, 9, 11263.	1.6	30
5740	Characterization of the complete chloroplast genome of <i>Suaeda salsa</i> (Amaranthaceae/Chenopodiaceae), an annual succulent halophyte. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2133-2134.	0.2	6
5741	The Oxymonad Genome Displays Canonical Eukaryotic Complexity in the Absence of a Mitochondrion. <i>Molecular Biology and Evolution</i> , 2019, 36, 2292-2312.	3.5	49
5742	Independent Evolution with the Gene Flux Originating from Multiple <i>Xanthomonas</i> Species Explains Genomic Heterogeneity in <i>Xanthomonas perforans</i> . <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	39
5743	Biogeography and Ecological Diversification of a Mayfly Clade in New Guinea. <i>Frontiers in Ecology and Evolution</i> , 2019, 7, .	1.1	13
5744	Phylogenetic Relationships in Orobanchaceae Inferred From Low-Copy Nuclear Genes: Consolidation of Major Clades and Identification of a Novel Position of the Non-photosynthetic Orobanche Clade Sister to All Other Parasitic Orobanchaceae. <i>Frontiers in Plant Science</i> , 2019, 10, 902.	1.7	18
5745	Fungal Planet description sheets: 868-950. <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2019, 42, 291-473.	1.6	124
5746	The Munduruku marmoset: a new monkey species from southern Amazonia. <i>PeerJ</i> , 2019, 7, e7019.	0.9	19
5747	Molecular and morphological evidence place <i>Pholiota psathyrelloides</i> from Patagonia within the ectomycorrhizal genus <i>Psathyroma</i> (Agaricales). <i>New Zealand Journal of Botany</i> , 2019, 57, 261-270.	0.8	0
5748	<i>Ptychomitrium subcrispatum</i> ThÄ©r. & P.de la Varde, an east southern African species excluded from the Cape Verde bryoflora. <i>Journal of Bryology</i> , 2019, 41, 281-284.	0.4	1
5749	A phylogenomic perspective on diversity, hybridization and evolutionary affinities in the stickleback genus <i>Pungitius</i> . <i>Molecular Ecology</i> , 2019, 28, 4046-4064.	2.0	39
5750	Metabolic Potential of As-yet-uncultured Archaeal Lineages of <i>Candidatus</i> Hydrothermarchaeota Thriving in Deep-sea Metal Sulfide Deposits. <i>Microbes and Environments</i> , 2019, 34, 293-303.	0.7	10
5751	The Complete Mitochondrial Genome of the Rhus Gall Aphid <i>Nurudea shiraii</i> (Hemiptera: Aphididae: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.2	1
5752	A Reverse Ecology Approach Based on a Biological Definition of Microbial Populations. <i>Cell</i> , 2019, 178, 820-834.e14.	13.5	118
5753	DNA-based approaches uncover cryptic diversity in the European <i>Lepidocyrtus lanuginosus</i> species group (Collembola: Entomobryidae). <i>Invertebrate Systematics</i> , 2019, , .	0.5	4
5754	Evolution and diversity of the courtship repertoire in the <i>Drosophila montium</i> species group (Diptera: Drosophilidae). <i>Journal of Evolutionary Biology</i> , 2019, 32, 1124-1140.	0.8	11
5755	Rapid phenotypic evolution in multidrug-resistant <i>Klebsiella pneumoniae</i> hospital outbreak strains. <i>Microbial Genomics</i> , 2019, 5, .	1.0	25
5756	A new marine prasinophyte genus alternates between a flagellate and a dominant benthic stage with microrhizoids for adhesion. <i>Journal of Phycology</i> , 2019, 55, 1210-1225.	1.0	5

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5757	DNA barcoding and molecular phylogeny indicate that three members of the "morning glory" (<i>Ipomoea</i>) Tj ETQc 0 0 0 rgBT /Overlo	0.8	0
5758	Evolution and losses of spines in slug caterpillars (Lepidoptera: Limacodidae). <i>Ecology and Evolution</i> , 2019, 9, 9827-9840.	0.8	13
5759	Four complete mitochondrial genomes of Saurogobio fishes (Cypriniformes: Gobionidae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2175-2176.	0.2	5
5760	Dicyemid Mesozoans: A Unique Parasitic Lifestyle and a Reduced Genome. <i>Genome Biology and Evolution</i> , 2019, 11, 2232-2243.	1.1	15
5761	Geologic legacy spanning >90% years explains unique Yellowstone hot spring geochemistry and biodiversity. <i>Environmental Microbiology</i> , 2019, 21, 4180-4195.	1.8	17
5762	Gene Modules Co-regulated with Biosynthetic Gene Clusters for Allelopathy between Rice and Barnyardgrass. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3846.	1.8	9
5763	Homoplasmy or plesiomorphy? Reconstruction of the evolutionary history of mitochondrial gene order rearrangements in the subphylum Neodermata. <i>International Journal for Parasitology</i> , 2019, 49, 819-829.	1.3	17
5764	MpsAB is important for <i>Staphylococcus aureus</i> virulence and growth at atmospheric CO ₂ levels. <i>Nature Communications</i> , 2019, 10, 3627.	5.8	22
5765	Complete chloroplast genome of <i>Cymbidium ensifolium</i> Orchidaceae. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2236-2237.	0.2	7
5766	Genetic Diversity in FUB Genes of <i>Fusarium oxysporum</i> f. sp. <i>cubense</i> Suggests Horizontal Gene Transfer. <i>Frontiers in Plant Science</i> , 2019, 10, 1069.	1.7	10
5767	Intergeneric Relationships within the Family Salicaceae s.l. based on Plastid Phylogenomics. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3788.	1.8	18
5768	Adaptation of host transmission cycle during <i>Clostridium difficile</i> speciation. <i>Nature Genetics</i> , 2019, 51, 1315-1320.	9.4	41
5769	Frankia-Enriched Metagenomes from the Earliest Diverging Symbiotic Frankia Cluster: They Come in Teams. <i>Genome Biology and Evolution</i> , 2019, 11, 2273-2291.	1.1	33
5770	A Novel Test for Absolute Fit of Evolutionary Models Provides a Means to Correctly Identify the Substitution Model and the Model Tree. <i>Genome Biology and Evolution</i> , 2019, 11, 2403-2419.	1.1	2
5771	Contrasting patterns of genetic structure and phylogeography in the marine agarophytes <i>Gelidiophycus divaricatus</i> and <i>G.</i> <i>freshwateri</i> (Gelidiales, Rhodophyta) from East Asia. <i>Journal of Phycology</i> , 2019, 55, 1319-1334.	1.0	24
5772	The genus <i>Marasmius</i> (Basidiomycota, Agaricales, Marasmiaceae) from Republic of São Tomé and Príncipe, West Africa. <i>Phytotaxa</i> , 2019, 414, 55-104.	0.1	5
5773	Rare coral under the genomic microscope: timing and relationships among Hawaiian <i>Montipora</i> . <i>BMC Evolutionary Biology</i> , 2019, 19, 153.	3.2	16
5774	Identification and assessment of variable single-copy orthologous (SCO) nuclear loci for low-level phylogenomics: a case study in the genus <i>Rosa</i> (Rosaceae). <i>BMC Evolutionary Biology</i> , 2019, 19, 152.	3.2	16

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5775	Deep south-north genetic divergence in Godlewski's bunting (<i>Emberiza godlewskii</i>) related to uplift of the Qinghai-Tibet Plateau and habitat preferences. <i>BMC Evolutionary Biology</i> , 2019, 19, 161.	3.2	22
5776	Molecular Systematics and Morphological Analyses of the Subgenus <i>Setihenricia</i> (<i>Echinodermata</i> : <i>Asteroidea</i> : <i>Henricia</i>) from Japan. <i>Species Diversity</i> , 2019, 24, 119-135.	0.1	3
5777	Identifying genetic markers for a range of phylogenetic utility—From species to family level. <i>PLoS ONE</i> , 2019, 14, e0218995.	1.1	12
5778	Relicts and radiations: Phylogenomics of an Australasian lizard clade with east Gondwanan origins (<i>Gekkota</i> : <i>Diplodactyloidea</i>). <i>Molecular Phylogenetics and Evolution</i> , 2019, 140, 106589.	1.2	24
5779	Comparative Complete Chloroplast Genome Analyses and Contribution to the Understanding of Chloroplast Phylogeny and Adaptive Evolution in Subgenus <i>Anguinum</i> . <i>Russian Journal of Genetics</i> , 2019, 55, 872-884.	0.2	2
5780	Species Boundaries within Morphologically Cryptic <i>Galagos</i> : Evidence from Acoustic and Genetic Data. <i>Folia Primatologica</i> , 2019, 90, 279-299.	0.3	8
5781	Genome-wide identification and analysis of the MADS-box gene family and its potential role in fruit development and ripening in red bayberry (<i>Morella rubra</i>). <i>Gene</i> , 2019, 717, 144045.	1.0	13
5782	Genome analysis of antimicrobial resistance, virulence, and plasmid presence in Turkish <i>Salmonella</i> serovar <i>Infantis</i> isolates. <i>International Journal of Food Microbiology</i> , 2019, 307, 108275.	2.1	37
5783	Unusual new species of <i>Styphelia</i> (<i>Ericaceae</i> , <i>Epacridoideae</i> , <i>Styphelieae</i>) from north-eastern Australia. <i>Australian Systematic Botany</i> , 2019, , .	0.3	1
5784	Characterization the complete chloroplast genome of the tomato (<i>Solanum lycopersicum</i> L.) from China. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1374-1376.	0.2	1
5785	Characterization of the complete chloroplast genome of <i>Pterygocalyx volubilis</i> (<i>Gentianaceae</i>). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2579-2580.	0.2	9
5786	Evolutionary lability of host associations promotes phylogenetic overdispersion of co-infecting blood parasites. <i>Journal of Animal Ecology</i> , 2019, 88, 1936-1949.	1.3	17
5787	Population dynamics of an <i>Escherichia coli</i> ST131 lineage during recurrent urinary tract infection. <i>Nature Communications</i> , 2019, 10, 3643.	5.8	76
5788	Multigene phylogeny of root-knot nematodes and molecular characterization of <i>Meloidogyne nataliei</i> Golden, Rose & Bird, 1981 (<i>Nematoda</i> : <i>Tylenchida</i>). <i>Scientific Reports</i> , 2019, 9, 11788.	1.6	31
5789	The phylogenomics of diversification on an island: applying anchored hybrid enrichment to New Zealand <i>Leptospermum scoparium</i> (<i>Myrtaceae</i>). <i>Botanical Journal of the Linnean Society</i> , 2019, 191, 1-17.	0.8	14
5790	Environmental latitudinal gradients and host-specificity shape <i>Symbiodiniaceae</i> distribution in Red Sea <i>Porites</i> corals. <i>Journal of Biogeography</i> , 2019, 46, 2323-2335.	1.4	39
5791	Comparative Genomics Reveals Ecological and Evolutionary Insights into Sponge-Associated <i>Thaumarchaeota</i> . <i>MSystems</i> , 2019, 4, .	1.7	59
5792	Class Id ribonucleotide reductase utilizes a Mn ² (IV,III) cofactor and undergoes large conformational changes on metal loading. <i>Journal of Biological Inorganic Chemistry</i> , 2019, 24, 863-877.	1.1	10

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5793	Morphology and molecular phylogeny of coccoid green algae <i>Coelastrella</i> sensu lato (Scenedesmales, Sphaeropeales), including the description of three new species and two new varieties. <i>Journal of Phycology</i> , 2019, 55, 1290-1305.	1.0	26
5794	High Genetic Diversity and Species Complexity of Diaporthe Associated With Grapevine Dieback in China. <i>Frontiers in Microbiology</i> , 2019, 10, 1936.	1.5	66
5795	Molecular cloning and expression pattern of IGFBP-2a in black porgy (<i>Acanthopagrus schlegelii</i>) and evolutionary analysis of IGFBP-2s in the species of Perciformes. <i>Fish Physiology and Biochemistry</i> , 2019, 45, 1731-1745.	0.9	3
5796	Diversity of bone-eating <i>Osedax</i> worms on the deep Atlantic whale falls—bathymetric variation and inter-basin distributions. <i>Marine Biodiversity</i> , 2019, 49, 2587-2599.	0.3	18
5797	Population genomic evidence for radiative divergence of four <i>Orychophragmus</i> (Brassicaceae) species in eastern Asia. <i>Botanical Journal of the Linnean Society</i> , 2019, 191, 18-29.	0.8	8
5798	Phylogeography and species delineation of the genus <i>Phoxinus</i> Rafinesque, 1820 (Actinopterygii). <i>Journal of Biogeography</i> , 2019, 57, 926-941.	0.6	28
5799	Challenges in funding and developing genomic software: roots and remedies. <i>Genome Biology</i> , 2019, 20, 147.	3.8	21
5800	The South American and Australian percichthyids and perciliids. What is new about them?. <i>Neotropical Ichthyology</i> , 2019, 17, .	0.5	9
5801	Phylogeographic Analysis and Genetic Structure of an Endemic Sino-Japanese Disjunctive Genus <i>Diabelia</i> (Caprifoliaceae). <i>Frontiers in Plant Science</i> , 2019, 10, 913.	1.7	12
5802	Global genetic diversity, lineage distribution, and <i>Wolbachia</i> infection of the alfalfa weevil <i>Hypera postica</i> (Coleoptera: Curculionidae). <i>Ecology and Evolution</i> , 2019, 9, 9546-9563.	0.8	9
5803	The origin of Humboldt and Bonpland's holotype of <i>Oncidium ornithorhynchum</i> , clarified using +200-year-old DNA. <i>Taxon</i> , 2019, 68, 471-480.	0.4	2
5804	Phylogeny, ecology and distribution of the rare Mediterranean species <i>Lactarius pseudoscrobiculatus</i> (Basidiomycota, Russulales). <i>Plant Systematics and Evolution</i> , 2019, 305, 755-764.	0.3	3
5805	Characterization of the complete chloroplast genome of the Hongkong kumquat (<i>Fortunella</i>). <i>Journal of Biotechnology</i> , 2019, 10, 9.	0.2	9
5806	Complete mitochondrial genome of the marine mysid <i>Siriella</i> sp. (Crustacea, Mysida, Mysidae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2400-2402.	0.2	1
5807	Comparison of single-nucleotide variants identified by Illumina and Oxford Nanopore technologies in the context of a potential outbreak of Shiga toxin-producing <i>Escherichia coli</i> . <i>GigaScience</i> , 2019, 8, .	3.3	42
5808	Cobble community DNA as a tool to monitor patterns of biodiversity within kelp forest ecosystems. <i>Molecular Ecology Resources</i> , 2019, 19, 1470-1485.	2.2	23
5809	Extreme diversity in fine-grained morphology reveals fourteen new species of conopeate <i>Nitzschia</i> (Bacillariophyta: Bacillariales). <i>Phytotaxa</i> , 2019, 401, 199.	0.1	19
5810	Insights into the Phylogeny and Evolution of Cold Shock Proteins: From Enteropathogenic <i>Yersinia</i> and <i>Escherichia coli</i> to Eubacteria. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4059.	1.8	20

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5811	Diversification history in the <i>Dendrocincla fuliginosa</i> complex (Aves: Dendrocolaptidae): Insights from broad geographic sampling. <i>Molecular Phylogenetics and Evolution</i> , 2019, 140, 106581.	1.2	10
5812	On the genus <i>Racekiela</i> in Mexico: molecular and morphological description of <i>Racekiela cresciscrystae</i> n. sp.. <i>Journal of Natural History</i> , 2019, 53, 1351-1368.	0.2	4
5813	Complete plastome of an endemic fern species from China: <i>Neocheiropteris palmatopedata</i> (Polypodiaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2394-2395.	0.2	2
5814	The complete mitochondrial genome of <i>Cervus elaphus kansuensis</i> (Artiodactyla: Cervidae) and its phylogenetic analysis. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1720-1722.	0.2	0
5815	The complete chloroplast genome sequence of <i>Achnatherum splendens</i> (Pooideae), a high-quality forage grass in Northern China. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1841-1843.	0.2	3
5816	The complete chloroplast genome of <i>Rosa lucidissima</i> , a critically endangered wild rose endemic to China. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1826-1827.	0.2	2
5817	The complete chloroplast genome of <i>Semenovia gyirongensis</i> (Tribe Tordylieae, Apiaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1863-1864.	0.2	4
5818	The complete chloroplast genome of <i>Magnolia omeiensis</i> , an endangered and endemic species in China. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1909-1910.	0.2	4
5819	Complete mitochondrial genome for the Mobile River Basin endemic Coal Darter, <i>Percina breviceuda</i> (Perciformes, Percidae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2031-2032.	0.2	1
5820	The complete mitochondrial genome of the sand-hopper <i>Trinorchestia longiramus</i> (Amphipoda): Tj ETQq1 1 0.784314 rgBT /Overlock 10 0,2 2	0.2	2
5821	The complete chloroplast genome of <i>Primula obconica</i> (Primulaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2189-2190.	0.2	4
5822	The complete plastid genome of the brown alga <i>Scytosiphon lomentaria</i> (scytosiphonaceae,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 0,2 1	0.2	1
5823	The complete mitochondrial genome of the New Zealand parasitic roundworm <i>Haemonchus contortus</i> (Trichostrongyloidea: Haemonchidae) field strain NZ_Hco_NP. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2208-2210.	0.2	16
5824	The complete chloroplast genome sequence of monotypic <i>Cyphotheca</i> (Melastomataceae), an endemic genus in China. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2295-2296.	0.2	1
5825	The complete chloroplast genome sequence of an Alpine flowering plant <i>Kuepferia otophora</i> (Gentianaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2308-2309.	0.2	0
5826	Lucerne (<i>Medicago sativa</i>) alters N2O-reducing communities associated with cocksfoot (<i>Dactylis</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 4,2 25 <i>Biology and Biochemistry</i> , 2019, 137, 107547.	4.2	25
5827	Somatic evolution and global expansion of an ancient transmissible cancer lineage. <i>Science</i> , 2019, 365, .	6.0	58
5828	Miracula Moenusica , a New Member of the Holocarpic Parasitoid Genus from the Invasive Freshwater Diatom <i>Pleurosira laevis</i> . <i>Fungal Systematics and Evolution</i> , 2019, 3, 219-224.	0.9	9

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5829	Multiple origins of prokaryotic and eukaryotic single-stranded DNA viruses from bacterial and archaeal plasmids. <i>Nature Communications</i> , 2019, 10, 3425.	5.8	127
5830	Complete mitochondrial genome of the intertidal hermit crab, <i>Pagurus similis</i> (Crustacea). <i>Tj ETQq1 1 0.784314 rgBT /5 Overloc</i>	0.2	5
5831	Population Gene Introgression and High Genome Plasticity for the Zoonotic Pathogen <i>Streptococcus agalactiae</i> . <i>Molecular Biology and Evolution</i> , 2019, 36, 2572-2590.	3.5	36
5832	An Integrative Approach Using Phylogenomics and High-Resolution X-Ray Computed Tomography for Species Delimitation in Cryptic Taxa. <i>Systematic Biology</i> , 2020, 69, 294-307.	2.7	15
5833	Indo-West Pacific species of <i>Trachinotus</i> with spots on their sides as adults, with description of a new species endemic to the Marquesas Islands (Teleostei: Carangidae). <i>Zootaxa</i> , 2019, 4651, zootaxa.4651.1.1.	0.2	3
5834	Transcriptome Surveys in Silverfish Suggest a Multistep Origin of the Insect Odorant Receptor Gene Family. <i>Frontiers in Ecology and Evolution</i> , 2019, 7, .	1.1	17
5835	Multifaceted mechanisms of colistin resistance revealed by genomic analysis of multidrug-resistant <i>Klebsiella pneumoniae</i> isolates from individual patients before and after colistin treatment. <i>Journal of Infection</i> , 2019, 79, 312-321.	1.7	24
5836	The effect of surface sterilization and the type of sterilizer on the genus composition of lichen-inhabiting fungi with notes on some frequently isolated genera. <i>Mycoscience</i> , 2019, 60, 331-342.	0.3	9
5837	Ancient DNA from a 2,500-year-old Caribbean fossil places an extinct bird (<i>Caracara creightoni</i>) in a phylogenetic context. <i>Molecular Phylogenetics and Evolution</i> , 2019, 140, 106576.	1.2	14
5838	The native European <i>Aedes geniculatus</i> mosquito species can transmit chikungunya virus. <i>Emerging Microbes and Infections</i> , 2019, 8, 962-972.	3.0	14
5839	Characterization of the complete mitochondrial genome of <i>Lepus comu</i> s, the endemic <i>Lepus</i> in China. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2217-2218.	0.2	0
5840	<i>Meloscaphander grandis</i> (Heterobranchia: Cephalaspidea), a deep-water species from the North Pacific: Redescription and taxonomic remarks. <i>Zootaxa</i> , 2019, 4646, zootaxa.4646.2.12.	0.2	22
5841	Widespread phenotypic hypervariation in the enigmatic anchialine shrimp <i>Barbouria cubensis</i> (Decapoda: Barbouriidae). <i>Zootaxa</i> , 2019, 4648, 1-26.	0.2	3
5842	Molecular and morphological data reveal three new tribes within the Scirpo-Caricoid Clade (Cyperoideae, Cyperaceae). <i>Taxon</i> , 2019, 68, 218-245.	0.4	10
5843	Immature stages of beetles representing the "Opatriinoid" clade (Coleoptera: Tenebrionidae): an overview of current knowledge of the larval morphology and some resulting taxonomic notes on <i>Blapstinina</i> . <i>Zoomorphology</i> , 2019, 138, 349-370.	0.4	15
5844	Phylogenetic relationships and characterization of the complete chloroplast genome of strawberry, <i>Fragaria x ananassa</i> (Rosaceae: <i>Fragaria</i>). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 916-918.	0.2	1
5845	They are young, and they are many: dating freshwater lineages in unicellular dinophytes. <i>Environmental Microbiology</i> , 2019, 21, 4125-4135.	1.8	17
5846	The utility of DNA barcoding as a tool to assess the success of ecological restoration using Hemiptera as a biological indicator. <i>Restoration Ecology</i> , 2019, 27, 1409-1419.	1.4	7

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5847	A novel member of the <i>Hemidactylus brookii</i> complex (Squamata: Gekkonidae) from the Western Ghats of Maharashtra, India. <i>Zootaxa</i> , 2019, 4646, zootaxa.4646.2.2.	0.2	5
5848	Active mode of excretion across digestive tissues predates the origin of excretory organs. <i>PLoS Biology</i> , 2019, 17, e3000408.	2.6	22
5849	Diversity, Distribution and Phylogeny of Hesionidae (Annelida) Colonizing Whale Falls: New Species of Sirsoe and Connections Between Ocean Basins. <i>Frontiers in Marine Science</i> , 2019, 6, .	1.2	12
5850	Phylogenetics. , 0, , .		0
5851	Metagenomics for broad and improved parasite detection: a proof-of-concept study using swine faecal samples. <i>International Journal for Parasitology</i> , 2019, 49, 769-777.	1.3	29
5852	Research on capacity optimization configuration of AC/DC hybrid microgrid interconnect converter. <i>IOP Conference Series: Earth and Environmental Science</i> , 2019, 227, 032041.	0.2	0
5853	Multiple components of plant diversity loss determine herbivore phylogenetic diversity in a subtropical forest experiment. <i>Journal of Ecology</i> , 2019, 107, 2697-2712.	1.9	33
5854	Anaerobic Degradation of Non-Methane Alkanes by <i>Candidatus</i> <i>Methanoliparia</i> in Hydrocarbon Seeps of the Gulf of Mexico. <i>MBio</i> , 2019, 10, .	1.8	63
5855	Species composition of arbuscular mycorrhizal communities changes with elevation in the Andes of South Ecuador. <i>PLoS ONE</i> , 2019, 14, e0221091.	1.1	14
5856	The complete chloroplast genome sequence of plumed cockscomb (<i>Celosia argentea</i> , Amaranthaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2123-2124.	0.2	0
5857	The complete chloroplast genome of a Chinese endemic ornamental plant <i>Sorbus unguiculata</i> Koehne (Rosaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2227-2228.	0.2	1
5858	The complete mitochondrial genome of <i>Barbatula nuda</i> and <i>B. toni</i> (Teleostei: Nemacheilidae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2585-2587.	0.2	2
5859	The chloroplast genome sequence of <i>Commelina communis</i> (Commelinaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2631-2632.	0.2	3
5860	Shifts in plant functional composition following long-term drought in grasslands. <i>Journal of Ecology</i> , 2019, 107, 2133-2148.	1.9	85
5861	Ecology and trophic role of <i>Oncholaimus dyvae</i> sp. nov. (Nematoda: Oncholaimidae) from the lucky strike hydrothermal vent field (Mid-Atlantic Ridge). <i>BMC Zoology</i> , 2019, 4, .	0.3	25
5862	Mapping 15 years of crayfish plague in the Iberian Peninsula: The impact of two invasive species on the endangered native crayfish. <i>PLoS ONE</i> , 2019, 14, e0219223.	1.1	30
5863	Transcriptomic Analysis of Marine Gastropod <i>Hemifusus tuba</i> Provides Novel Insights into Conotoxin Genes. <i>Marine Drugs</i> , 2019, 17, 466.	2.2	6
5864	Phylogeny of <i>Paullinia</i> L. (Paullinieae: Sapindaceae), a diverse genus of lianas with dynamic fruit evolution. <i>Molecular Phylogenetics and Evolution</i> , 2019, 140, 106577.	1.2	15

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5865	Genomic characterization of mumps viruses from a large-scale mumps outbreak in Arkansas, 2016. <i>Infection, Genetics and Evolution</i> , 2019, 75, 103965.	1.0	11
5866	Phylogenetic re-evaluation of previously identified <i>Chlamydomonas</i> (Chlorophyta.) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 707 To molecular data. <i>South African Journal of Botany</i> , 2019, 125, 16-23.	1.2	2
5867	Multilocus nuclear markers provide new insights into the origin and evolution of the blackbuck (<i>Antilope cervicapra</i> , Bovidae). <i>Molecular Phylogenetics and Evolution</i> , 2019, 139, 106560.	1.2	5
5868	Non-photosynthetic predators are sister to red algae. <i>Nature</i> , 2019, 572, 240-243.	13.7	107
5869	The complete chloroplast genome sequence of <i>Belosynapsis ciliata</i> (Blume) R. S. Rao (Commelinaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2373-2374.	0.2	2
5870	Trait-based functional dietary analysis provides a better insight into the foraging ecology of bats. <i>Journal of Animal Ecology</i> , 2019, 88, 1587-1600.	1.3	23
5871	Genome Sequences of an H9N2 Avian Influenza Virus Strain Found in Pakistan in 2017. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	1
5872	The evolutionary history of LysM-RLKs (LYKs/LYRs) in wild tomatoes. <i>BMC Evolutionary Biology</i> , 2019, 19, 141.	3.2	11
5873	The diversity, evolution and ecology of <i>Salmonella</i> in venomous snakes. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007169.	1.3	16
5874	A family AA5_2 carbohydrate oxidase from <i>Penicillium rubens</i> displays functional overlap across the AA5 family. <i>PLoS ONE</i> , 2019, 14, e0216546.	1.1	10
5875	Complex History of Codiversification and Host Switching of a Newfound Soricid-Borne Orthohantavirus in North America. <i>Viruses</i> , 2019, 11, 637.	1.5	5
5876	Is reproductive strategy a key factor in understanding the evolutionary history of Southern Ocean Asteroidea (Echinodermata)? <i>Ecology and Evolution</i> , 2019, 9, 8465-8478.	0.8	14
5877	Further analyses on the phylogeny of the subclass Scuticociliatia (Protozoa, Ciliophora) based on both nuclear and mitochondrial data. <i>Molecular Phylogenetics and Evolution</i> , 2019, 139, 106565.	1.2	33
5878	Ebony and the Mascarenes: the evolutionary relationships and biogeography of <i>Diospyros</i> (Ebenaceae) in the western Indian Ocean. <i>Botanical Journal of the Linnean Society</i> , 2019, 190, 359-373.	0.8	14
5879	A Systematist's Guide to Estimating Bayesian Phylogenies From Morphological Data. <i>Insect Systematics and Diversity</i> , 2019, 3, 2.	0.7	28
5880	Global distribution of Trebouxiophyceae diversity explored by high-throughput sequencing and phylogenetic approaches. <i>Environmental Microbiology</i> , 2019, 21, 3885-3895.	1.8	16
5881	Geomicrobiology of the carbon, nitrogen and sulphur cycles in Powell Lake: a permanently stratified water column containing ancient seawater. <i>Environmental Microbiology</i> , 2019, 21, 3927-3952.	1.8	10
5882	Phylogeny, host use, and diversification in the moth family Momphidae (Lepidoptera: Gelechioidea). <i>PLoS ONE</i> , 2019, 14, e0207833.	1.1	11

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5883	Approaches to metagenomic classification and assembly. , 2019, , .		1
5884	Exploring the Phylogeny and Species Diversity of Chelidoperca (Teleostei: Serranidae) From the Western Pacific Ocean by an Integrated Approach in Systematics, With Descriptions of Three New Species and a Redescription of <i>C. lecroi</i> Fourmanoir, 1982. <i>Frontiers in Marine Science</i> , 2019, 6, .	1.2	5
5885	Potential of Transcript Editing Across Mitogenomes of Early Land Plants Shows Novel and Familiar Trends. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2963.	1.8	12
5886	Costatone C��A New Halogenated Monoterpene from the New Zealand Red Alga <i>Plocamium angustum</i> . <i>Marine Drugs</i> , 2019, 17, 418.	2.2	8
5887	Speciation, gene flow, and seasonal migration in <i>Catharus</i> thrushes (Aves:Turdidae). <i>Molecular Phylogenetics and Evolution</i> , 2019, 139, 106564.	1.2	21
5888	In marine <i>Bacteroidetes</i> the bulk of glycan degradation during algae blooms is mediated by few clades using a restricted set of genes. <i>ISME Journal</i> , 2019, 13, 2800-2816.	4.4	125
5889	Head Shape Modulates Diversification of a Classic Cichlid Pharyngeal Jaw Innovation. <i>American Naturalist</i> , 2019, 194, 693-706.	1.0	7
5890	Speciation in <i>Howea</i> Palms Occurred in Sympatry, Was Preceded by Ancestral Admixture, and Was Associated with Edaphic and Phenological Adaptation. <i>Molecular Biology and Evolution</i> , 2019, 36, 2682-2697.	3.5	17
5891	Genomic analysis unveils important aspects of population structure, virulence, and antimicrobial resistance in <i>Klebsiella</i> <i>Aerogenes</i> . <i>FEBS Journal</i> , 2019, 286, 3797-3810.	2.2	27
5892	Efflux Pumps in <i>Chromobacterium</i> Species Increase Antibiotic Resistance and Promote Survival in a Coculture Competition Model. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	16
5893	Silicon limitation facilitates virus infection and mortality of marine diatoms. <i>Nature Microbiology</i> , 2019, 4, 1790-1797.	5.9	64
5894	A phylogenomic rodent tree reveals the repeated evolution of masseter architectures. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20190672.	1.2	34
5895	Convergent evolution of cytochrome P450s underlies independent origins of keto-carotenoid pigmentation in animals. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20191039.	1.2	28
5896	Metagenomic Next-Generation Sequencing of the 2014 Ebola Virus Disease Outbreak in the Democratic Republic of the Congo. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	1.8	17
5897	T-BAS Version 2.1: Tree-Based Alignment Selector Toolkit for Evolutionary Placement of DNA Sequences and Viewing Alignments and Specimen Metadata on Curated and Custom Trees. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	35
5898	First mitochondrial genomes of five hoverfly species of the genus <i>Eristalinu</i> s (Diptera): Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.9	11
5899	<i>Cobitis xui</i> , a new species of spined loach (Teleostei: Cobitidae) from the Pearl River drainage in southern China. <i>Zootaxa</i> , 2019, 4604, 161.	0.2	1
5900	Hidden diversity in waterfall environments: The genus <i>Acrorbis</i> (Gastropoda: Planorbidae) from the Upper-Paran�� Atlantic Forest. <i>PLoS ONE</i> , 2019, 14, e0220027.	1.1	2

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5901	Updates on Section <i>Pseudo-opuntia</i> of <i>Halimeda</i> : phylogenetic analyses of <i>H. soniae</i> sp. nov. (Bryopsidales, Chlorophyta) along the Brazilian coast. <i>Botanica Marina</i> , 2019, 62, 327-336.	0.6	3
5902	<i>Blastochloris tepida</i> , sp. nov., a thermophilic species of the bacteriochlorophyll b-containing genus <i>Blastochloris</i> . <i>Archives of Microbiology</i> , 2019, 201, 1351-1359.	1.0	18
5903	Establishment of mesophilic-like catalytic properties in a thermophilic enzyme without affecting its thermal stability. <i>Scientific Reports</i> , 2019, 9, 9346.	1.6	24
5904	The complete chloroplast genome of <i>Phoebe zhennan</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1564-1565.	0.2	1
5905	The re-sequencing and re-assembly of complete chloroplast genome of <i>Melastoma dodecandrum</i> (Melastomataceae) from Fujian, China. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2219-2220.	0.2	1
5906	Paleomicrobiology: Diagnosis and Evolution of Ancient Pathogens. <i>Annual Review of Microbiology</i> , 2019, 73, 639-666.	2.9	36
5907	DAIRYdb: a manually curated reference database for improved taxonomy annotation of 16S rRNA gene sequences from dairy products. <i>BMC Genomics</i> , 2019, 20, 560.	1.2	48
5908	Extensive chloroplast genome rearrangement amongst three closely related <i>Halamphora</i> spp. (Bacillariophyceae), and evidence for rapid evolution as compared to land plants. <i>PLoS ONE</i> , 2019, 14, e0217824.	1.1	16
5909	An Anomalous Phylogenetic Position for <i>Deraiotrema platacis</i> Machida, 1982 (Lepocreadiidae) from <i>Platax pinnatus</i> on the Great Barrier Reef. <i>Diversity</i> , 2019, 11, 104.	0.7	5
5910	Novel Molecular Synapomorphies Demarcate Different Main Groups/Subgroups of Plasmodium and Piroplasmida Species Clarifying Their Evolutionary Relationships. <i>Genes</i> , 2019, 10, 490.	1.0	4
5911	How does genome size affect the evolution of pollen tube growth rate, a haploid performance trait?. <i>American Journal of Botany</i> , 2019, 106, 1011-1020.	0.8	11
5912	Resolving intergeneric relationships in the aroid clade and the backbone of <i>Ptilotus</i> (Amaranthaceae): Evidence from whole plastid genomes and morphology. <i>Taxon</i> , 2019, 68, 297-314.	0.4	10
5913	Genetic diversity, virulence factors and farm-to-table spread pattern of <i>Vibrio parahaemolyticus</i> food-associated isolates. <i>Food Microbiology</i> , 2019, 84, 103270.	2.1	38
5914	TreeMerge: a new method for improving the scalability of species tree estimation methods. <i>Bioinformatics</i> , 2019, 35, i417-i426.	1.8	15
5915	HCV Phylogeography of the General Population and High-Risk Groups in Cyprus Identifies the Island as a Global Sink for and Source of Infection. <i>Scientific Reports</i> , 2019, 9, 10077.	1.6	5
5916	The complete mitochondrial genome of <i>Aquila nipalensis</i> and its phylogenetic position. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2152-2153.	0.2	1
5917	Evolution in action: habitat transition from sediment to the pelagial leads to genome streamlining in <i>Methylophilaceae</i> . <i>ISME Journal</i> , 2019, 13, 2764-2777.	4.4	81
5918	Complete mitochondrial genome of <i>Rhus</i> gall aphid <i>Meitanaphis microgallis</i> (Hemiptera: Tj ETQq1 1 0,784314rgBT /Over	0.2	4

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5919	Extensive Cryptic Diversity Within the <i>Physalaemus cuvieri</i> “ <i>Physalaemus ephippifer</i> Species Complex (Amphibia, Anura) Revealed by Cytogenetic, Mitochondrial, and Genomic Markers. <i>Frontiers in Genetics</i> , 2019, 10, 719.	1.1	9
5920	Targeted Capture of Hundreds of Nuclear Genes Unravels Phylogenetic Relationships of the Diverse Neotropical Palm Tribe Geonomateae. <i>Frontiers in Plant Science</i> , 2019, 10, 864.	1.7	40
5921	RAD sequencing rejects a long-distance disjunction in <i>Stellaria</i> (Caryophyllaceae) and yields support for a New southern Rocky Mountains endemic. <i>Taxon</i> , 2019, 68, 280-296.	0.4	12
5922	The first clawed lobster virus <i>Homarus gammarus nudivirus</i> (HgNV n. sp.) expands the diversity of the Nudiviridae. <i>Scientific Reports</i> , 2019, 9, 10086.	1.6	15
5923	Methane-fuelled biofilms predominantly composed of methanotrophic ANME-1 in Arctic gas hydrate-related sediments. <i>Scientific Reports</i> , 2019, 9, 9725.	1.6	33
5924	Characterization of the complete chloroplast genome sequence of <i>Blastus cochinchinensis</i> (Melastomataceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2185-2186.	0.2	1
5925	<i>Akanthomyces araneicola</i> , a new araneogenous species from Southwest China. <i>Phytotaxa</i> , 2019, 409, 227-232.	0.1	8
5926	Phylogeography of ants from the Brazilian Atlantic Forest. <i>Organisms Diversity and Evolution</i> , 2019, 19, 435-445.	0.7	7
5927	Circulation, Evolution and Transmission of H5N8 virus, 2016–2018. <i>Journal of Infection</i> , 2019, 79, 363-372.	1.7	6
5928	A demonstration of unsupervised machine learning in species delimitation. <i>Molecular Phylogenetics and Evolution</i> , 2019, 139, 106562.	1.2	67
5929	Diversification of African Tree Legumes in Miombo “Mopane Woodlands. <i>Plants</i> , 2019, 8, 182.	1.6	13
5930	<i>Petunia</i> - and <i>Arabidopsis</i> -Specific Root Microbiota Responses to Phosphate Supplementation. <i>Phytobiomes Journal</i> , 2019, 3, 112-124.	1.4	37
5931	Genome-Wide Signatures of Selection in <i>Colletotrichum kahawae</i> Reveal Candidate Genes Potentially Involved in Pathogenicity and Aggressiveness. <i>Frontiers in Microbiology</i> , 2019, 10, 1374.	1.5	13
5932	Evolutionary Implications of Anoxygenic Phototrophy in the Bacterial Phylum Candidatus Eremiobacterota (WPS-2). <i>Frontiers in Microbiology</i> , 2019, 10, 1658.	1.5	88
5933	Risk factors and dynamics of verotoxigenic <i>Escherichia coli</i> O157:H7 on cattle farms: An observational study combining information from questionnaires, spatial data and molecular analyses. <i>Preventive Veterinary Medicine</i> , 2019, 170, 104726.	0.7	7
5934	The role of cryptic diversity and its environmental correlates in global conservation status assessments: Insights from the threatened bird’s-eye primrose (<i>Primula farinosa</i> L.). <i>Diversity and Distributions</i> , 2019, 25, 1457-1471.	1.9	15
5935	<i>Wolbachia</i> Acquisition by <i>Drosophila yakuba</i> -Clade Hosts and Transfer of Incompatibility Loci Between Distantly Related <i>Wolbachia</i> . <i>Genetics</i> , 2019, 212, 1399-1419.	1.2	62
5936	Ultraconserved element (UCE) probe set design: Base genome and initial design parameters critical for optimization. <i>Ecology and Evolution</i> , 2019, 9, 6933-6948.	0.8	19

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5937	Modern Phylogenomics: Building Phylogenetic Trees Using the Multispecies Coalescent Model. <i>Methods in Molecular Biology</i> , 2019, 1910, 211-239.	0.4	30
5938	Real-time whole genome sequencing to control a <i>Streptococcus pyogenes</i> outbreak at a national orthopaedic hospital. <i>Journal of Hospital Infection</i> , 2019, 103, 21-26.	1.4	14
5939	Global-level population genomics reveals differential effects of geography and phylogeny on horizontal gene transfer in soil bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 15200-15209.	3.3	85
5940	Towards a Science Gateway for Bioinformatics: Experiences in the Brazilian System of High Performance Computing. , 2019, , .		1
5941	Diversifying Evolution of the Ubiquitin-26S Proteasome System in Brassicaceae and Poaceae. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3226.	1.8	13
5942	Seasonal development of a coastal microbial mat. <i>Scientific Reports</i> , 2019, 9, 9035.	1.6	26
5943	Community analysis of gut microbiota in hornets, the largest eusocial wasps, <i>Vespa mandarinia</i> and <i>V. simillima</i> . <i>Scientific Reports</i> , 2019, 9, 9830.	1.6	37
5944	Extensively Drug-Resistant <i>Pseudomonas aeruginosa</i> ST309 Harboring Tandem Guiana Extended Spectrum β -Lactamase Enzymes: A Newly Emerging Threat in the United States. <i>Open Forum Infectious Diseases</i> , 2019, 6, ofz273.	0.4	36
5945	East Asian origins of European holly oaks (<i>Quercus</i> section <i>Ilex</i> Loudon) via the Tibet-Himalaya. <i>Journal of Biogeography</i> , 2019, 46, 2203-2214.	1.4	53
5946	Dynamic virulence-related regions of the plant pathogenic fungus <i>Verticillium dahliae</i> display enhanced sequence conservation. <i>Molecular Ecology</i> , 2019, 28, 3482-3495.	2.0	34
5947	Boomeranging around Australia: Historical biogeography and population genomics of the anti-equatorial fish <i>Microcanthus strigatus</i> (Teleostei: Microcanthidae). <i>Molecular Ecology</i> , 2019, 28, 3771-3785.	2.0	17
5948	Activity and Phylogenetics of the Broadly Occurring Family of Microbial Nep1-Like Proteins. <i>Annual Review of Phytopathology</i> , 2019, 57, 367-386.	3.5	70
5949	<i>Fusarium volatile</i> , a new potential pathogen from a human respiratory sample. <i>Fungal Systematics and Evolution</i> , 2019, 4, 171-181.	0.9	7
5950	Alternative Functional rad21 Paralogs in <i>Fusarium oxysporum</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 1370.	1.5	3
5951	Ecotypic divergences of the alpine herb <i>Potentilla matsumurae</i> adapted to fellfield "snowbed" habitats across a series of mountain sky islands. <i>American Journal of Botany</i> , 2019, 106, 772-787.	0.8	14
5952	A customized nuclear target enrichment approach for developing a phylogenomic baseline for <i>Dioscorea</i> yams (Dioscoreaceae). <i>Applications in Plant Sciences</i> , 2019, 7, e11254.	0.8	49
5953	Hybridization preceded radiation in diploid wheats. <i>Molecular Phylogenetics and Evolution</i> , 2019, 139, 106554.	1.2	21
5954	Substrate specificity, regiospecificity, and processivity in glycoside hydrolase family 74. <i>Journal of Biological Chemistry</i> , 2019, 294, 13233-13247.	1.6	25

#	ARTICLE	IF	CITATIONS
5955	Further assessment of the Genus Neodon and the description of a new species from Nepal. PLoS ONE, 2019, 14, e0219157.	1.1	6
5956	Dissecting the Heterogeneous Population Genetic Structure of <i>Candida albicans</i> : Limitations and Constraints of the Multilocus Sequence Typing Scheme. Frontiers in Microbiology, 2019, 10, 1052.	1.5	9
5957	Insights into cryptic diversity and adaptive evolution of the clam <i>Coelomactra antiquata</i> (Spengler, 1845) from the Mediterranean Sea. BMC Evolutionary Biology, 2019, 19, 1007133.	0.3	2
5958	Genome resequencing of the orange-spotted grouper (<i>Epinephelus coioides</i>) for a genome-wide association study on ammonia tolerance. Aquaculture, 2019, 512, 734332.	1.7	24
5959	Gut Colonization Preceding Mucosal Barrier Injury Bloodstream Infection in Pediatric Hematopoietic Stem Cell Transplantation Recipients. Biology of Blood and Marrow Transplantation, 2019, 25, 2274-2280.	2.0	36
5960	Microbial life cycles link global modularity in regulation to mosaic evolution. Nature Ecology and Evolution, 2019, 3, 1184-1196.	3.4	18
5961	Genomic Features of <i>Vibrio parahaemolyticus</i> from Lebanon and Comparison to Globally Diverse Strains by Whole-Genome Sequencing. Foodborne Pathogens and Disease, 2019, 16, 778-787.	0.8	7
5962	Recent colonization and expansion through the Lesser Sundas by seven amphibian and reptile species. Zoologica Scripta, 2019, 48, 614-626.	0.7	7
5963	Per-sample immunoglobulin germline inference from B cell receptor deep sequencing data. PLoS Computational Biology, 2019, 15, e1007133.	1.5	51
5964	Origin and diversification of <i>Cristaria</i> (Malvaceae) parallel Andean orogeny and onset of hyperaridity in the Atacama Desert. Global and Planetary Change, 2019, 181, 102992.	1.6	18
5965	Cross-species transmission resulted in the emergence and establishment of circovirus in pig. Infection, Genetics and Evolution, 2019, 75, 103973.	1.0	6
5966	Genome and plasmid diversity of Extended-Spectrum β -Lactamase-producing <i>Escherichia coli</i> ST131 tracking phylogenetic trajectories with Bayesian inference. Scientific Reports, 2019, 9, 10291.	1.6	15
5967	Comparison of Four Complete Chloroplast Genomes of Medicinal and Ornamental <i>Meconopsis</i> Species: Genome Organization and Species Discrimination. Scientific Reports, 2019, 9, 10567.	1.6	29
5968	Genome and transcriptome evolve separately in recently hybridized <i>Trichosporon</i> fungi. Communications Biology, 2019, 2, 263.	2.0	9
5969	Depth distributions of nitrite reductase (<i>nirK</i>) gene variants reveal spatial dynamics of thaumarchaeal ecotype populations in coastal Monterey Bay. Environmental Microbiology, 2019, 21, 4032-4045.	1.8	14
5970	Salinity drives meiofaunal community structure dynamics across the Baltic ecosystem. Molecular Ecology, 2019, 28, 3813-3829.	2.0	31
5971	Phylogenetic Concepts and Tools Applied to Epidemiologic Investigations of Infectious Diseases. Microbiology Spectrum, 2019, 7, .	1.2	3
5972	Recurrent gene co-amplification on <i>Drosophila</i> X and Y chromosomes. PLoS Genetics, 2019, 15, e1008251.	1.5	41

#	ARTICLE	IF	CITATIONS
5973	Characterization and whole genome sequencing of closely related multidrug-resistant <i>Salmonella enterica</i> serovar Heidelberg isolates from imported poultry meat in the Netherlands. <i>PLoS ONE</i> , 2019, 14, e0219795.	1.1	30
5974	Genomic Analyses Reveal Evidence of Independent Evolution, Demographic History, and Extreme Environment Adaptation of Tibetan Plateau <i>Agaricus bisporus</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 1786.	1.5	14
5975	Molecular phylogeny and biogeography of the land snail subfamily Leptaxinae (Gastropoda: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 662 T	1.2	7
5976	Multiple auto- and allopolyploidisations marked the Pleistocene history of the widespread Eurasian steppe plant <i>Astragalus onobrychis</i> (Fabaceae). <i>Molecular Phylogenetics and Evolution</i> , 2019, 139, 106572.	1.2	27
5977	Molecular Interactions Between Smut Fungi and Their Host Plants. <i>Annual Review of Phytopathology</i> , 2019, 57, 411-430.	3.5	59
5978	Widespread selection and gene flow shape the genomic landscape during a radiation of monkeyflowers. <i>PLoS Biology</i> , 2019, 17, e3000391.	2.6	111
5979	Spatiotemporal Characteristics of the Largest HIV-1 CRF02_AG Outbreak in Spain: Evidence for Onward Transmissions. <i>Frontiers in Microbiology</i> , 2019, 10, 370.	1.5	9
5980	<i>Pseudomonas aeruginosa</i> populations in the cystic fibrosis lung lose susceptibility to newly applied β -lactams within 3 days. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 2916-2925.	1.3	17
5981	Benchmarking of alignment-free sequence comparison methods. <i>Genome Biology</i> , 2019, 20, 144.	3.8	147
5982	The complete chloroplast genome of <i>Pinus squamata</i> (Pinaceae), a critically endangered species in China. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2668-2669.	0.2	0
5983	Genotypic and Phenotypic Characterization of Antimicrobial Resistance in <i>Neisseria gonorrhoeae</i> : a Cross-Sectional Study of Isolates Recovered from Routine Urine Cultures in a High-Incidence Setting. <i>MSphere</i> , 2019, 4, .	1.3	8
5984	Comparative transcriptomics suggest unique molecular adaptations within tardigrade lineages. <i>BMC Genomics</i> , 2019, 20, 607.	1.2	68
5985	RPW8/HR repeats control NLR activation in <i>Arabidopsis thaliana</i> . <i>PLoS Genetics</i> , 2019, 15, e1008313.	1.5	56
5986	Paired RNA Radiocarbon and Sequencing Analyses Indicate the Importance of Autotrophy in a Shallow Alluvial Aquifer. <i>Scientific Reports</i> , 2019, 9, 10370.	1.6	1
5987	Two New Corticolous Buellioid Species from South Korea. <i>Mycobiology</i> , 2019, 47, 143-153.	0.6	1
5988	<i>Sulzbacheromyces sinensis</i> , an Unexpected Basidiolichen, was Newly Discovered from Korean Peninsula and Philippines, with a Phylogenetic Reconstruction of Genus <i>Sulzbacheromyces</i> . <i>Mycobiology</i> , 2019, 47, 191-199.	0.6	1
5989	Faster speciation of fig wasps than their host figs leads to decoupled speciation dynamics: Snapshots across the speciation continuum. <i>Molecular Ecology</i> , 2019, 28, 3958-3976.	2.0	14
5990	Genomic differentiation tracks earth-historic isolation in an Indo-Australasian archipelagic pitta (Pittidae; Aves) complex. <i>BMC Evolutionary Biology</i> , 2019, 19, 151.	3.2	14

#	ARTICLE	IF	CITATIONS
5991	Mycoheterotrophic Epirixanthes (Polygalaceae) has a typical angiosperm mitogenome but unorthodox plastid genomes. <i>Annals of Botany</i> , 2019, 124, 791-807.	1.4	14
5992	A Preliminary Phylogeny of Rhyacophilidae with Reference to Fansipangana and the Monophyly of Rhyacophila . <i>Zoosymposia</i> , 2019, 14, 189-192.	0.3	2
5993	Untangling the Hypogeococcus pungens species complex (Hemiptera: Pseudococcidae) for Argentina, Australia, and Puerto Rico based on host plant associations and genetic evidence. <i>PLoS ONE</i> , 2019, 14, e0220366.	1.1	14
5994	Inter- and intra-lineage genetic diversity of wild-type Zika viruses reveals both common and distinctive nucleotide variants and clusters of genomic diversity. <i>Emerging Microbes and Infections</i> , 2019, 8, 1126-1138.	3.0	20
5995	From Root to Tips: Sporulation Evolution and Specialization in <i>Bacillus subtilis</i> and the Intestinal Pathogen <i>Clostridioides difficile</i> . <i>Molecular Biology and Evolution</i> , 2019, 36, 2714-2736.	3.5	29
5996	Statistically consistent divide-and-conquer pipelines for phylogeny estimation using NJMerge. <i>Algorithms for Molecular Biology</i> , 2019, 14, 14.	0.3	16
5997	Patterns of Geographical and Potential Adaptive Divergence in the Genome of the Common Carp (<i>Cyprinus carpio</i>). <i>Frontiers in Genetics</i> , 2019, 10, 660.	1.1	12
5998	Novel Methicillin-Resistant <i>Staphylococcus aureus</i> CC8 Clone Identified in a Hospital Setting in Armenia. <i>Frontiers in Microbiology</i> , 2019, 10, 1592.	1.5	6
5999	Description and phylogenetic relationships of a new genus of sea cucumbers from Australia, with two new combinations (Holothuroidea, Stichopodidae). <i>Marine Biodiversity</i> , 2019, 49, 2499-2518.	0.3	2
6000	The relative importance of ecological drivers of arbuscular mycorrhizal fungal distribution varies with taxon phylogenetic resolution. <i>New Phytologist</i> , 2019, 224, 936-948.	3.5	17
6001	A Robust Phylogenomic Time Tree for Biotechnologically and Medically Important Fungi in the Genera <i>Aspergillus</i> and <i>Penicillium</i> . <i>MBio</i> , 2019, 10, .	1.8	106
6002	Identification and molecular epidemiology of methicillin resistant <i>Staphylococcus pseudintermedius</i> strains isolated from canine clinical samples in Argentina. <i>BMC Veterinary Research</i> , 2019, 15, 264.	0.7	25
6003	Genome sequencing and comparison of five <i>Tilletia</i> species to identify candidate genes for the detection of regulated species infecting wheat. <i>IMA Fungus</i> , 2019, 10, 11.	1.7	21
6004	Assessing Anthocyanin Biosynthesis in Solanaceae as a Model Pathway for Secondary Metabolism. <i>Genes</i> , 2019, 10, 559.	1.0	14
6005	Near full genome characterization of HIV-1 unique recombinant forms in Cameroon reveals dominant CRF02_AG and F2 recombination patterns. <i>Journal of the International AIDS Society</i> , 2019, 22, e25362.	1.2	7
6006	Island biogeography of the Macaronesian <i>Gesnouinia</i> and Mediterranean <i>Soleirolia</i> (Parietarieae.) <i>Tj ETQq1 1 0.784314 rgBT (Overlock</i>	0.4	8
6007	A new species of Branchellion Savigny, 1822 (Hirudinida: Piscicolidae), a marine leech parasitic on the giant electric ray <i>Narcine entemedor</i> Jordan & Starks (Batoidea: Narcinidae) off Oaxaca, Mexico. <i>Systematic Parasitology</i> , 2019, 96, 575-584.	0.5	1
6008	Placing <i>Eophila tellinii</i> (Oligochaeta, Lumbricidae) in a molecular phylogenetic context advances the century-old controversy around the problematic genus. <i>European Journal of Soil Biology</i> , 2019, 94, 103114.	1.4	12

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6009	Tarantula phylogenomics: A robust phylogeny of deep theraphosid clades inferred from transcriptome data sheds light on the prickly issue of urticating setae evolution. <i>Molecular Phylogenetics and Evolution</i> , 2019, 140, 106573.	1.2	31
6010	A multigene phylogeny to infer the evolutionary history of Chaetocerotaceae (Bacillariophyta). <i>Molecular Phylogenetics and Evolution</i> , 2019, 140, 106575.	1.2	16
6011	Genomic Features of High-Priority <i>Salmonella enterica</i> Serovars Circulating in the Food Production Chain, Brazil, 2000–2016. <i>Scientific Reports</i> , 2019, 9, 11058.	1.6	61
6012	Complete sequence of mitochondrial DNA of <i>Gloiopeltis furcata</i> (Postels and Ruprecht) J. Agardh. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2543-2544.	0.2	7
6013	Chance and predictability in evolution: The genomic basis of convergent dietary specializations in an adaptive radiation. <i>Molecular Ecology</i> , 2019, 28, 4028-4045.	2.0	21
6014	Two new species of Amphiglena (Sabellidae, Annelida), with an assessment of hidden diversity in the Mediterranean. <i>Zootaxa</i> , 2019, 4648, zootaxa.4648.2.8.	0.2	6
6015	A New Species of <i>Prosthlostomum</i> (Platyhelminthes: Polycladida) from Shirahama, Japan. <i>Species Diversity</i> , 2019, 24, 137-143.	0.1	2
6016	Scalable methods for analyzing and visualizing phylogenetic placement of metagenomic samples. <i>PLoS ONE</i> , 2019, 14, e0217050.	1.1	65
6017	The Parallel Molecular Adaptations to the Antarctic Cold Environment in Two Psychrophilic Green Algae. <i>Genome Biology and Evolution</i> , 2019, 11, 1897-1908.	1.1	19
6018	The genome assembly and annotation of yellowhorn (<i>Xanthoceras sorbifolium</i> Bunge). <i>GigaScience</i> , 2019, 8, .	3.3	37
6019	Symbiosis, Selection, and Novelty: Freshwater Adaptation in the Unique Sponges of Lake Baikal. <i>Molecular Biology and Evolution</i> , 2019, 36, 2462-2480.	3.5	22
6020	A mirage of cryptic species: Genomics uncover striking mitonuclear discordance in the butterfly <i>Thymelicus sylvestris</i> . <i>Molecular Ecology</i> , 2019, 28, 3857-3868.	2.0	75
6021	De novo assembly of the goldfish (<i>Carassius auratus</i>) genome and the evolution of genes after whole-genome duplication. <i>Science Advances</i> , 2019, 5, eaav0547.	4.7	182
6022	Plastid genome evolution in tribe Desmodieae (Fabaceae: Papilionoideae). <i>PLoS ONE</i> , 2019, 14, e0218743.	1.1	23
6023	Terpene Synthase Genes Originated from Bacteria through Horizontal Gene Transfer Contribute to Terpenoid Diversity in Fungi. <i>Scientific Reports</i> , 2019, 9, 9223.	1.6	31
6024	Polyploidy does not control all: Lineage-specific average chromosome length constrains genome size evolution in ferns. <i>Journal of Systematics and Evolution</i> , 2019, 57, 418-430.	1.6	16
6025	Long-Term Intra-host Evolution of Methicillin Resistant <i>Staphylococcus aureus</i> Among Cystic Fibrosis Patients With Respiratory Carriage. <i>Frontiers in Genetics</i> , 2019, 10, 546.	1.1	24
6026	Avian Genomics in Ecology and Evolution. , 2019, , .		4

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6027	Diversity of Wolbachia Associated with the Giant Turtle Ant, <i>Cephalotes atratus</i> . <i>Current Microbiology</i> , 2019, 76, 1330-1337.	1.0	19
6028	<i>Pseudosclerococcum golindoi</i> gen. et sp. nov., a new taxon with apothecial ascomata and a Chalara-like anamorph within the Sclerococcales (Eurotiomycetes). <i>Mycological Progress</i> , 2019, 18, 895-905.	0.5	8
6029	Comparative Genomics of Wild Bee and Flower Isolated <i>Lactobacillus</i> Reveals Potential Adaptation to the Bee Host. <i>Genome Biology and Evolution</i> , 2019, 11, 2151-2161.	1.1	38
6030	Effective Surveillance Using Multilocus Variable-Number Tandem-Repeat Analysis and Whole-Genome Sequencing for Enterohemorrhagic <i>Escherichia coli</i> O157. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	13
6031	Resolving the Avian Tree of Life from Top to Bottom: The Promise and Potential Boundaries of the Phylogenomic Era. , 2019, , 151-210.		27
6032	Transcriptome and organellar sequencing highlights the complex origin and diversification of allotetraploid <i>Brassica napus</i> . <i>Nature Communications</i> , 2019, 10, 2878.	5.8	78
6033	Building a DNA barcode library for the freshwater fishes of Bangladesh. <i>Scientific Reports</i> , 2019, 9, 9382.	1.6	16
6034	<i>Mycobacterium tuberculosis</i> whole genome sequencing provides insights into the Manila strain and drug-resistance mutations in the Philippines. <i>Scientific Reports</i> , 2019, 9, 9305.	1.6	33
6035	Genetic basis of species-specific genitalia reveals role in species diversification. <i>Science Advances</i> , 2019, 5, eaav9939.	4.7	22
6036	Penicillin-Binding Protein Typing, Antibiotic Resistance Gene Identification, and Molecular Phylogenetic Analysis of Meropenem-Resistant <i>Streptococcus pneumoniae</i> Serotype 19A-CC3111 Strains in Japan. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	1.4	13
6037	Isolation of Highly Pathogenic H5N1 Influenza Viruses in 2009–2013 in Vietnam. <i>Frontiers in Microbiology</i> , 2019, 10, 1411.	1.5	5
6038	Frequency of Hepatitis B Virus Resistance Mutations in Women Using Tenofovir Gel as Pre-Exposure Prophylaxis. <i>Viruses</i> , 2019, 11, 569.	1.5	2
6039	A new species of <i>Echinoderes</i> (Cyclorhagida: Echinoderidae) from the San Juan Islands, Washington State, USA, and insights into the kinorhynch transcriptome. <i>Zoologischer Anzeiger</i> , 2019, 282, 52-63.	0.4	4
6040	<i>Mortierella oedorhiza</i> , a new species forming a dichotomously branched rhizoid at the sporangiochore base. <i>Mycoscience</i> , 2019, 60, 361-365.	0.3	5
6041	A study on the non-monophyletic genera <i>Australothrix</i> and <i>Holostichides</i> based on multigene and morphological analyses with a reexamination of type materials (Protozoa: Ciliophora). <i>Molecular Phylogenetics and Evolution</i> , 2019, 139, 106538.	1.2	7
6042	Cyanobacteria and cyanophage contributions to carbon and nitrogen cycling in an oligotrophic oxygen-deficient zone. <i>ISME Journal</i> , 2019, 13, 2714-2726.	4.4	52
6043	De novo design of symmetric ferredoxins that shuttle electrons in vivo. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 14557-14562.	3.3	41
6044	Novel insights into endogenous RNA viral elements in <i>Ixodes scapularis</i> and other arbovirus vector genomes. <i>Virus Evolution</i> , 2019, 5, vez010.	2.2	34

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6045	First record of the bacterial endosymbiont <i>Wolbachia</i> for phytophagous hoverflies from genus <i>Merodon</i> (Diptera: Syrphidae). <i>Entomological Science</i> , 2019, 22, 283-296.	0.3	4
6046	Allopatric and sympatric diversification within roach (<i>Rutilus rutilus</i>) of large pre-Alpine lakes. <i>Journal of Evolutionary Biology</i> , 2019, 32, 1174-1185.	0.8	4
6047	Surveying seaweeds from the Ulvales and Fucales in the world's most frequently used artificial waterway, the Kiel Canal. <i>Botanica Marina</i> , 2019, 62, 51-61.	0.6	14
6048	A Novel Alphabaculovirus from the Soybean Looper, <i>Chrysodeixis includens</i> , that Produces Tetrahedral Occlusion Bodies and Encodes Two Copies of he65. <i>Viruses</i> , 2019, 11, 579.	1.5	3
6049	Hydrogeology of the deepest underwater cave in the world: Hranice Abyss, Czechia. <i>Hydrogeology Journal</i> , 2019, 27, 2325-2345.	0.9	7
6050	Core Metabolic Features and Hot Origin of Bathyarchaeota. <i>Engineering</i> , 2019, 5, 498-504.	3.2	42
6051	Genome Sequences Provide Insights into the Reticulate Origin and Unique Traits of Woody Bamboos. <i>Molecular Plant</i> , 2019, 12, 1353-1365.	3.9	116
6052	Sequencing and comparative analysis of three <i>Chlorella</i> genomes provide insights into strain-specific adaptation to wastewater. <i>Scientific Reports</i> , 2019, 9, 9514.	1.6	23
6053	Implications of a Dating Analysis of Hippoboscoidea (Diptera) for the Origins of Phoresis in Feather Lice (Psocodea: Phthiraptera: Philopteridae). <i>Insect Systematics and Diversity</i> , 2019, 3, .	0.7	7
6054	Ancient Hybridization and Adaptive Introgression of an Invadysin Gene in Schistosome Parasites. <i>Molecular Biology and Evolution</i> , 2019, 36, 2127-2142.	3.5	56
6056	Algicidal potential of cultivable bacteria from pelagic waters against the toxic dinoflagellate <i>Pyrodinium bahamense</i> (Dinophyceae). <i>Journal of Applied Phycology</i> , 2019, 31, 3721-3735.	1.5	9
6057	Cryptic species and independent origins of allochronic populations within a seabird species complex (<i>Hydrobates</i> spp.). <i>Molecular Phylogenetics and Evolution</i> , 2019, 139, 106552.	1.2	18
6058	Cryptic, alien and lost species: molecular diversity of <i>Ulva sensu lato</i> along the German coasts of the North and Baltic Seas. <i>European Journal of Phycology</i> , 2019, 54, 466-483.	0.9	43
6059	Phylogeny of the subgenus <i>Eumitria</i> in Tanzania. <i>Mycology</i> , 2019, 10, 250-260.	2.0	4
6060	Prevalence of viral photosynthesis genes along a freshwater to saltwater transect in Southeast USA. <i>Environmental Microbiology Reports</i> , 2019, 11, 672-689.	1.0	24
6061	New leaf and fruit disease of <i>Juglans regia</i> caused by <i>Juglanconis juglandina</i> in Xinjiang, China. <i>Forest Pathology</i> , 2019, 49, e12537.	0.5	3
6062	Expression and regulatory asymmetry of retained <i>Arabidopsis thaliana</i> transcription factor genes derived from whole genome duplication. <i>BMC Evolutionary Biology</i> , 2019, 19, 77.	3.2	20
6063	Plastome phylogenomics of <i>Saussurea</i> (Asteraceae: Cardueae). <i>BMC Plant Biology</i> , 2019, 19, 290.	1.6	34

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6064	Resurrection of <i>Carex ignota</i> (Cyperaceae, section <i>Laxiflorae</i>), a long overlooked sedge of the southern U.S.A.. <i>Brittonia</i> , 2019, 71, 253-267.	0.8	2
6065	New Ca. <i>Liberibacter psyllaourous</i> haplotype resurrected from a 49-year-old specimen of <i>Solanum umbelliferum</i> : a native host of the psyllid vector. <i>Scientific Reports</i> , 2019, 9, 9530.	1.6	32
6066	First record of the family Ameronothridae (Acari: Oribatida) from Japan – new species, juvenile morphology, ecology and biogeographic remarks. <i>International Journal of Acarology</i> , 2019, 45, 315-327.	0.3	7
6067	Two complete plastid genome sequences of Sapindales: <i>Zanthoxylum nitidum</i> and <i>Xanthoceras sorbifolium</i> , and phylogenetic analyses in Sapindales. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1716-1717.	0.2	0
6068	Complete Genomes of Symbiotic Cyanobacteria Clarify the Evolution of Vanadium-Nitrogenase. <i>Genome Biology and Evolution</i> , 2019, 11, 1959-1964.	1.1	45
6069	The evolution of endogenous retroviral envelope genes in bats and their potential contribution to host biology. <i>Virus Research</i> , 2019, 270, 197645.	1.1	10
6070	Draft genome sequence of cauliflower (<i>Brassica oleracea</i> L. var. <i>botrytis</i>) provides new insights into the C genome in Brassica species. <i>Horticulture Research</i> , 2019, 6, 82.	2.9	53
6071	Annual Thermal Stress Increases a Soft Coral's Susceptibility to Bleaching. <i>Scientific Reports</i> , 2019, 9, 8064.	1.6	21
6072	Prey, populations, and the pleistocene: evidence for low COI variation in a widespread North American leech. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2019, 30, 749-763.	0.7	8
6073	<i>Stenotrophomonas maltophilia</i> Encodes a VirB/VirD4 Type IV Secretion System That Modulates Apoptosis in Human Cells and Promotes Competition against Heterologous Bacteria, Including <i>Pseudomonas aeruginosa</i> . <i>Infection and Immunity</i> , 2019, 87, .	1.0	29
6074	Two new species of <i>Lerista</i> Bell, 1833 (Reptilia: Scincidae) from north Queensland populations formerly assigned to <i>Lerista storri</i> Greer, McDonald and Lawrie, 1983. <i>Zootaxa</i> , 2019, 4577, 473.	0.2	2
6075	Description of new chactine-bearing sponges provides insights into the higher classification of <i>Calcaronea</i> (Porifera: Calcarea). <i>Zootaxa</i> , 2019, 4615, zootaxa.4615.2.1.	0.2	6
6076	Evolutionary Analysis of Unicellular Species in Chlamydomonadales Through Chloroplast Genome Comparison With the Colonial Volvocine Algae. <i>Frontiers in Microbiology</i> , 2019, 10, 1351.	1.5	13
6077	Genome Characteristics and Evolution of Pseudorabies Virus Strains in Eastern China from 2017 to 2019. <i>Virologica Sinica</i> , 2019, 34, 601-609.	1.2	26
6078	Diversification of the gut fungi <i>Smittium</i> and allies (Harpellales) co-occurred with the origin of complete metamorphosis of their symbiotic insect hosts (lower Diptera). <i>Molecular Phylogenetics and Evolution</i> , 2019, 139, 106550.	1.2	8
6079	Diversity and evolution of chitin synthases in oomycetes (Straminipila: Oomycota). <i>Molecular Phylogenetics and Evolution</i> , 2019, 139, 106558.	1.2	14
6080	Phylogenetic Techniques in Geomicrobiology. , 2019, , 360-404.		0
6081	Genes functioned in kleptoplastids of <i>Dinophysis</i> are derived from haptophytes rather than from cryptophytes. <i>Scientific Reports</i> , 2019, 9, 9009.	1.6	15

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6082	Probing the geological source and biological fate of hydrogen in Yellowstone hot springs. <i>Environmental Microbiology</i> , 2019, 21, 3816-3830.	1.8	22
6083	A taxonomic revision of Cheilodactylidae and Latridae (Centrarchiformes: Cirrhitidae) using morphological and genomic characters. <i>Zootaxa</i> , 2019, 4585, zootaxa.4585.1.7.	0.2	9
6084	A new species of <i>Lerista</i> Bell, 1833 (Reptilia: Scincidae) from Cape York Peninsula, Queensland, belonging to the <i>Lerista allanae</i> clade but strongly disjunct from other members of the clade. <i>Zootaxa</i> , 2019, 4613, 161-171.	0.2	2
6085	Particle Migration and Clogging in Porous Media: A Convergent Flow Microfluidics Study. <i>Journal of Geophysical Research: Solid Earth</i> , 2019, 124, 9495-9504.	1.4	56
6086	Dissecting the molecular evolution of fluoroquinolone-resistant <i>Shigella sonnei</i> . <i>Nature Communications</i> , 2019, 10, 4828.	5.8	41
6087	Combined molecular and morphological phylogeny of <i>Myrtlemiris</i> , evolution of endosomal spicules, description of two new species and <i>Neomyrtlemiris</i> , gen. nov. (Insecta : Heteroptera : Miridae :). <i>Tj ETQq1 1 0.7843 14rgBT /Overlock 10</i>	0.7	10
6088	Phylogenomics reveals the evolutionary timing and pattern of butterflies and moths. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 22657-22663.	3.3	291
6089	The complete chloroplast genome of an endangered species <i>Cymbidium mastersii</i> (Orchidaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3068-3069.	0.2	4
6090	The Complete mitochondrial genome of <i>Marmota vancouverensis</i> (Vancouver Island Marmot). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3151-3152.	0.2	1
6091	Complete mitochondrial genome of <i>Schizothorax davidi</i> (Teleostei: Cypriniformes: Cyprinidae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3210-3211.	0.2	0
6092	PhyloMagnet: fast and accurate screening of short-read meta-omics data using gene-centric phylogenetics. <i>Bioinformatics</i> , 2020, 36, 1718-1724.	1.8	7
6093	Nematodes as evolutionary commuters between marine, freshwater and terrestrial habitats. <i>Biological Journal of the Linnean Society</i> , 2019, 128, 756-767.	0.7	39
6094	Evolution of Perine Morphology in the Thelypteridaceae. <i>International Journal of Plant Sciences</i> , 2019, 180, 1016-1035.	0.6	9
6095	Dark Ophiuroid Biodiversity in a Prospective Abyssal Mine Field. <i>Current Biology</i> , 2019, 29, 3909-3912.e3.	1.8	43
6096	Antibiotic resistance of <i>Mycobacterium tuberculosis</i> complex in Africa: A systematic review of current reports of molecular epidemiology, mechanisms and diagnostics. <i>Journal of Infection</i> , 2019, 79, 550-571.	1.7	15
6097	Whole genome sequencing of drug resistant <i>Mycobacterium tuberculosis</i> isolates from a high burden tuberculosis region of North West Pakistan. <i>Scientific Reports</i> , 2019, 9, 14996.	1.6	24
6098	ChromaClade: combined visualisation of phylogenetic and sequence data. <i>BMC Evolutionary Biology</i> , 2019, 19, 186.	3.2	7
6099	RADseq population genomics confirms divergence across closely related species in blue coral (<i>Heliopora coerulea</i>). <i>BMC Evolutionary Biology</i> , 2019, 19, 187.	3.2	12

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6100	Analysis of 1,000 Type-Strain Genomes Improves Taxonomic Classification of Bacteroidetes. <i>Frontiers in Microbiology</i> , 2019, 10, 2083.	1.5	1,281
6101	Investigating Evolutionary Rate Variation in Bacteria. <i>Journal of Molecular Evolution</i> , 2019, 87, 317-326.	0.8	31
6102	Polyclad phylogeny persists to be problematic. <i>Organisms Diversity and Evolution</i> , 2019, 19, 585-608.	0.7	20
6103	The Caribbean enigma: the presence of unusual cryptic diversity in intertidal mites (Arachnida, Acari). <i>Tj ETQq1 1 0.784314 rgBT /Over</i>	0.7	13
6104	Immobilization of dopamine on <i>Aspergillus niger</i> microspheres (AM/PDA) and its effect on the U(VI) adsorption capacity in aqueous solutions. <i>Colloids and Surfaces A: Physicochemical and Engineering Aspects</i> , 2019, 583, 123914.	2.3	23
6105	A high-quality <i>Actinidia chinensis</i> (kiwifruit) genome. <i>Horticulture Research</i> , 2019, 6, 117.	2.9	109
6106	A new species in the major malaria vector complex sheds light on reticulated species evolution. <i>Scientific Reports</i> , 2019, 9, 14753.	1.6	56
6107	Epidemiology, evolution and transmission of human metapneumovirus in Guangzhou China, 2013â€“2017. <i>Scientific Reports</i> , 2019, 9, 14022.	1.6	23
6108	The anatomy of an unstable node: a Levantine relict precipitates phylogenomic dissolution of higher-level relationships of the armoured harvestmen (Arachnida: Opiliones: Laniatores). <i>Invertebrate Systematics</i> , 2019, , .	0.5	12
6109	Genomeâ€“resolved metagenomics and metatranscriptomics reveal niche differentiation in functionally redundant microbial communities at deepâ€“sea hydrothermal vents. <i>Environmental Microbiology</i> , 2019, 21, 4395-4410.	1.8	51
6110	Rapid diversification of alpine bamboos associated with the uplift of the Hengduan Mountains. <i>Journal of Biogeography</i> , 2019, 46, 2678-2689.	1.4	52
6111	Yellow Fever Virus Reemergence and Spread in Southeast Brazil, 2016â€“2019. <i>Journal of Virology</i> , 2019, 94, .	1.5	62
6112	Supporting evidence for a human reservoir of invasive non-Typhoidal <i>Salmonella</i> from household samples in Burkina Faso. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007782.	1.3	36
6113	The mobile FOX AmpC beta-lactamases originated in <i>Aeromonas allosaccharophila</i> . <i>International Journal of Antimicrobial Agents</i> , 2019, 54, 798-802.	1.1	15
6114	The chromosome-scale reference genome of black pepper provides insight into piperine biosynthesis. <i>Nature Communications</i> , 2019, 10, 4702.	5.8	115
6115	The complete chloroplast genome of a commercially exploited ornamental plant, <i>Bougainvillea glabra</i> (Caryophyllales: Nyctaginaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3390-3391.	0.2	3
6116	Modeling Structural Constraints on Protein Evolution via Side-Chain Conformational States. <i>Molecular Biology and Evolution</i> , 2019, 36, 2086-2103.	3.5	10
6117	A phylogenetic approach to a global supraspecific taxonomy of <i>Cortinarius</i> (<i>Agaricales</i>) with an emphasis on the southern mycota. <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2019, 42, 261-290.	1.6	39

#	ARTICLE	IF	CITATIONS
6118	A novel molecular mechanism to explain mutations of the HCV protease associated with resistance against covalently bound inhibitors. <i>Virus Research</i> , 2019, 274, 197778.	1.1	9
6119	Variable genome evolution in fungi after transposon-mediated amplification of a housekeeping gene. <i>Mobile DNA</i> , 2019, 10, 37.	1.3	1
6120	Culturable plant pathogenic fungi associated with sugarcane in southern China. <i>Fungal Diversity</i> , 2019, 99, 1-104.	4.7	62
6121	Genetic diversity of <i>Mycobacterium tuberculosis</i> clinical isolates in Blantyre, Malawi. <i>Heliyon</i> , 2019, 5, e02638.	1.4	3
6122	Phylogenetic analysis provides insights into the evolution of Asian fireflies and adult bioluminescence. <i>Molecular Phylogenetics and Evolution</i> , 2019, 140, 106600.	1.2	24
6123	Can Insertion Sequences Proliferation Influence Genomic Plasticity? Comparative Analysis of <i>Acinetobacter baumannii</i> Sequence Type 78, a Persistent Clone in Italian Hospitals. <i>Frontiers in Microbiology</i> , 2019, 10, 2080.	1.5	23
6124	Genome-wide Identification and Characterization of a Superfamily of Bacterial Extracellular Contractile Injection Systems. <i>Cell Reports</i> , 2019, 29, 511-521.e2.	2.9	44
6125	Spatiotemporal dynamics of multidrug resistant bacteria on intensive care unit surfaces. <i>Nature Communications</i> , 2019, 10, 4569.	5.8	39
6126	Lassa virus circulating in Liberia: a retrospective genomic characterisation. <i>Lancet Infectious Diseases</i> , The, 2019, 19, 1371-1378.	4.6	30
6127	The <i>Prevotella copri</i> Complex Comprises Four Distinct Clades Underrepresented in Westernized Populations. <i>Cell Host and Microbe</i> , 2019, 26, 666-679.e7.	5.1	274
6128	New species of <i>Amanita</i> subgen. <i>Lepidella</i> from Guyana. <i>Fungal Systematics and Evolution</i> , 2019, 3, 1-12.	0.9	7
6129	The Acidophilic Methanotroph <i>Methylacidimicrobium tartarophylax</i> 4AC Grows as Autotroph on H ₂ Under Microoxic Conditions. <i>Frontiers in Microbiology</i> , 2019, 10, 2352.	1.5	28
6130	The allotetraploid origin and asymmetrical genome evolution of the common carp <i>Cyprinus carpio</i> . <i>Nature Communications</i> , 2019, 10, 4625.	5.8	156
6131	Disruption of <i>hmgA</i> by DNA Duplication is Responsible for Hyperpigmentation in a <i>Vibrio anguillarum</i> Strain. <i>Scientific Reports</i> , 2019, 9, 14589.	1.6	2
6132	A single-cell genome reveals diplonemid-like ancestry of kinetoplastid mitochondrial gene structure. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20190100.	1.8	13
6133	Comparative transcriptomics of <i>Gymnosporangium</i> spp. teliospores reveals a conserved genetic program at this specific stage of the rust fungal life cycle. <i>BMC Genomics</i> , 2019, 20, 723.	1.2	6
6134	A further study on <i>Franciscobasis Machado & Bed^ã</i> , 2016 (Odonata: Coenagrionidae), a newly described genus from Minas Gerais, Brazil. <i>PLoS ONE</i> , 2019, 14, e0223241.	1.1	6
6135	De Novo Assembly Discovered Novel Structures in Genome of Plastids and Revealed Divergent Inverted Repeats in <i>Mammillaria</i> (Cactaceae, Caryophyllales). <i>Plants</i> , 2019, 8, 392.	1.6	28

#	ARTICLE	IF	CITATIONS
6136	Large-scale phylogenomic analysis suggests three ancient superclades of the WUSCHEL-RELATED HOMEBOX transcription factor family in plants. <i>PLoS ONE</i> , 2019, 14, e0223521.	1.1	55
6137	Mapping benzimidazole resistance in trypanosomatids and exploring evolutionary histories of nitroreductases and ABCG transporter protein sequences. <i>Acta Tropica</i> , 2019, 200, 105161.	0.9	11
6138	The Eurasian steppe belt in time and space: Phylogeny and historical biogeography of the false flax (<i>Camelina</i> Crantz, <i>Camelineae</i> , <i>Brassicaceae</i>). <i>Flora: Morphology, Distribution, Functional Ecology of Plants</i> , 2019, 260, 151477.	0.6	22
6139	Convergent and parallel evolution in a voltage-gated sodium channel underlies TTX-resistance in the Greater Blue-ringed Octopus: <i>Hapalochlaena lunulata</i> . <i>Toxicon</i> , 2019, 170, 77-84.	0.8	18
6140	Phylogeny, origin and dispersal of <i>Saussurea</i> (<i>Asteraceae</i>) based on chloroplast genome data. <i>Molecular Phylogenetics and Evolution</i> , 2019, 141, 106613.	1.2	39
6141	Biogeographical, ecological, and phylogenetic analyses clarifying the evolutionary history of <i>Calibrachoa</i> in South American grasslands. <i>Molecular Phylogenetics and Evolution</i> , 2019, 141, 106614.	1.2	20
6142	The complete plastome of <i>Daphne laureola</i> L. (<i>Thymelaeaceae</i>). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3364-3365.	0.2	6
6143	Complex Evolutionary Origins of Specialized Metabolite Gene Cluster Diversity among the Plant Pathogenic Fungi of the <i>Fusarium graminearum</i> Species Complex. <i>Genome Biology and Evolution</i> , 2019, 11, 3106-3122.	1.1	24
6144	Genomic Analyses Identify Novel Molecular Signatures Specific for the <i>Caenorhabditis</i> and other Nematode Taxa Providing Novel Means for Genetic and Biochemical Studies. <i>Genes</i> , 2019, 10, 739.	1.0	2
6145	Novel Lineages of Oxymonad Flagellates from the Termite <i>Porotermes adamsoni</i> (<i>Stolotermitidae</i>): the Genera <i>Oxynympha</i> and <i>Termitimonas</i> . <i>Protist</i> , 2019, 170, 125683.	0.6	5
6146	Characterization of the complete plastome of medicinal plant <i>Saururus chinensis</i> (<i>Saururaceae</i>). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3206-3207.	0.2	2
6147	The complete chloroplast genome of <i>Salix psamaphila</i> , a desert shrub in northwest China. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3432-3433.	0.2	3
6148	Evolution of the visual sensory system in cichlid fishes from crater lake Barombi Mbo in Cameroon. <i>Molecular Ecology</i> , 2019, 28, 5010-5031.	2.0	29
6149	Origins and relationships of the Pleuronectoidei: Molecular and morphological analysis of living and fossil taxa. <i>Zoologica Scripta</i> , 2019, 48, 640-656.	0.7	13
6150	Comparative Mitochondrial Genome Analysis of Two Ectomycorrhizal Fungi (<i>Rhizopogon</i>) Reveals Dynamic Changes of Intron and Phylogenetic Relationships of the Subphylum Agaricomycotina. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5167.	1.8	65
6151	Phylogenomics in Cactaceae: A case study using the chollas sensu lato (<i>Cylindropuntia</i> spp.) <i>TJ ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50</i> <i>Journal of Botany</i> , 2019, 106, 1327-1345.	0.8	38
6152	Effects of taxon sampling and tree reconstruction methods on phylodiversity metrics. <i>Ecology and Evolution</i> , 2019, 9, 9479-9499.	0.8	23
6153	Population genetic structures of two ecologically distinct species <i>Betula platyphylla</i> and <i>B. Åermanii</i> inferred based on nuclear and chloroplast DNA markers. <i>Ecology and Evolution</i> , 2019, 9, 11406-11419.	0.8	1

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6154	The evolution of climate tolerance in conifer-feeding aphids in relation to their host's climatic niche. <i>Ecology and Evolution</i> , 2019, 9, 11657-11671.	0.8	7
6155	Genome Organization and Adaptive Potential of Archetypal Organophosphate Degrading <i>Sphingobium fuliginis</i> ATCC 27551. <i>Genome Biology and Evolution</i> , 2019, 11, 2557-2562.	1.1	12
6156	The Prevalence and Impact of Model Violations in Phylogenetic Analysis. <i>Genome Biology and Evolution</i> , 2019, 11, 3341-3352.	1.1	105
6157	Have Niche, Will Travel. New Means of Linking Diet and Ecomorphology Reveals Niche Conservatism in Freshwater Cottoid Fishes. <i>Integrative Organismal Biology</i> , 2019, 1, obz023.	0.9	11
6158	Complete mitochondrial genome of the super mealworm <i>Zophobas atratus</i> (Fab.) (Insecta: Coleoptera: Tj ETQq0 0,0rgBT /Overlock 10	0.2	18
6159	The complete plastid genome of <i>Magnolia omeiensis</i> (Magnoliaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1837-1838.	0.2	1
6160	The first complete chloroplast genome of <i>Alsophila costularis</i> (Cyatheaceae), a least concerned relict tree fern. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1897-1898.	0.2	2
6161	Complete mitochondrial genome sequence of <i>Emberiza pallasi</i> (Emberizidae: <i>Emberiza</i>). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2015-2016.	0.2	1
6162	The complete chloroplast genome of <i>Juniperus squamata</i> (Cupressaceae), a shrubby conifer from Asian Mountains. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2137-2139.	0.2	3
6163	Characteristic and phylogenetic analyses of chloroplast genome for an endangered species <i>Manglietia lucida</i> (Magnoliaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2285-2286.	0.2	0
6164	Analysis of <i>Poncirus polyandra</i> (Rutaceae) chloroplast genome and its phylogenetic implications. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2287-2288.	0.2	2
6165	Characterization of the complete chloroplast genome of <i>Amomum longiligulare</i> (Zingiberaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2431-2432.	0.2	3
6166	The complete chloroplast genome sequence of <i>Lycium ruthenicum</i> (Solanaceae), a traditional medicinal plant in China. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2495-2496.	0.2	1
6167	Characterization of the complete plastome of <i>Atriplex centralasiatica</i> (Chenopodiaceae), an annual halophytic herb. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2475-2476.	0.2	5
6168	Complete mitochondrial genome of <i>Capreolus pygargus</i> (Cervidae: Capreolinae), a protected and threatened species in China. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2469-2470.	0.2	1
6169	The complete plastid genome sequence of <i>Neopicrorhiza scrophulariiflora</i> (Plantaginaceae): an endangered species endemic to The Himalayas regions. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2504-2505.	0.2	1
6170	The complete chloroplast genome of <i>Epimedium sagittatum</i> (Sieb. Et Zucc.) Maxim. (Berberidaceae), a traditional Chinese herb. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2572-2573.	0.2	5
6171	Constraints on H_0 from WMAP and BAO Measurements*. <i>Communications in Theoretical Physics</i> , 2019, 71, 826.	1.1	20

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6172	Analytic Model and Assessment Framework for Data Quality Evaluation in State Grid. <i>Journal of Physics: Conference Series</i> , 2019, 1302, 022083.	0.3	1
6173	Excellent Rate Capability of NiCo ₂ O ₄ with Urchin-Like Nanostructure as Cathode for Asymmetric Supercapacitors. <i>IOP Conference Series: Earth and Environmental Science</i> , 2019, 281, 012038.	0.2	0
6174	Capacitive performance of carbon-based supercapacitors using sulfonated poly(ether ether ketone) membranes as separators: influences of casting solvents. <i>Materials Research Express</i> , 2019, 6, 115533.	0.8	2
6175	Genetic polymorphisms of ABCB1 (P-glycoprotein) as a covariate influencing daptomycin pharmacokinetics: a population analysis in patients with bone and joint infection. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 1012-1020.	1.3	12
6176	Inferring putative transmission clusters with Phydelity. <i>Virus Evolution</i> , 2019, 5, vez039.	2.2	18
6177	A new subfamily for a clade of opecoelids (Trematoda: Digenea) exploiting marine fishes as second-intermediate hosts, with the first report of opecoelid metacercariae from an elasmobranch. <i>Zoological Journal of the Linnean Society</i> , 0, , .	1.0	4
6178	The biodiversity benefit of native forests and mixed-species plantations over monoculture plantations. <i>Diversity and Distributions</i> , 2019, 25, 1721-1735.	1.9	50
6179	Contrasting Biogeographic Patterns of Bacterial and Archaeal Diversity in the Top- and Subsoils of Temperate Grasslands. <i>MSystems</i> , 2019, 4, .	1.7	24
6180	New perspectives on the plant PARP family: Arabidopsis PARP3 is inactive, and PARP1 exhibits predominant poly (ADP-ribose) polymerase activity in response to DNA damage. <i>BMC Plant Biology</i> , 2019, 19, 364.	1.6	24
6181	Effects of virtual reality-based planar motion exercises on upper extremity function, range of motion, and health-related quality of life: a multicenter, single-blinded, randomized, controlled pilot study. <i>Journal of NeuroEngineering and Rehabilitation</i> , 2019, 16, 122.	2.4	45
6182	A Chromosome-Scale Reference Assembly of a Tibetan Loach, <i>Triplophysa siluroides</i> . <i>Frontiers in Genetics</i> , 2019, 10, 991.	1.1	10
6183	The Complete Mitogenome of <i>Pyrrhocoris tibialis</i> (Hemiptera: Pyrrhocoridae) and Phylogenetic Implications. <i>Genes</i> , 2019, 10, 820.	1.0	8
6184	Generalized Hyers-Ulam Stability of the Pexider Functional Equation. <i>Mathematics</i> , 2019, 7, 280.	1.1	0
6185	Expression dynamics of autophagy-related genes in the cattle tick <i>Rhipicephalus microplus</i> during embryonic development and under increasing larval starvation. <i>Experimental and Applied Acarology</i> , 2019, 79, 255-266.	0.7	2
6186	Draft genome sequence data of <i>Cercospora kikuchii</i> , a causal agent of <i>Cercospora</i> leaf blight and purple seed stain of soybeans. <i>Data in Brief</i> , 2019, 27, 104693.	0.5	11
6187	Structural variation of the complete chloroplast genome and plastid phylogenomics of the genus <i>Asteropyrum</i> (Ranunculaceae). <i>Scientific Reports</i> , 2019, 9, 15285.	1.6	38
6188	The architecture of the <i>Plasmodiophora brassicae</i> nuclear and mitochondrial genomes. <i>Scientific Reports</i> , 2019, 9, 15753.	1.6	17
6189	Complete mitochondrial genome of the silkworm strain, Chilseongjam (<i>Bombyx mori</i>) (<i>Lepidoptera</i> : <i>Bombycidae</i>), with a unique larval body marking. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2853-2854.	0.2	2

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6190	The PATRIC Bioinformatics Resource Center: expanding data and analysis capabilities. <i>Nucleic Acids Research</i> , 2020, 48, D606-D612.	6.5	552
6191	DAY-LENGTH-DEPENDENT DELAYED-GREENING1, the Arabidopsis Homolog of the Cyanobacterial H ⁺ -Extrusion Protein, Is Essential for Chloroplast pH Regulation and Optimization of Non-Photochemical Quenching. <i>Plant and Cell Physiology</i> , 2019, 60, 2660-2671.	1.5	13
6192	Pleistocene glacial cycles drove lineage diversification and fusion in the Yosemite toad (<i>Anaxyrus</i>). <i>Trends in Ecology and Evolution</i> , 2019, 30, 101-110.	1.1	25
6193	Characteristics and Evolutionary Analysis of Photosynthetic Gene Clusters on Extrachromosomal Replicons: from Streamlined Plasmids to Chromids. <i>MSystems</i> , 2019, 4, .	1.7	13
6194	Comparison of chloroplast genomes of <i>Gynura</i> species: sequence variation, genome rearrangement and divergence studies. <i>BMC Genomics</i> , 2019, 20, 791.	1.2	8
6195	High-resolution mapping of tuberculosis transmission: Whole genome sequencing and phylogenetic modelling of a cohort from Valencia Region, Spain. <i>PLoS Medicine</i> , 2019, 16, e1002961.	3.9	62
6196	Molecular phylogenetic analyses show that <i>Amanita ovoidea</i> and <i>Amanita proxima</i> are distinct species and suggest their assignment to <i>Roanokenses</i> section. <i>Mycological Progress</i> , 2019, 18, 1275-1283.	0.5	4
6197	Landscape and Dynamics of Single Immune Cells in Hepatocellular Carcinoma. <i>Cell</i> , 2019, 179, 829-845.e20.	13.5	897
6198	The complete mitochondrial genome of <i>Apis mellifera unicolor</i> (Insecta: Hymenoptera: Apidae), the Malagasy honey bee. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3286-3287.	0.2	10
6199	Complete plastome sequence of <i>Tetrataenium Candicans</i> (tribe Tordylieae, Apiaceae): a medicinal plant. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3429-3431.	0.2	0
6200	What does mitogenomics tell us about the evolutionary history of the <i>Drosophila buzzatii</i> cluster (repleta group)? <i>PLoS ONE</i> , 2019, 14, e0220676.	1.1	12
6201	Freshwater Sordariomycetes. <i>Fungal Diversity</i> , 2019, 99, 451-660.	4.7	119
6202	Phylotranscriptomic analyses reveal asymmetrical gene duplication dynamics and signatures of ancient polyploidy in mints. <i>Genome Biology and Evolution</i> , 2019, 11, 3393-3408.	1.1	21
6203	Molecular phylogeny and divergence times of the genus <i>Hedysarum</i> (Fabaceae) with special reference to section <i>Multicaulia</i> in Southwest Asia. <i>Plant Systematics and Evolution</i> , 2019, 305, 1001-1017.	0.3	22
6204	Complete mitochondrial genome of <i>Prionailurus bengalensis</i> (Carnivora: Felidae), a protected species in China. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3072-3074.	0.2	1
6205	Successional trophic complexity and biogeographical structure of eukaryotic communities in waterworks' rapid sand filters. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	3
6206	Oral Microbiome Alterations Associated with Early Childhood Caries Highlight the Importance of Carbohydrate Metabolic Activities. <i>MSystems</i> , 2019, 4, .	1.7	56
6207	Phenotypic and genotypic characterization of clinical <i>Staphylococcus aureus</i> isolates from Kenya. <i>BMC Microbiology</i> , 2019, 19, 245.	1.3	19

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6208	Antimicrobial and antioxidant activities of endophytic fungi extracts isolated from <i>Carissa carandas</i> . <i>African Journal of Microbiology Research</i> , 2019, 13, 464-473.	0.4	4
6209	Molecular investigation of the natural transovarial transmission of tick-borne pathogens in Turkey. <i>Veterinary Parasitology</i> , 2019, 273, 97-104.	0.7	12
6210	The complete chloroplast genome sequence of <i>Abies chensiensis</i> (Pinaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3262-3263.	0.2	4
6211	The complete chloroplast genome of <i>Laurocerasus zippeliana</i> (Rosaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3264-3265.	0.2	1
6212	The complete chloroplast genome sequence of <i>Dendrobium zhenghuoense</i> (Orchidaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3326-3327.	0.2	0
6213	Characterization of the complete plastome of <i>Ophrys aveyronensis</i> , a Euro-Mediterranean orchid with an intriguing disjunct geographic distribution. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3256-3257.	0.2	8
6214	Complete chloroplast genome of an endangered endemic tree, <i>Handeliodendron bodinieri</i> (level.) rehd. (Sapindaceae) from karst forests of southwest China. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3272-3273.	0.2	1
6215	Characterization of the complete chloroplast genome of medicinal tea tree (<i>Melaleuca alternifolia</i>). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3307-3308.	0.2	2
6216	Complete mitochondrial genome of the silver striped skipper, <i>Leptalina unicolor</i> (Lepidoptera: Pieridae). <i>GenBank/Overlock 10.1101/2019.07.06.256000</i>	0.2	6
6217	Complete plastid genome of <i>Dendrobium naungmungense</i> (Orchidaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3423-3424.	0.2	0
6218	Phylogenetic revision of Gymnotidae (Teleostei: Gymnotiformes), with descriptions of six subgenera. <i>PLoS ONE</i> , 2019, 14, e0224599.	1.1	8
6219	Microbial metabolisms in an abyssal ferromanganese crust from the Takuyo-Daigo Seamount as revealed by metagenomics. <i>PLoS ONE</i> , 2019, 14, e0224888.	1.1	14
6220	The Family Placement of <i>Cyrtandromoea</i> . <i>Systematic Botany</i> , 2019, 44, 616-630.	0.2	7
6222	A comprehensive genome variation map of melon identifies multiple domestication events and loci influencing agronomic traits. <i>Nature Genetics</i> , 2019, 51, 1607-1615.	9.4	153
6223	The complete plastome of <i>Gymnotheca chinensis</i> (Saururaceae) and its phylogenetic analysis. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3202-3203.	0.2	0
6224	Pathogen-induced activation of disease-suppressive functions in the endophytic root microbiome. <i>Science</i> , 2019, 366, 606-612.	6.0	621
6225	Evidence for Adaptive Selection in the Mitogenome of a Mesoparasitic Monogenean Flatworm <i>Enterogyrus malmbergi</i> . <i>Genes</i> , 2019, 10, 863.	1.0	4
6226	Population-Specific Selection on Standing Variation Generated by Lateral Gene Transfers in a Grass. <i>Current Biology</i> , 2019, 29, 3921-3927.e5.	1.8	26

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6227	Cryptic diversity of a widespread global pathogen reveals expanded threats to amphibian conservation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 20382-20387.	3.3	86
6228	New species of <i>Galene</i> and <i>Howella</i> gen. nov. (Halymeniaceae, Rhodophyta) from the mesophotic zone off Bermuda. <i>Phycologia</i> , 2019, 58, 690-697.	0.6	10
6229	Complete chloroplast genome of <i>Lamium takesimense</i> Nakai (Lamiaceae): an endemic species in South Korea. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3216-3217.	0.2	0
6230	Gene Composition as a Potential Barrier to Large Recombinations in the Bacterial Pathogen <i>Klebsiella pneumoniae</i> . <i>Genome Biology and Evolution</i> , 2019, 11, 3240-3251.	1.1	18
6231	Chromosomal-level reference genome of Chinese peacock butterfly (<i>Papilio bianor</i>) based on third-generation DNA sequencing and Hi-C analysis. <i>GigaScience</i> , 2019, 8, .	3.3	26
6232	Genome-scale data resolve ancestral rock-inhabiting lifestyle in Dothideomycetes (Ascomycota). <i>IMA Fungus</i> , 2019, 10, 19.	1.7	17
6233	Nanopore Sequencing and De Novo Assembly of a Black-Shelled Pacific Oyster (<i>Crassostrea gigas</i>) Genome. <i>Frontiers in Genetics</i> , 2019, 10, 1211.	1.1	33
6234	Conservation Analysis of B-Cell Allergen Epitopes to Predict Clinical Cross-Reactivity Between Shellfish and Inhalant Invertebrate Allergens. <i>Frontiers in Immunology</i> , 2019, 10, 2676.	2.2	42
6236	Attenuated Fgf Signaling Underlies the Forelimb Heterochrony in the Emu <i>Dromaius novaehollandiae</i> . <i>Current Biology</i> , 2019, 29, 3681-3691.e5.	1.8	24
6237	<i>Opegrapha multipuncta</i> and <i>Schismatomma quercicola</i> (Arthoniomycetes) belong to the Lecanoromycetes. <i>Lichenologist</i> , 2019, 51, 395-405.	0.5	4
6238	<i>Arctoparmelia collatolica</i> (Parmeliaceae), a new species from Siberia, Russia. <i>Lichenologist</i> , 2019, 51, 407-417.	0.5	1
6239	Complete chloroplast genome of <i>Isoetes sinensis</i> , an endemic fern in China. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3276-3277.	0.2	2
6240	The mitochondrial genome of the Carniolan honey bee, <i>Apis mellifera carnica</i> (Insecta: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 262	0.2	5
6241	Characterization of the complete chloroplast genome of black soybeans, <i>Glycine max</i> (L.) Merr. (legume). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3309-3311.	0.2	0
6242	Characterization of the complete plastome of <i>Elymus tangutorum</i> (Poaceae: Triticeae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3356-3357.	0.2	2
6243	The complete chloroplast genome sequence of <i>Goodyera foliosa</i> (Orchidaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3477-3478.	0.2	2
6244	The complete chloroplast genome sequence of <i>Euscaphis japonica</i> (Staphyleaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3484-3485.	0.2	6
6245	Characterization of the complete chloroplast genome of <i>Sinosenecio oldhamianus</i> (Compositae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3496-3497.	0.2	2

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6246	Characterization of the complete chloroplast genome of <i>Saussurea integrifolia</i> (Compositae). Mitochondrial DNA Part B: Resources, 2019, 4, 3502-3503.	0.2	1
6247	An assessment of <i>Raphitoma</i> and allied genera (Neogastropoda: Raphitomidae). Journal of Molluscan Studies, 2019, 85, 413-424.	0.4	5
6248	First record of <i>Larsonella pumilus</i> (Teleostei: Gobiidae) from Japan, with phylogenetic placement of the genus <i>Larsonella</i> . Zootaxa, 2019, 4695, zootaxa.4695.4.4.	0.2	2
6249	Differences in Applied Redox Potential on Cathodes Enrich for Diverse Electrochemically Active Microbial Isolates From a Marine Sediment. Frontiers in Microbiology, 2019, 10, 1979.	1.5	24
6250	Positive Selection in Bifidobacterium Genes Drives Species-Specific Host-Bacteria Communication. Frontiers in Microbiology, 2019, 10, 2374.	1.5	5
6251	Evolution of the Genes Encoding Effector Candidates Within Multiple Pathotypes of <i>Magnaporthe oryzae</i> . Frontiers in Microbiology, 2019, 10, 2575.	1.5	31
6252	Can biochemical phenotype, obtained from herbarium samples, help taxonomic decisions? A case study using Gentianaceae. Taxon, 2019, 68, 771-782.	0.4	6
6253	The complete chloroplast genome of <i>Impatiens uliginosa</i> Franch., an endemic species in Southwest China. Mitochondrial DNA Part B: Resources, 2019, 4, 3846-3847.	0.2	3
6254	Mitochondrial genome in <i>Hypsizygus marmoreus</i> and its evolution in Dikarya. BMC Genomics, 2019, 20, 765.	1.2	22
6255	An Emerging Pathogen from Rotted Chestnut in China: <i>Gnomoniopsis daii</i> sp. nov.. Forests, 2019, 10, 1016.	0.9	23
6256	Phylogeny and biogeography of <i>Polygala</i> (Polygalaceae). Taxon, 2019, 68, 673-691.	0.4	19
6257	Latitudinal gradient of cyanobacterial diversity in tidal flats. PLoS ONE, 2019, 14, e0224444.	1.1	4
6258	Fine tuning the circumscription of <i>Fridericia</i> (Bignoniaceae, Bignoniaceae). Taxon, 2019, 68, 751-770.	0.4	17
6259	Genomes of Subaerial Zygnematophyceae Provide Insights into Land Plant Evolution. Cell, 2019, 179, 1057-1067.e14.	13.5	320
6260	Distinct Polysaccharide Utilization Profiles of Human Intestinal <i>Prevotella copri</i> Isolates. Cell Host and Microbe, 2019, 26, 680-690.e5.	5.1	115
6261	Genome-wide identification of ABC transporters in monogeneans. Molecular and Biochemical Parasitology, 2019, 234, 111234.	0.5	9
6262	Expansion of LINEs and species-specific DNA repeats drives genome expansion in Asian Gypsy Moths. Scientific Reports, 2019, 9, 16413.	1.6	8
6263	Deep Instability in the Phylogenetic Backbone of Heteroptera is Only Partly Overcome by Transcriptome-Based Phylogenomics. Insect Systematics and Diversity, 2019, 3, .	0.7	6

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6264	Adaptive Radiation Genomics of Two Ecologically Divergent Hawaiian Honeycreepers: The <i>Akaiapa</i> and the <i>Amakihi</i> . <i>Journal of Heredity</i> , 2020, 111, 21-32.	1.0	6
6265	Characterization of nAChRs in <i>Nematostella vectensis</i> supports neuronal and non-neuronal roles in the cnidarian-bilaterian common ancestor. <i>EvoDevo</i> , 2019, 10, 27.	1.3	18
6266	Molecular mechanism of azithromycin resistance among typhoidal <i>Salmonella</i> strains in Bangladesh identified through passive pediatric surveillance. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007868.	1.3	100
6267	Molecular epidemiological characteristics of dengue virus carried by 34 patients in Guangzhou in 2018. <i>PLoS ONE</i> , 2019, 14, e0224676.	1.1	2
6268	Molecular Phylogeny of Gobies (Teleostei, Gobiidae) from Iranian Water Bodies with a New Record. <i>Russian Journal of Marine Biology</i> , 2019, 45, 385-392.	0.2	0
6269	A new species of the coral associated barnacle (Thoracica: Pyrgomatidae: <i>Pyrgoma</i>) from a deep-sea oculinid coral in New Caledonian waters. <i>Zootaxa</i> , 2019, 4695, zootaxa.4695.1.2.	0.2	1
6270	First record of translocation in Culicidae (Diptera) mitogenomes: evidence from the tribe Sabethini. <i>BMC Genomics</i> , 2019, 20, 721.	1.2	16
6271	Microbial sulfidogenesis of arsenic in naturally contaminated wetland soil. <i>Geochimica Et Cosmochimica Acta</i> , 2019, 267, 33-50.	1.6	16
6272	An interbacterial toxin inhibits target cell growth by synthesizing (p)ppApp. <i>Nature</i> , 2019, 575, 674-678.	13.7	118
6273	Tissue-specific expression profiles and positive selection analysis in the tree swallow (<i>Tachycineta</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	1.6	39
6274	Characterization of the complete chloroplast genome of <i>Leptochilus decurrens</i> (Polypodiaceae), a least concern folk medicinal fern. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3346-3347.	0.2	3
6275	Complete chloroplast genome of the tiny marine diatom <i>Nanofrustulum shiloi</i> (Bacillariophyta) from the Adriatic Sea. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3374-3376.	0.2	5
6276	The complete plastome of <i>Ctenolophon englerianus</i> Mildbr. (Ctenolophonaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3379-3380.	0.2	1
6277	The complete chloroplast genome sequence of <i>Kandelia obovata</i> (Rhizophoraceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3494-3495.	0.2	4
6278	Historical allopatry and secondary contact or primary intergradation in the Puerto Rican crested anole, <i>Anolis cristatellus</i> , on Vieques Island in the Caribbean. <i>Biological Journal of the Linnean Society</i> , 0, , .	0.7	1
6279	Systematic revision of Mexican threatened tarantulas <i>Brachypelma</i> (Araneae: Theraphosidae:) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	1.0	5
6280	<i>Molecular systematics of the heteronemertean genus <i>Dushia</i> (Nemertea,)</i> Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 complex comb. nov. <i>Zootaxa</i> , 2019, 4691, 333-358.	0.2	7
6281	Host-range shift of H3N8 canine influenza virus: a phylodynamic analysis of its origin and adaptation from equine to canine host. <i>Veterinary Research</i> , 2019, 50, 87.	1.1	9

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6282	<i>Artemisia baxoiensis</i> (Asteraceae: Anthemideae), a Distinctive New Species from Xizang, China. <i>Systematic Botany</i> , 2019, 44, 424-432.	0.2	4
6283	Comparative Genomics of <i>Pandoraea</i> , a Genus Enriched in Xenobiotic Biodegradation and Metabolism. <i>Frontiers in Microbiology</i> , 2019, 10, 2556.	1.5	85
6284	Crustose Calicioid Lichens and Fungi in Mountain Cloud Forests of Tanzania. <i>Microorganisms</i> , 2019, 7, 491.	1.6	3
6285	A tale of worldwide success: Behind the scenes of <i>Carex</i> (Cyperaceae) biogeography and diversification. <i>Journal of Systematics and Evolution</i> , 2019, 57, 695-718.	1.6	70
6286	The effect of alignment uncertainty, substitution models and priors in building and dating the mammal tree of life. <i>BMC Evolutionary Biology</i> , 2019, 19, 203.	3.2	11
6287	A Simple and Robust Statistical Method to Define Genetic Relatedness of Samples Related to Outbreaks at the Genomic Scale – Application to Retrospective Salmonella Foodborne Outbreak Investigations. <i>Frontiers in Microbiology</i> , 2019, 10, 2413.	1.5	17
6288	Evolution and networks in ancient and widespread symbioses between Mucoromycotina and liverworts. <i>Mycorrhiza</i> , 2019, 29, 551-565.	1.3	20
6289	Evolutionary basis of high-frequency hearing in the cochleae of echolocators revealed by comparative genomics. <i>Genome Biology and Evolution</i> , 2020, 12, 3740-3753.	1.1	10
6290	<i>Sieverdingia</i> gen. nov., <i>S. tortuosa</i> comb. nov., and <i>Diversispora peloponnesiaca</i> sp. nov. in the Diversisporaceae (Glomeromycota). <i>Mycological Progress</i> , 2019, 18, 1363-1382.	0.5	14
6291	Evaluation of in vitro alpha-glucosidase inhibitory, antimicrobial, and cytotoxic activities of secondary metabolites from the endophytic fungus, <i>Nigrospora sphaerica</i> , isolated from <i>Helianthus annuus</i> . <i>Annals of Microbiology</i> , 2019, 69, 1397-1406.	1.1	8
6292	The wax gourd genomes offer insights into the genetic diversity and ancestral cucurbit karyotype. <i>Nature Communications</i> , 2019, 10, 5158.	5.8	94
6293	Mutations in Glucan, Water Dikinase Affect Starch Degradation and Gametophore Development in the Moss <i>Physcomitrella patens</i> . <i>Scientific Reports</i> , 2019, 9, 15114.	1.6	7
6294	Enhancement of Hippocampal Plasticity by Physical Exercise as a Polypill for Stress and Depression: A Review. <i>CNS and Neurological Disorders - Drug Targets</i> , 2019, 18, 294-306.	0.8	17
6295	Towards the Complete Goat Pan-Genome by Recovering Missing Genomic Segments From the Reference Genome. <i>Frontiers in Genetics</i> , 2019, 10, 1169.	1.1	29
6296	<i>Pleurotus eryngii</i> Genomes Reveal Evolution and Adaptation to the Gobi Desert Environment. <i>Frontiers in Microbiology</i> , 2019, 10, 2024.	1.5	19
6297	Evolutionary Conservation of the Orchid MYB Transcription Factors DIV, RAD, and DRIF. <i>Frontiers in Plant Science</i> , 2019, 10, 1359.	1.7	17
6298	The complete chloroplast genome of <i>Saxifraga sinomontana</i> (Saxifragaceae) and comparative analysis with other Saxifragaceae species. <i>Revista Brasileira De Botanica</i> , 2019, 42, 601-611.	0.5	7
6299	An identity crisis in the Indo-Pacific: molecular exploration of the genus <i>Koseiria</i> (Digenea: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	1.3	8

#	ARTICLE	IF	CITATIONS
6300	Complete mitochondrial genome of a leaf-mining beetle, <i>Argopistes tsekooni</i> (Coleoptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf,50 742 Td	0.2	2
6301	The complete chloroplast genome of <i>Livaria macrophylla</i> (Annonaceae). Mitochondrial DNA Part B: Resources, 2019, 4, 3012-3013.	0.2	1
6302	Complete plastome of <i>Houttuynia cordata</i> (Saururaceae), a medicinal and edible plant. Mitochondrial DNA Part B: Resources, 2019, 4, 3208-3209.	0.2	4
6303	The complete mitochondrial genome of <i>Gruberia lanceolata</i> (Gruber, 1884) Kahl, 1932 (Ciliophora: Heterotrichea). Mitochondrial DNA Part B: Resources, 2019, 4, 3443-3445.	0.2	3
6304	Extended studies of interspecific relationships in <i>Daucus</i> (Apiaceae) using DNA sequences from ten nuclear orthologues. Botanical Journal of the Linnean Society, 2019, 191, 164-187.	0.8	3
6305	Traces of Imidacloprid Induce Hormesis as a Stimulatory Conditioned Response of Sweetpotato Whitefly (Hemiptera: Aleyrodidae). Environmental Entomology, 2019, 48, 1418-1424.	0.7	3
6306	Incorporating phylogenetic metrics to microbial co-occurrence networks based on amplicon sequences to discern community assembly processes. Molecular Ecology Resources, 2019, 19, 1552-1564.	2.2	41
6307	Molecular and morphological evaluation of <i>Meconopsis georgei</i> and <i>M. castanea</i> in southwest China. Nordic Journal of Botany, 2019, 37, .	0.2	1
6308	Molecular epidemiological study of enterovirus D68 in hospitalised children in Hong Kong in 2014-2015 and their complete coding sequences. BMJ Open Respiratory Research, 2019, 6, e000437.	1.2	2
6309	Fluctuations in Fabaceae mitochondrial genome size and content are both ancient and recent. BMC Plant Biology, 2019, 19, 448.	1.6	32
6310	Duplicate divergence of two bacterial small heat shock proteins reduces the demand for Hsp70 in refolding of substrates. PLoS Genetics, 2019, 15, e1008479.	1.5	22
6311	Hinge Region in DNA Packaging Terminase pUL15 of Herpes Simplex Virus: A Potential Allosteric Target for Antiviral Drugs. Biomolecules, 2019, 9, 603.	1.8	5
6312	Transcriptomic Analysis Reveals the Roles of Detoxification Systems in Response to Mercury in <i>Chromera velia</i> . Biomolecules, 2019, 9, 647.	1.8	21
6313	A Multireference-Based Whole Genome Assembly for the Obligate Ant-Following Antbird, <i>Rhegmatorhina melanosticta</i> (Thamnophilidae). Diversity, 2019, 11, 144.	0.7	13
6314	Genetic Data Suggest Multiple Introductions of the Lionfish (<i>Pterois miles</i>) into the Mediterranean Sea. Diversity, 2019, 11, 149.	0.7	25
6315	Identification of a novel RIG-I isoform and its truncating variant in Japanese eel, <i>Anguilla japonica</i> . Fish and Shellfish Immunology, 2019, 94, 373-380.	1.6	9
6316	Puma genomes from North and South America provide insights into the genomic consequences of inbreeding. Nature Communications, 2019, 10, 4769.	5.8	55
6317	<i>Chloris circumfontinalis</i> (Poaceae): a recently discovered species from the saline scalds surrounding artesian springs in north-eastern Australia. Australian Systematic Botany, 2019, , .	0.3	0

#	ARTICLE	IF	CITATIONS
6318	Characterization of the complete plastid genome of an endangered species <i>Fortunearia sinensis</i> (Hamamelidaceae). Mitochondrial DNA Part B: Resources, 2019, 4, 1432-1434.	0.2	1
6319	Characterization of the plastid genome of the monotypic genus <i>Bryocarpum</i> (Primulaceae). Mitochondrial DNA Part B: Resources, 2019, 4, 3122-3123.	0.2	0
6320	Complete mitochondrial genome of the sea star <i>Archaster typicus</i> (Asteroidea: Archasteridae). Mitochondrial DNA Part B: Resources, 2019, 4, 3130-3132.	0.2	8
6321	The complete chloroplast genome of <i>Eichhornia crassipes</i> (Pontederiaceae) and phylogeny of commelinids. Mitochondrial DNA Part B: Resources, 2019, 4, 3186-3187.	0.2	4
6322	Characterization of the whole plastome of <i>Dipentodon Sinicus</i> (Dipentodontaceae). Mitochondrial DNA Part B: Resources, 2019, 4, 3149-3150.	0.2	0
6323	The complete chloroplast genome sequence of <i>Gelidocalamus xunwuensis</i> (Bambusoideae: Tj ETQq1 1 0.784314 rgBT /Overl... 3352-3353.	0.2	5
6324	Off-target capture data, endosymbiont genes and morphology reveal a relict lineage that is sister to all other singing cicadas. Biological Journal of the Linnean Society, 2019, 128, 865-886.	0.7	27
6325	Successful Invasions of Short Internally Deleted Elements (SIDs) and Its Partner CR1 in Lepidoptera Insects. Genome Biology and Evolution, 2019, 11, 2505-2516.	1.1	0
6326	Phylogenomic Analysis Reveals the Evolutionary Route of Resistant Genes in <i>Staphylococcus aureus</i> . Genome Biology and Evolution, 2019, 11, 2917-2926.	1.1	21
6327	Three-Dimensional Numerical Study of Particle Trajectory in Particle Charge and Size Analyzer Considering the Effects of System Parameters. IEEE Access, 2019, 7, 138136-138150.	2.6	0
6328	Data Distribution for Phylogenetic Inference with Site Repeats via Judicious Hypergraph Partitioning., 2019, , .		0
6329	Phylogeography of sand-burrowing amphipods (Haustoriidae) supports an ancient suture zone in the Gulf of Mexico. Journal of Biogeography, 2019, 46, 2532-2547.	1.4	8
6330	Contrasting scales of local persistence between monsoonal and arid biomes in closely related, low-dispersal vertebrates. Journal of Biogeography, 2019, 46, 2506-2519.	1.4	9
6331	Geographic range and habitat reconstructions shed light on palaeotropical intercontinental disjunction and regional diversification patterns in <i>Artabotrys</i> (Annonaceae). Journal of Biogeography, 2019, 46, 2690-2705.	1.4	11
6332	Reclustering the cluster flies (Diptera: Oestroidea, Polleniidae). Systematic Entomology, 2019, 44, 957-972.	1.7	24
6333	Total-evidence phylogeny of the owlflies (Neuroptera, Ascalaphidae) supports a new higher-level classification. Zoologica Scripta, 2019, 48, 761-782.	0.7	16
6334	Emergence of an NDM-5-Producing Hypervirulent <i>Klebsiella pneumoniae</i> Sequence Type 35 Strain with Chromosomal Integration of an Integrative and Conjugative Element, ICE Kp1. Antimicrobial Agents and Chemotherapy, 2019, 64, .	1.4	18
6335	Genomic and metabolic differences between <i>Pseudomonas putida</i> populations inhabiting sugarcane rhizosphere or bulk soil. PLoS ONE, 2019, 14, e0223269.	1.1	9

#	ARTICLE	IF	CITATIONS
6336	Phylogenomics Yields New Insight Into Relationships Within Vernonieae (Asteraceae). <i>Frontiers in Plant Science</i> , 2019, 10, 1224.	1.7	22
6337	Complete Chloroplast Genomes of <i>Ampelopsis humulifolia</i> and <i>Ampelopsis japonica</i> : Molecular Structure, Comparative Analysis, and Phylogenetic Analysis. <i>Plants</i> , 2019, 8, 410.	1.6	25
6338	How to build distylous flowers: comparative floral development and evolution of distylous species across the angiosperms. <i>American Journal of Botany</i> , 2019, 106, 1285-1299.	0.8	1
6339	Molecular phylogeny of the large South American genus <i>Eriosyce</i> (Notocactaceae, Cactaceae): Generic delimitation and proposed changes in infrageneric and species ranks. <i>Taxon</i> , 2019, 68, 557-573.	0.4	13
6340	Reinstatement and revision of the genus <i>Adelmeria</i> (Zingiberaceae) endemic to the Philippines. <i>Taxon</i> , 2019, 68, 499-521.	0.4	6
6341	Molecular phylogeny and taxonomic synopsis of the angraecoid genus <i>Ypsilopus</i> (Orchidaceae.) <i>Tj ETQq1 1 0.784314 rgBT /Overlock</i>	0.4	6
6342	Genomic insight into species diversification in a mountainous biodiversity hotspot. <i>Journal of Systematics and Evolution</i> , 2019, 57, 633-645.	1.6	25
6343	Massive Gene Flux Drives Genome Diversity between Sympatric <i>Streptomyces</i> Conspecifics. <i>MBio</i> , 2019, 10, .	1.8	41
6344	Genomic Variation among Strains of <i>Crithidia bombi</i> and <i>C. expoeiki</i> . <i>MSphere</i> , 2019, 4, .	1.3	7
6345	<i>Ganoderma shanxiense</i> , a new species from northern China based on morphological and molecular evidence. <i>Phytotaxa</i> , 2019, 406, 129-136.	0.1	9
6346	<i>Pennellia yalaensis</i> (Brassicaceae: Halimolobeae), a New Species from the Andes of Northern Argentina. <i>Systematic Botany</i> , 2019, 44, 355-362.	0.2	2
6347	Genome-Wide Analysis of NAC Gene Family in <i>Betula pendula</i> . <i>Forests</i> , 2019, 10, 741.	0.9	44
6348	Cytochrome-C Oxidase I Gene-Based Genetic Divergence and Molecular Phylogeny Among the Species of Fish Genus <i>Channa</i> . <i>Proceedings of the National Academy of Sciences India Section B - Biological Sciences</i> , 2019, 89, 1455-1463.	0.4	4
6349	Molecular systematics of the arctiine tribe Syntomini (Lepidoptera, Erebidae). <i>Systematic Entomology</i> , 2019, 44, 624-637.	1.7	9
6350	Phylogenetic re-evaluation of <i>Thielavia</i> with the introduction of a new family <i>Podosporeaceae</i> . <i>Studies in Mycology</i> , 2019, 93, 155-252.	4.5	50
6351	Complete sequence of wild <i>Physalis philadelphica</i> chloroplast genome. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3295-3297.	0.2	6
6352	The Analysis of Resistivity Characteristics and Mineral Composition of Qinghai Meteorolite. <i>IOP Conference Series: Earth and Environmental Science</i> , 2019, 310, 032004.	0.2	0
6353	Repeated evolution of bacteriocytes in lygaeoid stinkbugs. <i>Environmental Microbiology</i> , 2019, 21, 4378-4394.	1.8	18

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6354	Genetic diversity of primate strongylid nematodes: Do sympatric nonhuman primates and humans share their strongylid worms?. <i>Molecular Ecology</i> , 2019, 28, 4786-4797.	2.0	11
6355	<p><p>A new species of rock-dwelling gecko (Gekkonidae: Gehyra) from the Mt Surprise region of northern Queensland, Australia </p>. <i>Zootaxa</i>, 2019, 4688, 503-518.</p>	0.2	0
6356	The RNA-binding ubiquitin ligase MKRN1 functions in ribosome-associated quality control of poly(A) translation. <i>Genome Biology</i> , 2019, 20, 216.	3.8	29
6357	Hidden biodiversity revealed by integrated morphology and genetic species delimitation of spring dwelling water mite species (Acari, Parasitengona: Hydrachnidia). <i>Parasites and Vectors</i> , 2019, 12, 492.	1.0	24
6358	Remnants of ancestral larval eyes in an eyeless mollusk? Molecular characterization of photoreceptors in the scaphopod <i>Antalis entalis</i> . <i>EvoDevo</i> , 2019, 10, 25.	1.3	3
6359	Comparative Genomic and Phylogenomic Analyses Clarify Relationships Within and Between <i>Bacillus cereus</i> and <i>Bacillus thuringiensis</i> : Proposal for the Recognition of Two <i>Bacillus thuringiensis</i> Genomovars. <i>Frontiers in Microbiology</i> , 2019, 10, 1978.	1.5	33
6360	Phylogeny of the gall midges (Diptera, Cecidomyiidae, Cecidomyiinae): Systematics, evolution of feeding modes and diversification rates. <i>Molecular Phylogenetics and Evolution</i> , 2019, 140, 106602.	1.2	33
6361	Six new epibiotic <i>Proschkinia</i> (Bacillariophyta) species and new insights into the genus phylogeny. <i>European Journal of Phycology</i> , 2019, 54, 609-631.	0.9	17
6362	Mitochondrial genome of <i>Murina shuipuensis</i> (Chiroptera: Vespertilionidae) from Shuifu Village, Guizhou, China (type locality). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2588-2590.	0.2	2
6363	Bioinformatics analysis of diversity in bacterial glycan chain-termination chemistry and organization of carbohydrate-binding modules linked to ABC transporters. <i>Glycobiology</i> , 2019, 29, 822-838.	1.3	5
6364	Origin and Evolution of Diploid and Allopolyploid <i>Camelina</i> Genomes was Accompanied by Chromosome Shattering. <i>Plant Cell</i> , 2019, 31, tpc.00366.2019.	3.1	61
6365	An integrated pathway for building regional phylogenies for ecological studies. <i>Global Ecology and Biogeography</i> , 2019, 28, 1899-1911.	2.7	9
6366	Detection and Molecular Characterization of Novel dsRNA Viruses Related to the Totiviridae Family in <i>Umbelopsis ramanniana</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 249.	1.8	9
6367	Phylogenetic Analysis of Multi-Drug Resistant <i>Klebsiella pneumoniae</i> Strains From Duodenoscope Biofilm: Microbiological Surveillance and Reprocessing Improvements for Infection Prevention. <i>Frontiers in Public Health</i> , 2019, 7, 219.	1.3	14
6368	Ophiostomatoid fungi associated with the spruce bark beetle <i>Ips typographus</i> , including 11 new species from China. <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2019, 42, 50-74.	1.6	28
6369	Evaluating methodologies for species delimitation: the mismatch between phenotypes and genotypes in lichenized fungi (<i>Bryoria</i> sect. <i>Implexae</i> , <i>Parmeliaceae</i>). <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2019, 42, 75-100.	1.6	44
6370	Re-evaluation of <i>Mycoleptodiscus</i> species and morphologically similar fungi. <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2019, 42, 205-227.	1.6	37
6371	Butterfly Mimicry Polymorphisms Highlight Phylogenetic Limits of Gene Reuse in the Evolution of Diverse Adaptations. <i>Molecular Biology and Evolution</i> , 2019, 36, 2842-2853.	3.5	30

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6372	The discovery of Rock Geckos (<i>Cnemaspis</i>) Strauch, 1887 (Squamata: Gekkonidae) in the Tanintharyi Region, Myanmar with the description of two new species . <i>Zootaxa</i> , 2019, 4661, 40-64.	0.2	21
6373	Old World and New World Phasmatodea: Phylogenomics Resolve the Evolutionary History of Stick and Leaf Insects. <i>Frontiers in Ecology and Evolution</i> , 2019, 7, .	1.1	80
6374	A new species of tree snake (<i>Dipsadoboa</i> , Serpentes: Colubridae) from "sky island"™ forests in northern Mozambique, with notes on other members of the <i>Dipsadoboa wernerii</i> group. <i>Zootaxa</i> , 2019, 4646, zootaxa.4646.3.6.	0.2	6
6375	Chance, luck and a fortunate finding: a new species of watersnake of the genus <i>Helicops</i> Wagler, 1828 (Serpentes: Xenodontinae), from the Brazilian Pantanal wetlands. <i>Zootaxa</i> , 2019, 4651, 445-470.	0.2	6
6376	Why the monophyly of Nymphaeaceae currently remains indeterminate: an assessment based on gene-wise plastid phylogenomics. <i>Plant Systematics and Evolution</i> , 2019, 305, 827-836.	0.3	13
6377	Evolution and Genetic Diversity of Porcine Circovirus 3 in China. <i>Viruses</i> , 2019, 11, 786.	1.5	19
6378	Defining a Core Genome for the Herpesvirales and Exploring their Evolutionary Relationship with the Caudovirales. <i>Scientific Reports</i> , 2019, 9, 11342.	1.6	8
6379	The specific status of <i>Melastoma kudoii</i> (Melastomataceae, Melastomeae). , 2019, 60, 5.		3
6380	New genus and species record of reef coral <i>Micromussa amakusensis</i> in the southern South China Sea. <i>Marine Biodiversity Records</i> , 2019, 12, .	1.2	6
6381	Travel Surveillance and Genomics Uncover a Hidden Zika Outbreak during the Waning Epidemic. <i>Cell</i> , 2019, 178, 1057-1071.e11.	13.5	68
6382	<i>Hygrocybe pseudoacutoconica</i> (Hygrocybeae, Hygrocyboideae, Hygrophoraceae), a new species from a South China Sea island. <i>Phytotaxa</i> , 2019, 400, 23.	0.1	1
6383	<i>Podonectria sichuanensis</i> , a potentially mycopathogenic fungus from Sichuan Province in China. <i>Phytotaxa</i> , 2019, 402, 219.	0.1	5
6384	Processive Recoding and Metazoan Evolution of Selenoprotein P: Up to 132 UGAs in Molluscs. <i>Journal of Molecular Biology</i> , 2019, 431, 4381-4407.	2.0	18
6385	Complete chloroplast genome sequences of four <i>Allium</i> species: comparative and phylogenetic analyses. <i>Scientific Reports</i> , 2019, 9, 12250.	1.6	71
6386	Genome-Wide Reinforcement of DNA Methylation Occurs during Somatic Embryogenesis in Soybean. <i>Plant Cell</i> , 2019, 31, 2315-2331.	3.1	55
6387	<i>Acricotopus</i> indet. morphotype <i>incurvatus</i> : Description and genetics of a new Orthocladinae (Diptera: Chironomidae) larval morphotype from the Tibetan Plateau. <i>Zootaxa</i> , 2019, 4656, zootaxa.4656.3.10.	0.2	6
6388	TreeCluster: Clustering biological sequences using phylogenetic trees. <i>PLoS ONE</i> , 2019, 14, e0221068.	1.1	99
6389	Whole-Genome Sequencing of <i>Salmonella</i> Mississippi and Typhimurium Definitive Type 160, Australia and New Zealand. <i>Emerging Infectious Diseases</i> , 2019, 25, 1690-1697.	2.0	10

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6390	The first two complete mitochondrial genome of <i>Dacus bivittatus</i> and <i>Dacus ciliatus</i> (Diptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 747 International Journal of Biological Macromolecules, 2019, 140, 469-476.	3.6	5
6391	Do mosses really exhibit so large distribution ranges? Insights from the integrative taxonomic study of the <i>Lewinskya affinis</i> complex (Orthotrichaceae, Bryopsida). <i>Molecular Phylogenetics and Evolution</i> , 2019, 140, 106598.	1.2	23
6392	Baltic Sea methanogens compete with acetogens for electrons from metallic iron. <i>ISME Journal</i> , 2019, 13, 3011-3023.	4.4	45
6393	Niche differentiation among annually recurrent coastal Marine Group II Euryarchaeota. <i>ISME Journal</i> , 2019, 13, 3024-3036.	4.4	41
6394	Mitochondrial genomes of the bird genus <i>Piranga</i> : rates of sequence evolution, and discordance between mitochondrial and nuclear markers. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2566-2569.	0.2	7
6395	Characterization and genetic analysis of the complete chloroplast genome of <i>Schisandra chinensis</i> (Magnoliaceae: <i>Schisandra</i>), an herbal medicine from China. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2428-2430.	0.2	1
6396	The complete chloroplast genome sequence of <i>Quercus gilva</i> (Fagaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2493-2494.	0.2	6
6397	The complete mitochondrial genome of the critically endangered Lesser Antillean iguana (<i>Iguana</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 747	0.2	7
6398	The plastid genome of <i>Klainedoxa gabonensis</i> Pierre ex Engl. (Malpighiales). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2541-2542.	0.2	1
6399	The complete chloroplast genome of <i>Calanthe arcuata</i> , an endemic terrestrial orchid in China. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2629-2630.	0.2	5
6400	The complete chloroplast genome sequence of <i>Polypodiodes amoena</i> (Polypodiaceae), an important medical fern. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2633-2634.	0.2	0
6401	Characterization of the complete chloroplast genome of Sanming wild banana (<i>Musa itinerans</i>) and phylogenetic relationships. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2614-2616.	0.2	6
6402	Allopatric Speciation in Asia Contributed to the Diversity Anomaly between Eastern Asia and Eastern North America: Evidence from Anchored Phylogenomics of <i>Stewartia</i> (Theaceae). <i>International Journal of Plant Sciences</i> , 2019, 180, 768-777.	0.6	4
6403	The Application of Convolutional Neural Network in Security Code Recognition. <i>Journal of Physics: Conference Series</i> , 2019, 1187, 042064.	0.3	1
6404	Source tracking on a dairy farm reveals a high occurrence of subclinical mastitis due to hypervirulent <i>Listeria monocytogenes</i> clonal complexes. <i>Journal of Applied Microbiology</i> , 2019, 127, 1349-1361.	1.4	20
6405	A new case of kleptoplasty in animals: Marine flatworms steal functional plastids from diatoms. <i>Science Advances</i> , 2019, 5, eaaw4337.	4.7	46
6406	Three new species, new combinations and a key to known species of <i>Lobothallia</i> (Megasporaceae). <i>Lichenologist</i> , 2019, 51, 301-322.	0.5	12
6407	The complete chloroplast genome of <i>Pyrrosia calvata</i> (Polypodiaceae), a traditional Chinese medicinal fern only restricted to Guangxi, China. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1757-1758.	0.2	2

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6408	The complete chloroplast genome of <i>Lilium Lankongense</i> Franchet (Liliaceae). Mitochondrial DNA Part B: Resources, 2019, 4, 1824-1825.	0.2	2
6409	The complete chloroplast genome of <i>Rheum rhabarbarum</i> . Mitochondrial DNA Part B: Resources, 2019, 4, 1965-1966.	0.2	1
6410	The complete chloroplast genome of <i>Gentiana urnula</i> (Gentianaceae). Mitochondrial DNA Part B: Resources, 2019, 4, 2148-2149.	0.2	0
6411	The mitochondrial genome of the gold-ringed cowry <i>Monetaria annulus</i> (Mollusca: Gastropoda): Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 187 Td (Plet 2305-2307.	0.2	4
6412	The complete chloroplast genome of <i>Zabelia dielsii</i> (Graebn.) Rehd. (Caprifoliaceae), an important horticultural plant in China. Mitochondrial DNA Part B: Resources, 2019, 4, 2379-2380.	0.2	0
6413	Characterization of the complete chloroplast genome of a purple passion flower variety 'Pingtang No.1' (Passiflora edulia Sims) in China and phylogenetic relationships. Mitochondrial DNA Part B: Resources, 2019, 4, 2649-2651.	0.2	3
6414	Analysis on Geological Conditions of Chang 7 Shale Gas Accumulation in Longdong Area in Ordos Basin. IOP Conference Series: Earth and Environmental Science, 2019, 300, 022093.	0.2	0
6415	Phylogenomics Reveals Clear Cases of Misclassification and Genus-Wide Phylogenetic Markers for <i>Acinetobacter</i> . Genome Biology and Evolution, 2019, 11, 2531-2541.	1.1	60
6416	De novo profiling of RNA viruses in <i>Anopheles malaria</i> vector mosquitoes from forest ecological zones in Senegal and Cambodia. BMC Genomics, 2019, 20, 664.	1.2	22
6417	A unique cluster of roo insertions in the promoter region of a stress response gene in <i>Drosophila melanogaster</i> . Mobile DNA, 2019, 10, 10.	1.3	8
6418	bla _{NDM-5} carried by a hypervirulent <i>Klebsiella pneumoniae</i> with sequence type 29. Antimicrobial Resistance and Infection Control, 2019, 8, 140.	1.5	36
6419	The complete chloroplast genome of <i>Rungia pectinata</i> (Acanthaceae). Mitochondrial DNA Part B: Resources, 2019, 4, 2736-2737.	0.2	2
6420	The innovation of the final moult and the origin of insect metamorphosis. Philosophical Transactions of the Royal Society B: Biological Sciences, 2019, 374, 20180415.	1.8	34
6421	Sequence capture phylogenomics of historical ethanol-preserved museum specimens: Unlocking the rest of the vault. Molecular Ecology Resources, 2019, 19, 1531-1544.	2.2	74
6422	Bony labyrinth morphometry reveals hidden diversity in lungless salamanders (Family) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 187 Td (Plet Evolution; International Journal of Organic Evolution, 2019, 73, 2135-2150.	1.1	10
6423	Maple phylogeny and biogeography inferred from phylogenomic data. Journal of Systematics and Evolution, 2019, 57, 594-606.	1.6	51
6424	Assessing the viral content of uncultured picoeukaryotes in the global ocean by single cell genomics. Molecular Ecology, 2019, 28, 4272-4289.	2.0	25
6425	Whole-Genome Sequencing To Identify Drivers of Carbapenem-Resistant <i>Klebsiella pneumoniae</i> Transmission within and between Regional Long-Term Acute-Care Hospitals. Antimicrobial Agents and Chemotherapy, 2019, 63, .	1.4	24

#	ARTICLE	IF	CITATIONS
6426	A revision of <i>Hynobius stejnegeri</i> , a lotic breeding salamander from western Japan, with a description of three new species (Amphibia, Caudata, Hynobiidae). <i>Zootaxa</i> , 2019, 4651, zootaxa.4651.3.1.	0.2	6
6427	Species Delimitation and Phylogeny of <i>Epithelantha</i> (Cactaceae). <i>Systematic Botany</i> , 2019, 44, 600-615.	0.2	12
6428	<i>Mutoviaspermum krassilovii</i> gen. et sp. nov.: A Peculiar Compound Ovuliferous Conifer Cone from the Lopingian (Late Permian) of European Russia (Vologda Region). <i>International Journal of Plant Sciences</i> , 2019, 180, 779-799.	0.6	4
6429	Plastome Reduction in the Only Parasitic Gymnosperm <i>Parasitaxus</i> Is Due to Losses of Photosynthesis but Not Housekeeping Genes and Apparently Involves the Secondary Gain of a Large Inverted Repeat. <i>Genome Biology and Evolution</i> , 2019, 11, 2789-2796.	1.1	31
6430	Comparative genomic analysis of six <i>Glossina</i> genomes, vectors of African trypanosomes. <i>Genome Biology</i> , 2019, 20, 187.	3.8	71
6431	Comparative Genomic Analysis of the 2016 <i>Vibrio cholerae</i> Outbreak in South Korea. <i>Frontiers in Public Health</i> , 2019, 7, 228.	1.3	10
6432	Nuclear Orthologs Derived from Whole Genome Sequencing Indicate Cryptic Diversity in the <i>Bemisia tabaci</i> (Insecta: Aleyrodidae) Complex of Whiteflies. <i>Diversity</i> , 2019, 11, 151.	0.7	39
6433	Mitochondrial Genomes of Two <i>Thaparocleidus</i> Species (Platyhelminthes: Monogenea) Reveal the First rRNA Gene Rearrangement among the Neodermata. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4214.	1.8	7
6434	Morphology and molecules reveal two new species of <i>Porites</i> (Scleractinia, Poritidae) from the Red Sea and the Gulf of Aden. <i>Systematics and Biodiversity</i> , 2019, 17, 491-508.	0.5	12
6435	Morphology and metabarcoding: a test with stream diatoms from Mexico highlights the complementarity of identification methods. <i>Freshwater Science</i> , 2019, 38, 448-464.	0.9	31
6436	Evolution of Outbreak-Causing Carbapenem-Resistant <i>Klebsiella pneumoniae</i> ST258 at a Tertiary Care Hospital over 8 Years. <i>MBio</i> , 2019, 10, .	1.8	66
6437	A Genome-Based Species Taxonomy of the <i>Lactobacillus</i> Genus Complex. <i>MSystems</i> , 2019, 4, .	1.7	50
6438	A herpetological survey of the Kathmandu Valley, Nepal, and phylogenetic identification of <i>Megophrys</i> (<i>Xenophrys</i>) <i>zhangii</i> . <i>Journal of Natural History</i> , 2019, 53, 1421-1437.	0.2	2
6439	<i>Streptococcus pneumoniae</i> Evades Host Cell Phagocytosis and Limits Host Mortality Through Its Cell Wall Anchoring Protein PfbA. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 301.	1.8	22
6440	Faecal Virome Analysis of Wild Animals from Brazil. <i>Viruses</i> , 2019, 11, 803.	1.5	51
6441	Characterization of the complete chloroplast genome of <i>Nitraria tangutorum</i> , a desert shrub. <i>Journal of Genetics</i> , 2019, 98, 1.	0.4	8
6442	A Tale of Two Setae: How Morphology and ITS2 Help Delimit a Cryptic Species Complex in Eulophidae (Hymenoptera: Chalcidoidea). <i>Insect Systematics and Diversity</i> , 2019, 3, .	0.7	6
6443	Analyzing and Characterizing the Chloroplast Genome of <i>Salix wilsonii</i> . <i>BioMed Research International</i> , 2019, 2019, 1-14.	0.9	20

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6444	Transcriptome and gene expression analysis of three developmental stages of the coffee berry borer, <i>Hypothenemus hampei</i> . <i>Scientific Reports</i> , 2019, 9, 12804.	1.6	17
6445	Total-evidence phylogeny of the Rhinomirini, taxonomic review of its subgroupings (Insecta: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Linnean Society, 2019, 187, 1196-1252.	1.0	13
6446	Multiple convergent events created a nominal widespread species: <i>Triplophysa stoliczkae</i> (Steindachner, 1866) (Cobitoidea: Nemacheilidae). <i>BMC Evolutionary Biology</i> , 2019, 19, 177.	3.2	13
6447	Similarities and differences in patterns of germline mutation between mice and humans. <i>Nature Communications</i> , 2019, 10, 4053.	5.8	79
6448	Whole-genome sequencing-based epidemiological analysis of anti-tuberculosis drug resistance genes in Japan in 2007: Application of the Genome Research for Asian Tuberculosis (GRaT) database. <i>Scientific Reports</i> , 2019, 9, 12823.	1.6	10
6449	Potential Interactions between Clade SUP05 Sulfur-Oxidizing Bacteria and Phages in Hydrothermal Vent Sponges. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	22
6450	Evolution of mantis shrimp telson armour and its role in ritualized fighting. <i>Journal of the Royal Society Interface</i> , 2019, 16, 20190203.	1.5	15
6451	The timing of Malvales evolution: Incorporating its extensive fossil record to inform about lineage diversification. <i>Molecular Phylogenetics and Evolution</i> , 2019, 140, 106606.	1.2	34
6452	Shallow genetic divergence and distinct phenotypic differences between two Andean hummingbirds: Speciation with gene flow?. <i>Auk</i> , 2019, 136, .	0.7	18
6453	Multilocus data reveal cryptic species in the Atlantic seabob shrimp <i>Xiphopenaeus kroyeri</i> (Crustacea: Tj ETQq1 1 0.784314 rgBT /Overlock 10 16	0.7	16
6454	Molecular characterization of carbapenem-resistant <i>Acinetobacter baumannii</i> using WGS revealed missed transmission events in Germany from 2012â€“15. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 3473-3480.	1.3	15
6455	Graph Splitting: A Graph-Based Approach for Superfamily-Scale Phylogenetic Tree Reconstruction. <i>Systematic Biology</i> , 2020, 69, 265-279.	2.7	12
6456	Broad Heterochromatic Domains Open in Gonocyte Development Prior to De Novo DNA Methylation. <i>Developmental Cell</i> , 2019, 51, 21-34.e5.	3.1	26
6457	Cryptic species diversity in ticks that transmit disease in Australia. <i>International Journal for Parasitology: Parasites and Wildlife</i> , 2019, 10, 125-131.	0.6	4
6458	Post K-Pg diversification of the mammalian order Eulipotyphla as suggested by phylogenomic analyses of ultra-conserved elements. <i>Molecular Phylogenetics and Evolution</i> , 2019, 141, 106605.	1.2	8
6459	<i>Dictyota falklandica</i> sp. nov. (Dictyotales, Phaeophyceae) from the Falkland Islands and southernmost South America. <i>Phycologia</i> , 2019, 58, 640-647.	0.6	6
6460	Capability for arsenic mobilization in groundwater is distributed across broad phylogenetic lineages. <i>PLoS ONE</i> , 2019, 14, e0221694.	1.1	15
6461	Comparative genomics reveals the origin of fungal hyphae and multicellularity. <i>Nature Communications</i> , 2019, 10, 4080.	5.8	80

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6462	Key evolutionary events in the emergence of a globally disseminated, carbapenem resistant clone in the Escherichia coli ST410 lineage. Communications Biology, 2019, 2, 322.	2.0	36
6463	The complete plastid genome of Zenia insignis Chun (Leguminosae). Mitochondrial DNA Part B: Resources, 2019, 4, 2926-2927.	0.2	2
6464	The <i>foraging</i> Gene and Its Behavioral Effects: Pleiotropy and Plasticity. Annual Review of Genetics, 2019, 53, 373-392.	3.2	49
6465	Isolation of five Enterobacteriaceae species harbouring blaNDM-1 and mcr-1 plasmids from a single paediatric patient. PLoS ONE, 2019, 14, e0221960.	1.1	19
6466	Phylogeography of the Bradyrhizobium spp. Associated With Peanut, Arachis hypogaea: Fellow Travelers or New Associations?. Frontiers in Microbiology, 2019, 10, 2041.	1.5	11
6467	Taxonomic revision of black salamanders of the <i>Aneides flavipunctatus</i> complex (Caudata:) Tj ETQq1 1 0.784314 rgBT /Overlock 1 0.9 3	0.9	3
6468	Stress Adapted Mollusca and Nematoda Exhibit Convergently Expanded Hsp70 and AIG1 Gene Families. Journal of Molecular Evolution, 2019, 87, 289-297.	0.8	12
6469	Carbon assimilation profiles of mucoralean fungi show their metabolic versatility. Scientific Reports, 2019, 9, 11864.	1.6	17
6470	A subfamily roadmap of the evolutionarily diverse glycoside hydrolase family 16 (GH16). Journal of Biological Chemistry, 2019, 294, 15973-15986.	1.6	118
6471	The first known fossil Uma: ecological evolution and the origins of North American fringe-toed lizards. BMC Evolutionary Biology, 2019, 19, 178.	3.2	9
6472	Phylotranscriptomics resolves interspecific relationships and indicates multiple historical out-of-North America dispersals through the Bering Land Bridge for the genus Picea (Pinaceae). Molecular Phylogenetics and Evolution, 2019, 141, 106610.	1.2	22
6473	Phylogenetic and taxonomic study of the complete mitochondrial genome of <i>Spodoptera frugiperda</i> . Mitochondrial DNA Part B: Resources, 2019, 4, 2759-2761.	0.2	4
6474	Hospital-based Surveillance Provides Insights Into the Etiology of Pediatric Bacterial Meningitis in Yaoundé, Cameroon, in the Post-Vaccine Era. Clinical Infectious Diseases, 2019, 69, S148-S155.	2.9	4
6475	The Impact of Natural Selection on the Evolution and Function of Placentally Expressed Galectins. Genome Biology and Evolution, 2019, 11, 2574-2592.	1.1	16
6476	The Genomic Substrate for Adaptive Radiation: Copy Number Variation across 12 Tribes of African Cichlid Species. Genome Biology and Evolution, 2019, 11, 2856-2874.	1.1	7
6477	A Laurasian origin for a pantropical bird radiation is supported by genomic and fossil data (Aves:) Tj ETQq1 1 0.784314 rgBT /Overlock 1 1.2 25	1.2	25
6478	<i>Worm-riding clam: description of Montacutona sigalionidcola</i> sp. nov. (Bivalvia: Heterodonta: Galeommatidae) from Japan and its phylogenetic position. Zootaxa, 2019, 4652, 473-486.	0.2	0
6479	Strigolactone synthesis is ancestral in land plants, but canonical strigolactone signalling is a flowering plant innovation. BMC Biology, 2019, 17, 70.	1.7	92

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6480	Gene Tags Assessment by Comparative Genomics (GTACG): A User-Friendly Framework for Bacterial Comparative Genomics. <i>Frontiers in Genetics</i> , 2019, 10, 725.	1.1	4
6481	Catabolism of Alkylphenols in <i>Rhodococcus</i> via a Meta-Cleavage Pathway Associated With Genomic Islands. <i>Frontiers in Microbiology</i> , 2019, 10, 1862.	1.5	14
6482	Phylogeny of Hawaiian Melicope (Rutaceae): RAD-seq Resolves Species Relationships and Reveals Ancient Introgression. <i>Frontiers in Plant Science</i> , 2019, 10, 1074.	1.7	35
6483	The Genomics of <i>Streptococcus Pneumoniae</i> Carriage Isolates from UK Children and Their Household Contacts, Pre-PCV7 to Post-PCV13. <i>Genes</i> , 2019, 10, 687.	1.0	16
6484	Two new genera of Acanthaceae from tropical Africa. <i>Kew Bulletin</i> , 2019, 74, 1.	0.4	4
6485	PRC2.1 and PRC2.2 Synergize to Coordinate H3K27 Trimethylation. <i>Molecular Cell</i> , 2019, 76, 437-452.e6.	4.5	137
6486	Pediatric Bacterial Meningitis Surveillance in Niger: Increased Importance of <i>Neisseria meningitidis</i> Serogroup C, and a Decrease in <i>Streptococcus pneumoniae</i> Following 13-Valent Pneumococcal Conjugate Vaccine Introduction. <i>Clinical Infectious Diseases</i> , 2019, 69, S133-S139.	2.9	10
6487	A global metabarcoding analysis expands molecular diversity of Platyhelminthes and reveals novel early-branching clades. <i>Biology Letters</i> , 2019, 15, 20190182.	1.0	6
6488	A revision of the French Trichobrachidae (Polychaeta), with descriptions of nine new species. <i>Zootaxa</i> , 2019, 4664, zootaxa.4664.2.1.	0.2	12
6489	<i>Cinetorhynchus gabonensis</i> , a new species of hinge-beak shrimp (Crustacea: Decapoda: Rhynchocinetidae) from the eastern Atlantic. <i>Zootaxa</i> , 2019, 4664, 191-205.	0.2	1
6490	Morphology and SSU rDNA sequences of four ciliates from China, with description of a new species (Protista, Ciliophora, Phyllopharyngea). <i>Zootaxa</i> , 2019, 4664, zootaxa.4664.2.3.	0.2	6
6491	Entry of bunyaviruses into plants and vectors. <i>Advances in Virus Research</i> , 2019, 104, 65-96.	0.9	23
6492	Adaptive Evolution Is Common in Rapid Evolutionary Radiations. <i>Current Biology</i> , 2019, 29, 3081-3086.e5.	1.8	32
6493	Phylogenomics resolves major relationships and reveals significant diversification rate shifts in the evolution of silk moths and relatives. <i>BMC Evolutionary Biology</i> , 2019, 19, 182.	3.2	49
6494	Gene expression vs. sequence divergence: comparative transcriptome sequencing among natural <i>Rhinolophus ferrumequinum</i> populations with different acoustic phenotypes. <i>Frontiers in Zoology</i> , 2019, 16, 37.	0.9	13
6495	The complete mitochondrial genome of <i>Calyptogenia marissinica</i> (Heterodonta: Veneroida: Tj ETQq1 1 0.784314 rgBT /Overlock 10 TTS 26	2.1	26
6496	Delayed peak of human infections and ongoing reassortment of H7N9 avian influenza virus in the newly affected western Chinese provinces during Wave Five. <i>International Journal of Infectious Diseases</i> , 2019, 88, 80-87.	1.5	2
6497	Euopisthobranch mollusks of the order Cephalaspidea (Gastropoda: Heterobranchia) of the Kuril-Kamchatka Trench and the adjacent Pacific abyssal plain with descriptions of three new species of the genus <i>Spiraphiline</i> (Philinidae). <i>Progress in Oceanography</i> , 2019, 178, 102185.	1.5	14

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6498	Spidroins and Silk Fibers of Aquatic Spiders. <i>Scientific Reports</i> , 2019, 9, 13656.	1.6	21
6499	Phylogeographic analysis of Iranian wildcats (<i>Felis lybica</i> / <i>Felis silvestris</i>) as revealed by mitochondrial cytochrome <i>b</i> gene. <i>Zoology in the Middle East</i> , 2019, 65, 293-306.	0.2	1
6500	Etiology of Pediatric Bacterial Meningitis Pre- and Post-PCV13 Introduction Among Children Under 5 Years Old in Lomé, Togo. <i>Clinical Infectious Diseases</i> , 2019, 69, S97-S104.	2.9	9
6501	Two new species of <i>Bambusicola</i> (Bambusicolaceae, Pleosporales) on <i>Phyllostachys heteroclada</i> from Sichuan, China. <i>Nova Hedwigia</i> , 2019, 108, 527-545.	0.2	13
6502	The mitochondrial genome of <i>Leuctra</i> sp. (Plecoptera: Leuctridae) and its performance in phylogenetic analyses. <i>Zootaxa</i> , 2019, 4671, zootaxa.4671.4.8.	0.2	7
6503	Metaviromics Reveals Unknown Viral Diversity in the Biting Midge <i>Culicoides impunctatus</i> . <i>Viruses</i> , 2019, 11, 865.	1.5	11
6504	New plectosphaerellaceous species from Dutch garden soil. <i>Mycological Progress</i> , 2019, 18, 1135-1154.	0.5	15
6505	Virus- and Interferon Alpha-Induced Transcriptomes of Cells from the Microbat <i>Myotis daubentonii</i> . <i>iScience</i> , 2019, 19, 647-661.	1.9	37
6506	Admixture between old lineages facilitated contemporary ecological speciation in Lake Constance stickleback. <i>Nature Communications</i> , 2019, 10, 4240.	5.8	49
6507	Complete mitochondrial genome of the taxonomically notorious sea star, <i>Henricia leviuscula</i> (Asteroidea, Spinulosida, Echinasteridae), from South Korea. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2656-2657.	0.2	0
6508	The complete chloroplast genome of an endangered endemic herb species in China, <i>Primula filchnerae</i> (Primulaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2746-2747.	0.2	2
6509	The complete mitochondrial genome of <i>Cerithidea sinensis</i> (Philippi, 1848). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2742-2743.	0.2	3
6510	Complete mitogenome of the invasive bivalve <i>Rangia cuneata</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2794-2795.	0.2	1
6511	The complete mitochondrial genome of the New Zealand parasitic roundworm <i>Teladorsagia circumcincta</i> (Trichostrongyloidea: Haemonchidae) field strain NZ_Teci_NP. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2869-2871.	0.2	11
6512	The complete chloroplast genome of a medicinal resource plant (<i>Rumex crispus</i>). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2800-2801.	0.2	3
6513	Complete chloroplast genome sequence of bamboo <i>Dendrocalamopsis vario-striata</i> (Gramineae) Tj ETQq1 1,0,784314,rgBT /Ove	0.2	2
6514	Complete chloroplast genome of <i>Arundina graminifolia</i> (Orchidaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2898-2899.	0.2	5
6515	Chloroplast genome structure and phylogenetic position of <i>Ruppia sinensis</i> Shuo Yu & den Hartog. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2916-2917.	0.2	3

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6516	The complete plastome of bloodroot (<i>Sanguinaria canadensis</i> , Papaveraceae), a spring ephemeral from eastern North America. Mitochondrial DNA Part B: Resources, 2019, 4, 2944-2945.	0.2	0
6517	The complete mitochondrial genome of <i>Sapajus flavus</i> Blonde Capuchini. Mitochondrial DNA Part B: Resources, 2019, 4, 2970-2971.	0.2	1
6518	The complete chloroplast genome of <i>Sesbania cannabina</i> . Mitochondrial DNA Part B: Resources, 2019, 4, 2952-2953.	0.2	1
6519	Characterization of the complete chloroplast genome of Chinese rose, <i>Rosa chinensis</i> (Rosaceae: Rosa). Mitochondrial DNA Part B: Resources, 2019, 4, 2984-2985.	0.2	4
6520	High-coverage genomes to elucidate the evolution of penguins. GigaScience, 2019, 8, .	3.3	18
6521	The conundrum of species delimitation: a genomic perspective on a mitogenetically super-variable butterfly. Proceedings of the Royal Society B: Biological Sciences, 2019, 286, 20191311.	1.2	37
6522	A shrimp out of place. New genus of Atyidae (Crustacea: Decapoda) in subterranean waters of southeastern Europe, with some remarks on Atyidae taxonomy. Zoologischer Anzeiger, 2019, 283, 111-123.	0.4	2
6523	Hybrid de novo genome assembly of Chinese chestnut (<i>Castanea mollissima</i>). GigaScience, 2019, 8, .	3.3	55
6524	On the systematic status of <i>Isopericlimenaeus</i> Marin, 2012 and its type species, <i>Periclimenaeus gorgonidarum</i> (Balss, 1913) (Crustacea: Decapoda: Palaemonidae). Zootaxa, 2019, 4614, 353.	0.2	6
6525	The molecular clock of <i>Mycobacterium tuberculosis</i> . PLoS Pathogens, 2019, 15, e1008067.	2.1	107
6526	Genome Sequence of <i>Striga asiatica</i> Provides Insight into the Evolution of Plant Parasitism. Current Biology, 2019, 29, 3041-3052.e4.	1.8	109
6527	Whole genome sequence analysis reveals high genetic variation of newly isolated <i>Acidithiobacillus ferrooxidans</i> IO-2C. Scientific Reports, 2019, 9, 13049.	1.6	10
6528	Large-Scale Molecular Evolutionary Analysis Uncovers a Variety of Polynucleotide Kinase Clp1 Family Proteins in the Three Domains of Life. Genome Biology and Evolution, 2019, 11, 2713-2726.	1.1	6
6529	Genetic Similarity of Gonococcal Homologs to Meningococcal Outer Membrane Proteins of Serogroup B Vaccine. MBio, 2019, 10, .	1.8	29
6530	Molecular taxonomy reveals the sexual morph of <i>Nodulosphaeria digitalis</i> in Phaeosphaeriaceae from <i>Campanula trachelium</i> in Italy. Phytotaxa, 2019, 400, 1.	0.1	4
6531	A new species of <i>Conocybe</i> (Bolbitaceae) from Punjab, Pakistan. Phytotaxa, 2019, 402, 251.	0.1	2
6532	Two species of <i>Agaricus</i> subg. <i>Minorioopsis</i> from Mexico. Phytotaxa, 2019, 404, 91.	0.1	4
6533	Notes on the phytogeography and conservation status of the genus <i>Acanthopsis</i> (Acantheae, Acanthaceae) . Phytotaxa, 2019, 415, 157-178.	0.1	2

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6534	Rapid evolution of Mexican H7N3 highly pathogenic avian influenza viruses in poultry. PLoS ONE, 2019, 14, e0222457.	1.1	20
6535	Species-Specific Marker Discovery in Tilapia. Scientific Reports, 2019, 9, 13001.	1.6	20
6536	Hortiboletus kohistanensis (Boletaceae), a new bolete species from temperate and subalpine oak forests of Pakistan. Phytotaxa, 2019, 388, 239.	0.1	4
6537	The holomorph of Neoroussoella alishanense sp. nov. (Roussoellaceae, Pleosporales) on Pennisetum purpureum (Poaceae). Phytotaxa, 2019, 406, 218-236.	0.1	9
6538	Micareia fennica, a new lignicolous lichen species from Finland. Phytotaxa, 2019, 409, 179-188.	0.1	11
6539	Amanita mansehraensis, a new species in section Vaginatae from Pakistan. Phytotaxa, 2019, 409, 189-201.	0.1	7
6540	Sphaeropezia leucocheila sp. nov. (Stictidaceae): a liverwort pathogen from New Zealand. Phytotaxa, 2019, 409, 222-226.	0.1	2
6541	Wicklowia submersa sp. nov. (Wicklowiaceae, Pleosporales), a second species in a monotypic family. Phytotaxa, 2019, 411, 73-83.	0.1	4
6542	Two new species of Pachyphlodes from China. Phytotaxa, 2019, 411, 105-115.	0.1	1
6543	New species discovered from old collections, the case of Hedysarum wangii sp. nov. (Fabaceae,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 0.1	0.1	4
6544	New records of Pluteus section Hispidoderma in Turkey Based on Morphological Characteristics and Molecular Data. Phytotaxa, 2019, 413, 175-206.	0.1	4
6545	A new species of Tashiroea (Melastomataceae, Sonerileae) from Guangxi, China. Phytotaxa, 2019, 414, 269-279.	0.1	0
6546	Hydnaceous fungi of China 7. Morphological and molecular characterization of Phellodon subconfluens sp. nov. from temperate, deciduous forests. Phytotaxa, 2019, 414, 280-288.	0.1	5
6547	Aphanomyces brasiliensis sp. nov. (Verrucalvaceae,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 0.1	0.1	4
6548	Marasmiellus griseobrunneus sp. nov. (Omphalotaceae) from Kerala State, India. Phytotaxa, 2019, 416, 25-33.	0.1	3
6549	Arcanumophis, a new genus and generic allocation for Erythrolamprus problematicus (Myers 1986), Xenodontinae (Colubridae) from the Cordillera de Carabaya, southern Peru. Zootaxa, 2019, 4671, 129-138.	0.2	4
6550	A new species of snook, Centropomus (Teleostei: Centropomidae), from northern South America, with notes on the geographic distribution of other species of the genus. Zootaxa, 2019, 4671, zootaxa.4671.1.6.	0.2	5
6551	Distribution and Community Assembly of Trees Along an Andean Elevational Gradient. Plants, 2019, 8, 326.	1.6	11

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6552	Diet-driven ecological radiation and allopatric speciation result in high species diversity in a temperate-cold water marine genus <i>Dendronotus</i> (Gastropoda: Nudibranchia). <i>Molecular Phylogenetics and Evolution</i> , 2019, 141, 106609.	1.2	35
6553	An overview of <i>Antrodiella</i> and related genera of Polyporales from the Neotropics. <i>Mycologia</i> , 2019, 111, 813-831.	0.8	10
6554	Hydraulically Fractured Natural-Gas Well Microbial Communities Contain Genomic Halogenation and Dehalogenation Potential. <i>Environmental Science and Technology Letters</i> , 2019, 6, 585-591.	3.9	6
6555	<i>Neofavolus subpurpurascens</i> comb. nov., with new records from the Neotropics. <i>Phytotaxa</i> , 2019, 405, 180.	0.1	3
6556	<i>Parasola psathyrelloides</i> (Psathyrellaceae), a new species from Kerala State, India. <i>Phytotaxa</i> , 2019, 405, 255-262.	0.1	3
6557	Multi-gene phylogeny and morphotaxonomy of <i>Phaeosphaeria ampeli</i> sp. nov. from <i>Ficus ampelas</i> and a new record of <i>P. musae</i> from <i>Roystonea regia</i> . <i>Phytotaxa</i> , 2019, 406, 111-128.	0.1	9
6558	Broad geographic sampling and DNA barcoding do not support the presence of <i>Helobdella stagnalis</i> (Linnaeus, 1758) (Clitellata: Glossiphoniidae) in North America. <i>Zootaxa</i> , 2019, 4671, zootaxa.4671.1.1.	0.2	9
6559	<i>Labrys khuzestanensis</i> n. sp. (Nematoda, Tylenchidae), a new member of the genus with large labial plate. <i>Zootaxa</i> , 2019, 4671, zootaxa.4671.2.7.	0.2	10
6560	Chloroplast Genomes and Comparative Analyses among Thirteen Taxa within Myrsinaceae s.str. Clade (Myrsinoideae, Primulaceae). <i>International Journal of Molecular Sciences</i> , 2019, 20, 4534.	1.8	17
6561	<i>Thyrostroma ephedricola</i> sp. nov. (Dothidotthiaceae) and proposal for <i>Thyrostroma jaczewskii</i> comb. nov. <i>Phytotaxa</i> , 2019, 416, 243-256.	0.1	7
6562	Revision of <i>Hyalopale</i> (Chrysopetalidae; Phyllodocida; Annelida): an amphi-Atlantic <i>Hyalopale bispinosa</i> species complex and five new species from reefs of the Caribbean Sea and Indo-Pacific Oceans. <i>Zootaxa</i> , 2019, 4671, 339-368.	0.2	2
6563	New records of <i>Swiftia</i> (Cnidaria, Anthozoa, Octocorallia) from off the Pacific Costa Rican margin, including a new species from methane seeps. <i>Zootaxa</i> , 2019, 4671, 407-419.	0.2	6
6564	Characterization of the endogenous retrovirus insertion in CYP19A1 associated with henny feathering in chicken. <i>Mobile DNA</i> , 2019, 10, 38.	1.3	15
6565	The Draft Genome of the Endangered Sichuan Partridge (<i>Arborophila rufipectus</i>) with Evolutionary Implications. <i>Genes</i> , 2019, 10, 677.	1.0	8
6566	Resurrection of <i>Paraisaria</i> in the Ophiocordycipitaceae with three new species from Thailand. <i>Mycological Progress</i> , 2019, 18, 1213-1230.	0.5	17
6567	Complete chloroplast genome sequences of <i>Poikilospermum lanceolatum</i> (Urticeae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2131-2132.	0.2	1
6568	Complete chloroplast genome of <i>Chloranthus henryi</i> (chloranthaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2964-2965.	0.2	4
6569	Characterization of the complete chloroplast genome of <i>Gerbera jamesonii</i> Bolus in China and phylogenetic relationships. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2706-2707.	0.2	0

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6570	The complete chloroplast genome sequence of the medicinal shrub <i>Daphne Giraldii</i> Nitsche. (Thymelaeaceae). Mitochondrial DNA Part B: Resources, 2019, 4, 2685-2686.	0.2	8
6571	The complete chloroplast genome of <i>Ophiopogon japonicus</i> , an ornamental and medicinal plant. Mitochondrial DNA Part B: Resources, 2019, 4, 2843-2844.	0.2	1
6572	The complete chloroplast genome of an annual halophyte herb, <i>Suaeda glauca</i> (Amaranthaceae). Mitochondrial DNA Part B: Resources, 2019, 4, 2780-2781.	0.2	5
6573	Complete plastid genome sequence of a medical herb, <i>Anisomeles indica</i> (L.) Kuntze (Lamiaceae). Mitochondrial DNA Part B: Resources, 2019, 4, 2782-2783.	0.2	1
6574	Complete plastome of the medicinally important plant, <i>Alstonia scholaris</i> (<i>Apocynaceae</i>). Mitochondrial DNA Part B: Resources, 2019, 4, 2896-2897.	0.2	1
6575	Characterization of the complete chloroplast genome of Taibaisanqi (<i>Tongoloa silaifolia</i>). Mitochondrial DNA Part B: Resources, 2019, 4, 2912-2913.	0.2	0
6576	The complete mitochondrial genomes of two endangered bitterling <i>Acheilognathus tabira tohokuensis</i> and <i>A. tabira erythropterus</i> (Cyprinidae, Acheilognathinae). Mitochondrial DNA Part B: Resources, 2019, 4, 2865-2866.	0.2	2
6577	The complete mitochondrial genome of <i>Neritina violacea</i> . Mitochondrial DNA Part B: Resources, 2019, 4, 2942-2943.	0.2	5
6578	Complete mitochondrial genome of the Antarctic fur seal (<i>Arctocephalus gazella</i>). Mitochondrial DNA Part B: Resources, 2019, 4, 2936-2937.	0.2	2
6579	The complete chloroplast genome sequence of <i>Rubus eucalyptus</i> (Rosaceae). Mitochondrial DNA Part B: Resources, 2019, 4, 2976-2977.	0.2	4
6580	The Evolution of Reverse Gyrase Suggests a Nonhyperthermophilic Last Universal Common Ancestor. <i>Molecular Biology and Evolution</i> , 2019, 36, 2737-2747.	3.5	29
6581	Machine-Learning Classification Suggests That Many Alphaproteobacterial Prophages May Instead Be Gene Transfer Agents. <i>Genome Biology and Evolution</i> , 2019, 11, 2941-2953.	1.1	24
6582	<i>Epinephelus fuscomarginatus</i> (Perciformes: Epinephelidae), a new species of grouper from off the Great Barrier Reef, Australia. <i>Zootaxa</i> , 2019, 4674, zootaxa.4674.3.2.	0.2	4
6583	Complete Sequence, Multichromosomal Architecture and Transcriptome Analysis of the <i>Solanum tuberosum</i> Mitochondrial Genome. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4788.	1.8	44
6584	Evolution, Origin of Life, Concepts and Methods. , 2019, , .		4
6585	Evaluation of the rust fungus <i>Puccinia rapipes</i> for biological control of <i>Lycium ferocissimum</i> (African boxthorn) in Australia: Life cycle, taxonomy and pathogenicity. <i>Fungal Biology</i> , 2019, 123, 811-823.	1.1	11
6586	Supergene validation: A model-based protocol for assessing the accuracy of non-model-based supergene methods. <i>MethodsX</i> , 2019, 6, 2181-2188.	0.7	1
6587	Molecular characterisation of a cellular conveyor belt in <i>Clytia</i> medusae. <i>Developmental Biology</i> , 2019, 456, 212-225.	0.9	17

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6588	Phylogeography of the second plague pandemic revealed through analysis of historical <i>Yersinia pestis</i> genomes. <i>Nature Communications</i> , 2019, 10, 4470.	5.8	113
6589	The near-complete mitogenome of the critically endangered <i>Pseudocleopatra dartevellei</i> (Caenogastropoda: Paludomidae) from the Congo River assembled from historical museum material. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3229-3231.	0.2	5
6590	Adenoviral Infections in Singapore: Should New Antiviral Therapies and Vaccines Be Adopted?. <i>Journal of Infectious Diseases</i> , 2019, 221, 566-577.	1.9	13
6591	<i>Dispora speciosa</i> , a new addition to the genus <i>Parallela</i> and the first coccoïd member of the family Microsporaceae. <i>Phytotaxa</i> , 2019, 419, 63-76.	0.1	1
6592	Genome expansion by allopolyploidization in the fungal strain <i>Coniochaeta</i> 2T2.1 and its exceptional lignocellulolytic machinery. <i>Biotechnology for Biofuels</i> , 2019, 12, 229.	6.2	12
6593	Museomics Clarifies the Classification of <i>Aloidendron</i> (Asphodelaceae), the Iconic African Tree Aloes. <i>Frontiers in Plant Science</i> , 2019, 10, 1227.	1.7	9
6594	The Canine Morbillivirus Strain Associated with An Epizootic in Caspian Seals Provides New Insights into the Evolutionary History of this Virus. <i>Viruses</i> , 2019, 11, 894.	1.5	19
6595	A hybrid sub-lineage of <i>Listeria monocytogenes</i> comprising hypervirulent isolates. <i>Nature Communications</i> , 2019, 10, 4283.	5.8	76
6596	An evolutionary signal to fungal succession during plant litter decay. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	30
6597	Amplified fragment length polymorphism and whole genome sequencing: a comparison of methods in the investigation of a nosocomial outbreak with vancomycin resistant enterococci. <i>Antimicrobial Resistance and Infection Control</i> , 2019, 8, 153.	1.5	5
6598	Morphological plasticity in a Fijian Seagrass: <i>Halophila ovalis</i> subsp. <i>bullosa</i> . <i>Regional Studies in Marine Science</i> , 2019, 32, 100809.	0.4	5
6599	Molecular systematics of <i>Pampus</i> (Perciformes: Stromateidae) based on thousands of nuclear loci using target-gene enrichment. <i>Molecular Phylogenetics and Evolution</i> , 2019, 140, 106595.	1.2	13
6600	The sequence and de novo assembly of <i>Takifugu bimaculatus</i> genome using PacBio and Hi-C technologies. <i>Scientific Data</i> , 2019, 6, 187.	2.4	29
6601	Repeated species radiations in the recent evolution of the key marine phytoplankton lineage <i>Gephyrocapsa</i> . <i>Nature Communications</i> , 2019, 10, 4234.	5.8	61
6602	The herophile species group of <i>Calisto</i> (Lepidoptera : Nymphalidae : Satyrinae), new taxa and historical biogeography. <i>Invertebrate Systematics</i> , 2019, , .	0.5	1
6603	Macrolepiota in Korea: New Records and a New Species. <i>Mycobiology</i> , 2019, 47, 368-377.	0.6	5
6604	Unraveling the functional role of the orphan solute carrier, SLC22A24 in the transport of steroid conjugates through metabolomic and genome-wide association studies. <i>PLoS Genetics</i> , 2019, 15, e1008208.	1.5	23
6605	Characterization of <i>Bifidobacterium</i> species in feaces of the Egyptian fruit bat: Description of <i>B. vespertilionis</i> sp. nov. and <i>B. roussetti</i> sp. nov.. <i>Systematic and Applied Microbiology</i> , 2019, 42, 126017.	1.2	22

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6606	Environmental DNA Metabarcoding: A Promising Tool for Ballast Water Monitoring. <i>Environmental Science & Technology</i> , 2019, 53, 11849-11859.	4.6	25
6607	The distinction of CPR bacteria from other bacteria based on protein family content. <i>Nature Communications</i> , 2019, 10, 4173.	5.8	112
6608	Characterisation of three novel Î ² -1,3 glucanases from the medically important house dust mite <i>Dermatophagoides pteronyssinus</i> (airmid). <i>Insect Biochemistry and Molecular Biology</i> , 2019, 115, 103242.	1.2	6
6609	ICEKp2: description of an integrative and conjugative element in <i>Klebsiella pneumoniae</i> , co-occurring and interacting with ICEKp1. <i>Scientific Reports</i> , 2019, 9, 13892.	1.6	10
6610	Quartet-based inference of cell differentiation trees from ChIP-Seq histone modification data. <i>PLoS ONE</i> , 2019, 14, e0221270.	1.1	3
6611	TaAPO-A1, an ortholog of rice ABERRANT PANICLE ORGANIZATION 1, is associated with total spikelet number per spike in elite European hexaploid winter wheat (<i>Triticum aestivum</i> L.) varieties. <i>Scientific Reports</i> , 2019, 9, 13853.	1.6	55
6612	<i>Rhizoglyphus dalpeae</i> , <i>R. maiae</i> , and <i>R. silesianum</i> , new species. <i>Mycologia</i> , 2019, 111, 965-980.	0.8	12
6613	Looks can be deceiving: the deceptive milkcaps (<i>Lactifluus</i> , Russulaceae) exhibit low morphological variance but harbour high genetic diversity. <i>IMA Fungus</i> , 2019, 10, 14.	1.7	13
6614	Evaluating Population Genetic Structure and Demographic History of <i>Quercus spinosa</i> (Fagaceae) Based on Specific Length Amplified Fragment Sequencing. <i>Frontiers in Genetics</i> , 2019, 10, 965.	1.1	14
6615	Thallus ontogeny, morphology and molecular phylogeny of <i>Madagascaria atlantica</i> sp. nov. (Compsopogonophyceae, Rhodophyta), a diminutive crustose species uncovered in the Atlantic Ocean. <i>Aquatic Botany</i> , 2019, 159, 103152.	0.8	3
6616	The complete chloroplast genome of a traditional medicinal and food plant, <i>Polygonatum humile</i> (Asparagaceae, Asparagales). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3184-3185.	0.2	2
6617	Assexon: Assembling Exon Using Gene Capture Data. <i>Evolutionary Bioinformatics</i> , 2019, 15, 117693431987479.	0.6	15
6618	Maternal phylogeographic patterns and coalescent times of <i>Arabidopsis thaliana</i> based on chloroplast DNA analyses. <i>Genes and Genetic Systems</i> , 2019, 94, 151-158.	0.2	0
6619	Characterization of the Complete Chloroplast Genome of an Endemic Perennial Grass <i>Orinus intermedius</i> and Its Phylogenetic Analysis in Poaceae. <i>Cytology and Genetics</i> , 2019, 53, 418-423.	0.2	0
6620	Genomic Analysis of Î ³ -Hexachlorocyclohexane-Degrading <i>Sphingopyxis lindanitolerans</i> WS5A3p Strain in the Context of the Pangenome of <i>Sphingopyxis</i> . <i>Genes</i> , 2019, 10, 688.	1.0	13
6621	<i>Chenopodium ficifolium</i> flowers under long days without upregulation of FLOWERING LOCUS T (FT) homologs. <i>Planta</i> , 2019, 250, 2111-2125.	1.6	16
6622	Phylogenomics disentangles the evolutionary history of spruces (<i>Picea</i>) in the Qinghai-Tibetan Plateau: Implications for the design of population genetic studies and species delimitation of conifers. <i>Molecular Phylogenetics and Evolution</i> , 2019, 141, 106612.	1.2	14
6623	Phylogenomic species delimitation in microendemic frogs of the Brazilian Atlantic Forest. <i>Molecular Phylogenetics and Evolution</i> , 2019, 141, 106627.	1.2	16

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6624	Transcriptomic data support a nocturnal bottleneck in the ancestor of gecko lizards. <i>Molecular Phylogenetics and Evolution</i> , 2019, 141, 106639.	1.2	21
6625	Phage Predation Shapes the Population Structure of Shiga-Toxigenic <i>Escherichia coli</i> O157:H7 in the UK: An Evolutionary Perspective. <i>Frontiers in Genetics</i> , 2019, 10, 763.	1.1	7
6626	<i>Paramoeba aparasomata</i> n. sp., a symbiont-free species, and its relative <i>Paramoeba karteshi</i> n. sp. (Amoebozoa, Dactylopodida). <i>European Journal of Protistology</i> , 2019, 71, 125630.	0.5	8
6627	Assembly and comparative analyses of the mitochondrial genome of <i>Castanospermum australe</i> (Papilionoideae, Leguminosae). <i>Australian Systematic Botany</i> , 2019, 32, 484-494.	0.3	4
6628	Isolation of New Thermophilic Sulfidogens from Microbial Mat Associated with Groundwater Discharge in the Tunkin Valley. <i>Microbiology</i> , 2019, 88, 642-645.	0.5	2
6629	<i>Infundibulicybe kotanensis</i> sp. nov. (Tricholomataceae), a new species from Buner, Pakistan. <i>Phytotaxa</i> , 2019, 418, 195-202.	0.1	5
6630	Morphological and phylogenetic characterization of novel <i>Metarhizium</i> species in Guizhou, China. <i>Phytotaxa</i> , 2019, 419, 189-196.	0.1	5
6631	Genomic analysis of the tryptome reveals molecular mechanisms of gland cell evolution. <i>EvoDevo</i> , 2019, 10, 23.	1.3	21
6632	<i>Vannella samoroda</i> n. sp. (Amoebozoa) – First member of the genus from a continental saline habitat placed in a molecular tree. <i>European Journal of Protistology</i> , 2019, 71, 125634.	0.5	7
6633	Diversity and distribution of Ischnomesidae (Crustacea: Isopoda: Asellota) along the Kuril-Kamchatka Trench – A genetic perspective. <i>Progress in Oceanography</i> , 2019, 178, 102174.	1.5	19
6634	Comprehensive codon usage analysis of porcine deltacoronavirus. <i>Molecular Phylogenetics and Evolution</i> , 2019, 141, 106618.	1.2	13
6635	Single cell ecogenomics reveals mating types of individual cells and ssDNA viral infections in the smallest photosynthetic eukaryotes. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20190089.	1.8	11
6636	An African <i>Salmonella</i> Typhimurium ST313 sublineage with extensive drug-resistance and signatures of host adaptation. <i>Nature Communications</i> , 2019, 10, 4280.	5.8	80
6637	The genus <i>Prototheca</i> (Trebouxiophyceae, Chlorophyta) revisited: Implications from molecular taxonomic studies. <i>Algal Research</i> , 2019, 43, 101639.	2.4	47
6638	Nemerteans from the deep-sea expedition KuramBio II with descriptions of three new hoplonemerteans from the Kuril-Kamchatka Trench. <i>Progress in Oceanography</i> , 2019, 178, 102148.	1.5	27
6639	Extracting phylogenetic signal from phylogenomic data: Higher-level relationships of the nightbirds (Strisores). <i>Molecular Phylogenetics and Evolution</i> , 2019, 141, 106611.	1.2	11
6640	Geography Shapes the Population Genomics of <i>Salmonella enterica</i> Dublin. <i>Genome Biology and Evolution</i> , 2019, 11, 2220-2231.	1.1	23
6641	Taxonomic and Metabolic Incongruence in the Ancient Genus <i>Streptomyces</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 2170.	1.5	40

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6642	Phylogeny and Biogeography of Branchipolynoe (Polynoidae, Phyllodocida, Aciculata, Annelida), with Descriptions of Five New Species from Methane Seeps and Hydrothermal Vents. <i>Diversity</i> , 2019, 11, 153.	0.7	12
6643	Transposable element discovery and characterization of LTR-retrotransposon evolutionary lineages in the tropical fruit species <i>Passiflora edulis</i> . <i>Molecular Biology Reports</i> , 2019, 46, 6117-6133.	1.0	8
6644	Diversity of exotic ectomycorrhizal <i>Rhizopogon</i> from pine plantations in Patagonia. <i>Mycologia</i> , 2019, 111, 782-792.	0.8	1
6645	Complete mitochondrial genomes of two scaphopod molluscs. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3161-3162.	0.2	1
6646	Chromosome-level assembly of the mustache toad genome using third-generation DNA sequencing and Hi-C analysis. <i>GigaScience</i> , 2019, 8, .	3.3	25
6647	Geochemical and Metagenomic Characterization of Jinata Onsen, a Proterozoic-Analog Hot Spring, Reveals Novel Microbial Diversity including Iron-Tolerant Phototrophs and Thermophilic Lithotrophs. <i>Microbes and Environments</i> , 2019, 34, 278-292.	0.7	48
6648	Machine Learning Predicts Accurately <i>Mycobacterium tuberculosis</i> Drug Resistance From Whole Genome Sequencing Data. <i>Frontiers in Genetics</i> , 2019, 10, 922.	1.1	51
6649	Molecular phylogeny of the diatom genera <i>Amphora</i> and <i>Halamphora</i> (Bacillariophyta) with a focus on morphological and ecological evolution. <i>Journal of Phycology</i> , 2019, 55, 442-456.	1.0	40
6650	Genomes of Three Closely Related Caribbean Amazons Provide Insight for Species History and Conservation. <i>Genes</i> , 2019, 10, 54.	1.0	8
6651	Characterization of post-pandemic influenza virus circulation in southern region of Romania during 2010–2014. <i>Infection, Genetics and Evolution</i> , 2019, 69, 85-92.	1.0	1
6652	Effects of missing data and data type on phylotranscriptomic analysis of stony corals (Cnidaria: Scleractinia). <i>Frontiers in Marine Science</i> , 2019, 6, 14.	1.2	14
6653	Penaeid shrimp genome provides insights into benthic adaptation and frequent molting. <i>Nature Communications</i> , 2019, 10, 356.	5.8	328
6654	The first complete chloroplast genome of <i>Zelkova schneideriana</i> Hand.-Mazz. (Ulmaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 378-379.	0.2	2
6655	The complete chloroplast genome of <i>Rhizophora stylosa</i> and its phylogenetic implications. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 374-375.	0.2	7
6656	Phylogeny and phylogeography of the genus <i>Luciobarbus</i> (Haeckel, 1843) in Algeria inferred from mitochondrial DNA sequence variation. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2019, 30, 332-344.	0.7	6
6657	The formation of lunule-like hollows in shells of the acorn barnacle <i>Tetraclitella chinensis</i> (Nilsson-Cantell, 1921), with a reappraisal of the taxonomic status of <i>T. multicostata</i> (Nilsson-Cantell). <i>Journal of Eukaryotic Microbiology</i> , 2019, 66, 694-706.	0.7	14
6658	Black aspergilli: A remaining challenge in fungal taxonomy?. <i>Medical Mycology</i> , 2019, 57, 773-780.	0.3	30
6659	Morphology, Morphogenesis and Molecular Phylogeny of a New Obligately Halophilic Ciliate, <i>Schmidtella ultrahalophila</i> gen. nov., spec. nov. (Ciliophora, Hypotrichia) Isolated from a Volcanic Crater on Sal (Cape Verde Islands). <i>Journal of Eukaryotic Microbiology</i> , 2019, 66, 694-706.	0.8	15

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6660	Causes and analytical impacts of missing data in RADseq phylogenetics: Insights from an African frog (<i>Afrivalus</i>). <i>Zoologica Scripta</i> , 2019, 48, 157-167.	0.7	30
6661	The co-transfer of plasmid-borne colistin-resistant genes <i>mcr-1</i> and <i>mcr-3.5</i> , the carbapenemase gene <i>bla_{NDM-5}</i> and the 16S methylase gene <i>rmtB</i> from <i>Escherichia coli</i> . <i>Scientific Reports</i> , 2019, 9, 696.	1.6	48
6662	Comparative analyses identify genomic features potentially involved in the evolution of birds-of-paradise. <i>GigaScience</i> , 2019, 8, .	3.3	22
6663	A new classification for deep-sea opecoelid trematodes based on the phylogenetic position of some unusual taxa from shallow-water, herbivorous fishes off south-west Australia. <i>Zoological Journal of the Linnean Society</i> , 2019, 186, 385-413.	1.0	22
6664	<i>Chlorococcum turfosum</i> comb. nov. (Volvocales, Chlorophyceae) and visualization of chimeric sequences. <i>Phycological Research</i> , 2019, 67, 239-243.	0.8	5
6665	Biogeography of Korea's top predator, the yellow-throated Marten: evolutionary history and population dynamics. <i>BMC Evolutionary Biology</i> , 2019, 19, 23.	3.2	2
6666	A journey on plate tectonics sheds light on European crayfish phylogeography. <i>Ecology and Evolution</i> , 2019, 9, 1957-1971.	0.8	22
6667	Predictable genome-wide sorting of standing genetic variation during parallel adaptation to basic versus acidic environments in stickleback fish. <i>Evolution Letters</i> , 2019, 3, 28-42.	1.6	41
6668	Potential for Heightened Sulfur-Metabolic Capacity in Coastal Subtropical Microalgae. <i>IScience</i> , 2019, 11, 450-465.	1.9	23
6669	Megaphages infect <i>Prevotella</i> and variants are widespread in gut microbiomes. <i>Nature Microbiology</i> , 2019, 4, 693-700.	5.9	141
6670	Day and Night: Metabolic Profiles and Evolutionary Relationships of Six Axenic Non-Marine Cyanobacteria. <i>Genome Biology and Evolution</i> , 2019, 11, 270-294.	1.1	35
6671	Diverse Lineages of <i>Candida albicans</i> Live on Old Oaks. <i>Genetics</i> , 2019, 211, 277-288.	1.2	54
6672	A Single Interacting Species Leads to Widespread Parallel Evolution of the Stickleback Genome. <i>Current Biology</i> , 2019, 29, 530-537.e6.	1.8	33
6673	Single-cell amplified genomes of two uncultivated members of the deltaproteobacterial SEEP-SRB1 clade, isolated from marine sediment. <i>Marine Genomics</i> , 2019, 46, 66-69.	0.4	14
6674	Ancient origin of a dipteromimid mayfly family endemic to the Japanese Islands and its genetic differentiation across tectonic faults. <i>Biological Journal of the Linnean Society</i> , 2019, 126, 555-573.	0.7	28
6675	Seed size evolution and biogeography of <i>Plukenetia</i> (Euphorbiaceae), a pantropical genus with traditionally cultivated oilseed species. <i>BMC Evolutionary Biology</i> , 2019, 19, 29.	3.2	16
6676	Phylogenetic relationships in two African <i>Cedreloideae</i> tree genera (Meliaceae) reveal multiple rain/dry forest transitions. <i>Perspectives in Plant Ecology, Evolution and Systematics</i> , 2019, 37, 1-10.	1.1	13
6677	The complete chloroplast genome of <i>Isoetes yunguiensis</i> (Isoetaceae), a rare and endangered fern endemic to China. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 563-564.	0.2	4

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6678	Transcriptional Reprogramming of Rice Cells by <i>Xanthomonas oryzae</i> TALEs. <i>Frontiers in Plant Science</i> , 2019, 10, 162.	1.7	38
6679	Comparative Epigenomics Reveals that RNA Polymerase II Pausing and Chromatin Domain Organization Control Nematode piRNA Biogenesis. <i>Developmental Cell</i> , 2019, 48, 793-810.e6.	3.1	37
6680	A new species of the <i>Amphisbaena</i> (<i>Squamata</i> , <i>Amphisbaenidae</i>) from the Brazilian Cerrado with a key for the two-pored species. <i>Zootaxa</i> , 2019, 4550, 301-320.	0.2	7
6681	Two new species of lotic breeding salamanders (<i>Amphibia</i> , <i>Caudata</i> , <i>Hynobiidae</i>) from western Japan. <i>Zootaxa</i> , 2019, 4550, 525-544.	0.2	9
6682	<i>Staphylococcus pseudintermedius</i> septicemia in puppies after elective cesarean section: confirmed transmission via dam's milk. <i>BMC Veterinary Research</i> , 2019, 15, 41.	0.7	16
6683	Hiding in the lianas of the tree of life: Molecular phylogenetics and species delimitation reveal considerable cryptic diversity of New World Vine Snakes. <i>Molecular Phylogenetics and Evolution</i> , 2019, 134, 61-65.	1.2	3
6684	Imaginal disc growth factor 4 regulates development and temperature adaptation in <i>Bactrocera dorsalis</i> . <i>Scientific Reports</i> , 2019, 9, 931.	1.6	17
6685	The complete chloroplast genome sequence of <i>Plantago lagopus</i> L.. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 382-383.	0.2	2
6686	JmjC Domain-Encoding Genes Are Conserved in Highly Regenerative Metazoans and Are Associated with Planarian Whole-Body Regeneration. <i>Genome Biology and Evolution</i> , 2019, 11, 552-564.	1.1	6
6687	Prot-SpaM: fast alignment-free phylogeny reconstruction based on whole-proteome sequences. <i>GigaScience</i> , 2019, 8, .	3.3	19
6688	Plant DNA barcode library and community phylogeny for a semi-arid East African savanna. <i>Molecular Ecology Resources</i> , 2019, 19, 838-846.	2.2	30
6689	Genomic resources for the Neotropical tree genus <i>Cedrela</i> (<i>Meliaceae</i>) and its relatives. <i>BMC Genomics</i> , 2019, 20, 58.	1.2	15
6690	Significance of the goby <i>Zosterisessor ophiocephalus</i> as a sentinel species for Venice Lagoon contamination: Combining biomarker responses and bioaccumulation. <i>Science of the Total Environment</i> , 2019, 660, 959-973.	3.9	1
6691	The complete chloroplast genome of <i>Juniperus tibetica</i> (<i>Cupressaceae</i>), the conifer that occupies the highest known treeline in the Northern Hemisphere. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 609-611.	0.2	5
6692	Diversity of opisthokont septin proteins reveals structural constraints and conserved motifs. <i>BMC Evolutionary Biology</i> , 2019, 19, 4.	3.2	15
6693	Origin and diversification of the plasminogen activation system among chordates. <i>BMC Evolutionary Biology</i> , 2019, 19, 27.	3.2	31
6694	Defining novel plant polyamine oxidase subfamilies through molecular modeling and sequence analysis. <i>BMC Evolutionary Biology</i> , 2019, 19, 28.	3.2	16
6695	Further analyses of variation of ribosome DNA copy number and polymorphism in ciliates provide insights relevant to studies of both molecular ecology and phylogeny. <i>Science China Life Sciences</i> , 2019, 62, 203-214.	2.3	73

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6696	Cultural characterization and chlamydospore function of the Ganodermataceae present in the eastern United States. <i>Mycologia</i> , 2019, 111, 1-12.	0.8	10
6697	Endemic, endangered and evolutionarily significant: cryptic lineages in Seychelles TM frogs (Anura: Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.7	11
6698	Molecular digitization of a botanical garden: high-depth whole-genome sequencing of 689 vascular plant species from the Ruili Botanical Garden. <i>GigaScience</i> , 2019, 8, .	3.3	39
6699	Origin of Gibberellin-Dependent Transcriptional Regulation by Molecular Exploitation of a Transactivation Domain in DELLA Proteins. <i>Molecular Biology and Evolution</i> , 2019, 36, 908-918.	3.5	38
6700	New Phylogenomic Analysis of the Enigmatic Phylum Telonemia Further Resolves the Eukaryote Tree of Life. <i>Molecular Biology and Evolution</i> , 2019, 36, 757-765.	3.5	93
6701	One Health Genomic Surveillance of <i>Escherichia coli</i> Demonstrates Distinct Lineages and Mobile Genetic Elements in Isolates from Humans versus Livestock. <i>MBio</i> , 2019, 10, .	1.8	130
6702	Lectin Sequence Distribution in QTLs from Rice (<i>Oryza sativa</i>) Suggest A Role in Morphological Traits and Stress Responses. <i>International Journal of Molecular Sciences</i> , 2019, 20, 437.	1.8	9
6703	The new genus <i>Symphycladiella</i> gen. nov. (Ceramiales, Rhodophyta) based on <i>S. bartlingiana</i> comb. nov. from the Pacific Ocean. <i>Phycologia</i> , 2019, 58, 9-17.	0.6	7
6704	Newly discovered molecular and ecological diversity within the widely distributed green algal genus <i>Pseudorhizoclonium</i> (Cladophorales, Ulvophyceae). <i>Phycologia</i> , 2019, 58, 83-94.	0.6	6
6705	Gut Virome Analysis of Cameroonians Reveals High Diversity of Enteric Viruses, Including Potential Interspecies Transmitted Viruses. <i>MSphere</i> , 2019, 4, .	1.3	57
6706	Plastome Sequences Help to Resolve Deep-Level Relationships of <i>Populus</i> in the Family Salicaceae. <i>Frontiers in Plant Science</i> , 2019, 10, 5.	1.7	38
6707	Taxonomy of the <i>Sphaerostilbella broomeana</i> -group (Hypocreales, Ascomycota). <i>Mycological Progress</i> , 2019, 18, 77-89.	0.5	10
6708	Molecular detection of a novel <i>Babesia</i> sp. and pathogenic spotted fever group rickettsiae in ticks collected from hedgehogs in Turkey: <i>Haemaphysalis erinacei</i> , a novel candidate vector for the genus <i>Babesia</i> . <i>Infection, Genetics and Evolution</i> , 2019, 69, 190-198.	1.0	18
6709	A molecular survey of <i>Ralfsia</i> sensu stricto (Ralfsiales, Phaeophyceae) in Canada uncovers three new species: <i>R. robertii</i> sp. nov., <i>R. tenebris</i> sp. nov., and <i>R. unimaculata</i> sp. nov.. <i>Botany</i> , 2019, 97, 135-147.	0.5	4
6710	Comparative plastid genomics of Synurophyceae: inverted repeat dynamics and gene content variation. <i>BMC Evolutionary Biology</i> , 2019, 19, 20.	3.2	27
6711	Contrasting evolutionary origins of two mountain endemics: <i>Saxifraga wahlenbergii</i> (Western) Tj ETQq1 1 0.784314 rgBT /Overlock 10	3.25	15
6712	Odontogenic ameloblast-associated (ODAM) is inactivated in toothless/enamelless placental mammals and toothed whales. <i>BMC Evolutionary Biology</i> , 2019, 19, 31.	3.2	22
6713	Highly Resolved Phylogenetic Relationships within Order Acipenseriformes According to Novel Nuclear Markers. <i>Genes</i> , 2019, 10, 38.	1.0	18

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6714	Symbiont type and environmental factors affect transcriptome-wide gene expression in the coral <i>Montipora capitata</i> . <i>Ecology and Evolution</i> , 2019, 9, 378-392.	0.8	9
6715	High frequency and diversity of parechovirus A in a cohort of Malawian children. <i>Archives of Virology</i> , 2019, 164, 799-806.	0.9	18
6716	Hydrogen-based metabolism as an ancestral trait in lineages sibling to the Cyanobacteria. <i>Nature Communications</i> , 2019, 10, 463.	5.8	87
6717	The antimicrobial potential of <i>Streptomyces</i> from insect microbiomes. <i>Nature Communications</i> , 2019, 10, 516.	5.8	222
6718	Genomic regions of speciation and adaptation among three species of grouse. <i>Scientific Reports</i> , 2019, 9, 812.	1.6	8
6719	Rapid Genetic Code Evolution in Green Algal Mitochondrial Genomes. <i>Molecular Biology and Evolution</i> , 2019, 36, 766-783.	3.5	22
6720	Fungal Endophyte Communities of Three Agricultural Important Grass Species Differ in Their Response Towards Management Regimes. <i>Microorganisms</i> , 2019, 7, 37.	1.6	14
6721	Repeated Evolution of Asexuality Involves Convergent Gene Expression Changes. <i>Molecular Biology and Evolution</i> , 2019, 36, 350-364.	3.5	26
6722	Taxon-specific expansion and loss of tektins inform metazoan ciliary diversity. <i>BMC Evolutionary Biology</i> , 2019, 19, 40.	3.2	5
6723	Morphological and molecular characterization of a new species <i>Myxobolus gutturocola</i> n. sp. (Myxozoa: Myxobolidae) from the throat of <i>Hypophthalmichthys molitrix</i> in China. <i>Parasitology Research</i> , 2019, 118, 773-781.	0.6	9
6724	Domain structure and expression along the midgut and carcass of peritrophins and cuticle proteins analogous to peritrophins in insects with and without peritrophic membrane. <i>Journal of Insect Physiology</i> , 2019, 114, 1-9.	0.9	15
6725	Assessing phylogenetic information to reveal uncertainty in historical data: An example using Goodeinae (Teleostei: Cyprinodontiformes: Goodeidae). <i>Molecular Phylogenetics and Evolution</i> , 2019, 134, 282-290.	1.2	6
6726	One fold, two functions: cytochrome P460 and cytochrome <i>c</i> from the methanotroph <i>Methylococcus capsulatus</i> (Bath). <i>Chemical Science</i> , 2019, 10, 3031-3041.	3.7	13
6727	Phylogenetic and morphological analyses of the mycoparasitic genus <i>Piptocephalis</i> . <i>Mycologia</i> , 2019, 111, 54-68.	0.8	9
6728	Integrative taxonomy reveals phenotypic plasticity in the freshwater mussel <i>Conradens contradens</i> (Bivalvia: Unionidae) in Thailand, with a description of a new species. <i>Systematics and Biodiversity</i> , 2019, 17, 134-147.	0.5	17
6729	Global survey of mobile DNA horizontal transfer in arthropods reveals Lepidoptera as a prime hotspot. <i>PLoS Genetics</i> , 2019, 15, e1007965.	1.5	41
6730	Tandem gene duplication and recombination at the AT3 locus in the Solanaceae, a gene essential for capsaicinoid biosynthesis in <i>Capsicum</i> . <i>PLoS ONE</i> , 2019, 14, e0210510.	1.1	11
6731	De novo assembly of white poplar genome and genetic diversity of white poplar population in Irtys River basin in China. <i>Science China Life Sciences</i> , 2019, 62, 609-618.	2.3	55

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6732	Phylogeny and molecular species delimitation of long-nosed armadillos (<i>Dasybus: Cingulata</i>) supports morphology-based taxonomy. <i>Zoological Journal of the Linnean Society</i> , 2019, 186, 813-825.	1.0	27
6733	Comparative transcriptomics of 3 high-altitude passerine birds and their low-altitude relatives. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 11851-11856.	3.3	63
6734	The complete plastid genome of carnivorous pitcher plant <i>Cephalotus follicularis</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2025-2027.	0.2	5
6735	Stress-Free Evolution: The Nrf-Coordinated Oxidative Stress Response in Early Diverging Metazoans. <i>Integrative and Comparative Biology</i> , 2019, 59, 799-810.	0.9	9
6736	Structure and evolution of the 4-helix bundle domain of Zuotin, a J-domain protein co-chaperone of Hsp70. <i>PLoS ONE</i> , 2019, 14, e0217098.	1.1	8
6737	Naked <i>Chrysochromulina</i> (Haptophyta) isolates from lake and river ecosystems: An electron microscopic comparison including new observations on the type species of this taxon. <i>Algal Research</i> , 2019, 40, 101492.	2.4	4
6738	The complete organelle genomes of <i>Physochlaina orientalis</i> : Insights into short sequence repeats across seed plant mitochondrial genomes. <i>Molecular Phylogenetics and Evolution</i> , 2019, 137, 274-284.	1.2	19
6739	Phylogeography of <i>Sodreaninae</i> harvestmen (Arachnida: Opiliones: Gonyleptidae): Insights into the biogeography of the southern Brazilian Atlantic Forest. <i>Molecular Phylogenetics and Evolution</i> , 2019, 138, 1-16.	1.2	18
6740	Multiple Lineages of Dengue Virus Serotype 2 Cosmopolitan Genotype Caused a Local Dengue Outbreak in Hangzhou, Zhejiang Province, China, in 2017. <i>Scientific Reports</i> , 2019, 9, 7345.	1.6	11
6741	Phylogenomics, biogeography and evolution in the American genus <i>Brahea</i> (Arecaceae). <i>Botanical Journal of the Linnean Society</i> , 2019, 190, 242-259.	0.8	14
6742	Morphology, phylogeny and taxonomy of the genus <i>Sectonema</i> (Nematoda, Aporcelaimidae). <i>Zoologica Scripta</i> , 2019, 48, 535-544.	0.7	4
6743	Morphological Plasticity in a Sulfur-Oxidizing Marine Bacterium from the SUP05 Clade Enhances Dark Carbon Fixation. <i>MBio</i> , 2019, 10, .	1.8	24
6744	Genomic evidence of the illumination response mechanism and evolutionary history of magnetotactic bacteria within the <i>Rhodospirillaceae</i> family. <i>BMC Genomics</i> , 2019, 20, 407.	1.2	8
6745	New insights from <i>Opisthorchis felinus</i> genome: update on genomics of the epidemiologically important liver flukes. <i>BMC Genomics</i> , 2019, 20, 399.	1.2	29
6746	Genome-wide identification of MST, SUT and SWEET family sugar transporters in root parasitic angiosperms and analysis of their expression during host parasitism. <i>BMC Plant Biology</i> , 2019, 19, 196.	1.6	26
6747	Proteome and allergenome of the European house dust mite <i>Dermatophagoides pteronyssinus</i> . <i>PLoS ONE</i> , 2019, 14, e0216171.	1.1	26
6748	Early Sex-Chromosome Evolution in the Diploid Dioecious Plant <i>Mercurialis annua</i> . <i>Genetics</i> , 2019, 212, 815-835.	1.2	53
6749	<i>Parakarstenia phyllostachydis</i> , a new genus and species of non-lichenized <i>Odontotremataceae</i> (Ostropales, Ascomycota). <i>Mycological Progress</i> , 2019, 18, 833-845.	0.5	12

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6750	Drivers of sociality in Gobiodon fishes: An assessment of phylogeny, ecology and life-history. <i>Molecular Phylogenetics and Evolution</i> , 2019, 137, 263-273.	1.2	6
6751	Higher-level phylogenetic affinities of the Neotropical genus <i>Mastigodryas</i> Amaral, 1934 (Serpentes: Colubridae), species-group definition and description of a new genus for <i>Mastigodryas bifossatus</i> . <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2019, 57, 205-239.	0.6	8
6752	Diversity and evolution of African Grass Rats (Muridae: <i>Arvicanthis</i>) – From radiation in East Africa to repeated colonization of northwestern and southeastern savannas. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2019, 57, 970-988.	0.6	34
6753	Differences in flowering time maintain species boundaries in a continental radiation of <i>Viburnum</i> . <i>American Journal of Botany</i> , 2019, 106, 833-849.	0.8	19
6754	Recent emergence and extinction of the protection of telomeres 1c gene in <i>Arabidopsis thaliana</i> . <i>Plant Cell Reports</i> , 2019, 38, 1081-1097.	2.8	6
6755	The pioneer lichen <i>Placopsis</i> in maritime Antarctica: Genetic diversity of their mycobionts and green algal symbionts, and their correlation with deglaciation time. <i>Symbiosis</i> , 2019, 79, 1-24.	1.2	19
6756	Advanced understanding of phylogenetic relationships, morphological evolution and biogeographic history of the mega-diverse plant genus <i>Myrcia</i> and its relatives (Myrtaceae: Myrteae). <i>Molecular Phylogenetics and Evolution</i> , 2019, 138, 65-88.	1.2	24
6757	Role of geography and climatic oscillations in governing into-India dispersal of freshwater snails of the family: Viviparidae. <i>Molecular Phylogenetics and Evolution</i> , 2019, 138, 174-181.	1.2	12
6758	Genome Plasticity in Papillomaviruses and De Novo Emergence of E5 Oncogenes. <i>Genome Biology and Evolution</i> , 2019, 11, 1602-1617.	1.1	14
6759	Natural <i>Wolbachia</i> infections are common in the major malaria vectors in Central Africa. <i>Evolutionary Applications</i> , 2019, 12, 1583-1594.	1.5	36
6760	Genetic variation of the most abundant forest-dwelling rodents in Central Africa (<i>Praomys</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 3 of Biogeography, 2019, 46, 1466-1478.	1.4	27
6761	Global phylodynamic analysis of avian paramyxovirus-1 provides evidence of inter-host transmission and intercontinental spatial diffusion. <i>BMC Evolutionary Biology</i> , 2019, 19, 108.	3.2	38
6762	Sequence-based identification of <i>Anopheles</i> species in eastern Ethiopia. <i>Malaria Journal</i> , 2019, 18, 135.	0.8	24
6763	A century of gray: A genomic locus found in 2 distinct <i>Pseudomonas</i> spp. is associated with historical and contemporary color defects in dairy products worldwide. <i>Journal of Dairy Science</i> , 2019, 102, 5979-6000.	1.4	20
6764	NCP activates chloroplast transcription by controlling phytochrome-dependent dual nuclear and plastidial switches. <i>Nature Communications</i> , 2019, 10, 2630.	5.8	38
6765	Genomic signatures of heterokaryosis in the oomycete pathogen <i>Bremia lactucae</i> . <i>Nature Communications</i> , 2019, 10, 2645.	5.8	67
6766	Orb-weaving spider <i>Araneus ventricosus</i> genome elucidates the spidroin gene catalogue. <i>Scientific Reports</i> , 2019, 9, 8380.	1.6	76
6767	Characterization of the complete chloroplast genome of <i>Incarvillea arguta</i> (Bignoniaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1603-1604.	0.2	2

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6768	The complete chloroplast genome sequence of <i>Actinidia cylindrica</i> C. F. Liang. Mitochondrial DNA Part B: Resources, 2019, 4, 1694-1695.	0.2	0
6769	Mitochondrial Architecture Rearrangements Produce Asymmetrical Nonadaptive Mutational Pressures That Subvert the Phylogenetic Reconstruction in Isopoda. Genome Biology and Evolution, 2019, 11, 1797-1812.	1.1	31
6770	Recombination-Aware Phylogenomics Reveals the Structured Genomic Landscape of Hybridizing Cat Species. Molecular Biology and Evolution, 2019, 36, 2111-2126.	3.5	98
6771	Genetic and Genomic Analyses Reveal Boundaries between Species Closely Related to <i>Cryptococcus</i> Pathogens. MBio, 2019, 10, .	1.8	37
6772	Genetic Analysis and Evolutionary Changes of the Torque teno sus Virus. International Journal of Molecular Sciences, 2019, 20, 2881.	1.8	17
6773	<i>Umbilicaria subpolyphylla</i> Oxner: the correct name for <i>U. iberica</i> Sancho & Krzewicka and its bipolar distribution pattern. Lichenologist, 2019, 51, 205-220.	0.5	7
6774	Characterisation of <i>Nesoa latifolia</i> (Halymeniaceae, Rhodophyta) from Europe with emphasis on cystocarp development and description of <i>Nesoa mediterranea</i> sp. nov. Phycologia, 2019, 58, 393-404.	0.6	7
6775	DNA barcoding of the rodent genus <i>Oligoryzomys</i> (Cricetidae: Sigmodontinae): mitochondrial-anchored database and identification of nuclear mitochondrial translocations (Numts). Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2019, 30, 702-712.	0.7	6
6776	Aquatic Adaptation and Depleted Diversity: A Deep Dive into the Genomes of the Sea Otter and Giant Otter. Molecular Biology and Evolution, 2019, 36, 2631-2655.	3.5	48
6777	Identifying Clusters of High Confidence Homologies in Multiple Sequence Alignments. Molecular Biology and Evolution, 2019, 36, 2340-2351.	3.5	108
6778	Genetic changes associated with the temporal shift in invasive non-typhoidal Salmonella serovars in Bamako Mali. PLoS Neglected Tropical Diseases, 2019, 13, e0007297.	1.3	4
6779	<i>Bacillus cereus</i> "Attributable Primary Cutaneous Anthrax-Like Infection in Newborn Infants, India. Emerging Infectious Diseases, 2019, 25, 1261-1270.	2.0	15
6780	Insight into picophytoplankton diversity of the subarctic White Sea "The first recording of Pedinophyceae in environmental DNA. MicrobiologyOpen, 2019, 8, e892.	1.2	5
6781	Using INC Within Divide-and-Conquer Phylogeny Estimation. Lecture Notes in Computer Science, 2019, , 167-178.	1.0	5
6782	Taxonomy and the evolutionary history of Micropeltidaceae. Fungal Diversity, 2019, 97, 393-436.	4.7	17
6783	<i>Chlamydia buteonis</i> , a new <i>Chlamydia</i> species isolated from a red-shouldered hawk. Systematic and Applied Microbiology, 2019, 42, 125997.	1.2	45
6784	Ancient introgression drives adaptation to cooler and drier mountain habitats in a cypress species complex. Communications Biology, 2019, 2, 213.	2.0	64
6785	Complete plastome of <i>Toricellia tiliifolia</i> (Toricelliaceae), a relict plant. Mitochondrial DNA Part B: Resources, 2019, 4, 1535-1536.	0.2	0

#	ARTICLE	IF	CITATIONS
6786	Towards a new classification of tribe Stachydeae (Lamiaceae): naming clades using molecular evidence. <i>Botanical Journal of the Linnean Society</i> , 2019, 190, 345-358.	0.8	14
6787	'Candidatus <i>Ornithobacterium hominis</i> ': insights gained from draft genomes obtained from nasopharyngeal swabs. <i>Microbial Genomics</i> , 2019, 5, .	1.0	16
6788	Molecular phylogeny of <i>Himalopsyche</i> (Trichoptera, Rhyacophilidae). <i>Systematic Entomology</i> , 2019, 44, 973-984.	1.7	4
6789	Relict distribution of <i>Microhyla</i> (Amphibia: Microhylidae) in the Ryukyu Archipelago: High diversity in East Asia maintained by insularization. <i>Zoologica Scripta</i> , 2019, 48, 440-453.	0.7	12
6790	Large-scale ruminant genome sequencing provides insights into their evolution and distinct traits. <i>Science</i> , 2019, 364, .	6.0	266
6791	Biological adaptations in the Arctic cervid, the reindeer (<i>Rangifer tarandus</i>). <i>Science</i> , 2019, 364, .	6.0	58
6792	Phylogenomics Provides New Insights into Gains and Losses of Selenoproteins among Archaeplastida. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3020.	1.8	10
6793	A Next-Generation Sequencing-Based Approach to Identify Genetic Determinants of Antibiotic Resistance in Cambodian <i>Helicobacter pylori</i> Clinical Isolates. <i>Journal of Clinical Medicine</i> , 2019, 8, 858.	1.0	52
6794	Embryonic development of a parthenogenetic vertebrate, the mourning gecko (<i>Lepidodactylus</i>). <i>Journal of Herpetology</i> , 2019, 53, 101-109.	0.8	19
6795	The Dancing Star: Reinvestigation of <i>Artodiscus saltans</i> (Variosea, Amoebozoa) Penard 1890. <i>Protist</i> , 2019, 170, 349-357.	0.6	4
6796	Multiple historical processes obscure phylogenetic relationships in a taxonomically difficult group (Lobariaceae, Ascomycota). <i>Scientific Reports</i> , 2019, 9, 8968.	1.6	32
6797	Pulcherrimin formation controls growth arrest of the <i>Bacillus subtilis</i> biofilm. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 13553-13562.	3.3	46
6798	Delimitation of sympatric <i>Palaemon</i> (Decapoda, Palaemonidae) species of the Laguna Madre, Mexico. <i>Zoologica Scripta</i> , 2019, 48, 667-678.	0.7	3
6799	For common community phylogenetic analyses, go ahead and use synthesis phylogenies. <i>Ecology</i> , 2019, 100, e02788.	1.5	80
6800	Infection Rates and Alkaloid Patterns of Different Grass Species with Systemic <i>Epichloa</i> Endophytes. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	18
6801	Fierce Selection and Interference in B-Cell Repertoire Response to Chronic HIV-1. <i>Molecular Biology and Evolution</i> , 2019, 36, 2184-2194.	3.5	46
6802	Chloroplast phylogenomic data support Eocene amphipacific early radiation for the Asian Palmate core Araliaceae. <i>Journal of Systematics and Evolution</i> , 2019, 57, 547-560.	1.6	49
6803	Phylogeny of the ciliate family Psilotrichidae (Protista, Ciliophora), a curious and poorly-known taxon, with notes on two algae-bearing psilotrichids from Guam, USA. <i>BMC Evolutionary Biology</i> , 2019, 19, 125.	3.2	32

#	ARTICLE	IF	CITATIONS
6804	Emergence of phylogenetically diverse and fluoroquinolone resistant Salmonella Enteritidis as a cause of invasive nontyphoidal Salmonella disease in Ghana. PLoS Neglected Tropical Diseases, 2019, 13, e0007485.	1.3	30
6805	Revalidation and redescription of Steindachnerina nigrotaenia and redescription of <i>S. insculpta</i> (Characiformes: Curimatidae). Neotropical Ichthyology, 2019, 17, .	0.5	1
6806	The Four FAD-Dependent Histone Demethylases of Arabidopsis Are Differently Involved in the Control of Flowering Time. Frontiers in Plant Science, 2019, 10, 669.	1.7	21
6807	Psychoactive plant- and mushroom-associated alkaloids from two behavior modifying cicada pathogens. Fungal Ecology, 2019, 41, 147-164.	0.7	55
6808	The origins and adaptation of European potatoes reconstructed from historical genomes. Nature Ecology and Evolution, 2019, 3, 1093-1101.	3.4	73
6809	Thermal Niche Differentiation in the Benthic Diatom <i>Cylindrotheca closterium</i> (Bacillariophyceae) Complex. Frontiers in Microbiology, 2019, 10, 1395.	1.5	21
6810	Fungal diversity notes 1036–1150: taxonomic and phylogenetic contributions on genera and species of fungal taxa. Fungal Diversity, 2019, 96, 1-242.	4.7	148
6811	Genomic identification of cryptic susceptibility to penicillins and β -lactamase inhibitors in methicillin-resistant <i>Staphylococcus aureus</i> . Nature Microbiology, 2019, 4, 1680-1691.	5.9	47
6812	Whole-genome comparative analysis of <i>Campylobacter jejuni</i> strains isolated from patients with diarrhea in northeastern Poland. Gut Pathogens, 2019, 11, 32.	1.6	24
6813	Evolution of protein kinase substrate recognition at the active site. PLoS Biology, 2019, 17, e3000341.	2.6	52
6814	<i>Araucaria angustifolia</i> chloroplast genome sequence and its relation to other Araucariaceae. Genetics and Molecular Biology, 2019, 42, 671-676.	0.6	6
6815	Genetic diversity of Hepatozoon (Apicomplexa) from domestic cats in South Africa, with a global reassessment of <i>Hepatozoon felis</i> diversity. Journal of the South African Veterinary Association, 2019, 90, e1-e6.	0.2	5
6816	A Genetically Tractable, Natural Mouse Model of Cryptosporidiosis Offers Insights into Host Protective Immunity. Cell Host and Microbe, 2019, 26, 135-146.e5.	5.1	72
6817	Mosaic origin of the eukaryotic kinetochore. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 12873-12882.	3.3	76
6818	Phylogenomic Analysis of a Putative Missing Link Sparks Reinterpretation of Leech Evolution. Genome Biology and Evolution, 2019, 11, 3082-3093.	1.1	22
6819	When Is A Lineage A Species? A Case Study In <i>Myxocorys</i> gen. nov. (Synechococcales) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T 2019, 55, 976-996.	1.0	51
6820	<i>Begonia balangcodiae</i> sp. nov. from northern Luzon, the Philippines and its natural hybrid with <i>B. crispipila</i> , <i>B. kapangan</i> nothosp. nov.. Phytotaxa, 2019, 407, 5-21.	0.1	7
6821	Serotype-specific evolutionary patterns of antimicrobial-resistant <i>Salmonella enterica</i> . BMC Evolutionary Biology, 2019, 19, 132.	3.2	20

#	ARTICLE	IF	CITATIONS
6822	Long-read based de novo assembly of low-complexity metagenome samples results in finished genomes and reveals insights into strain diversity and an active phage system. <i>BMC Microbiology</i> , 2019, 19, 143.	1.3	104
6823	A new record of <i>Lamellibrachia columna</i> (Siboglinidae, Annelida) from cold seeps off New Zealand, and an assessment of its presence in the western Pacific Ocean. <i>Marine Biodiversity Records</i> , 2019, 12, .	1.2	10
6824	Comparative genome analysis indicates high evolutionary potential of pathogenicity genes in <i>Colletotrichum tanacetii</i> . <i>PLoS ONE</i> , 2019, 14, e0212248.	1.1	19
6825	Species delimitation and evolutionary reconstruction within an integrative taxonomic framework: A case study on <i>Rhinolophus macrotis</i> complex (Chiroptera: Rhinolophidae). <i>Molecular Phylogenetics and Evolution</i> , 2019, 139, 106544.	1.2	15
6826	Expansion of vomeronasal receptor genes (OlfC) in the evolution of fright reaction in Ostariophysan fishes. <i>Communications Biology</i> , 2019, 2, 235.	2.0	16
6827	The ecology and evolution of autotomy. <i>Biological Reviews</i> , 2019, 94, 1881-1896.	4.7	58
6828	Variability in Genomic and Virulent Properties of <i>Porphyromonas gingivalis</i> Strains Isolated From Healthy and Severe Chronic Periodontitis Individuals. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 246.	1.8	19
6829	A comparison of termite assemblages from West African savannah and forest ecosystems using morphological and molecular markers. <i>PLoS ONE</i> , 2019, 14, e0216986.	1.1	8
6830	High-Quality Library Preparation for NGS-Based Immunoglobulin Germline Gene Inference and Repertoire Expression Analysis. <i>Frontiers in Immunology</i> , 2019, 10, 660.	2.2	55
6831	Phylogenetic conservation of bacterial responses to soil nitrogen addition across continents. <i>Nature Communications</i> , 2019, 10, 2499.	5.8	48
6832	Characterization of the complete chloroplast genome of <i>Camellia rensanxiangiae</i> (Theaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1490-1491.	0.2	1
6833	HCV resistance compartmentalization within tumoral and non-tumoral liver in transplanted patients with hepatocellular carcinoma. <i>Liver International</i> , 2019, 39, 1986-1998.	1.9	6
6834	A mitochondrial genome phylogeny of Mytilidae (Bivalvia: Mytilida). <i>Molecular Phylogenetics and Evolution</i> , 2019, 139, 106533.	1.2	41
6835	Sequence capture using AFLP-generated baits: A cost-effective method for high-throughput phylogenetic and phylogeographic analysis. <i>Ecology and Evolution</i> , 2019, 9, 5925-5937.	0.8	4
6836	Whole-genome sequencing reveals recent and frequent genetic recombination between clonal lineages of <i>Cryphonectria parasitica</i> in western Europe. <i>Fungal Genetics and Biology</i> , 2019, 130, 122-133.	0.9	16
6837	Beneath the surface: Evolution of methane activity in the bacterial multicomponent monooxygenases. <i>Molecular Phylogenetics and Evolution</i> , 2019, 139, 106527.	1.2	12
6838	Untangling a mess of worms: Species delimitations reveal morphological crypsis and variability in Southeast Asian semi-aquatic earthworms (Almidae, Glyphidrilus). <i>Molecular Phylogenetics and Evolution</i> , 2019, 139, 106531.	1.2	12
6839	Comparative genomics provides new insights into the remarkable adaptations of the African wild dog (<i>Lycaon pictus</i>). <i>Scientific Reports</i> , 2019, 9, 8329.	1.6	23

#	ARTICLE	IF	CITATIONS
6840	The antenna-like domain of the cyanobacterial ferrochelatase can bind chlorophyll and carotenoids in an energy-dissipative configuration. <i>Journal of Biological Chemistry</i> , 2019, 294, 11131-11143.	1.6	21
6841	The complete chloroplast genome of <i>Malus sieversii</i> (Rosaceae), a wild apple tree in Xinjiang, China. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 983-984.	0.2	3
6842	The Globe Artichoke Genome. <i>Compendium of Plant Genomes</i> , 2019, , .	0.3	1
6843	Ancient Mitogenomes Reveal the Evolutionary History and Biogeography of Sloths. <i>Current Biology</i> , 2019, 29, 2031-2042.e6.	1.8	99
6844	Isolation and characterization of a thermophilic sulfur- and iron-reducing thaumarchaeote from a terrestrial acidic hot spring. <i>ISME Journal</i> , 2019, 13, 2465-2474.	4.4	26
6845	Shortcomings of Phylogenetic Studies on Recent Radiated Insular Groups: A Meta-Analysis Using Cabo Verde Biodiversity. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2782.	1.8	10
6847	High rate of occult hepatitis B virus infection in hemodialysis units of KwaZulu-Natal, South Africa. <i>Journal of Medical Virology</i> , 2019, 91, 1797-1803.	2.5	3
6848	Type I interferon induced by TLR2-TLR4-MyD88-TRIF-IRF3 controls <i>Mycobacterium abscessus</i> subsp. <i>abscessus</i> persistence in murine macrophages via nitric oxide. <i>International Journal of Medical Microbiology</i> , 2019, 309, 307-318.	1.5	16
6849	The Genomic and Immune Landscapes of Lethal Metastatic Breast Cancer. <i>Cell Reports</i> , 2019, 27, 2690-2708.e10.	2.9	95
6850	A multigene timescale and diversification dynamics of Ciliophora evolution. <i>Molecular Phylogenetics and Evolution</i> , 2019, 139, 106521.	1.2	37
6851	Identification of 13 <i>Spirogyra</i> species (Zygnemataceae) by traits of sexual reproduction induced under laboratory culture conditions. <i>Scientific Reports</i> , 2019, 9, 7458.	1.6	17
6852	Phenology in a warming world: differences between native and non-native plant species. <i>Ecology Letters</i> , 2019, 22, 1253-1263.	3.0	62
6853	Exploring the Biodiversity of Understudied Benthic Taxa at Mesophotic and Deeper Depths: Examples From the Order Zoantharia (Anthozoa: Hexacorallia). <i>Frontiers in Marine Science</i> , 2019, 6, .	1.2	16
6854	Proteomic fingerprinting for the fast and accurate identification of species in the Polyporoid and Hymenochaetoid fungi clades. <i>Journal of Proteomics</i> , 2019, 203, 103390.	1.2	7
6855	NOTES ON CYRTANDRA (GESNERIACEAE) FROM JAPAN, TAIWAN AND BATAN ISLAND (PHILIPPINES). <i>Edinburgh Journal of Botany</i> , 2019, 76, 333-344.	0.4	3
6856	Mitochondrial gene rearrangement and phylogenetic relationships in the Amphilepidida and Ophiacanthida (Echinodermata, Ophiuroidea). <i>Marine Biology Research</i> , 2019, 15, 26-35.	0.3	8
6857	The characteristics and phylogenetic relationship of two complete mitochondrial genomes of <i>Matrona basilaris</i> (Odonata: Zygoptera: Calopterygidae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1745-1747.	0.2	4
6858	The complete chloroplast genome sequence of <i>Castanopsis carlesii</i> (Fagaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2076-2077.	0.2	1

#	ARTICLE	IF	CITATIONS
6859	Unprecedented Parallel Photosynthetic Losses in a Heterotrophic Orchid Genus. <i>Molecular Biology and Evolution</i> , 2019, 36, 1884-1901.	3.5	38
6860	A Fast Likelihood Method to Reconstruct and Visualize Ancestral Scenarios. <i>Molecular Biology and Evolution</i> , 2019, 36, 2069-2085.	3.5	153
6861	Presence and genetic variability of <i>Piscine orthoreovirus</i> genotype 1 (PRV α) in wild salmonids in Northern Europe and North Atlantic Ocean. <i>Journal of Fish Diseases</i> , 2019, 42, 1107-1118.	0.9	11
6862	Two Coxsackievirus B3 outbreaks associated with hand, foot, and mouth disease in China and the evolutionary history worldwide. <i>BMC Infectious Diseases</i> , 2019, 19, 466.	1.3	23
6863	A Systematic Approach to Identify and Characterize the Effectiveness and Safety of Novel Probiotic Strains to Control Foodborne Pathogens. <i>Frontiers in Microbiology</i> , 2019, 10, 1108.	1.5	37
6864	Mitochondrial genetic population structure and variation of the littoral earthworm <i>Pontodrilus longissimus</i> Seesamut and Panha, 2018 along the coast of Thailand. <i>European Journal of Soil Biology</i> , 2019, 93, 103091.	1.4	6
6865	Revision of freshwater shrimps belonging to <i>Caridina weberi</i> complex (Crustacea: Decapoda: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 815-847.	0.2	1
6866	Complete chloroplast genome sequence of <i>Dracaena cochinchinensis</i> : genome structure and genomic resources. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1750-1751.	0.2	3
6867	The complete chloroplast genome sequence and phylogenetic analysis of <i>Flaveria bidentis</i> (L.) Kuntze, an invasive alien plant species in China. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2021-2022.	0.2	0
6868	A key metabolic gene for recurrent freshwater colonization and radiation in fishes. <i>Science</i> , 2019, 364, 886-889.	6.0	109
6869	Phylogenomic Approaches to DNA Barcoding of Herbal Medicines: Developing Clade-Specific Diagnostic Characters for Berberis. <i>Frontiers in Plant Science</i> , 2019, 10, 586.	1.7	28
6870	Genetic analysis and evolutionary changes of Porcine circovirus 2. <i>Molecular Phylogenetics and Evolution</i> , 2019, 139, 106520.	1.2	36
6871	Diversification in gravel beaches: A radiation of interstitial clingfish (<i>Gouania</i> , Gobiesocidae) in the Mediterranean Sea. <i>Molecular Phylogenetics and Evolution</i> , 2019, 139, 106525.	1.2	14
6872	Detection and characterization of a novel marine birnavirus isolated from Asian seabass in Singapore. <i>Virology Journal</i> , 2019, 16, 71.	1.4	13
6873	Mitochondrial genome diversity and evolution in Branchiopoda (Crustacea). <i>Zoological Letters</i> , 2019, 5, 15.	0.7	16
6874	Exploring protein myristoylation in <i>Toxoplasma gondii</i> . <i>Experimental Parasitology</i> , 2019, 203, 8-18.	0.5	11
6875	Unraveling the phylogenetic relationships of the extinct bovid <i>Myotragus balearicus</i> Bate 1909 from the Balearic Islands. <i>Quaternary Science Reviews</i> , 2019, 215, 185-195.	1.4	21
6876	<i>Chromulinavorax destructans</i> , a pathogen of microzooplankton that provides a window into the enigmatic candidate phylum <i>Dependentiae</i> . <i>PLoS Pathogens</i> , 2019, 15, e1007801.	2.1	59

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6877	Genome Analysis of <i>Hypomyces perniciosus</i> , the Causal Agent of Wet Bubble Disease of Button Mushroom (<i>Agaricus bisporus</i>). <i>Genes</i> , 2019, 10, 417.	1.0	17
6878	A comparative genomics approach for identifying host-range determinants in <i>Streptococcus thermophilus</i> bacteriophages. <i>Scientific Reports</i> , 2019, 9, 7991.	1.6	26
6879	Phylogenetic relationships of <i>Phaeochorella parinari</i> and recognition of a new family, Phaeochorellaceae (Diaporthales). <i>Mycologia</i> , 2019, 111, 660-675.	0.8	11
6880	Combing Transcriptomes for Secrets of Deep-Sea Survival: Environmental Diversity Drives Patterns of Protein Evolution. <i>Integrative and Comparative Biology</i> , 2019, 59, 786-798.	0.9	4
6881	A global survey of arsenic-related genes in soil microbiomes. <i>BMC Biology</i> , 2019, 17, 45.	1.7	70
6882	Isolation of Subtype 3c, 3e and 3f-Like Hepatitis E Virus Strains Stably Replicating to High Viral Loads in an Optimized Cell Culture System. <i>Viruses</i> , 2019, 11, 483.	1.5	32
6883	Metabolic versatility in a modern lineage of cyanobacteria from terrestrial hot springs. <i>Free Radical Biology and Medicine</i> , 2019, 140, 224-232.	1.3	20
6884	Phylogenomic analyses reveal intractable evolutionary history of a temperate bamboo genus (Poaceae: <i>Tj ETQq1 1,0,784314,rgBT /Oe</i>). <i>Plant Systematics and Evolution</i> , 2019, 263, 1483-1494.	1.8	14
6885	Metabolic Consequences of Cobalamin Scarcity in the Diatom <i>Thalassiosira pseudonana</i> as Revealed Through Metabolomics. <i>Protist</i> , 2019, 170, 328-348.	0.6	33
6886	Speciation across mountains: Phylogenomics, species delimitation and taxonomy of the <i>Liolaemus leopardinus</i> clade (Squamata, Liolaemidae). <i>Molecular Phylogenetics and Evolution</i> , 2019, 139, 106524.	1.2	28
6887	Recent Secondary Contacts, Linked Selection, and Variable Recombination Rates Shape Genomic Diversity in the Model Species <i>Anolis carolinensis</i> . <i>Genome Biology and Evolution</i> , 2019, 11, 2009-2022.	1.1	29
6888	Genome-wide SNP Data Reveal an Overestimation of Species Diversity in a Group of Hawkmoths. <i>Genome Biology and Evolution</i> , 2019, 11, 2136-2150.	1.1	35
6889	Phylogenomic analyses and distribution of terpene synthases among <i>Streptomyces</i> . <i>Beilstein Journal of Organic Chemistry</i> , 2019, 15, 1181-1193.	1.3	28
6890	Realgar (As ₄ S ₄) bioprecipitation in microcosm fed by a natural groundwater and organic matter. <i>Environmental Science and Pollution Research</i> , 2019, 26, 18766-18776.	2.7	8
6891	Metagenomic analysis exhibited the co-metabolism of polycyclic aromatic hydrocarbons by bacterial community from estuarine sediment. <i>Environment International</i> , 2019, 129, 308-319.	4.8	93
6892	Ancient <i>Yersinia pestis</i> genomes from across Western Europe reveal early diversification during the First Pandemic (541â€“750). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 12363-12372.	3.3	100
6893	Complex Gene Loss and Duplication Events Have Facilitated the Evolution of Multiple Loricrin Genes in Diverse Bird Species. <i>Genome Biology and Evolution</i> , 2019, 11, 984-1001.	1.1	12
6894	Phylogenomics Reveals an Ancient Hybrid Origin of the Persian Walnut. <i>Molecular Biology and Evolution</i> , 2019, 36, 2451-2461.	3.5	79

#	ARTICLE	IF	CITATIONS
6895	Diversification of light capture ability was accompanied by the evolution of phycobiliproteins in cryptophyte algae. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20190655.	1.2	24
6896	Identification of Y chromosome scaffolds of the Queensland fruit fly reveals a duplicated <i>gyf</i> gene paralogue common to many <i>Bactrocera</i> pest species. <i>Insect Molecular Biology</i> , 2019, 28, 873-886.	1.0	10
6897	Hybrid enrichment of poorly preserved museum specimens refines homology hypotheses in a group of minute litter bugs (Hemiptera: Dipsocoromorpha: Schizopteridae). <i>Systematic Entomology</i> , 2019, 44, 985-995.	1.7	5
6898	Revision of the genus <i>Exsuperantia</i> Zdikmen, 2009 (Tetractinellida: Phymaraphiniidae) with description of a new species from the Atlantic Ocean. <i>Zootaxa</i> , 2019, 4613, zootaxa.4613.1.7.	0.2	4
6899	Comparative Genomics of <i>Thiohalobacter thiocyanaticus</i> HRh1T and <i>Guyarkeria</i> sp. SCN-R1, Halophilic Chemolithoautotrophic Sulfur-Oxidizing Gammaproteobacteria Capable of Using Thiocyanate as Energy Source. <i>Frontiers in Microbiology</i> , 2019, 10, 898.	1.5	20
6900	Proteases Underground: Analysis of the Maize Root Apoplast Identifies Organ Specific Papain-Like Cysteine Protease Activity. <i>Frontiers in Plant Science</i> , 2019, 10, 473.	1.7	15
6901	The population history of northeastern Siberia since the Pleistocene. <i>Nature</i> , 2019, 570, 182-188.	13.7	259
6902	On the occurrence of cytochrome P450 in viruses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 12343-12352.	3.3	45
6903	The male and female complete mitochondrial genomes of the threatened freshwater pearl mussel <i>Margaritifera margaritifera</i> (Linnaeus, 1758) (Bivalvia: Margaritiferidae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1417-1420.	0.2	8
6904	A natural point mutation in the bitter taste receptor TAS2R16 causes inverse agonism of arbutin in lemur gustation. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20190884.	1.2	10
6905	Diversification of Hawaiian <i>Cyrtandra</i> (Gesneriaceae) under the influence of incomplete lineage sorting and hybridization. <i>Journal of Systematics and Evolution</i> , 2019, 57, 561-578.	1.6	32
6906	Species delimitation of neotropical Characins (Stevardiinae): Implications for taxonomy of complex groups. <i>PLoS ONE</i> , 2019, 14, e0216786.	1.1	31
6907	The Exaptation of HERV-H: Evolutionary Analyses Reveal the Genomic Features of Highly Transcribed Elements. <i>Frontiers in Immunology</i> , 2019, 10, 1339.	2.2	18
6908	Phylogeny of Coussareeae (Rubioidae, Rubiaceae). <i>Plant Systematics and Evolution</i> , 2019, 305, 293-304.	0.3	11
6909	First Report of a Novel Hepatozoon sp. in Giant Pandas (<i>Ailuropoda melanoleuca</i>). <i>EcoHealth</i> , 2019, 16, 338-345.	0.9	2
6910	An emerging new fowl adenovirus genotype. <i>Heliyon</i> , 2019, 5, e01732.	1.4	38
6911	Origin and divergence of Afro-Indian Picrodendraceae: linking pollen morphology, dispersal modes, fossil records, molecular dating and paleogeography. <i>Grana</i> , 2019, 58, 227-275.	0.4	9
6912	Extensive regional endemism and cryptic diversity in the Tennessee and Kentucky, USA populations of the burrowing crayfish <i>Cambarus deweesae</i> (Bouchard & Etnier, 1979) (Decapoda: Astacidea: Tj ETQq1 1 0.784314 rgBT /Overlo	0.4	9

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6913	Habitat preference modulates trans-oceanic dispersal in a terrestrial vertebrate. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20182575.	1.2	21
6914	Positive Feedback Defines the Timing, Magnitude, and Robustness of Angiogenesis. <i>Cell Reports</i> , 2019, 27, 3139-3151.e5.	2.9	27
6915	Restriction-site associated DNA markers provide new insights into the evolutionary history of the bark beetle genus <i>Dendroctonus</i> . <i>Molecular Phylogenetics and Evolution</i> , 2019, 139, 106528.	1.2	12
6916	Genome skimming provides well resolved plastid and nuclear phylogenies, showing patterns of deep reticulate evolution in the tropical carnivorous plant genus <i>Nepenthes</i> (Caryophyllales). <i>Australian Systematic Botany</i> , 2019, , .	0.3	2
6917	The complete chloroplast genome of <i>Blastus auriculatus</i> (Melastomataceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1177-1178.	0.2	11
6918	First extensive multilocus phylogeny of the genus <i>Milnesium</i> (Tardigrada) reveals no congruence between genetic markers and morphological traits. <i>Zoological Journal of the Linnean Society</i> , 0, , .	1.0	16
6919	Plastome phylogenomics of sugarcane and relatives confirms the segregation of the genus <i>Tripidium</i> (Poaceae: Andropogoneae). <i>Taxon</i> , 2019, 68, 246-267.	0.4	26
6920	Phylogeography of the Rufous Vanga and the role of bioclimatic transition zones in promoting speciation within Madagascar. <i>Molecular Phylogenetics and Evolution</i> , 2019, 139, 106535.	1.2	7
6921	Kistamicin biosynthesis reveals the biosynthetic requirements for production of highly crosslinked glycopeptide antibiotics. <i>Nature Communications</i> , 2019, 10, 2613.	5.8	48
6922	Integrative taxonomy widens our knowledge of the diversity, distribution and biology of the genus <i>Plakina</i> (Homosclerophorida: Plakinidae). <i>Invertebrate Systematics</i> , 2019, , .	0.5	18
6923	Phylogeny of the <i>Echinoderes coulli</i> -group (Kinorhyncha : Cyclorhagida : Echinoderidae) – a cosmopolitan species group trapped in the intertidal. <i>Invertebrate Systematics</i> , 2019, , .	0.5	3
6924	Optimizing the Production of Nursery-Based Biological Soil Crusts for Restoration of Arid Land Soils. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	24
6925	Evaluation of chloroplast genome annotation tools and application to analysis of the evolution of coffee species. <i>PLoS ONE</i> , 2019, 14, e0216347.	1.1	31
6926	Microbial communities across a hillslope-riparian transect shaped by proximity to the stream, groundwater table, and weathered bedrock. <i>Ecology and Evolution</i> , 2019, 9, 6869-6900.	0.8	24
6927	Classification and enzyme kinetics of formate dehydrogenases for biomanufacturing via CO ₂ utilization. <i>Biotechnology Advances</i> , 2019, 37, 107408.	6.0	58
6928	Updated unified phylogenetic classification system and revised nomenclature for Newcastle disease virus. <i>Infection, Genetics and Evolution</i> , 2019, 74, 103917.	1.0	227
6929	Characterization of the complete mitochondrial genome and phylogenetic analysis of <i>Otus sunia</i> (Strigiformes: Strigidae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 804-805.	0.2	2
6930	Improved phylogenomic sampling of free-living nematodes enhances resolution of higher-level nematode phylogeny. <i>BMC Evolutionary Biology</i> , 2019, 19, 121.	3.2	78

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6931	A Rare Deep-Rooting D0 African Y-Chromosomal Haplogroup and Its Implications for the Expansion of Modern Humans Out of Africa. <i>Genetics</i> , 2019, 212, 1421-1428.	1.2	35
6932	Clustering of <i>Vibrio parahaemolyticus</i> Isolates Using MLST and Whole-Genome Phylogenetics and Protein Motif Fingerprinting. <i>Frontiers in Public Health</i> , 2019, 7, 66.	1.3	8
6933	Genome Resequencing. <i>Compendium of Plant Genomes</i> , 2019, , 205-218.	0.3	0
6934	The first survey of Cystobasidiomycete yeasts in the lichen genus <i>Cladonia</i> ; with the description of <i>Lichenzyma pisutiana</i> gen. nov., sp. nov.. <i>Fungal Biology</i> , 2019, 123, 625-637.	1.1	28
6935	Genetic characterization of susceptible and multi-drug resistant <i>Mannheimia haemolytica</i> isolated from high-risk stocker calves prior to and after antimicrobial metaphylaxis. <i>Veterinary Microbiology</i> , 2019, 235, 110-117.	0.8	11
6936	The application of high-throughput sequencing for taxonomy: The case of <i>Plantago</i> subg. <i>Plantago</i> (Plantaginaceae). <i>Molecular Phylogenetics and Evolution</i> , 2019, 138, 156-173.	1.2	27
6937	Phylogeny of the genus <i>Hypophthalmus</i> Cuvier, 1829 (Pimelodidae " Siluriformes), based on a multilocus analysis, indicates diversification and introgression in the Amazon basin. <i>Molecular Phylogenetics and Evolution</i> , 2019, 137, 285-292.	1.2	6
6938	A fossil-calibrated phylogenomic analysis of <i>Daphnia</i> and the Daphniidae. <i>Molecular Phylogenetics and Evolution</i> , 2019, 137, 250-262.	1.2	43
6939	Patterns of inter- and intrasubspecific homologous recombination inform eco-evolutionary dynamics of <i>Xylella fastidiosa</i> . <i>ISME Journal</i> , 2019, 13, 2319-2333.	4.4	55
6940	Mediterranean grassland soil C-N compound turnover is dependent on rainfall and depth, and is mediated by genomically divergent microorganisms. <i>Nature Microbiology</i> , 2019, 4, 1356-1367.	5.9	170
6941	A metaanalysis of bat phylogenetics and positive selection based on genomes and transcriptomes from 18 species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 11351-11360.	3.3	57
6942	Sharpening species boundaries in the <i>Micarea prasina</i> group, with a new circumscription of the type species <i>M. prasina</i> . <i>Mycologia</i> , 2019, 111, 574-592.	0.8	22
6943	Evolutionary and functional analysis of RBMY1 gene copy number variation on the human Y chromosome. <i>Human Molecular Genetics</i> , 2019, 28, 2785-2798.	1.4	9
6944	The Taxonomy and Phylogeny of the Poorly known Heterotrich Ciliate <i>Ampullofolliculina lageniformis</i> Hadâ³i, 1951 (Ciliophora: Heterotrichea). <i>Journal of Eukaryotic Microbiology</i> , 2019, 66, 925-936.	0.8	9
6945	Genetic diversity of <i>Pseudomonas syringae</i> pv. <i>actinidiae</i> , pathogen of kiwifruit bacterial canker. <i>Plant Pathology</i> , 2019, 68, 1235-1248.	1.2	41
6946	Shotgun Metagenomics Reveals the Benthic Microbial Community Response to Plastic and Bioplastic in a Coastal Marine Environment. <i>Frontiers in Microbiology</i> , 2019, 10, 1252.	1.5	128
6947	New Poroid Hymenochaetaceae (Basidiomycota, Hymenochaetales) from Chile. <i>Mycological Progress</i> , 2019, 18, 865-877.	0.5	16
6948	Genomics, Biology and Phylogeny <i>Aurantiochytrium acetophilum</i> sp. nov. (Thraustochytriaceae), Including First Evidence of Sexual Reproduction. <i>Protist</i> , 2019, 170, 209-232.	0.6	27

#	ARTICLE	IF	CITATIONS
6949	Uncultured <i>Nitrospina</i> -like species are major nitrite oxidizing bacteria in oxygen minimum zones. <i>ISME Journal</i> , 2019, 13, 2391-2402.	4.4	67
6950	The complete mitochondrial genome of the Madagascan plowshare tortoise <i>Astrochelys yniphora</i> (Testudines, Testudinidae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1778-1779.	0.2	0
6951	The complete chloroplast genome of <i>aquilegia rockii</i> , an endemic herb plant in Western China. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1737-1738.	0.2	1
6952	Whole genome sequencing <i>Mycobacterium tuberculosis</i> directly from sputum identifies more genetic diversity than sequencing from culture. <i>BMC Genomics</i> , 2019, 20, 389.	1.2	56
6953	Extensive loss of cell-cycle and DNA repair genes in an ancient lineage of bipolar budding yeasts. <i>PLoS Biology</i> , 2019, 17, e3000255.	2.6	116
6954	Genomic comparison of Newcastle disease viruses isolated in Nigeria between 2002 and 2015 reveals circulation of highly diverse genotypes and spillover into wild birds. <i>Archives of Virology</i> , 2019, 164, 2031-2047.	0.9	28
6955	Coalescent-based species delimitation in the sand lizards of the <i>Liolaemus wiegmannii</i> complex (Squamata: Liolaemidae). <i>Molecular Phylogenetics and Evolution</i> , 2019, 138, 89-101.	1.2	16
6956	Molecules and morphology reveal a new widespread North American freshwater mussel species (Bivalvia: Unionidae). <i>Molecular Phylogenetics and Evolution</i> , 2019, 138, 182-192.	1.2	14
6957	A systematic study towards evolutionary and epidemiological dynamics of currently predominant H5 highly pathogenic avian influenza viruses in Vietnam. <i>Scientific Reports</i> , 2019, 9, 7723.	1.6	15
6958	The chloroplast genome of an endangered tree <i>Artocarpus nanchuanensis</i> (Moraceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 893-894.	0.2	2
6959	A haplotype-resolved draft genome of the European sardine (<i>Sardina pilchardus</i>). <i>GigaScience</i> , 2019, 8, .	3.3	14
6960	Comparative Functional and Phylogenomic Analyses of Host Association in the Remoras (Echeneidae), a Family of Hitchhiking Fishes. <i>Integrative Organismal Biology</i> , 2019, 1, obz007.	0.9	7
6961	Ancestral Admixture Is the Main Determinant of Global Biodiversity in Fission Yeast. <i>Molecular Biology and Evolution</i> , 2019, 36, 1975-1989.	3.5	50
6962	MICROBIAL1Z is a user-friendly web server for the analysis of large-scale microbial genomics data. <i>Nucleic Acids Research</i> , 2019, 47, W88-W92.	6.5	86
6963	Isolation and Characterization of Live Yeast Cells from Ancient Vessels as a Tool in Bio-Archaeology. <i>MBio</i> , 2019, 10, .	1.8	27
6964	Genome-wide study on genetic diversity and phylogeny of five species in the genus <i>Cervus</i> . <i>BMC Genomics</i> , 2019, 20, 384.	1.2	22
6965	Population genetic differentiation of the hydrothermal vent crab <i>Austinochela alayseae</i> (Crustacea: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.1	11
6966	Multiloci analyses suggest synonymy among <i>Rhomboplites</i> , <i>Ocyurus</i> and <i>Lutjanus</i> and reveal the phylogenetic position of <i>Lutjanus alexandrei</i> (Lutjanidae: Perciformes). <i>Neotropical Ichthyology</i> , 2019, 17, .	0.5	8

#	ARTICLE	IF	CITATIONS
6967	In-Depth Genomic and Phenotypic Characterization of the Antarctic Psychrotolerant Strain <i>Pseudomonas</i> sp. MPC6 Reveals Unique Metabolic Features, Plasticity, and Biotechnological Potential. <i>Frontiers in Microbiology</i> , 2019, 10, 1154.	1.5	36
6968	Hiding in plain sight: invasive coral <i>Tubastraea tagusensis</i> (Scleractinia:Hexacorallia) in the Gulf of Mexico. <i>Coral Reefs</i> , 2019, 38, 395-403.	0.9	16
6969	Towards a global DNA barcode reference library for quarantine identifications of lepidopteran stemborers, with an emphasis on sugarcane pests. <i>Scientific Reports</i> , 2019, 9, 7039.	1.6	16
6970	PhyloToL: A Taxon/Gene-Rich Phylogenomic Pipeline to Explore Genome Evolution of Diverse Eukaryotes. <i>Molecular Biology and Evolution</i> , 2019, 36, 1831-1842.	3.5	23
6971	Biosynthesis of Long Chain Alkyl Diols and Long Chain Alkenols in <i>Nannochloropsis</i> spp. (Eustigmatophyceae). <i>Plant and Cell Physiology</i> , 2019, 60, 1666-1682.	1.5	9
6972	Discovery and Characterization of Novel Bat Coronavirus Lineages from Kazakhstan. <i>Viruses</i> , 2019, 11, 356.	1.5	11
6973	Paleogenome Reveals Genetic Contribution of Extinct Giant Panda to Extant Populations. <i>Current Biology</i> , 2019, 29, 1695-1700.e6.	1.8	22
6974	Illumina and Nanopore methods for whole genome sequencing of hepatitis B virus (HBV). <i>Scientific Reports</i> , 2019, 9, 7081.	1.6	75
6975	RAxML-NG: a fast, scalable and user-friendly tool for maximum likelihood phylogenetic inference. <i>Bioinformatics</i> , 2019, 35, 4453-4455.	1.8	2,287
6976	Positive Selection Evidence in Xylose-Related Genes Suggests Methylglyoxal Reductase as a Target for the Improvement of Yeasts' Fermentation in Industry. <i>Genome Biology and Evolution</i> , 2019, 11, 1923-1938.	1.1	11
6977	Return to the Sea, Get Huge, Beat Cancer: An Analysis of Cetacean Genomes Including an Assembly for the Humpback Whale (<i>Megaptera novaeangliae</i>). <i>Molecular Biology and Evolution</i> , 2019, 36, 1746-1763.	3.5	75
6978	Lineage specific histories of <i>Mycobacterium tuberculosis</i> dispersal in Africa and Eurasia. <i>Molecular Ecology</i> , 2019, 28, 3241-3256.	2.0	86
6979	Evaluation of species boundaries in sympatric and parapatric populations of Mesoamerican toads. <i>Zoologica Scripta</i> , 2019, 48, 454-465.	0.7	4
6980	Fat body-specific vitellogenin expression regulates host-seeking behaviour in the mosquito <i>Aedes albopictus</i> . <i>PLoS Biology</i> , 2019, 17, e3000238.	2.6	22
6981	Comparative Analysis of Tools and Approaches for Source Tracking <i>Listeria monocytogenes</i> in a Food Facility Using Whole-Genome Sequence Data. <i>Frontiers in Microbiology</i> , 2019, 10, 947.	1.5	61
6982	Genomic Epidemiology and Phenotyping Reveal on-Farm Persistence and Cold Adaptation of Raw Milk Outbreak-Associated <i>Yersinia pseudotuberculosis</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 1049.	1.5	13
6983	Dual colonization of European high-altitude areas from Asia by <i>Callianthemum</i> (Ranunculaceae). <i>Plant Systematics and Evolution</i> , 2019, 305, 431-443.	0.3	8
6984	Genomic signatures accompanying the dietary shift to phytophagy in polyphagan beetles. <i>Genome Biology</i> , 2019, 20, 98.	3.8	27

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6985	Applied shotgun metagenomics approach for the genetic characterization of dengue viruses. <i>Journal of Biotechnology</i> , 2019, 306, 100009.	1.9	6
6986	Community dynamics of Neocallimastigomycetes in the rumen of yak feeding on wheat straw revealed by different primer sets. <i>Fungal Ecology</i> , 2019, 41, 34-44.	0.7	2
6987	Molecular identification of late and terminal Pleistocene <i>Equus ovodovi</i> from northeastern China. <i>PLoS ONE</i> , 2019, 14, e0216883.	1.1	15
6988	Contraction of the ROS Scavenging Enzyme Glutathione <i>S</i> -Transferase Gene Family in Cetaceans. <i>C3: Genes, Genomes, Genetics</i> , 2019, 9, 2303-2315.	0.8	13
6989	Phylogenetic Characterization of the Palyam Serogroup Orbiviruses. <i>Viruses</i> , 2019, 11, 446.	1.5	10
6990	The monocotyledonous underground: global climatic and phylogenetic patterns of geophyte diversity. <i>American Journal of Botany</i> , 2019, 106, 850-863.	0.8	44
6991	Cryptic speciation in the Chinese white pine (<i>Pinus armandii</i>): Implications for the high species diversity of conifers in the Hengduan Mountains, a global biodiversity hotspot. <i>Molecular Phylogenetics and Evolution</i> , 2019, 138, 114-125.	1.2	27
6992	Evaluation of a concatenated protein phylogeny for classification of tailed double-stranded DNA viruses belonging to the order Caudovirales. <i>Nature Microbiology</i> , 2019, 4, 1306-1315.	5.9	69
6993	Integrative taxonomy of the cave-dwelling mysids of the genus <i>Hemimysis</i> . <i>Systematics and Biodiversity</i> , 2019, 17, 245-259.	0.5	0
6994	Whole-Genome Sequencing Analysis of Nontyphoidal <i>Salmonella enterica</i> of Chicken Meat and Human Origin Under Surveillance in Sri Lanka. <i>Foodborne Pathogens and Disease</i> , 2019, 16, 531-537.	0.8	16
6995	Metagenomic recovery of two distinct comammox <i>Nitrospira</i> from the terrestrial subsurface. <i>Environmental Microbiology</i> , 2019, 21, 3627-3637.	1.8	69
6996	Gradual evolution towards flightlessness in steamer ducks*. <i>Evolution; International Journal of Organic Evolution</i> , 2019, 73, 1916-1926.	1.1	21
6997	Connecting the morphological and molecular species concepts to facilitate species identification within the genus <i>Fragilaria</i> (Bacillariophyta). <i>Journal of Phycology</i> , 2019, 55, 948-970.	1.0	28
6999	High abundance of Amphidomataceae (Dinophyceae) during the 2015 spring bloom of the Argentinean Shelf and a new, non-toxicogenic ribotype of <i>Azadinium spinosum</i> . <i>Harmful Algae</i> , 2019, 84, 244-260.	2.2	16
7000	Nitrate Consumers in Arctic Marine Eukaryotic Communities: Comparative Diversities of 18S rRNA, 18S rRNA Genes, and Nitrate Reductase Genes. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	14
7001	East African cichlid lineages (Teleostei: Cichlidae) might be older than their ancient host lakes: new divergence estimates for the east African cichlid radiation. <i>BMC Evolutionary Biology</i> , 2019, 19, 94.	3.2	33
7002	Consequences of breed formation on patterns of genomic diversity and differentiation: the case of highly diverse peripheral Iberian cattle. <i>BMC Genomics</i> , 2019, 20, 334.	1.2	11
7003	The plastid genome and its implications in barcoding specific-chemotypes of the medicinal herb <i>Pogostemon cablin</i> in China. <i>PLoS ONE</i> , 2019, 14, e0215512.	1.1	11

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7004	Comparative Analysis of the Two <i>Acinetobacter baumannii</i> Multilocus Sequence Typing (MLST) Schemes. <i>Frontiers in Microbiology</i> , 2019, 10, 930.	1.5	133
7005	First detection of TBE virus in ticks and sero-reactivity in goats in a non-endemic region in the southern part of Switzerland (Canton of Ticino). <i>Ticks and Tick-borne Diseases</i> , 2019, 10, 868-874.	1.1	29
7006	Complete chloroplast genome of <i>Euphorbia hainanensis</i> (Euphorbiaceae), a rare cliff top boskage endemic to China. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1325-1326.	0.2	4
7007	An empirical pipeline for choosing the optimal clustering threshold in RADseq studies. <i>Molecular Ecology Resources</i> , 2019, 19, 1195-1204.	2.2	53
7008	Evolution of hybridogenetic lineages in <i>Cataglyphis</i> ants. <i>Molecular Ecology</i> , 2019, 28, 3073-3088.	2.0	6
7009	Pervasive hybridizations in the history of wheat relatives. <i>Science Advances</i> , 2019, 5, eaav9188.	4.7	79
7010	Identification of Novel Mobilized Colistin Resistance Gene <i>mcr-9</i> in a Multidrug-Resistant, Colistin-Susceptible <i>Salmonella enterica</i> Serotype Typhimurium Isolate. <i>MBio</i> , 2019, 10, .	1.8	406
7011	Sequential horizontal gene transfers from different hosts in a widespread Eurasian parasitic plant, <i>Cynomorium coccineum</i> . <i>American Journal of Botany</i> , 2019, 106, 679-689.	0.8	18
7012	Ice-Age Climate Adaptations Trap the Alpine Marmot in a State of Low Genetic Diversity. <i>Current Biology</i> , 2019, 29, 1712-1720.e7.	1.8	27
7013	A brief overview of the concepts, methods and computational tools used in phylogenetic tree construction and gene prediction. <i>Meta Gene</i> , 2019, 21, 100586.	0.3	8
7014	Molecular phylogeny of the Pectinoidea (Bivalvia) indicates Propeamussiidae to be a non-monophyletic family with one clade sister to the scallops (Pectinidae). <i>Molecular Phylogenetics and Evolution</i> , 2019, 137, 293-299.	1.2	10
7015	Phylogeographical and cross-species transmission dynamics of SAT1 and SAT2 foot-and-mouth disease virus in Eastern Africa. <i>Molecular Ecology</i> , 2019, 28, 2903-2916.	2.0	19
7016	Complete Assembly of <i>Escherichia coli</i> Sequence Type 131 Genomes Using Long Reads Demonstrates Antibiotic Resistance Gene Variation within Diverse Plasmid and Chromosomal Contexts. <i>MSphere</i> , 2019, 4, .	1.3	27
7017	Exploiting the natural poly(3-hydroxyalkanoates) production capacity of Antarctic <i>Pseudomonas</i> strains: from unique phenotypes to novel biopolymers. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2019, 46, 1139-1153.	1.4	25
7018	Active seafloor microbial communities from Mariana back-arc venting fluids share metabolic strategies across different thermal niches and taxa. <i>ISME Journal</i> , 2019, 13, 2264-2279.	4.4	38
7019	Match and mismatch between dietary switches and microbial partners in plant sap-feeding insects. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20190065.	1.2	13
7020	<i>Snf2</i> controls pulcherriminic acid biosynthesis and antifungal activity of the biocontrol yeast <i>Metschnikowia pulcherrima</i> . <i>Molecular Microbiology</i> , 2019, 112, 317-332.	1.2	64
7021	On the phylogenetic position and systematics of extant and fossil Aclopinæ (Coleoptera: Tj ETQq1 1 0.784314 rgBTj/Overlock 10 Tf 50	1.7	10

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7022	MGERT: a pipeline to retrieve coding sequences of mobile genetic elements from genome assemblies. <i>Mobile DNA</i> , 2019, 10, 21.	1.3	2
7023	Mitigating Anticipated Effects of Systematic Errors Supports Sister-Group Relationship between Xenacoelomorpha and Ambulacraria. <i>Current Biology</i> , 2019, 29, 1818-1826.e6.	1.8	120
7024	Loss of Fitness of Mexican H7N3 Highly Pathogenic Avian Influenza Virus in Mallards after Circulating in Chickens. <i>Journal of Virology</i> , 2019, 93, .	1.5	13
7025	Comparative genomics of Bifidobacterium species isolated from marmosets and humans. <i>American Journal of Primatology</i> , 2019, 81, e983.	0.8	12
7026	Phylogenomic analyses reveal an exceptionally high number of evolutionary shifts in a florally diverse clade of African legumes. <i>Molecular Phylogenetics and Evolution</i> , 2019, 137, 156-167.	1.2	17
7027	Historical biogeography of the fern genus <i>Polystichum</i> (Dryopteridaceae) in Austral South America. <i>Molecular Phylogenetics and Evolution</i> , 2019, 137, 168-189.	1.2	5
7028	Evolution of organellar genes of chlorophyte algae: Relevance to phylogenetic inference. <i>PLoS ONE</i> , 2019, 14, e0216608.	1.1	4
7029	Assessing the Diversity of Endogenous Viruses Throughout Ant Genomes. <i>Frontiers in Microbiology</i> , 2019, 10, 1139.	1.5	28
7030	Kinetid Structure of Aphelidium and Paraphelidium (Aphelida) Suggests the Features of the Common Ancestor of Fungi and Opisthosporidia. <i>Journal of Eukaryotic Microbiology</i> , 2019, 66, 911-924.	0.8	9
7031	Phylogenomic analysis suggests Coreidae and Alydidae (Hemiptera: Heteroptera) are not monophyletic. <i>Zoologica Scripta</i> , 2019, 48, 520-534.	0.7	33
7032	Functional diversification of horizontally acquired glycoside hydrolase family 45 (GH45) proteins in Phytophaga beetles. <i>BMC Evolutionary Biology</i> , 2019, 19, 100.	3.2	30
7033	The Water Microbiome Through a Pilot Scale Advanced Treatment Facility for Direct Potable Reuse. <i>Frontiers in Microbiology</i> , 2019, 10, 993.	1.5	36
7034	New phagotrophic euglenids from deep sea and surface waters of the Atlantic Ocean (Keelungia) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 2 102-116.	0.5	12
7035	Family of neural wiring receptors in bilaterians defined by phylogenetic, biochemical, and structural evidence. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 9837-9842.	3.3	21
7036	Phylogenomic Investigation of IncI1-Î³ Plasmids Harboring <i>bla</i> _{CMY-2} and <i>bla</i> _{SHV-12} in Salmonella enterica and Escherichia coli in Multiple Countries. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	1.4	14
7037	A Mutagenic Screen Identifies a TonB-Dependent Receptor Required for the Lanthanide Metal Switch in the Type I Methanotroph <i>Methylothermobacter buryatense</i> 5GB1C. <i>Journal of Bacteriology</i> , 2019, 201, .	1.0	32
7038	Characterisation of HIV-1 molecular transmission clusters among newly diagnosed individuals infected with non-B subtypes in Italy. <i>Sexually Transmitted Infections</i> , 2019, 95, 619-625.	0.8	18
7039	Genomic and Epidemiological Evidence of a Dominant Panton-Valentine Leucocidin-Positive Methicillin Resistant Staphylococcus aureus Lineage in Sri Lanka and Presence Among Isolates From the United Kingdom and Australia. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 123.	1.8	7

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7040	Phylogeny of Chinese <i>Allium</i> Species in Section <i>Daghestanica</i> and Adaptive Evolution of <i>Allium</i> (<i>Amaryllidaceae</i> , <i>Allioideae</i>) Species Revealed by the Chloroplast Complete Genome. <i>Frontiers in Plant Science</i> , 2019, 10, 460.	1.7	64
7041	Hiding in plain sight on Gunung Muria: A new species and first record of rock gecko (<i>Cnemaspis</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 11	0.2	3
7042	Islands of retroelements are major components of <i>Drosophila</i> centromeres. <i>PLoS Biology</i> , 2019, 17, e3000241.	2.6	124
7043	Molecular Data Reveal Multiple Lineages in Piranhas of the Genus <i>Pygocentrus</i> (Teleostei,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	1.0	10
7044	Bioprospecting microalgae from natural algal bloom for sustainable biomass and biodiesel production. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 5447-5458.	1.7	21
7045	A molecular approach to identification of protonemata helps assess biodiversity of extremely acidic freshwaters. <i>Limnology</i> , 2019, 20, 225-231.	0.8	0
7046	Hidden species diversity in <i>Pachyhynobius</i> : A multiple approaches species delimitation with mitogenomes. <i>Molecular Phylogenetics and Evolution</i> , 2019, 137, 138-145.	1.2	18
7047	A dated molecular perspective of eucalypt taxonomy, evolution and diversification. <i>Australian Systematic Botany</i> , 2019, 32, 29-48.	0.3	79
7048	Shared species of crocodylian trypanosomes carried by tabanid flies in Africa and South America, including the description of a new species from caimans, <i>Trypanosoma kaiowa</i> n. sp.. <i>Parasites and Vectors</i> , 2019, 12, 225.	1.0	21
7049	No Signs of Genetic Erosion in a 19th Century Genome of the Extinct Paradise Parrot (<i>Psephotellus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 11	0.7	11
7050	ORTHOSCOPE Analysis Reveals the Presence of the Cellulose Synthase Gene in All Tunicate Genomes but Not in Other Animal Genomes. <i>Genes</i> , 2019, 10, 294.	1.0	10
7051	Integrating Culture-based Antibiotic Resistance Profiles with Whole-genome Sequencing Data for 11,087 Clinical Isolates. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 169-182.	3.0	8
7052	A multiobjective adaptive approach for the inference of evolutionary relationships in protein-based scenarios. <i>Information Sciences</i> , 2019, 485, 281-300.	4.0	5
7053	Ploeotids Represent Much of the Phylogenetic Diversity of Euglenids. <i>Protist</i> , 2019, 170, 233-257.	0.6	12
7054	Candidate Phyla Radiation Roizmanbacteria From Hot Springs Have Novel and Unexpectedly Abundant CRISPR-Cas Systems. <i>Frontiers in Microbiology</i> , 2019, 10, 928.	1.5	36
7055	Exploring the sequence, function, and evolutionary space of protein superfamilies using sequence similarity networks and phylogenetic reconstructions. <i>Methods in Enzymology</i> , 2019, 620, 315-347.	0.4	13
7056	Two new mitogenomes of Picidae (Aves, Piciformes): Sequence, structure and phylogenetic analyses. <i>International Journal of Biological Macromolecules</i> , 2019, 133, 683-692.	3.6	13
7057	Evolution of folate biosynthesis and metabolism across algae and land plant lineages. <i>Scientific Reports</i> , 2019, 9, 5731.	1.6	35

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7058	Improved geographic sampling provides further evidence for the separation of <i>Glossiphonia complanata</i> and <i>Glossiphonia elegans</i> (Annelida: Clitellata: Glossiphoniidae). <i>Journal of Natural History</i> , 2019, 53, 335-350.	0.2	11
7059	A new species of <i>Orobdella</i> (Hirudinida: Arhynchobdellida: Orobdellidae) from Primorye Territory, Russian Far East. <i>Journal of Natural History</i> , 2019, 53, 351-364.	0.2	3
7060	The complete mitochondrial genome of <i>Xystrocera globosa</i> (Coleoptera: Cerambycidae) and its phylogeny. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1647-1649.	0.2	5
7061	DNA barcoding of shrimps from a mangrove biodiversity hotspot. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2019, 30, 618-625.	0.7	14
7062	Variation in the Internal Transcribed Spacer Region of <i>Phakopsora pachyrhizi</i> and Implications for Molecular Diagnostic Assays. <i>Plant Disease</i> , 2019, 103, 2237-2245.	0.7	11
7063	Sequence capture across large phylogenetic scales by using pooled PCR-generated baits: A case study of Lepidoptera. <i>Molecular Ecology Resources</i> , 2019, 19, 1037-1051.	2.2	18
7064	A new species of <i>Piaractus</i> (Characiformes: Serrasalminidae) from the Orinoco Basin with a redescription of <i>Piaractus brachypomus</i> . <i>Journal of Fish Biology</i> , 2019, 95, 411-427.	0.7	16
7065	Redescription of <i>Milnesium alpigenum</i> Ehrenberg, 1853 (Tardigrada: Apochela) and a description of <i>Milnesium inceptum</i> sp. nov., a tardigrade laboratory model. <i>Zootaxa</i> , 2019, 4586, zootaxa.4586.1.2.	0.2	55
7066	Nosocomial bloodstream infection and the emerging carbapenem-resistant pathogen <i>Ralstonia insidiosa</i> . <i>BMC Infectious Diseases</i> , 2019, 19, 334.	1.3	33
7067	Genomic Analysis of <i>Pseudomonas</i> sp. Strain SCT, an Iodate-Reducing Bacterium Isolated from Marine Sediment, Reveals a Possible Use for Bioremediation. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1321-1329.	0.8	6
7068	Whole Genome Sequencing and Re-sequencing of the Sable Antelope (<i>Hippotragus niger</i>): A Resource for Monitoring Diversity in <i>ex Situ</i> and <i>in Situ</i> Populations. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1785-1793.	0.8	18
7069	Systematic Identification and Evolution Analysis of Sox Genes in <i>Coturnix japonica</i> Based on Comparative Genomics. <i>Genes</i> , 2019, 10, 314.	1.0	10
7070	Metabolic potential of uncultured bacteria and archaea associated with petroleum seepage in deep-sea sediments. <i>Nature Communications</i> , 2019, 10, 1816.	5.8	118
7071	Geographic separation and genetic differentiation of populations are not coupled with niche differentiation in threatened Kaiser's spotted newt (<i>Neurergus kaiseri</i>). <i>Scientific Reports</i> , 2019, 9, 6239.	1.6	26
7072	The horse Y chromosome as an informative marker for tracing sire lines. <i>Scientific Reports</i> , 2019, 9, 6095.	1.6	39
7073	The complete chloroplast genome sequence of <i>Calanthe delavayi</i> (Orchidaceae), an endemic to China. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1562-1563.	0.2	4
7074	Genes Associated With Psychrotolerant <i>Bacillus cereus</i> Group Isolates. <i>Frontiers in Microbiology</i> , 2019, 10, 662.	1.5	6
7075	A Whole-genome Sequencing Analysis of <i>Neisseria gonorrhoeae</i> Isolates in China: An Observational Study. <i>EClinicalMedicine</i> , 2019, 7, 47-54.	3.2	45

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7076	Genome-wide annotation and comparative analysis of cuticular protein genes in the noctuid pest <i>Spodoptera litura</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2019, 110, 90-97.	1.2	33
7077	The complete chloroplast genome sequence of an endemic species Pearl chestnut (<i>Castanea</i>) Tj ETQq1 1 0.784314 rgBT /Overlock	0.2	5
7078	The complete chloroplast sequence of <i>Roscoea humeana</i> (Zingiberaceae): an alpine ginger in the Hengduan Mountains, China. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1398-1399.	0.2	2
7079	Multiple colonizations, hybridization and uneven diversification in <i>Cyrtandra</i> (Gesneriaceae) lineages on Hawai'i Island. <i>Journal of Biogeography</i> , 2019, 46, 1178-1196.	1.4	20
7080	Aerosol Transmission of Gull-Origin Iceland Subtype H10N7 Influenza A Virus in Ferrets. <i>Journal of Virology</i> , 2019, 93, .	1.5	17
7081	Whole-Genome Analysis of Human Papillomavirus Type 16 Prevalent in Japanese Women with or without Cervical Lesions. <i>Viruses</i> , 2019, 11, 350.	1.5	10
7082	Genome analysis of <i>Paenibacillus polymyxa</i> A18 gives insights into the features associated with its adaptation to the termite gut environment. <i>Scientific Reports</i> , 2019, 9, 6091.	1.6	16
7083	Genome analyses of the new model protist <i>Euplotes vannus</i> focusing on genome rearrangement and resistance to environmental stressors. <i>Molecular Ecology Resources</i> , 2019, 19, 1292-1308.	2.2	69
7084	High-resolution QTL mapping in <i>Tetranychus urticae</i> reveals acaricide-specific responses and common target-site resistance after selection by different MET-I acaricides. <i>Insect Biochemistry and Molecular Biology</i> , 2019, 110, 19-33.	1.2	62
7085	Use of online tools for antimicrobial resistance prediction by whole-genome sequencing in methicillin-resistant <i>Staphylococcus aureus</i> (MRSA) and vancomycin-resistant enterococci (VRE). <i>Journal of Global Antimicrobial Resistance</i> , 2019, 19, 136-143.	0.9	17
7086	3RAD-based systematics of the transitional Nearctic-Neotropical lubber grasshopper genus <i>Taeniopoda</i> (Orthoptera: Romaleidae). <i>Molecular Phylogenetics and Evolution</i> , 2019, 137, 64-75.	1.2	7
7087	<i>In silico</i> prediction and characterisation of secondary metabolite clusters in the plant pathogenic fungus <i>Verticillium dahliae</i> . <i>FEMS Microbiology Letters</i> , 2019, 366, .	0.7	14
7088	Clonal expansion and spread of the ceftriaxone-resistant <i>Neisseria gonorrhoeae</i> strain FC428, identified in Japan in 2015, and closely related isolates. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 1812-1819.	1.3	50
7089	Running in circles in phylomorphospace: host environment constrains morphological diversification in parasitic wasps. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20182352.	1.2	14
7090	Superimposing incident sexually transmitted infections on HIV phylogram to investigate possible misclassification of men who have sex with men as heterosexuals in a cohort in Antwerp, Belgium. <i>International Journal of STD and AIDS</i> , 2019, 30, 486-495.	0.5	0
7091	Origin of angiosperms and the puzzle of the Jurassic gap. <i>Nature Plants</i> , 2019, 5, 461-470.	4.7	467
7092	The complete chloroplast genome sequence of <i>Cenchrus purpureus</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 51-52.	0.2	4
7093	The complete chloroplast genome sequence of a medicinal mangrove tree <i>Ceriops tagal</i> and its phylogenetic analysis. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 267-268.	0.2	7

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7094	Complete mitochondrial genome of <i>Callogorgia cf. gracilis</i> (Octocorallia: Calcaxonia: Primnoidae). Mitochondrial DNA Part B: Resources, 2019, 4, 361-362.	0.2	2
7095	Complete chloroplast genome sequence of <i>Asplenium nidus</i> (Aspleniaceae), an economically important foliage fern. Mitochondrial DNA Part B: Resources, 2019, 4, 923-924.	0.2	1
7096	The complete chloroplast genome sequence of an endangered species, <i>Oncodostigma hainanense</i> . Mitochondrial DNA Part B: Resources, 2019, 4, 721-722.	0.2	0
7097	The chloroplast genome of a landscape tree <i>Zelkova serrata</i> (Ulmaceae). Mitochondrial DNA Part B: Resources, 2019, 4, 227-228.	0.2	0
7098	Characterization of the complete chloroplast genome of <i>Magnolia odoratissima</i> (Magnoliaceae), an endangered and endemic species in China. Mitochondrial DNA Part B: Resources, 2019, 4, 386-388.	0.2	1
7099	Complete mitochondrial genomes of three troglophile cave spiders (<i>Mesabolivar</i> , pholcidae). Mitochondrial DNA Part B: Resources, 2019, 4, 251-252.	0.2	3
7100	The complete mitochondrial genome of a European fire-bellied toad (<i>Bombina bombina</i>) from Germany. Mitochondrial DNA Part B: Resources, 2019, 4, 498-500.	0.2	3
7101	The complete chloroplast genome sequence of <i>Podocarpus imbricatus</i> (Podocarpaceae) and its phylogenetic analysis. Mitochondrial DNA Part B: Resources, 2019, 4, 368-369.	0.2	1
7102	The complete chloroplast genome sequence of <i>Actinidia zhejiangensis</i> . Mitochondrial DNA Part B: Resources, 2019, 4, 690-691.	0.2	1
7103	Next-generation sequencing yields the complete chloroplast genome of <i>Abies fanjingshanensis</i> , an Endangered species from South China. Mitochondrial DNA Part B: Resources, 2019, 4, 880-881.	0.2	3
7104	Two new complete mitochondrial genomes (<i>Paradoxornis gularis</i> and <i>Niltava davidi</i>) and their phylogenetic and taxonomic implications. Mitochondrial DNA Part B: Resources, 2019, 4, 820-821.	0.2	2
7105	Genomic Plasticity Mediated by Transposable Elements in the Plant Pathogenic Fungus <i>Colletotrichum higginsianum</i> . <i>Genome Biology and Evolution</i> , 2019, 11, 1487-1500.	1.1	47
7106	Two Independent Plastid accD Transfers to the Nuclear Genome of <i>Gnetum</i> and Other Insights on Acetyl-CoA Carboxylase Evolution in Gymnosperms. <i>Genome Biology and Evolution</i> , 2019, 11, 1691-1705.	1.1	15
7107	Species-level predation network uncovers high prey specificity in a Neotropical army ant community. <i>Molecular Ecology</i> , 2019, 28, 2423-2440.	2.0	33
7108	Nuclear and plastid DNA phylogeny of tribe Cardueae (Compositae) with Hyb-Seq data: A new subtribal classification and a temporal diversification framework. <i>Molecular Phylogenetics and Evolution</i> , 2019, 137, 313-332.	1.2	58
7109	Methylamine-specific methyltransferase paralogs in <i>Methanosarcina</i> are functionally distinct despite frequent gene conversion. <i>ISME Journal</i> , 2019, 13, 2173-2182.	4.4	6
7110	Transcriptome Analysis Reveals Unique Relationships Among <i>Eleusine</i> Species and Heritage of <i>Eleusine coracana</i> . <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2029-2036.	0.8	18
7111	Genomic analysis on pygmy hog reveals extensive interbreeding during wild boar expansion. <i>Nature Communications</i> , 2019, 10, 1992.	5.8	38

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7112	Lost and Found: Return of the Inverted Repeat in the Legume Clade Defined by Its Absence. <i>Genome Biology and Evolution</i> , 2019, 11, 1321-1333.	1.1	67
7113	The genomes of pecan and Chinese hickory provide insights into <i>Carya</i> evolution and nut nutrition. <i>GigaScience</i> , 2019, 8, .	3.3	88
7114	Evolutionary shifts in fruit dispersal syndromes in Apiaceae tribe Scandiceae. <i>Plant Systematics and Evolution</i> , 2019, 305, 401-414.	0.3	19
7115	Intercontinental spread of Asian-origin H7 avian influenza viruses by captive bird trade in 1990's. <i>Infection, Genetics and Evolution</i> , 2019, 73, 146-150.	1.0	6
7116	Three phylogenetic groups have driven the recent population expansion of <i>Cryptococcus neoformans</i> . <i>Nature Communications</i> , 2019, 10, 2035.	5.8	47
7117	The complete plastid genome of marula (<i>Sclerocarya birrea</i>). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1111-1113.	0.2	1
7118	The complete mitochondrial genome of the polychaete, <i>Marphysa tamurai</i> (Eunicida, Eunicidae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1055-1056.	0.2	2
7119	The complete chloroplast genome of a wild onion species <i>Allium monanthum</i> (Alliaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 854-855.	0.2	3
7120	Complete mitochondrial genome of sea cucumber, <i>Holothuria (Stauropora) pervicax</i> (Holothuroidea). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf</i> 1047-1048.	0.2	3
7121	The complete mitochondrial genome of grey-headed canary-flycatcher (<i>Culicicapa ceylonensis</i>). <i>Tj ETQq1 1 0,784314 rgBT /Over</i>	0,2	2
7122	The complete mitochondrial genome of <i>Thaumatosmylus hainanus</i> (Neuroptera: Osmylidae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1202-1203.	0.2	1
7123	Quantitative proteomics reveals the key molecular events occurring at different cell cycle phases of the in situ blooming dinoflagellate cells. <i>Science of the Total Environment</i> , 2019, 676, 62-71.	3.9	14
7124	Complete arsenic-based respiratory cycle in the marine microbial communities of pelagic oxygen-deficient zones. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 9925-9930.	3.3	38
7125	Complete chloroplast genome sequence of <i>Carpinus oblongifolia</i> (Betulaceae) and phylogenetic analysis. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1304-1305.	0.2	0
7126	Early consequences of allopolyploidy alter floral evolution in <i>Nicotiana</i> (Solanaceae). <i>BMC Plant Biology</i> , 2019, 19, 162.	1.6	9
7127	Plasticity of opsin gene expression in the adult red shiner (<i>Cyprinella lutrensis</i>) in response to turbid habitats. <i>PLoS ONE</i> , 2019, 14, e0215376.	1.1	10
7128	Dicyemida and Orthonectida: Two Stories of Body Plan Simplification. <i>Frontiers in Genetics</i> , 2019, 10, 443.	1.1	37
7129	Methanethiol and Dimethylsulfide Cycling in Stiffkey Saltmarsh. <i>Frontiers in Microbiology</i> , 2019, 10, 1040.	1.5	23

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7130	Does the Enigmatic <i>Wightia</i> Belong to Paulowniaceae (Lamiales)? <i>Frontiers in Plant Science</i> , 2019, 10, 528.	1.7	18
7131	Tracing the Evolution of the Plastome and Mitogenome in the Chloropicophyceae Uncovered Convergent tRNA Gene Losses and a Variant Plastid Genetic Code. <i>Genome Biology and Evolution</i> , 2019, 11, 1275-1292.	1.1	20
7132	Molecular Identity of <i>Holomastigotes</i> (Spirotrichonymphea, Parabasalia) with Descriptions of <i>Holomastigotes flavipes</i> n. sp. and <i>Holomastigotes tibialis</i> n. sp.. <i>Journal of Eukaryotic Microbiology</i> , 2019, 66, 882-891.	0.8	6
7133	Red Sea SAR11 and <i>Prochlorococcus</i> Single-Cell Genomes Reflect Globally Distributed Pangenomes. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	11
7134	A human infection with a novel reassortant H3N2 swine virus in China. <i>Journal of Infection</i> , 2019, 79, 174-187.	1.7	20
7135	The phylogenetic position of species of <i>Lecanora</i> s. l. containing calycin and usnic acid, with the description of <i>Lecanora solaris</i> Yakovchenko & Davydov sp. nov.. <i>Lichenologist</i> , 2019, 51, 147-156.	0.5	9
7136	Reiterative Synthesis by the Ribosome and Recognition of the N-Terminal Formyl Group by Biosynthetic Machinery Contribute to Evolutionary Conservation of the Length of Antibiotic Microcin C Peptide Precursor. <i>MBio</i> , 2019, 10, .	1.8	6
7137	Using Bioinformatics and Molecular Biology to Streamline Construction of Effector Libraries for Phytopathogenic <i>Pseudomonas syringae</i> Strains. <i>Methods in Molecular Biology</i> , 2019, 1991, 1-12.	0.4	2
7138	Tracking Five Millennia of Horse Management with Extensive Ancient Genome Time Series. <i>Cell</i> , 2019, 177, 1419-1435.e31.	13.5	195
7139	Interpreting Viral Deep Sequencing Data with GLUE. <i>Viruses</i> , 2019, 11, 323.	1.5	29
7140	Tracking temporal shifts in area, biomes, and pollinators in the radiation of <i>Salvia</i> (sages) across continents: leveraging anchored hybrid enrichment and targeted sequence data. <i>American Journal of Botany</i> , 2019, 106, 573-597.	0.8	76
7141	2018 Ebola virus disease outbreak in <i>Å</i> %uateur Province, Democratic Republic of the Congo: a retrospective genomic characterisation. <i>Lancet Infectious Diseases</i> , The, 2019, 19, 641-647.	4.6	27
7142	A brainstorm on the systematics of <i>Turnera</i> (Turneraceae, Malpighiales) caused by insights from molecular phylogenetics and morphological evolution. <i>Molecular Phylogenetics and Evolution</i> , 2019, 137, 44-63.	1.2	11
7143	Linear Mitochondrial Genome in Anthozoa (Cnidaria): A Case Study in <i>Ceriantharia</i> . <i>Scientific Reports</i> , 2019, 9, 6094.	1.6	29
7144	Cardinalfishes (Apogonidae) show visual system adaptations typical of nocturnally and diurnally active fish. <i>Molecular Ecology</i> , 2019, 28, 3025-3041.	2.0	24
7145	Phylogeography of the Assassin Bug <i>Sphephanolestes impressicollis</i> in East Asia Inferred From Mitochondrial and Nuclear Gene Sequences. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1234.	1.8	9
7146	The species identity and biogeography of <i>Blanus</i> (Amphisbaenia: Blanidae) in Lebanon. <i>Zoology in the Middle East</i> , 2019, 65, 208-214.	0.2	7
7147	Characterization of the complete chloroplast genome of <i>Eriobotrya japonica</i> in China and phylogenetic relationships. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1367-1369.	0.2	2

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7148	Whole-Genome Sequencing of the Opportunistic Yeast Pathogen <i>Candida inconspicua</i> Uncovers Its Hybrid Origin. <i>Frontiers in Genetics</i> , 2019, 10, 383.	1.1	63
7149	Identification and characterization of <i>Septoria steviae</i> as the causal agent of <i>Septoria</i> leaf spot disease of <i>stevia</i> in North Carolina. <i>Mycologia</i> , 2019, 111, 456-465.	0.8	7
7150	Characterization of the complete chloroplast genome of <i>Taxillus nigrans</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 472-473.	0.2	3
7151	Are Pheromones Key to Unlocking Cryptic Lizard Diversity?. <i>American Naturalist</i> , 2019, 194, 168-182.	1.0	29
7152	Molecular convergence and positive selection associated with the evolution of symbiont transmission mode in stony corals. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20190111.	1.2	5
7153	In-depth transcriptome characterization uncovers distinct gene family expansions for <i>Cupressus gigantea</i> important to this long-lived species's adaptability to environmental cues. <i>BMC Genomics</i> , 2019, 20, 213.	1.2	12
7154	Analysis of the recombination landscape of hexaploid bread wheat reveals genes controlling recombination and gene conversion frequency. <i>Genome Biology</i> , 2019, 20, 69.	3.8	79
7155	Unprecedented bacterial community richness in soybean nodules vary with cultivar and water status. <i>Microbiome</i> , 2019, 7, 63.	4.9	51
7156	Morphological evolution and classification of the red algal order Ceramiales inferred using plastid phylogenomics. <i>Molecular Phylogenetics and Evolution</i> , 2019, 137, 76-85.	1.2	17
7157	Biogeography of <i>Mesalina</i> (Reptilia: Lacertidae), with special emphasis on the <i>Mesalina adramitana</i> group from Arabia and the Socotra Archipelago. <i>Molecular Phylogenetics and Evolution</i> , 2019, 137, 300-312.	1.2	12
7158	Ultraconserved elements resolve genus-level relationships in a major Australasian bird radiation (Aves: Meliphagidae). <i>Emu</i> , 2019, 119, 218-232.	0.2	21
7159	Whole-Genome Analyses Resolve the Phylogeny of Flightless Birds (Palaeognathae) in the Presence of an Empirical Anomaly Zone. <i>Systematic Biology</i> , 2019, 68, 937-955.	2.7	88
7160	The Origins and Diversification of the Exceptionally Rich Gernsnakes (Colubroidea: Lamprophiidae:). <i>Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50</i>	2.7	22
7161	Bacterial Genome-Wide Association Identifies Novel Factors That Contribute to Ethionamide and Prothionamide Susceptibility in <i>Mycobacterium tuberculosis</i> . <i>MBio</i> , 2019, 10, .	1.8	39
7162	Variation in secondary metabolite production potential in the <i>Fusarium incarnatum-equiseti</i> species complex revealed by comparative analysis of 13 genomes. <i>BMC Genomics</i> , 2019, 20, 314.	1.2	68
7163	Metabolite profiling of the <i>Cladonia</i> lichens using gas chromatography-mass spectrometry. <i>Biochemical Systematics and Ecology</i> , 2019, 85, 3-12.	0.6	7
7164	Functions of cyclins and CDKs in mammalian gametogenesis. <i>Biological Journal of the Linnean Society</i> , 2019, 101, 591-601.	1.2	36
7165	Systematics, biogeography and ancestral state of the Australian marsupial genus <i>Antechinus</i> (Dasyuromorphia: Dasyuridae). <i>Zoological Journal of the Linnean Society</i> , 2019, 186, 553-568.	1.0	12

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7166	Microbial Diversity and Connectivity in Deep-Sea Sediments of the South Atlantic Polar Front. <i>Frontiers in Microbiology</i> , 2019, 10, 665.	1.5	32
7167	Molecular Epidemiology of HIV-1 Subtype G in the Russian Federation. <i>Viruses</i> , 2019, 11, 348.	1.5	9
7168	A new karst-dwelling gecko of the <i>Gekko petricolus</i> group (Reptilia: Gekkonidae) from Phitsanulok Province, central Thailand. <i>Journal of Natural History</i> , 2019, 53, 557-576.	0.2	0
7169	Complete mitochondrial genome of the leaf-rolling-weevil, <i>Apoderus jekelii</i> Roelofs, 1874 (Coleoptera: Tj ETQq1 1 0.784314 rgBT /Over	0.2	1
7170	Sexual Dichromatism Drives Diversification within a Major Radiation of African Amphibians. <i>Systematic Biology</i> , 2019, 68, 859-875.	2.7	41
7171	Learning mutational graphs of individual tumour evolution from single-cell and multi-region sequencing data. <i>BMC Bioinformatics</i> , 2019, 20, 210.	1.2	25
7172	<i>Aestuariusphingobium litorale</i> gen. nov., sp. nov., a novel proteobacterium isolated from a water sample of Pearl River estuary. <i>Antonie Van Leeuwenhoek</i> , 2019, 112, 1357-1367.	0.7	8
7173	Genome-informed Bradyrhizobium taxonomy: where to from here?. <i>Systematic and Applied Microbiology</i> , 2019, 42, 427-439.	1.2	62
7174	The complete chloroplast genome sequence of <i>Morella salicifolia</i> (Myricaceae): characterization and phylogenetic analysis. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 963-964.	0.2	2
7175	Ancient Polyploidy and Genome Evolution in Palms. <i>Genome Biology and Evolution</i> , 2019, 11, 1501-1511.	1.1	25
7176	CONTRIBUTIONS TO THE KNOWLEDGE OF CAMBODIAN CYPERACEAE. <i>Edinburgh Journal of Botany</i> , 2019, 76, 197-220.	0.4	0
7177	A review of <i>Sulcospira</i> (Gastropoda: Pachychilidae) from China, with description of two new species. <i>Molluscan Research</i> , 2019, 39, 241-252.	0.2	2
7178	Brood parasitism in eusocial insects (Hymenoptera): role of host geographical range size and phylogeny. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20180203.	1.8	9
7179	Social genes are selection hotspots in kin groups of a soil microbe. <i>Science</i> , 2019, 363, 1342-1345.	6.0	32
7180	New species and records of lichens from Bolivia. <i>Phytotaxa</i> , 2019, 397, 257.	0.1	14
7181	New records from the southern North Sea and first records from the Baltic Sea of <i>Kornmannia leptoderma</i> . <i>Botanica Marina</i> , 2019, 62, 63-73.	0.6	3
7182	Local Diversification of Methicillin- Resistant <i>Staphylococcus aureus</i> ST239 in South America After Its Rapid Worldwide Dissemination. <i>Frontiers in Microbiology</i> , 2019, 10, 82.	1.5	20
7183	Species Boundaries and Parapatric Speciation in the Complex of Alpine Shrubs, <i>Rosa sericea</i> (Rosaceae), Based on Population Genetics and Ecological Tolerances. <i>Frontiers in Plant Science</i> , 2019, 10, 321.	1.7	19

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7184	Allopatric separation represents an overlooked cryptic species in the <i>Anania hortulata</i> species complex (Lepidoptera: Crambidae: Pyraustinae): congruence between genetic and morphological evidence. <i>Canadian Entomologist</i> , 2019, 151, 163-186.	0.4	4
7185	Genomic analysis of ant domatia-associated melanized fungi (Chaetothyriales, Ascomycota). <i>Mycological Progress</i> , 2019, 18, 541-552.	0.5	17
7186	<i>OsAGO2</i> controls ROS production and the initiation of tapetal PCD by epigenetically regulating <i>OsHKK1</i> expression in rice anthers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 7549-7558.	3.3	102
7187	Inadvertent Paralog Inclusion Drives Artifactual Topologies and Timetree Estimates in Phylogenomics. <i>Molecular Biology and Evolution</i> , 2019, 36, 1344-1356.	3.5	56
7188	On and off the rocks: persistence and ecological diversification in a tropical Australian lizard radiation. <i>BMC Evolutionary Biology</i> , 2019, 19, 81.	3.2	13
7189	The Patchy Distribution of Restriction Modification System Genes and the Conservation of Orphan Methyltransferases in Halobacteria. <i>Genes</i> , 2019, 10, 233.	1.0	27
7190	Detection of vancomycin-resistant <i>Enterococcus faecium</i> hospital-adapted lineages in municipal wastewater treatment plants indicates widespread distribution and release into the environment. <i>Genome Research</i> , 2019, 29, 626-634.	2.4	40
7191	<i>Gelidium guimaraesiae</i> sp. nov. (Gelidiaceae, Rhodophyta) from the Western Atlantic segregated from <i>G. floridanum</i> by morphological and molecular evidence. <i>Phytotaxa</i> , 2019, 388, 275.	0.1	4
7192	Phylogeography of <i>Bellamyia</i> (Mollusca: Gastropoda: Viviparidae) snails on different continents: contrasting patterns of diversification in China and East Africa. <i>BMC Evolutionary Biology</i> , 2019, 19, 82.	3.2	14
7193	Benthic Diatom Communities in an Alpine River Impacted by Waste Water Treatment Effluents as Revealed Using DNA Metabarcoding. <i>Frontiers in Microbiology</i> , 2019, 10, 653.	1.5	55
7194	Four new monorchiids from the golden trevally, <i>Gnathanodon speciosus</i> (Forsskål) (Perciformes): Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	0.5	13
7195	Evolution and Diversification of Kiwifruit Mitogenomes through Extensive Whole-Genome Rearrangement and Mosaic Loss of Intergenic Sequences in a Highly Variable Region. <i>Genome Biology and Evolution</i> , 2019, 11, 1192-1206.	1.1	43
7196	Differential gene expression associated with fungal trophic shifts along the senescence gradient of the moss <i>Dicranum scoparium</i> . <i>Environmental Microbiology</i> , 2019, 21, 2273-2289.	1.8	11
7197	Untangling the <i>Echiniscus</i> Gordian knot: paraphyly of the <i>arctomys</i> group (Heterotardigrada: Echiniscidae). <i>Cladistics</i> , 2019, 35, 633-653.	1.5	40
7198	Complete subspecies-level phylogeny of the Oriolidae (Aves: Passeriformes): Out of Australasia and return. <i>Molecular Phylogenetics and Evolution</i> , 2019, 137, 200-209.	1.2	18
7199	Diversified local CRISPR-Cas immunity to viruses of <i>Sulfolobus islandicus</i> . <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20180093.	1.8	32
7200	Genomic Characterization of Candidate Division LCP-89 Reveals an Atypical Cell Wall Structure, Microcompartment Production, and Dual Respiratory and Fermentative Capacities. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	14
7201	A new genus and species of the trematode family Gyliauchenidae Fukui, 1929 from an unexpected, but plausible, host, <i>Kyphosus cornelii</i> (Perciformes: Kyphosidae). <i>Parasitology</i> , 2019, 146, 937-946.	0.7	8

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7202	Pyrite formation from FeS and H ₂ S is mediated through microbial redox activity. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 6897-6902.	3.3	106
7203	The first complete chloroplast genome of <i>Pontederia cordata</i> (Pontederiaceae). Mitochondrial DNA Part B: Resources, 2019, 4, 555-557.	0.2	3
7204	Revisiting the North American freshwater mussel genus <i>Quadrula</i> sensu lato (Bivalvia). Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 662	0.7	21
7205	Misturatosphaeria viridibrunnea sp. nov. (Teichosporaceae, Pleosporales) from Thailand. Phytotaxa, 2019, 388, 123.	0.1	2
7206	Phylogenetic and morphological analyses of species of the Entolomataceae (Agaricales). Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 582 Td (B	0.1	11
7207	Hermatomyces trangensis sp. nov., a new dematiaceous hyphomycete (Hermatomycetaceae). Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 10 T	0.1	5
7208	Paris lihengiana (Melanthiaceae: Parideae), a new species from Yunnan, China. Phytotaxa, 2019, 392, 45.	0.1	8
7209	Reappraisal of Tashiroea as a genus independent of Bredia (Melastomataceae) based on molecular data. Phytotaxa, 2019, 392, 75.	0.1	6
7210	New insights on Hygrophorus penarioides and H. penarius (Agaricales, Hygrophoraceae) from Hungary. Phytotaxa, 2019, 392, 127.	0.1	3
7211	Laccaria violaceotincta: a new species from tropical India based on morphology and molecular phylogeny. Phytotaxa, 2019, 392, 140.	0.1	11
7212	Neopestalotiopsis alpapicalis sp. nov. a new endophyte from tropical mangrove trees in Krabi Province (Thailand). Phytotaxa, 2019, 393, 251.	0.1	19
7213	Phylogeny and a new species of the genus Arachnomyces (Arachnomycetaceae). Phytotaxa, 2019, 394, 89.	0.1	7
7214	A broader circumscription of Bulbostylis including Nenum (Abildgaardieae: Cyperaceae). Phytotaxa, 2019, 395, 199.	0.1	26
7215	A new species of Bothrops (Serpentes: Viperidae: Crotalinae) from Pampas del Heath, southeastern Peru, with comments on the systematics of the Bothrops neuwiedi species group. Zootaxa, 2019, 4565, zootaxa.4565.3.1.	0.2	14
7216	Distribution and status of Turdus thrushes in white-sand areas of eastern Colombia, with a new subspecies of T. leucomelas. Zootaxa, 2019, 4567, 161.	0.2	1
7217	Extensive allopolyploidy in the neotropical genus <i>Lachemilla</i> (Rosaceae) revealed by PCR-based target enrichment of the nuclear ribosomal DNA cistron and plastid phylogenomics. American Journal of Botany, 2019, 106, 415-437.	0.8	14
7218	Galactitol catabolism in Sinorhizobium meliloti is dependent on a chromosomally encoded sorbitol dehydrogenase and a pSymB-encoded operon necessary for tagatose catabolism. Molecular Genetics and Genomics, 2019, 294, 739-755.	1.0	6
7219	The transition to selfing in Azorean Tolpis (Asteraceae). Plant Systematics and Evolution, 2019, 305, 305-317.	0.3	16

#	ARTICLE	IF	CITATIONS
7220	Comparative mitogenomic and phylogenetic analysis of <i>Apalone spinifera</i> and <i>Apalone ferox</i> (Testudines: Trionychidae). <i>Genetica</i> , 2019, 147, 165-176.	0.5	5
7221	A novel species and a new combination of <i>Daldinia</i> from Ban Hua Thung community forest in the northern part of Thailand. <i>Mycological Progress</i> , 2019, 18, 553-564.	0.5	8
7222	Megaphylogeny resolves global patterns of mushroom evolution. <i>Nature Ecology and Evolution</i> , 2019, 3, 668-678.	3.4	187
7223	An automated Raman-based platform for the sorting of live cells by functional properties. <i>Nature Microbiology</i> , 2019, 4, 1035-1048.	5.9	170
7224	Draft genome of the brown alga, <i>Nemacystus decipiens</i> , Onna-1 strain: Fusion of genes involved in the sulfated fucan biosynthesis pathway. <i>Scientific Reports</i> , 2019, 9, 4607.	1.6	33
7225	Genomes of skipper butterflies reveal extensive convergence of wing patterns. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 6232-6237.	3.3	86
7226	The complete chloroplast genome of <i>Prunus incisa</i> , and phylogenetic analysis with Prunoideae species. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 895-896.	0.2	0
7227	Diversity, Prevalence, and Virulence of <i>Colletotrichum</i> Species Associated with Lima Bean in Brazil. <i>Plant Disease</i> , 2019, 103, 1961-1966.	0.7	10
7228	Ancestral range reconstruction of remote oceanic island species of <i>Plantago</i> (Plantaginaceae) reveals differing scales and modes of dispersal. <i>Journal of Biogeography</i> , 2019, 46, 706-722.	1.4	21
7229	Reticulate evolution in nuclear Middle America causes discordance in the phylogeny of palmâ€špitvipers (Viperidae: <i>Bothriechis</i>). <i>Journal of Biogeography</i> , 2019, 46, 833-844.	1.4	24
7230	The making of elaborate petals in <i>Nigella</i> through developmental repatterning. <i>New Phytologist</i> , 2019, 223, 385-396.	3.5	21
7231	Genomic and Functional Analysis of Emerging Virulent and Multidrug-Resistant <i>Escherichia coli</i> Lineage Sequence Type 648. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	1.4	71
7232	Early Genomic Detection of Cosmopolitan Genotype of Dengue Virus Serotype 2, Angola, 2018. <i>Emerging Infectious Diseases</i> , 2019, 25, 784-787.	2.0	36
7233	<i>Klebsiella pneumoniae</i> ST307 with bla _{OXA-181} South Africa, 2014â€“2016. <i>Emerging Infectious Diseases</i> , 2019, 25, 739-747.	2.0	74
7234	Morphological and Molecular Analysis of Australian Earwigs (Dermaptera) Points to Unique Species and Regional Endemism in the Anisolabididae Family. <i>Insects</i> , 2019, 10, 72.	1.0	7
7235	Description of adults and larvae of <i>Orientelmis parvula</i> (Nomura & Baba, 1961) (Coleoptera: Tj ETQq1 1 0,784314,rgBT /Over	0,2	
7236	Hospital outbreak due to <i>Clostridium difficile</i> ribotype 018 (RT018) in Southern Germany. <i>International Journal of Medical Microbiology</i> , 2019, 309, 189-193.	1.5	16
7237	Discovery and ecogenomic context of a global <i>Caldiserica</i> -related phylum active in thawing permafrost, <i>Candidatus Cryoserica</i> phylum nov., <i>Ca. Cryoserica</i> class nov., <i>Ca. Cryosericales</i> ord. nov., <i>Ca. Cryoseriaceae</i> fam. nov., comprising the four species <i>Cryosericum septentrionale</i> gen. nov. sp. nov., <i>Ca. C. hinesii</i> sp. nov., <i>Ca. C. odellii</i> sp. nov., <i>Ca. C. terrychapinii</i> sp. nov.. <i>Systematic and Applied Microbiology</i> , 2019, 42, 54-66.	1.2	42

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7238	Diversified secondary metabolite biosynthesis gene repertoire revealed in symbiotic dinoflagellates. <i>Scientific Reports</i> , 2019, 9, 1204.	1.6	21
7239	Blast Fungal Genomes Show Frequent Chromosomal Changes, Gene Gains and Losses, and Effector Gene Turnover. <i>Molecular Biology and Evolution</i> , 2019, 36, 1148-1161.	3.5	42
7240	Systematic Identification of Pathogenic <i>Streptomyces</i> sp. AMCC400023 That Causes Common Scab and Genomic Analysis of Its Pathogenicity Island. <i>Phytopathology</i> , 2019, 109, 1115-1128.	1.1	11
7241	Physical gills in Elmidae (Coleoptera: Byrrhoidea): Structure and evolutionary pattern of plastron in <i>Stenelmis</i> and related genera. <i>Entomological Science</i> , 2019, 22, 157-160.	0.3	4
7242	The evolution of functional complexity within the β -amylase gene family in land plants. <i>BMC Evolutionary Biology</i> , 2019, 19, 66.	3.2	47
7243	More pieces to a huge puzzle: Two new <i>Escovopsis</i> species from fungus gardens of attine ants. <i>MycKeys</i> , 2019, 46, 97-118.	0.8	8
7244	Genome-wide analysis reveals the genomic features of the turkey vulture (<i>Cathartes aura</i>) as a scavenger. <i>Molecular Genetics and Genomics</i> , 2019, 294, 679-692.	1.0	10
7245	The complete plastid genomes of four species from Brassicales. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 124-125.	0.2	1
7246	The complete chloroplast genome of <i>Helichrysum italicum</i> (Roth) G. Don (Asteraceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1036-1037.	0.2	5
7247	Rapid morphological evolution in placental mammals post-dates the origin of the crown group. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20182418.	1.2	29
7248	A phylum-wide survey reveals multiple independent gains of head regeneration in Nemertea. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20182524.	1.2	30
7249	A review of the <i>Barbatula</i> loaches (Teleostei: Nemacheilidae) from north-eastern China, with the description of four new species. <i>Zootaxa</i> , 2019, 4565, zootaxa.4565.1.1.	0.2	5
7250	Genomic analysis of <i>Leptospira interrogans</i> serovar Paidjan and Dadas isolates from carrier dogs and comparative genomic analysis to detect genes under positive selection. <i>BMC Genomics</i> , 2019, 20, 168.	1.2	8
7251	Gene Selection and Evolutionary Modeling Affect Phylogenomic Inference of Neuropterida Based on Transcriptome Data. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1072.	1.8	8
7252	The transcriptome of the veiled chameleon (<i>Chamaeleo calytratus</i>): A resource for studying the evolution and development of vertebrates. <i>Developmental Dynamics</i> , 2019, 248, 702-708.	0.8	26
7253	The Genome of <i>Cucurbita argyrosperma</i> (Silver-Seed Gourd) Reveals Faster Rates of Protein-Coding Gene and Long Noncoding RNA Turnover and Neofunctionalization within <i>Cucurbita</i> . <i>Molecular Plant</i> , 2019, 12, 506-520.	3.9	48
7254	Owls lack UV-sensitive cone opsin and red oil droplets, but see UV light at night: Retinal transcriptomes and ocular media transmittance. <i>Vision Research</i> , 2019, 158, 109-119.	0.7	32
7255	Genomics-based diversity analysis of <i>Vanilla</i> species using a <i>Vanilla planifolia</i> draft genome and Genotyping-By-Sequencing. <i>Scientific Reports</i> , 2019, 9, 3416.	1.6	36

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7256	The complete chloroplast genome of <i>Tetraena mongolica</i> (Zygophyllaceae), an endangered shrub endemic to China. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1030-1031.	0.2	5
7257	Cloudy with a chance of speciation: integrative taxonomy reveals extraordinary divergence within a Mesoamerican cloud forest bird. <i>Biological Journal of the Linnean Society</i> , 2019, 126, 1-15.	0.7	28
7258	Identification of the novel class D Î²-lactamase OXA-679 involved in carbapenem resistance in <i>Acinetobacter calcoaceticus</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 1494-1502.	1.3	7
7259	The emergence of the multi-species NIP1 effector in <i>Rhynchosporium</i> was accompanied by high rates of gene duplications and losses. <i>Environmental Microbiology</i> , 2019, 21, 2677-2695.	1.8	19
7260	When do herbivorous insects compete? A phylogenetic meta-analysis. <i>Ecology Letters</i> , 2019, 22, 875-883.	3.0	23
7261	Climate change, extinction, and Sky Island biogeography in a montane lizard. <i>Molecular Ecology</i> , 2019, 28, 2610-2624.	2.0	40
7262	Constrained incremental tree building: new absolute fast converging phylogeny estimation methods with improved scalability and accuracy. <i>Algorithms for Molecular Biology</i> , 2019, 14, 2.	0.3	9
7263	Diversity and Distribution of Sulfur Oxidation-Related Genes in <i>Thioalkalivibrio</i> , a Genus of Chemolithoautotrophic and Haloalkaliphilic Sulfur-Oxidizing Bacteria. <i>Frontiers in Microbiology</i> , 2019, 10, 160.	1.5	56
7264	New sporocarpic taxa in the phylum Glomeromycota: <i>Sclerocarpum amazonicum</i> gen. et sp. nov. in the family Glomeraceae (Glomerales) and <i>Diversispora sporocarpia</i> sp. nov. in the Diversisporaceae (Diversisporales). <i>Mycological Progress</i> , 2019, 18, 369-384.	0.5	19
7265	The phylogenetic position of the morphologically unusual <i>Pleurostichidium falkenbergii</i> (Rhodomelaceae, Rhodophyta) based on plastid phylogenomics. <i>Phycologia</i> , 2019, 58, 319-325.	0.6	4
7266	Genomic Organization and Phylogeny of MHC Class II Loci in Cetaceans. <i>Journal of Heredity</i> , 2019, 110, 332-339.	1.0	6
7267	Promiscuous terpene synthases from <i>Prunella vulgaris</i> highlight the importance of substrate and compartment switching in terpene synthase evolution. <i>New Phytologist</i> , 2019, 223, 323-335.	3.5	26
7268	The complex geography of domestication of the African rice <i>Oryza glaberrima</i> . <i>PLoS Genetics</i> , 2019, 15, e1007414.	1.5	30
7269	Genomic, epidemiological and digital surveillance of Chikungunya virus in the Brazilian Amazon. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007065.	1.3	75
7270	Utility of Hybrid Transferrin Binding Protein Antigens for Protection Against Pathogenic <i>Neisseria</i> Species. <i>Frontiers in Immunology</i> , 2019, 10, 247.	2.2	32
7271	The complete chloroplast genome sequence of watercress (<i>Nasturtium officinale</i> R. Br.): Genome organization, adaptive evolution and phylogenetic relationships in Cardamineae. <i>Gene</i> , 2019, 699, 24-36.	1.0	55
7272	The complete plastid genome sequence of <i>Aconitum brachypodum</i> (Ranunculaceae): an Endangered species endemic to China. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 130-131.	0.2	1
7273	Morphological Polymorphism Associated with Alternative Reproductive Tactics in a Plethodontid Salamander. <i>American Naturalist</i> , 2019, 193, 608-618.	1.0	10

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7274	CMY-1/MOX-family AmpC β -lactamases MOX-1, MOX-2 and MOX-9 were mobilized independently from three <i>Aeromonas</i> species. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 1202-1206.	1.3	17
7275	Illuminating the obscured phylogenetic radiation of South American <i>Sylvilagus</i> Gray, 1867 (Lagomorpha: Leporidae). <i>Journal of Mammalogy</i> , 2019, 100, 31-44.	0.6	13
7276	Bayesian Estimation of Species Divergence Times Using Correlated Quantitative Characters. <i>Systematic Biology</i> , 2019, 68, 967-986.	2.7	27
7277	Does reproductive behaviour reflect phylogenetic relationships? An example from Central European <i>Alopecosa</i> wolf spiders (Araneae: Lycosidae). <i>Zoological Journal of the Linnean Society</i> , 2019, 185, 1039-1056.	1.0	5
7278	Conidae phylogenomics and evolution. <i>Zoologica Scripta</i> , 2019, 48, 194-214.	0.7	21
7279	Mycobiome Profiles in Breast Milk from Healthy Women Depend on Mode of Delivery, Geographic Location, and Interaction with Bacteria. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	76
7280	Identification of the OXA-48 Carbapenemase Family by Use of Tryptic Peptides and Liquid Chromatography-Tandem Mass Spectrometry. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	1.8	15
7281	Taxonomic novelties in grammitid ferns (Polypodiaceae) from the Neotropics and Madagascar supported by molecular data. <i>Phytotaxa</i> , 2019, 394, 176.	0.1	2
7282	Transcriptomic analysis confirms differences among nuclear genomes of cryptic earthworm lineages living in sympatry. <i>BMC Evolutionary Biology</i> , 2019, 19, 50.	3.2	18
7283	Evolution of plastid genomes of <i>Holcoglossum</i> (Orchidaceae) with recent radiation. <i>BMC Evolutionary Biology</i> , 2019, 19, 63.	3.2	47
7284	The golden death bacillus <i>Chryseobacterium nematophagum</i> is a novel matrix digesting pathogen of nematodes. <i>BMC Biology</i> , 2019, 17, 10.	1.7	12
7285	Phylogenetic relationships within the primitive acanthomorph fish genus <i>Polymixia</i> , with changes to species composition and geographic distributions. <i>PLoS ONE</i> , 2019, 14, e0212954.	1.1	4
7286	Congruent phylogenetic relationships of <i>Melaphidina</i> aphids (Aphididae: Eriosomatinae: Fordini) according to nuclear and mitochondrial DNA data with taxonomic implications on generic limits. <i>PLoS ONE</i> , 2019, 14, e0213181.	1.1	17
7287	Comparative genomics sheds light on the predatory lifestyle of accipitrids and owls. <i>Scientific Reports</i> , 2019, 9, 2249.	1.6	14
7288	Deep genetic differentiation between two morphologically similar species of wolf herrings (Teleostei, Tj ETQq0 0 0 rgBT /Overlock 10 Tf	0.8	1
7289	Evolutionary history of the buildup and breakdown of the heterostylous syndrome in <i>Plumbaginaceae</i> . <i>New Phytologist</i> , 2019, 224, 1278-1289.	3.5	17
7290	<i>Ionosporus</i> : a new genus for <i>Boletus longipes</i> (Boletaceae), with a new species, <i>I. australis</i> , from Australia. <i>Mycological Progress</i> , 2019, 18, 439-451.	0.5	15
7291	Extreme mito-nuclear discordance in a peninsular lizard: the role of drift, selection, and climate. <i>Heredity</i> , 2019, 123, 359-370.	1.2	24

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7292	Co-occurring genomic capacity for anaerobic methane and dissimilatory sulfur metabolisms discovered in the Korarchaeota. <i>Nature Microbiology</i> , 2019, 4, 614-622.	5.9	91
7293	Expanding anaerobic alkane metabolism in the domain of Archaea. <i>Nature Microbiology</i> , 2019, 4, 595-602.	5.9	133
7294	Evolutionary genomics of anthroponosis in <i>Cryptosporidium</i> . <i>Nature Microbiology</i> , 2019, 4, 826-836.	5.9	99
7295	Genome mining identifies cepacin as a plant-protective metabolite of the biopesticidal bacterium <i>Burkholderia ambifaria</i> . <i>Nature Microbiology</i> , 2019, 4, 996-1005.	5.9	106
7296	The complete mitochondrial genome of <i>Gryposmylus pennyi</i> (Neuroptera: Osmylidae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 870-871.	0.2	1
7297	The Draft Genome of an Octocoral, <i>Dendronephthya gigantea</i> . <i>Genome Biology and Evolution</i> , 2019, 11, 949-953.	1.1	44
7298	Primary Production in the Water Column as Major Structuring Element of the Biogeographical Distribution and Function of Archaea in Deep-Sea Sediments of the Central Pacific Ocean. <i>Archaea</i> , 2019, 2019, 1-12.	2.3	9
7299	Urban metagenomics uncover antibiotic resistance reservoirs in coastal beach and sewage waters. <i>Microbiome</i> , 2019, 7, 35.	4.9	109
7300	Host Phylogeny, Geographic Overlap, and Roost Sharing Shape Parasite Communities in European Bats. <i>Frontiers in Ecology and Evolution</i> , 2019, 7, .	1.1	34
7301	Uncovering carbohydrate metabolism through a genotype-phenotype association study of 56 lactic acid bacteria genomes. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 3135-3152.	1.7	61
7302	Characterization of the complete chloroplast genome of <i>Rosa chinensis</i> "Old Blush" (Rosaceae), an important cultivated Chinese rose. <i>Acta Horticulturae</i> , 2019, , 119-124.	0.1	3
7303	Being in the right place at the right time? Parallel diversification bursts favored by the persistence of ancient epizoochorous traits and hidden factors in Cynoglossoidae. <i>American Journal of Botany</i> , 2019, 106, 438-452.	0.8	12
7304	Adaptive Strategies of the Candidate Probiotic <i>E.Âcoli</i> Nissle in the Mammalian Gut. <i>Cell Host and Microbe</i> , 2019, 25, 499-512.e8.	5.1	94
7305	Reverse Evolution of a Classic Gene Network in Yeast Offers a Competitive Advantage. <i>Current Biology</i> , 2019, 29, 1126-1136.e5.	1.8	26
7306	Ecology, not distance, explains community composition in parasites of sky-island Audubon's Warblers. <i>International Journal for Parasitology</i> , 2019, 49, 437-448.	1.3	19
7307	Molecular epidemiology of hepatitis B virus in Paraguay. <i>Infection, Genetics and Evolution</i> , 2019, 71, 91-97.	1.0	12
7308	Pathogenicity and transmission of virulent Newcastle disease virus from the 2018-2019 California outbreak and related viruses in young and adult chickens. <i>Virology</i> , 2019, 531, 203-218.	1.1	28
7309	Spatio-temporal evolution of climbing habit in the <i>Dahlia-Hidalgoa</i> group (Coreopsidae, Asteraceae). <i>Molecular Phylogenetics and Evolution</i> , 2019, 135, 166-176.	1.2	8

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7310	Long-term seasonal and interannual variability of marine aerobic anoxygenic photoheterotrophic bacteria. <i>ISME Journal</i> , 2019, 13, 1975-1987.	4.4	32
7311	Anaerobic oxidation of ethane by archaea from a marine hydrocarbon seep. <i>Nature</i> , 2019, 568, 108-111.	13.7	149
7312	Insight into the genome and brackish water adaptation strategies of toxic and bloom-forming Baltic Sea <i>Dolichospermum</i> sp. UHCC 0315. <i>Scientific Reports</i> , 2019, 9, 4888.	1.6	14
7313	Nuclear phylogeny and hypothesized allopolyploidization events in the Subtribe Otachyriinae (Paspaleae, Poaceae). <i>Systematics and Biodiversity</i> , 2019, 17, 277-294.	0.5	6
7314	Diversity of Saint Helena Island and zoogeography of zoantharians in the Atlantic Ocean: Jigsaw falling into place. <i>Systematics and Biodiversity</i> , 2019, 17, 165-178.	0.5	10
7315	Complete chloroplast genome sequence of the Oriental oak, <i>Quercus variabilis</i> (Fagaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 203-204.	0.2	2
7316	The complete chloroplast genome of <i>Justicia leptostachya</i> (Acanthaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1114-1115.	0.2	2
7317	Characterization of the complete chloroplast genome of <i>Juniperus recurva</i> (Cupressaceae), the Drooping Juniper from the Himalaya. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1219-1220.	0.2	5
7318	Phylogenetics, classification and typification of extant horsetails (<i>Equisetum</i> , Equisetaceae). <i>Botanical Journal of the Linnean Society</i> , 2019, 189, 311-352.	0.8	23
7319	Duplications in Corneous Beta Protein Genes and the Evolution of Gecko Adhesion. <i>Integrative and Comparative Biology</i> , 2019, 59, 193-202.	0.9	15
7320	Parallel Speciation of Wild Rice Associated with Habitat Shifts. <i>Molecular Biology and Evolution</i> , 2019, 36, 875-889.	3.5	31
7321	Green Fluorescent Protein Transformation Sheds More Light on a Widespread Mycoparasitic Interaction. <i>Phytopathology</i> , 2019, 109, 1404-1416.	1.1	14
7322	A process of convergent amplification and tissue-specific expression dominates the evolution of toxin and toxin-like genes in sea anemones. <i>Molecular Ecology</i> , 2019, 28, 2272-2289.	2.0	48
7323	A New Species of Scutigera (Anura: Megophryidae) from the Gaoligongshan Mountain Range, China. <i>Copeia</i> , 2019, 107, 10.	1.4	8
7324	Major Traditional Probiotics: Comparative Genomic Analyses and Roles in Gut Microbiome of Eight Cohorts. <i>Frontiers in Microbiology</i> , 2019, 10, 712.	1.5	13
7325	Sequencing and Phylogenetic Analysis of Chloroplast Genes in Freshwater Raphidophytes. <i>Genes</i> , 2019, 10, 245.	1.0	3
7326	Essentials of Bioinformatics, Volume I., 2019, .		8
7327	Olfactomedin domain-containing proteins: evolution, functional divergence, expression patterns and damaging SNPs. <i>Molecular Genetics and Genomics</i> , 2019, 294, 875-885.	1.0	9

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7328	New family and genus for Dendrilla-like sponges with characters of Verongiida. Part I redescription of <i>Dendrilla lacunosa</i> Hentschel 1912, diagnosis of the new family Ernstiliidae and <i>Ernstilla</i> n. g.. <i>Zoologischer Anzeiger</i> , 2019, 280, 14-20.	0.4	14
7329	Phylogenomics shows lignotuber state is taxonomically informative in closely related eucalypts. <i>Molecular Phylogenetics and Evolution</i> , 2019, 135, 236-248.	1.2	14
7330	Museum genomics reveals the speciation history of <i>Dendrortyx</i> wood-partridges in the Mesoamerican highlands. <i>Molecular Phylogenetics and Evolution</i> , 2019, 136, 29-34.	1.2	21
7331	Restriction-site associated DNA sequencing supports a sister group relationship of <i>Nigritella</i> and <i>Gymnadenia</i> (Orchidaceae). <i>Molecular Phylogenetics and Evolution</i> , 2019, 136, 21-28.	1.2	24
7332	An integrated whole genome analysis of <i>Mycobacterium tuberculosis</i> reveals insights into relationship between its genome, transcriptome and methylome. <i>Scientific Reports</i> , 2019, 9, 5204.	1.6	26
7333	Systematic congruence in Polycladida (Platyhelminthes, Rhabditophora): are DNA and morphology telling the same story?. <i>Zoological Journal of the Linnean Society</i> , 2019, 186, 865-891.	1.0	27
7334	An <i>scpr</i> package and online resource for macroevolutionary studies using the ray-finned fish tree of life. <i>Methods in Ecology and Evolution</i> , 2019, 10, 1118-1124.	2.2	85
7335	Genetic and morphological variations of the lichenized fungus <i>Steinera intricata</i> (Arctomiaceae.) <i>Tj ETQq1 1 0.784314 rgBT /Overlock</i> 907-918.	0.5	0
7336	<i>Myxotrichum albicans</i> , a new slowly-growing species isolated from forest litters in China. <i>Mycoscience</i> , 2019, 60, 232-236.	0.3	1
7337	Incorporation of deep-sea and small-sized species provides new insights into gastropods phylogeny. <i>Molecular Phylogenetics and Evolution</i> , 2019, 135, 136-147.	1.2	21
7338	Complete chloroplast genome of the diatom <i>Skeletonema pseudocostatum</i> from the Western Mediterranean coast of Algeria. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1091-1092.	0.2	2
7339	Cluster-Transition Determining Sites Underlying the Antigenic Evolution of Seasonal Influenza Viruses. <i>Molecular Biology and Evolution</i> , 2019, 36, 1172-1186.	3.5	13
7340	Multiple radiations of spiny mice (Rodentia: Acomys) in dry open habitats of Afro-Arabia: evidence from a multi-locus phylogeny. <i>BMC Evolutionary Biology</i> , 2019, 19, 69.	3.2	31
7341	Assessing the role of transmission chains in the spread of HIV-1 among men who have sex with men in Quebec, Canada. <i>PLoS ONE</i> , 2019, 14, e0213366.	1.1	7
7342	A multilocus phylogeny of the fish genus <i>Poeciliopsis</i> : Solving taxonomic uncertainties and preliminary evidence of reticulation. <i>Ecology and Evolution</i> , 2019, 9, 1845-1857.	0.8	13
7343	Genomic, ecological, and morphological approaches to investigating species limits: A case study in modern taxonomy from Tropical Eastern Pacific surgeonfishes. <i>Ecology and Evolution</i> , 2019, 9, 4001-4012.	0.8	6
7344	Nine new RNA viruses associated with the fire ant <i>Solenopsis invicta</i> from its native range. <i>Virus Genes</i> , 2019, 55, 368-380.	0.7	22
7345	Evolution of the eyes of vipers with and without infrared-sensing pit organs. <i>Biological Journal of the Linnean Society</i> , 2019, 126, 796-823.	0.7	22

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7346	Resolving Phylogenetic Relationships for <i>Streptococcus mitis</i> and <i>Streptococcus oralis</i> through Core- and Pan-Genome Analyses. <i>Genome Biology and Evolution</i> , 2019, 11, 1077-1087.	1.1	34
7347	Aneuploidy and Ethanol Tolerance in <i>Saccharomyces cerevisiae</i> . <i>Frontiers in Genetics</i> , 2019, 10, 82.	1.1	71
7348	Phylogenomics of the Major Tropical Plant Family Annonaceae Using Targeted Enrichment of Nuclear Genes. <i>Frontiers in Plant Science</i> , 2018, 9, 1941.	1.7	100
7349	Integrative taxonomy refutes a species hypothesis: The asymmetric hybrid origin of <i>Arsapnia arapahoe</i> (Plecoptera, Capniidae). <i>Ecology and Evolution</i> , 2019, 9, 1364-1377.	0.8	6
7350	The genome of the jellyfish <i>Clytia hemisphaerica</i> and the evolution of the cnidarian life-cycle. <i>Nature Ecology and Evolution</i> , 2019, 3, 801-810.	3.4	135
7351	Flower visitors of the licuri palm (<i>Syagrus coronata</i>): brood pollinators coexist with a diverse community of antagonists and mutualists. <i>Biological Journal of the Linnean Society</i> , 2019, 126, 666-687.	0.7	31
7352	Phylogenetic Clustering by Linear Integer Programming (PhyCLIP). <i>Molecular Biology and Evolution</i> , 2019, 36, 1580-1595.	3.5	54
7353	The origins and dispersal history of the trichaline net-winged beetles in Southeast Asia, Wallacea, New Guinea and Australia. <i>Zoological Journal of the Linnean Society</i> , 2019, 185, 1079-1094.	1.0	22
7354	The plant Pontin and Reptin homologues, RuvBL1 and RuvBL2a, colocalize with TERT and TRB proteins <i>in vivo</i> , and participate in telomerase biogenesis. <i>Plant Journal</i> , 2019, 98, 195-212.	2.8	18
7355	Inflorescence evolution in Santalales: integrating morphological characters and molecular phylogenetics. <i>American Journal of Botany</i> , 2019, 106, 402-414.	0.8	27
7356	Updated phylogenetic and systematics of the <i>Acrapex albivena</i> Hampson, 1910 and <i>A. stygiata</i> (Hampson, 1910) species groups (Lepidoptera, Noctuidae, Noctuinae, Apameini, Sesamiina), with the description of nine new species from the Afrotropics. <i>Annales De La Societe Entomologique De France</i> , 2019, 55, 219-248.	0.4	4
7357	Persistence of a Geographically-Stable Hybrid Zone in Puerto Rican Dwarf Geckos. <i>Journal of Heredity</i> , 2019, 110, 523-534.	1.0	14
7358	Draft Genome Sequences of Eight <i>Vibrio</i> sp. Clinical Isolates from across the United States That Form a Basal Sister Clade to <i>Vibrio cholerae</i> . <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	5
7359	Genome Sequencing Illustrates the Genetic Basis of the Pharmacological Properties of <i>Gloeostereum incarnatum</i> . <i>Genes</i> , 2019, 10, 188.	1.0	33
7360	<i>Geosmithia</i> species in southeastern USA and their affinity to beetle vectors and tree hosts. <i>Fungal Ecology</i> , 2019, 39, 168-183.	0.7	14
7361	Structures of Class Id Ribonucleotide Reductase Catalytic Subunits Reveal a Minimal Architecture for Deoxynucleotide Biosynthesis. <i>Biochemistry</i> , 2019, 58, 1845-1860.	1.2	10
7362	A new genomic blueprint of the human gut microbiota. <i>Nature</i> , 2019, 568, 499-504.	13.7	901
7363	Taming extreme morphological variability through coupling of molecular phylogeny and quantitative phenotype analysis as a new avenue for taxonomy. <i>Scientific Reports</i> , 2019, 9, 2429.	1.6	7

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7364	Acquisition and Loss of Secondary Metabolites Shaped the Evolutionary Path of Three Emerging Phytopathogens of Wheat. <i>Genome Biology and Evolution</i> , 2019, 11, 890-905.	1.1	22
7365	Genomic changes underlying host specialization in the bee gut symbiont <i>Lactobacillus Firm5</i> . <i>Molecular Ecology</i> , 2019, 28, 2224-2237.	2.0	45
7366	Reconstruction of ancestral genome reveals chromosome evolution history for selected legume species. <i>New Phytologist</i> , 2019, 223, 2090-2103.	3.5	40
7367	<i>Mycobacterium ulcerans</i> Population Genomics To Inform on the Spread of Buruli Ulcer across Central Africa. <i>MSphere</i> , 2019, 4, .	1.3	14
7368	Gene Expansion and Positive Selection as Bacterial Adaptations to Oligotrophic Conditions. <i>MSphere</i> , 2019, 4, .	1.3	28
7369	The complete genome sequence of an alphabaculovirus from <i>Spodoptera exempta</i> , an agricultural pest of major economic significance in Africa. <i>PLoS ONE</i> , 2019, 14, e0209937.	1.1	5
7370	Mycological Diversity Description II. <i>Acta Botanica Brasilica</i> , 2019, 33, 163-173.	0.8	5
7371	Near Full-length Genomic Sequencing and Molecular Analysis of HIVInfected Individuals in a Network-based Intervention (TRIP) in Athens, Greece: Evidence that Transmissions Occur More Frequently from those with High HIV-RNA. <i>Current HIV Research</i> , 2019, 16, 345-353.	0.2	3
7372	Phylogeography of a widespread eastern North American shrub, <i>Viburnum lantanoides</i> . <i>American Journal of Botany</i> , 2019, 106, 389-401.	0.8	26
7373	Bioinformatics applied to biotechnology: A review towards bioenergy research. <i>Biomass and Bioenergy</i> , 2019, 123, 195-224.	2.9	17
7374	Evolution of hierarchy in bacterial metabolic networks. <i>BioSystems</i> , 2019, 180, 71-78.	0.9	3
7375	Phylogenetic relationships and regional spread of meningococcal strains in the meningitis belt, 2011–2016. <i>EBioMedicine</i> , 2019, 41, 488-496.	2.7	17
7376	Root endophytic fungi show low levels of interspecific competition in planta. <i>Fungal Ecology</i> , 2019, 39, 184-191.	0.7	13
7377	<i>Plagiorchis</i> sp. in small mammals of Senegal and the potential emergence of a zoonotic trematodiasis. <i>International Journal for Parasitology: Parasites and Wildlife</i> , 2019, 8, 164-170.	0.6	6
7378	A new species of <i>Lactifluus</i> (Russulales, Agaricomycetes) from the Brazilian caatinga semiarid region. <i>New Zealand Journal of Botany</i> , 2019, 57, 169-178.	0.8	7
7379	DNA barcoding of <i>Sialis</i> sp. (Megaloptera) in Portugal: the missing tool to species identification. <i>Aquatic Insects</i> , 2019, 40, 173-184.	0.6	5
7380	Mitochondrial genome of <i>Parborlasia corrugatus</i> (Nemertea: Lineidae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 332-334.	0.2	1
7381	Relationships between Tertiary relict and circumboreal woodland floras: a case study in <i>Chimaphila</i> (Ericaceae). <i>Annals of Botany</i> , 2019, 123, 1089-1098.	1.4	5

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7382	A congruent topology for deep gastropod relationships. Proceedings of the Royal Society B: Biological Sciences, 2019, 286, 20182776.	1.2	66
7383	Acoel genome reveals the regulatory landscape of whole-body regeneration. Science, 2019, 363, .	6.0	125
7384	Comparative genomics of plant pathogenic Botrytis species with distinct host specificity. BMC Genomics, 2019, 20, 203.	1.2	53
7385	Contingency in the convergent evolution of a regulatory network: Dosage compensation in Drosophila. PLoS Biology, 2019, 17, e3000094.	2.6	26
7386	Mixed infection by Histoplasma capsulatum isolates with different mating types in Brazilian AIDS-patients. Revista Do Instituto De Medicina Tropical De Sao Paulo, 2019, 61, e8.	0.5	3
7388	Survival Mechanisms of Campylobacter hepaticus Identified by Genomic Analysis and Comparative Transcriptomic Analysis of in vivo and in vitro Derived Bacteria. Frontiers in Microbiology, 2019, 10, 107.	1.5	21
7389	ProtParCon: A Framework for Processing Molecular Data and Identifying Parallel and Convergent Amino Acid Replacements. Genes, 2019, 10, 181.	1.0	4
7390	Insertion Hot Spots of DIRS1 Retrotransposon and Chromosomal Diversifications among the Antarctic Teleosts Nototheniidae. International Journal of Molecular Sciences, 2019, 20, 701.	1.8	10
7391	Digging for the spiny rat and hutia phylogeny using a gene capture approach, with the description of a new mammal subfamily. Molecular Phylogenetics and Evolution, 2019, 136, 241-253.	1.2	32
7392	Crystal structures of human lysosomal EPDR1 reveal homology with the superfamily of bacterial lipoprotein transporters. Communications Biology, 2019, 2, 52.	2.0	18
7393	Identification of evolutionarily conserved virulence factor by selective pressure analysis of Streptococcus pneumoniae. Communications Biology, 2019, 2, 96.	2.0	26
7394	Principles of plastid reductive evolution illuminated by nonphotosynthetic chrysophytes. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 6914-6923.	3.3	96
7395	Leaf shape and size track habitat transitions across forest-grassland boundaries in the grass family (Poaceae). Evolution; International Journal of Organic Evolution, 2019, 73, 927-946.	1.1	44
7396	A molecular phylogeny of chafers revisits the polyphyly of Tanyproctini (Scarabaeidae.) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 22 0.7 12	0.7	12
7397	Emergence of New Delhi Metallo-β-Lactamase (NDM-5) in Klebsiella quasipneumoniae from Neonates in a Nigerian Hospital. MSphere, 2019, 4, .	1.3	37
7398	Interspecific delimitation and relationships among four Ostrya species based on plastomes. BMC Genetics, 2019, 20, 33.	2.7	3
7399	Genetic diversity and relationship between cultivated, weedy and wild rye species as revealed by chloroplast and mitochondrial DNA non-coding regions analysis. PLoS ONE, 2019, 14, e0213023.	1.1	21
7400	Cryptic Diversity, but to What Extent? Discordance Between Single-Locus Species Delimitation Methods Within Mainland Anoles (Squamata: Dactyloidae) of Northern Central America. Frontiers in Genetics, 2019, 10, 11.	1.1	34

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7401	Distinct Genetic and Functional Traits of Human Intestinal <i>Prevotella copri</i> Strains Are Associated with Different Habitual Diets. <i>Cell Host and Microbe</i> , 2019, 25, 444-453.e3.	5.1	229
7402	Sponges Lack ParaHox Genes. <i>Genome Biology and Evolution</i> , 2019, 11, 1250-1257.	1.1	11
7403	Narrow habitat breadth and late-summer emergence increases extinction vulnerability in Central European bees. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20190316.	1.2	24
7404	Na ⁺ /K ⁺ -ATPase gene duplications in clitellate annelids are associated with freshwater colonization. <i>Journal of Evolutionary Biology</i> , 2019, 32, 580-591.	0.8	6
7405	Description of a new diminutive, rupicolous species of day-gecko (Squamata: Gekkonidae: Cnemaspis) from southern Sri Lanka. <i>Zootaxa</i> , 2019, 4565, 223.	0.2	8
7406	Hidden in plain sight: reassessment of the pig-footed bandicoot, <i>Chaeropus ecaudatus</i> (Peramelemorphia, Chaeropodidae), with a description of a new species from central australia, and use of the fossil record to trace its past distribution. <i>Zootaxa</i> , 2019, 4566, zootaxa.4566.1.1.	0.2	23
7407	A new glass sponge genus (Hexactinellida: Euplectellidae) from abyssal depth of the Yap Trench, northwestern Pacific Ocean. <i>Zootaxa</i> , 2019, 4567, zootaxa.4567.2.9.	0.2	7
7408	The complete chloroplast genome of wild diploid potato species <i>Solanum chacoense</i> bitter. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1127-1128.	0.2	0
7409	The lichen family Teloschistaceae in the Altai-Sayan region (Central Asia). <i>Phytotaxa</i> , 2019, 396, 1.	0.1	17
7410	Taxonomic status of the barbastelles (Chiroptera: Vespertilionidae: <i>Barbastella</i>) from the Japanese archipelago and Kunashir Island. <i>Zootaxa</i> , 2019, 4567, 461.	0.2	6
7411	The Molecular Basis of pH-Modulated HIV gp120 Binding Revealed. <i>Evolutionary Bioinformatics</i> , 2019, 15, 117693431983130.	0.6	4
7412	First report, along with nomenclature adjustments, of <i>Ulva ohnoi</i> , <i>U. tepida</i> and <i>U. torta</i> (Ulviceae, Ulvales, Chlorophyta) from northwestern Mexico. <i>Botanica Marina</i> , 2019, 62, 113-123.	0.6	14
7413	Diversity and Evolution of Viral Pathogen Community in Cave Nectar Bats (<i>Eonycteris spelaea</i>). <i>Viruses</i> , 2019, 11, 250.	1.5	22
7414	Genome analysis of a <i>Bacillus subtilis</i> strain reveals genetic mutations determining biocontrol properties. <i>World Journal of Microbiology and Biotechnology</i> , 2019, 35, 52.	1.7	17
7415	Filamentous phages: masters of a microbial sharing economy. <i>EMBO Reports</i> , 2019, 20, .	2.0	128
7416	Molecular Analysis of Evolution and Origins of Cultivated Hawthorn (<i>Crataegus</i> spp.) and Related Species in China. <i>Frontiers in Plant Science</i> , 2019, 10, 443.	1.7	21
7417	Effects of Different Pretreatments of DNA Extraction from Dried Specimens of Ladybird Beetles (Coleoptera: Coccinellidae). <i>Insects</i> , 2019, 10, 91.	1.0	5
7418	<i>Coprinopsis neocinerea</i> sp. nov., an ammonia fungus from Southern Vietnam. <i>Mycoscience</i> , 2019, 60, 307-312.	0.3	1

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7419	Spatial segregation of the biological soil crust microbiome around its foundational cyanobacterium, <i>Microcoleus vaginatus</i> , and the formation of a nitrogen-fixing cyanosphere. <i>Microbiome</i> , 2019, 7, 55.	4.9	74
7420	Wild Origins of Macadamia Domestication Identified Through Intraspecific Chloroplast Genome Sequencing. <i>Frontiers in Plant Science</i> , 2019, 10, 334.	1.7	47
7421	Genetic resiliency and the Black Death: No apparent loss of mitogenomic diversity due to the Black Death in medieval London and Denmark. <i>American Journal of Physical Anthropology</i> , 2019, 169, 240-252.	2.1	15
7423	Saffron (<i>Crocus sativus</i>) is an autotriploid that evolved in Attica (Greece) from wild <i>Crocus cartwrightianus</i> . <i>Molecular Phylogenetics and Evolution</i> , 2019, 136, 14-20.	1.2	62
7424	Chloroplast genome analysis of box-ironbark Eucalyptus. <i>Molecular Phylogenetics and Evolution</i> , 2019, 136, 76-86.	1.2	32
7425	Insights into ecological role of a new deltaproteobacterial order <i>Candidatus</i> <i>Acidulodesulfobacterales</i> by metagenomics and metatranscriptomics. <i>ISME Journal</i> , 2019, 13, 2044-2057.	4.4	112
7426	Mitogenomics of historical type specimens of Australasian turtles: clarification of taxonomic confusion and old mitochondrial introgression. <i>Scientific Reports</i> , 2019, 9, 5841.	1.6	20
7427	Integrative taxonomic revision of <i>Dendrobaena veneta</i> (Rosa, 1886) sensu lato with description of a new species and resurrection of <i>Dendrobaena succinta</i> (Rosa, 1905) (Megadrili: Tj ETQq1 1 0.784314 rgBT /Overlock 10 T F 2	0.8	7
7428	Complete mitogenome of a Baltic Sea specimen of the non-indigenous polychaete <i>Marenzelleria neglecta</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 581-582.	0.2	2
7429	Characterization of the complete chloroplast genome of the Phoebe zhennan S. Lee. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 856-857.	0.2	1
7430	The mitochondrial genome of a slit limpet <i>Pseudorimula</i> sp. (Vetigastropoda: Lepetodrilidae) from hydrothermal vent on the Southwest Indian Ridge. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1189-1190.	0.2	2
7431	Sequencing the Obligate Intracellular <i>Rhodochloromyces helveticus</i> within Its Tick Host <i>Ixodes ricinus</i> to Investigate Their Symbiotic Relationship. <i>Genome Biology and Evolution</i> , 2019, 11, 1334-1344.	1.1	21
7432	Genomics overrules mitochondrial DNA, siding with morphology on a controversial case of species delimitation. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20182924.	1.2	40
7433	<i>Pinjata ruminata</i> gen. et sp. n. "A New Member of Centrohelid Family Yogsothothidae (Haptista: Tj ETQq1 1 0.784314 rgBT /Overlock 10 T F 2	0.8	7
7434	Phosphate-limited ocean regions select for bacterial populations enriched in the carbon-phosphorus lyase pathway for phosphonate degradation. <i>Environmental Microbiology</i> , 2019, 21, 2402-2414.	1.8	73
7435	<i>gyrA</i> and <i>parC</i> mutations in fluoroquinolone-resistant <i>Neisseria gonorrhoeae</i> isolates from Kenya. <i>BMC Microbiology</i> , 2019, 19, 76.	1.3	17
7436	Substrate specificity and promiscuity of horizontally transferred UDP-glycosyltransferases in the generalist herbivore <i>Tetranychus urticae</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2019, 109, 116-127.	1.2	38
7437	Chronology of emergence of the genus <i>Leptosira</i> and over-representation of gene families enriched by vitamin B2, B12 biosynthesis, cell adhesion and external encapsulating structure in <i>L. interrogans</i> isolates from asymptomatic dogs. <i>Infection, Genetics and Evolution</i> , 2019, 73, 7-12.	1.0	2

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7438	The reclassification of 37 strains from The Mosonmagyaróvár Algal Culture Collection, Hungary, which were previously identified as <i>Anabaena</i> (Cyanobacteria, Nostocaceae). <i>South African Journal of Botany</i> , 2019, 123, 333-340.	1.2	0
7439	Evaluation of 16S next-generation sequencing of hypervariable region 4 in wastewater samples: An unsuitable approach for bacterial enteric pathogen identification. <i>Science of the Total Environment</i> , 2019, 670, 1111-1124.	3.9	44
7440	Evolutionary origin of a periodical mass-flowering plant. <i>Ecology and Evolution</i> , 2019, 9, 4373-4381.	0.8	10
7441	A comprehensive kelp phylogeny sheds light on the evolution of an ecosystem. <i>Molecular Phylogenetics and Evolution</i> , 2019, 136, 138-150.	1.2	62
7442	High quality reference genomes for toxigenic and non-toxicogenic <i>Vibrio cholerae</i> serogroup O139. <i>Scientific Reports</i> , 2019, 9, 5865.	1.6	13
7443	Characterization of the complete chloroplast genome of <i>Sparganium stoloniferum</i> (Poales: Typhaceae) and phylogenetic analysis. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1402-1403.	0.2	9
7444	The complete mitochondrial genomes of three species of <i>Macridiscus</i> Dall, 1902 (Bivalvia: Veneroidea). <i>Tj ETQq0 0 0 rgBT /Overlock 10 T</i>	0.4	4
7445	The complete chloroplast genome sequence of Chengal (<i>Neobalanocarpus heimii</i>) <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50</i>	0.2	4
7446	The complete chloroplast genome of <i>Casuarina glauca</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 357-358.	0.2	2
7447	The complete plastome of <i>Bennettiodendron brevipes</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 395-396.	0.2	1
7448	Complete chloroplast genome of an endangered plant, <i>Hopea hainanensis</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 505-506.	0.2	1
7449	Complete mitochondrial genome of plant pathogen <i>Monilinia fructicola</i> (Sclerotiniaceae). <i>Tj ETQq1 1 0.784314 rgBT /Overlock 1</i>	0.2	7
7450	Complete chloroplast genome of <i>Caragana kozlowii</i> , an alpine shrub endemic to China. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 715-716.	0.2	0
7451	New genera and species from the Equatorial Pacific provide phylogenetic insights into deep-sea Polynoidae (Annelida). <i>Zoological Journal of the Linnean Society</i> , 2019, 185, 555-635.	1.0	32
7452	Welcome back Janolidae and <i>Antiopella</i> : Improving the understanding of Janolidae and Madrellidae (Cladobronchia, Heterobronchia) with description of four new species. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2019, 57, 345-368.	0.6	5
7453	Ultraconserved elements put the final nail in the coffin of traditional use of the genus <i>Meliphaga</i> (Aves: Meliphagidae). <i>Zoologica Scripta</i> , 2019, 48, 411-418.	0.7	4
7454	Anupama: a new genus of Biannulariaceae (Agaricales) from tropical India. <i>Mycological Progress</i> , 2019, 18, 659-669.	0.5	7
7455	<i>Gelidium adriaticum</i> sp. nov. and <i>Gelidium carolinianum</i> sp. nov. (Gelidiales, Rhodophyta) from the Mediterranean Sea. <i>Phycologia</i> , 2019, 58, 359-373.	0.6	9

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7456	Novel contributions to the peritrich family Vaginicolidae (Protista: Ciliophora), with morphological and phylogenetic analyses of poorly known species of Pyxicola, Cothurnia and Vaginicola. Zoological Journal of the Linnean Society, 2019, 187, 1-30.	1.0	26
7457	Critical predictors of functional, phylogenetic and taxonomic diversity are geographically structured in lichen epiphytic communities. Journal of Ecology, 2019, 107, 2303-2316.	1.9	24
7458	Identification and pathogenicity of <i>Macrophomina</i> species collected from weeds in melon fields in Northeastern Brazil. Journal of Phytopathology, 2019, 167, 326-337.	0.5	20
7459	Toward Spider Glue: Long Read Scaffolding for Extreme Length and Repetitious Silk Family Genes AgSp1 and AgSp2 with Insights into Functional Adaptation. G3: Genes, Genomes, Genetics, 2019, 9, 1909-1919.	0.8	28
7460	Reestablishment of <i>Protium cordatum</i> (Burseraceae) based on integrative taxonomy. Taxon, 2019, 68, 34-46.	0.4	17
7461	Phylogeny of the Eurasian genus <i>Jurinea</i> (Asteraceae: Cardueae): Support for a monophyletic genus concept and a first hypothesis on overall species relationships. Taxon, 2019, 68, 112-131.	0.4	10
7462	Three new Phylloporus species from tropical China and Thailand. Mycological Progress, 2019, 18, 603-614.	0.5	9
7463	How to resurrect ancestral proteins as proxies for ancient biogeochemistry. Free Radical Biology and Medicine, 2019, 140, 260-269.	1.3	45
7464	Phylogenomics clarifies biogeographic and evolutionary history, and conservation status of West Indian tremblers and thrashers (Aves: Mimidae). Molecular Phylogenetics and Evolution, 2019, 136, 196-205.	1.2	5
7465	Morphology and genome of a snailfish from the Mariana Trench provide insights into deep-sea adaptation. Nature Ecology and Evolution, 2019, 3, 823-833.	3.4	99
7466	Signatures of Divergence, Invasiveness, and Terrestrialization Revealed by Four Apple Snail Genomes. Molecular Biology and Evolution, 2019, 36, 1507-1520.	3.5	65
7467	Biogeography of the xerophytic genus <i>Anabasis</i> L. (Chenopodiaceae). Ecology and Evolution, 2019, 9, 3539-3552.	0.8	12
7468	Spatiotemporal distributions and environmental drivers of diversity and community structure of nosZ-type denitrifiers and anammox bacteria in sediments of the Bohai Sea and North Yellow Sea, China. Journal of Oceanology and Limnology, 2019, 37, 1211-1228.	0.6	6
7469	Sequencing of Tuta absoluta genome to develop SNP genotyping assays for species identification. Journal of Pest Science, 2019, 92, 1397-1407.	1.9	24
7470	Analyses of 202 plastid genomes elucidate the phylogeny of Solanum section Petota. Scientific Reports, 2019, 9, 4454.	1.6	34
7471	The complete chloroplast genome of <i>Ampelocalamus actinotrichus</i> (Bambusoideae): Tj ETQq1 1 0.784314 rgBT /Overlock 10 TFS 6,2		
7472	Complete plastome sequence of an endangered species, Calocedrus rupestris (Cupressaceae). Mitochondrial DNA Part B: Resources, 2019, 4, 762-763.	0.2	12
7473	The complete chloroplast genome sequence of a typical alpine fern Lepisorus waltonii (Ching) S. L. Yu in Polypodiaceae. Mitochondrial DNA Part B: Resources, 2019, 4, 801-803.	0.2	1

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7474	The complete chloroplast genome of <i>Ranunculus Cantoniensis</i> . Mitochondrial DNA Part B: Resources, 2019, 4, 1095-1096.	0.2	8
7475	Complete chloroplast genome of the economically important crop, <i>Amorphophallus konjac</i> (Araceae). Mitochondrial DNA Part B: Resources, 2019, 4, 1097-1098.	0.2	2
7476	Efficacy of novel recombinant fowlpox vaccine against recent Mexican H7N3 highly pathogenic avian influenza virus. Vaccine, 2019, 37, 2232-2243.	1.7	18
7477	Molecular phylogeny of Paraonidae (Annelida). Molecular Phylogenetics and Evolution, 2019, 136, 1-13.	1.2	11
7478	Secondary Metabolite Dereplication and Phylogenetic Analysis Identify Various Emerging Mycotoxins and Reveal the High Intra-Species Diversity in <i>Aspergillus flavus</i> . Frontiers in Microbiology, 2019, 10, 667.	1.5	24
7479	Plastome based phylogenetics and younger crown node age in <i>Pelargonium</i> . Molecular Phylogenetics and Evolution, 2019, 137, 33-43.	1.2	19
7480	Genetic analysis of admixture and hybrid patterns of <i>Populus hopeiensis</i> and <i>P. tomentosa</i> . Scientific Reports, 2019, 9, 4821.	1.6	15
7481	The genome of the arapaima (<i>Arapaima gigas</i>) provides insights into gigantism, fast growth and chromosomal sex determination system. Scientific Reports, 2019, 9, 5293.	1.6	25
7482	Morphology, phylogeny, and sexual stage of <i>Fusarium caatingaense</i> and <i>Fusarium pernambucanum</i> , new species of the <i>Fusarium incarnatum-equiseti</i> species complex associated with insects in Brazil. Mycologia, 2019, 111, 244-259.	0.8	36
7483	Validation and phylogenetic placement of the Placentophoraceae fam. nov. (Gigartinales). Tj ETQq1 1 0.784314 rgBT /Overloc 0,6		
7484	Complete plastome sequences of 14 African yam species (<i>Dioscorea</i> spp.). Mitochondrial DNA Part B: Resources, 2019, 4, 74-76.	0.2	4
7485	Population structure of <i>Betula albosinensis</i> and <i>Betula platyphylla</i> : evidence for hybridization and a cryptic lineage. Annals of Botany, 2019, 123, 1179-1189.	1.4	28
7486	Detection of Aminoglycoside Resistant Bacteria in Sludge Samples From Norwegian Drinking Water Treatment Plants. Frontiers in Microbiology, 2019, 10, 487.	1.5	16
7487	Tools and Methods in the Analysis of Simple Sequences. , 2019, , 127-153.		0
7488	The complete mitochondrial genome of <i>Dryophytes versicolor</i> : Phylogenetic relationship among Hylidae and mitochondrial protein-coding gene expression in response to freezing and anoxia. International Journal of Biological Macromolecules, 2019, 132, 461-469.	3.6	16
7489	Multigene phylogenetic and morphological evidence for seven new species of <i>Aquanectria</i> and <i>Gliocladiopsis</i> (Ascomycota, Hypocreales) from tropical areas. Mycologia, 2019, 111, 299-318.	0.8	4
7490	Hce2 domain-containing effectors contribute to the full virulence of <i>Valsa mali</i> in a redundant manner. Molecular Plant Pathology, 2019, 20, 843-856.	2.0	20
7491	Multi-locus DNA sequence analysis, antifungal agent susceptibility, and fungal keratitis outcome in horses from Southeastern United States. PLoS ONE, 2019, 14, e0214214.	1.1	8

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7492	Variation among human, veterinary and environmental <i>Mycobacterium chelonae-abscessus</i> complex isolates observed using core genome phylogenomic analysis, targeted gene comparison, and anti-microbial susceptibility patterns. <i>PLoS ONE</i> , 2019, 14, e0214274.	1.1	12
7493	Proposals to recognize <i>Petalonia tenella</i> comb. nov. and to resurrect <i>Hapterophycus canaliculatus</i> (Scytosiphonaceae, Phaeophyceae). <i>Botanica Marina</i> , 2019, 62, 149-153.	0.6	3
7494	El dominio STK de la proteína de resistencia a la bacteriosis vascular de yuca RXAM1 interactúa con una E3 Ubiquitin Ligasa. <i>Acta Biologica Colombiana</i> , 2019, 24, 139-149.	0.1	0
7495	A New Species of <i>Trillium</i> (Melanthiaceae) from Central Georgia and its Phylogenetic Position in subgenus <i>Sessilium</i> . <i>Systematic Botany</i> , 2019, 44, 107-114.	0.2	5
7496	Viral complementation of immunodeficiency confers protection against enteric pathogens via interferon- λ . <i>Nature Microbiology</i> , 2019, 4, 1120-1128.	5.9	83
7497	Metagenomic analysis of colorectal cancer datasets identifies cross-cohort microbial diagnostic signatures and a link with choline degradation. <i>Nature Medicine</i> , 2019, 25, 667-678.	15.2	602
7498	Broad-spectrum enzymatic inhibition of CRISPR-Cas12a. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 315-321.	3.6	99
7499	Earth history and the passerine superradiation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 7916-7925.	3.3	238
7500	Low pathogenic avian influenza (H7N6) virus causing an outbreak in commercial Turkey farms in Chile. <i>Emerging Microbes and Infections</i> , 2019, 8, 479-485.	3.0	12
7501	WGS of 1058 <i>Enterococcus faecium</i> from Copenhagen, Denmark, reveals rapid clonal expansion of vancomycin-resistant clone ST80 combined with widespread dissemination of a vanA-containing plasmid and acquisition of a heterogeneous accessory genome. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 1776-1785.	1.3	43
7502	Phylogenomics using low-depth whole genome sequencing: A case study with the olive tribe. <i>Molecular Ecology Resources</i> , 2019, 19, 877-892.	2.2	48
7503	Plastome Phylogenetics of Tribe Eriachneae and Evolution of C ₄ Photosynthesis in Subfamily Mircalroideae (Poaceae). <i>Systematic Botany</i> , 2019, 44, 32-40.	0.2	4
7504	Character Evolution and Recircumscription of the Northern Andean <i>Begonia</i> Section <i>Casparya</i> (Begoniaceae). <i>Systematic Botany</i> , 2019, 44, 52-65.	0.2	4
7505	Into Africa via docked India: a fossil climbing perch from the Oligocene of Tibet helps solve the anabantid biogeographical puzzle. <i>Science Bulletin</i> , 2019, 64, 455-463.	4.3	15
7506	Novel insights into pasteurellosis in captive pinnipeds. <i>Veterinary Microbiology</i> , 2019, 231, 232-237.	0.8	6
7507	A high-quality apple genome assembly reveals the association of a retrotransposon and red fruit colour. <i>Nature Communications</i> , 2019, 10, 1494.	5.8	254
7508	Systematic study of truffles in the genus <i>Ruhlandiella</i> , with the description of two new species from Patagonia. <i>Mycologia</i> , 2019, 111, 477-492.	0.8	11
7509	Two New Species of the Genus <i>Candelariella</i> from China and Korea. <i>Mycobiology</i> , 2019, 47, 40-49.	0.6	3

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7510	Life in wood: preliminary phylogeny of deep-sea wood-boring bivalves (Xylophagaidae), with descriptions of three new genera and one new species. <i>Journal of Molluscan Studies</i> , 2019, 85, 232-243.	0.4	21
7511	Adaptations of <i>Alteromonas</i> sp. 76-1 to Polysaccharide Degradation: A CAZyme Plasmid for Ulvan Degradation and Two Alginate Lytic Systems. <i>Frontiers in Microbiology</i> , 2019, 10, 504.	1.5	30
7512	Comparative genomics of 10 new <i>Caenorhabditis</i> species. <i>Evolution Letters</i> , 2019, 3, 217-236.	1.6	106
7513	HIV-1 remission following CCR5 ^{Δ32/Δ32} haematopoietic stem-cell transplantation. <i>Nature</i> , 2019, 568, 244-248.	13.7	447
7514	A widespread coral-infecting apicomplexan with chlorophyll biosynthesis genes. <i>Nature</i> , 2019, 568, 103-107.	13.7	102
7515	Repertoires of G protein-coupled receptors for <i>Ciona</i> -specific neuropeptides. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 7847-7856.	3.3	39
7516	Rampant introgressive hybridization in <i>Pogoniulus</i> tinkerbirds (Piciformes: Lybiidae) despite millions of years of divergence. <i>Biological Journal of the Linnean Society</i> , 2019, 127, 125-142.	0.7	9
7517	A <i>Toxoplasma</i> Prolyl Hydroxylase Mediates Oxygen Stress Responses by Regulating Translation Elongation. <i>MBio</i> , 2019, 10, .	1.8	14
7519	Thinking outside of the cell: Secreted protein kinases in bacteria, parasites, and mammals. <i>IUBMB Life</i> , 2019, 71, 749-759.	1.5	9
7520	Complete mitogenome of the giant invasive hammerhead flatworm <i>Bipalium kewense</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1343-1344.	0.2	10
7521	Sexually Antagonistic Mitonuclear Coevolution in Duplicate Oxidative Phosphorylation Genes. <i>Integrative and Comparative Biology</i> , 2019, 59, 864-874.	0.9	9
7522	Parallel Miocene dispersal events explain the cosmopolitan distribution of the Hypogymnioid lichens. <i>Journal of Biogeography</i> , 2019, 46, 945-955.	1.4	6
7523	Convergent regulatory evolution and loss of flight in paleognathous birds. <i>Science</i> , 2019, 364, 74-78.	6.0	189
7524	Rapid Replacement of <i>Acinetobacter baumannii</i> Strains Accompanied by Changes in Lipooligosaccharide Loci and Resistance Gene Repertoire. <i>MBio</i> , 2019, 10, .	1.8	28
7525	Characterization of Two <i>Pseudomonas aeruginosa</i> Viruses vB_PaeM_SCUT-S1 and vB_PaeM_SCUT-S2. <i>Viruses</i> , 2019, 11, 318.	1.5	30
7526	Ancient pathogen genomics as an emerging tool for infectious disease research. <i>Nature Reviews Genetics</i> , 2019, 20, 323-340.	7.7	195
7527	No signal of deleterious mutation accumulation in conserved gene sequences of extant asexual hexapods. <i>Scientific Reports</i> , 2019, 9, 5338.	1.6	17
7528	Whole genome sequencing identifies bacterial factors affecting transmission of multidrug-resistant tuberculosis in a high-prevalence setting. <i>Scientific Reports</i> , 2019, 9, 5602.	1.6	25

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7529	Characterization of the complete chloroplast genome of an important Southeast Asian medicinal plant, <i>Eurycoma longifolia</i> (Simaroubaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 128-129.	0.2	1
7530	Comparative Genomics Reveals the Genetic Mechanisms of Musk Secretion and Adaptive Immunity in Chinese Forest Musk Deer. <i>Genome Biology and Evolution</i> , 2019, 11, 1019-1032.	1.1	17
7531	Multilocus phylogeny and a new classification for African, Asian and Indian supple and writhing skinks (Scincidae: Lygosominae). <i>Zoological Journal of the Linnean Society</i> , 2019, 186, 1067-1096.	1.0	15
7532	Trophic interactions and abiotic factors drive functional and phylogenetic structure of vertebrate herbivore communities across the Arctic tundra biome. <i>Ecography</i> , 2019, 42, 1152-1163.	2.1	23
7533	Molecular phylogeny of the Paleogene fungus gnat tribe Exechiini (Diptera: Mycetophilidae) revisited: Monophyly of genera established and rapid radiation confirmed. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2019, 57, 806-821.	0.6	10
7534	Loss and Gain in the Evolution of the <i>Salmonella enterica</i> Serovar Gallinarum Biovar Pullorum Genome. <i>MSphere</i> , 2019, 4, .	1.3	23
7535	Genome-wide analysis of <i>Fusarium verticillioides</i> reveals inter-kingdom contribution of horizontal gene transfer to the expansion of metabolism. <i>Fungal Genetics and Biology</i> , 2019, 128, 60-73.	0.9	8
7536	The first species of <i>Cotithene</i> Voss (Coleoptera: Curculionidae: Curculioninae) from Amazonian Brazil, with notes on its role as a pollinator of <i>Evodianthus funifer</i> (Poit.) Lindm. (Cyclanthaceae). <i>Zootaxa</i> , 2019, 4576, zootaxa.4576.3.3.	0.2	5
7537	Pharmacological and molecular dynamics analyses of differences in inhibitor binding to human and nematode PDE4: Implications for management of parasitic nematodes. <i>PLoS ONE</i> , 2019, 14, e0214554.	1.1	7
7538	Molecular and Morphological Analyses Support the Transfer of <i>Gleadovia kwangtungensis</i> to <i>Christisonia</i> (Orobanchaceae). <i>Systematic Botany</i> , 2019, 44, 74-82.	0.2	1
7539	Phylogenetic relationships among species of <i>Barleria</i> (Acanthaceae, Lamiales): Molecular data reveal complex patterns of morphological evolution and support a revised classification. <i>Taxon</i> , 2019, 68, 92-111.	0.4	17
7540	An integrative taxonomic study reveals carychiid microsnails of the troglobitic genus <i>Zospeum</i> in the Eastern and Dinaric Alps (Gastropoda, Ellobioidea, Carychiinae). <i>Organisms Diversity and Evolution</i> , 2019, 19, 135-177.	0.7	12
7541	Phylogenetic inference for the study of within-host HIV-1 dynamics and persistence on antiretroviral therapy. <i>Lancet HIV</i> , 2019, 6, e325-e333.	2.1	7
7542	Surviving the marine environment: two new species of <i>Mallomonas</i> (Synurophyceae). <i>Phycologia</i> , 2019, 58, 276-286.	0.6	5
7543	The Immature Stages, Biology, and Phylogenetic Relationships of <i>Rotunda rotundapex</i> (Lepidoptera: Tj ETQq0 0 0 ggBT /Overlock 10 Tf 0.6	0.6	6
7544	Identification of two new core chromosome-encoded superantigens in <i>Streptococcus pyogenes</i> ; speQ and speR. <i>Journal of Infection</i> , 2019, 78, 358-363.	1.7	15
7545	Reconstructing evolution at the community level: A case study on Mediterranean amphibians. <i>Molecular Phylogenetics and Evolution</i> , 2019, 134, 211-225.	1.2	21
7546	Phylogenomic reappraisal of the Neotropical catfish family Loricariidae (Teleostei: Siluriformes) using ultraconserved elements. <i>Molecular Phylogenetics and Evolution</i> , 2019, 135, 148-165.	1.2	71

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7547	Four new epiphytic species in the <i>Micarea prasina</i> group from Europe. <i>Lichenologist</i> , 2019, 51, 7-25.	0.5	26
7548	Reticulate evolution in eukaryotes: Origin and evolution of the nitrate assimilation pathway. <i>PLoS Genetics</i> , 2019, 15, e1007986.	1.5	21
7549	Integrative taxonomy of commercially important deep water penaeoid shrimps from India. <i>Journal of Genetics</i> , 2019, 98, 1.	0.4	2
7550	Phylogenomic conflict resulting from ancient introgression following species diversification in <i>Stewartia s.l.</i> (Theaceae). <i>Molecular Phylogenetics and Evolution</i> , 2019, 135, 1-11.	1.2	43
7551	Translocation of promoter-conserved hatching enzyme genes with intron-loss provides a new insight in the role of retrocopy during teleostean evolution. <i>Scientific Reports</i> , 2019, 9, 2448.	1.6	3
7552	The complete chloroplast genome sequence of <i>Pemphis acidula</i> (Lythraceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 912-913.	0.2	4
7553	Rapid Divergence Followed by Adaptation to Contrasting Ecological Niches of Two Closely Related Columbine Species <i>Aquilegia japonica</i> and <i>A. oxysepala</i> . <i>Genome Biology and Evolution</i> , 2019, 11, 919-930.	1.1	7
7554	Phylogenomic analysis of Calyptratae: resolving the phylogenetic relationships within a major radiation of Diptera. <i>Cladistics</i> , 2019, 35, 605-622.	1.5	51
7555	Evolutionary rate covariation analysis of E-cadherin identifies Raskol as a regulator of cell adhesion and actin dynamics in <i>Drosophila</i> . <i>PLoS Genetics</i> , 2019, 15, e1007720.	1.5	30
7556	Comparative Genomic Analyses Reveal Core-Genome-Wide Genes Under Positive Selection and Major Regulatory Hubs in Outlier Strains of <i>Pseudomonas aeruginosa</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 53.	1.5	36
7557	Genetic Evolution and Molecular Selection of the HE Gene of Influenza C Virus. <i>Viruses</i> , 2019, 11, 167.	1.5	27
7558	Statistical binning leads to profound model violation due to gene tree error incurred by trying to avoid gene tree error. <i>Molecular Phylogenetics and Evolution</i> , 2019, 134, 164-171.	1.2	20
7559	Diverse anaerobic methane- and multi-carbon alkane-metabolizing archaea coexist and show activity in Guaymas Basin hydrothermal sediment. <i>Environmental Microbiology</i> , 2019, 21, 1344-1355.	1.8	25
7560	Evolutionary Implications of the microRNA- and piRNA Complement of <i>Lepidodermella squamata</i> (Gastrotricha). <i>Non-coding RNA</i> , 2019, 5, 19.	1.3	5
7561	Origin and evolution of the octoploid strawberry genome. <i>Nature Genetics</i> , 2019, 51, 541-547.	9.4	469
7562	OrthoMaM v10: Scaling-Up Orthologous Coding Sequence and Exon Alignments with More than One Hundred Mammalian Genomes. <i>Molecular Biology and Evolution</i> , 2019, 36, 861-862.	3.5	64
7563	Genome plasticity favours double chromosomal Tn4401b-blaKPC-2 transposon insertion in the <i>Pseudomonas aeruginosa</i> ST235 clone. <i>BMC Microbiology</i> , 2019, 19, 45.	1.3	24
7564	Gall disease in the alginophyte <i>Lessonia berteroana</i> : A pathogenic interaction linked with host adulthood in a seasonal-dependant manner. <i>Algal Research</i> , 2019, 39, 101435.	2.4	4

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7565	Evolution and a revised nomenclature of P4 ATPases, a eukaryotic family of lipid flippases. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2019, 1861, 1135-1151.	1.4	46
7566	A Likely Ancient Genome Duplication in the Speciose Reef-Building Coral Genus, <i>Acropora</i> . <i>IScience</i> , 2019, 13, 20-32.	1.9	11
7567	Atypical influenza A(H1N1)pdm09 strains caused an influenza virus outbreak in Saudi Arabia during the 2009–2011 pandemic season. <i>Journal of Infection and Public Health</i> , 2019, 12, 557-567.	1.9	5
7568	A Chromosome-Scale Genome Assembly of Paper Mulberry (<i>Broussonetia papyrifera</i>) Provides New Insights into Its Forage and Papermaking Usage. <i>Molecular Plant</i> , 2019, 12, 661-677.	3.9	83
7569	Target sequence capture in the Brazil nut family (Lecythidaceae): Marker selection and in silico capture from genome skimming data. <i>Molecular Phylogenetics and Evolution</i> , 2019, 135, 98-104.	1.2	25
7570	Phylogenomics of the superfamily Dytiscoidea (Coleoptera: Adepaga) with an evaluation of phylogenetic conflict and systematic error. <i>Molecular Phylogenetics and Evolution</i> , 2019, 135, 270-285.	1.2	36
7571	GeM-Pro: a tool for genome functional mining and microbial profiling. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 3123-3134.	1.7	13
7572	Antibodies Against Egg- and Cell-Grown Influenza A(H3N2) Viruses in Adults Hospitalized During the 2017–2018 Influenza Season. <i>Journal of Infectious Diseases</i> , 2019, 219, 1904-1912.	1.9	37
7573	Deconstructing an infamous extinction crisis: Survival of <i>Partula</i> species on Moorea and Tahiti. <i>Evolutionary Applications</i> , 2019, 12, 1017-1033.	1.5	8
7574	Evolutionary Relationships Between the Laccase Genes of Polyporales: Orthology-Based Classification of Laccase Isozymes and Functional Insight From <i>Trametes hirsuta</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 152.	1.5	25
7575	The complete chloroplast genome of the threatened <i>Dipentodon sinicus</i> (Dipentodontaceae). <i>Journal of Genetics</i> , 2019, 98, 1.	0.4	2
7576	Compositional heterogeneity and outgroup choice influence the internal phylogeny of the ants. <i>Molecular Phylogenetics and Evolution</i> , 2019, 134, 111-121.	1.2	73
7577	Tracking the origin of two genetic components associated with transposable element bursts in domesticated rice. <i>Nature Communications</i> , 2019, 10, 641.	5.8	34
7578	24-nt reproductive phasiRNAs are broadly present in angiosperms. <i>Nature Communications</i> , 2019, 10, 627.	5.8	106
7579	Mercury methylating microbial communities of boreal forest soils. <i>Scientific Reports</i> , 2019, 9, 518.	1.6	53
7580	Marine <i>Synechococcus</i> isolates representing globally abundant genomic lineages demonstrate a unique evolutionary path of genome reduction without a decrease in GC content. <i>Environmental Microbiology</i> , 2019, 21, 1677-1686.	1.8	28
7581	A conserved molecular switch in Class F receptors regulates receptor activation and pathway selection. <i>Nature Communications</i> , 2019, 10, 667.	5.8	56
7582	Identification of novel autoinducer-2 receptors in Clostridia reveals plasticity in the binding site of the LsrB receptor family. <i>Journal of Biological Chemistry</i> , 2019, 294, 4450-4463.	1.6	24

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7583	Resolving the backbone of the Brassicaceae phylogeny for investigating trait diversity. <i>New Phytologist</i> , 2019, 222, 1638-1651.	3.5	123
7584	Transcriptome, proteome and draft genome of <i>Euglena gracilis</i> . <i>BMC Biology</i> , 2019, 17, 11.	1.7	98
7585	Evolution of the modular, disordered stress proteins known as dehydrins. <i>PLoS ONE</i> , 2019, 14, e0211813.	1.1	28
7586	Absence of adaptive evolution is the main barrier against influenza emergence in horses in Asia despite frequent virus interspecies transmission from wild birds. <i>PLoS Pathogens</i> , 2019, 15, e1007531.	2.1	12
7587	The long journey of <i>Orthotrichum shevockii</i> (Orthotrichaceae, Bryopsida): From California to Macaronesia. <i>PLoS ONE</i> , 2019, 14, e0211017.	1.1	12
7588	First isolation of West Nile virus in Brazil. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2019, 114, e180332.	0.8	33
7589	Characterization of Emetic and Diarrheal <i>Bacillus cereus</i> Strains From a 2016 Foodborne Outbreak Using Whole-Genome Sequencing: Addressing the Microbiological, Epidemiological, and Bioinformatic Challenges. <i>Frontiers in Microbiology</i> , 2019, 10, 144.	1.5	101
7590	Neither <i>Diplectanum</i> nor specific: a dramatic twist to the taxonomic framework of <i>Diplectanum</i> (Monogenea: Diplectanidae). <i>International Journal for Parasitology</i> , 2019, 49, 365-374.	1.3	10
7591	Putting keyhole limpets on the map: phylogeny and biogeography of the globally distributed marine family Fissurellidae (Vetigastropoda, Mollusca). <i>Molecular Phylogenetics and Evolution</i> , 2019, 135, 249-269.	1.2	11
7592	Dual β -Lactam Combinations Highly Active against <i>Mycobacterium abscessus</i> Complex <i>In Vitro</i> . <i>MBio</i> , 2019, 10, .	1.8	51
7593	Genes expression and in silico studies of functions of trehalases, a highly dispersed <i>Anisakis simplex</i> s. l. specific gene family. <i>International Journal of Biological Macromolecules</i> , 2019, 129, 957-964.	3.6	10
7594	High contiguity genome sequence of a multidrug-resistant hospital isolate of <i>Enterobacter hormaechei</i> . <i>Gut Pathogens</i> , 2019, 11, 3.	1.6	26
7595	Mitochondrial Genomes from New Zealand's Extinct Adzebills (Aves: Aptornithidae: Aptornis) Support a Sister-Taxon Relationship with the Afro-Madagascan Sarothruridae. <i>Diversity</i> , 2019, 11, 24.	0.7	22
7596	Molecular phylogenetic relationships among populations of <i>Sagittaria aginashi</i> Makino (Alismataceae) and endemic Chinese species. <i>Journal of Asia-Pacific Biodiversity</i> , 2019, 12, 106-114.	0.2	1
7597	Mitogenomic evidence of close relationships between New Zealand's extinct giant raptors and small-sized Australian sister-taxa. <i>Molecular Phylogenetics and Evolution</i> , 2019, 134, 122-128.	1.2	17
7598	Carboxydrotrophy potential of uncultivated Hydrothermarchaeota from the subseafloor crustal biosphere. <i>ISME Journal</i> , 2019, 13, 1457-1468.	4.4	31
7599	Evolutionary dynamics of linc RNA transcription in nine citrus species. <i>Plant Journal</i> , 2019, 98, 912-927.	2.8	43
7600	The Environment and Cyanophage Diversity: Insights From Environmental Sequencing of DNA Polymerase. <i>Frontiers in Microbiology</i> , 2019, 10, 167.	1.5	14

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7601	Unusual AT-skew of <i>Sinorhodeus microlepis</i> mitogenome provides new insights into mitogenome features and phylogenetic implications of bitterling fishes. <i>International Journal of Biological Macromolecules</i> , 2019, 129, 339-350.	3.6	17
7602	Solution structure and novel insights into phylogeny and mode of action of the Neosartorya (<i>Aspergillus</i>) <i>fischeri</i> antifungal protein (NFAP). <i>International Journal of Biological Macromolecules</i> , 2019, 129, 511-522.	3.6	16
7603	Phylogenomic analyses of brachyuran crabs support early divergence of primary freshwater crabs. <i>Molecular Phylogenetics and Evolution</i> , 2019, 135, 62-66.	1.2	35
7604	Plastomes resolve generic limits within tribe Clusiaceae (<i>Clusiaceae</i>) and reveal the new genus <i>Arawakia</i> . <i>Molecular Phylogenetics and Evolution</i> , 2019, 134, 142-151.	1.2	19
7605	Systematic analysis of the caridean shrimp superfamily Pandaloidea (Crustacea: Decapoda) based on molecular and morphological evidence. <i>Molecular Phylogenetics and Evolution</i> , 2019, 134, 200-210.	1.2	16
7606	Bioinformatic discovery of a toxin family in <i>Chryseobacterium piperi</i> with sequence similarity to botulinum neurotoxins. <i>Scientific Reports</i> , 2019, 9, 1634.	1.6	31
7607	Identification of non-specific Lipid Transfer Protein gene family members in <i>Solanum lycopersicum</i> and insights into the features of Sola l 3 protein. <i>Scientific Reports</i> , 2019, 9, 1607.	1.6	42
7608	A multi-gene phylogeny of Australian <i>Monomorium</i> Mayr (Hymenoptera : Formicidae) results in reinterpretation of the genus and resurrection of <i>Chelaner</i> Emery. <i>Invertebrate Systematics</i> , 2019, , .	0.5	8
7609	Phylogeny, evolution and systematic revision of the mite harvestman family Neogoveidae (Opiliones) Tj ETQq0 0 0 0.5 rgBT /Overlock 10 Tf	0.5	2
7610	Combining morphological and molecular data resolves the phylogeny of Squilloidea (Crustacea :) Tj ETQq1 1 0.784314 rgBT /Overlock 1	0.5	5
7611	A new species of Tithaeidae (Arachnida: Opiliones: Laniatores) from Mindanao reveals contemporaneous colonisation of the Philippines by Sunda Shelf opiliofauna. <i>Invertebrate Systematics</i> , 2019, , .	0.5	4
7612	The complete chloroplast genome of <i>Eriocaulon sexangulare</i> (<i>Eriocaulaceae</i>). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 666-667.	0.2	2
7613	Plastomes of Betulaceae and phylogenetic implications. <i>Journal of Systematics and Evolution</i> , 2019, 57, 508-518.	1.6	24
7614	Isolation by instability: Historical climate change shapes population structure and genomic divergence of treefrogs in the Neotropical Cerrado savanna. <i>Molecular Ecology</i> , 2019, 28, 1748-1764.	2.0	38
7615	Circulation of Plasmids Harboring Resistance Genes to Quinolones and/or Extended-Spectrum Cephalosporins in Multiple <i>Salmonella enterica</i> Serotypes from Swine in the United States. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	1.4	16
7616	Resurrection of <i>Caltoris ranrunna</i> (Sonan) from synonymy as a skipper endemic to Taiwan based on COI barcode and morphology. <i>Zootaxa</i> , 2019, 4555, 56.	0.2	0
7617	The genome of the soybean cyst nematode (<i>Heterodera glycines</i>) reveals complex patterns of duplications involved in the evolution of parasitism genes. <i>BMC Genomics</i> , 2019, 20, 119.	1.2	55
7618	Hybridization is a recurrent evolutionary stimulus in wild yeast speciation. <i>Nature Communications</i> , 2019, 10, 923.	5.8	62

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7619	Characterization of the complete chloroplast genome of the Chinese <i>Kadsura vine</i> <i>Kadsura longipedunculata</i> (Schisandraceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 476-477.	0.2	2
7620	Complete mitochondrial genome sequences of a deep-sea holothurian species of the genus <i>Scotoplanes</i> (Elasipodida: Elpidiidae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 112-113.	0.2	3
7621	The complete chloroplast genome sequence of <i>Rubus leucanthus</i> Hance (Rosaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 376-377.	0.2	3
7622	Tracing the Impact of Public Health Interventions on HIV-1 Transmission in Portugal Using Molecular Epidemiology. <i>Journal of Infectious Diseases</i> , 2019, 220, 233-243.	1.9	23
7623	An integrative phylogenomic approach illuminates the evolutionary history of cockroaches and termites (Blattodea). <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20182076.	1.2	143
7624	Big data for a large clade: Bioregionalization and ancestral range estimation in the daisy family (Asteraceae). <i>Journal of Biogeography</i> , 2019, 46, 255-267.	1.4	19
7625	Red And far-red regulation of filament movement correlates with the expression of phytochrome and <i>FHY1</i> genes in <i>Spirogyra varians</i> (Zygnematales, Streptophyta). <i>Journal of Phycology</i> , 2019, 55, 688-699.	1.0	10
7626	Whole-Genome Sequencing Analysis of Multidrug-Resistant Serotype 15A <i>Streptococcus pneumoniae</i> in Japan and the Emergence of a Highly Resistant Serotype 15A-ST9084 Clone. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	1.4	32
7627	Genus-Wide Comparative Genomics Analysis of <i>Neisseria</i> to Identify New Genes Associated with Pathogenicity and Niche Adaptation of <i>Neisseria</i> Pathogens. <i>International Journal of Genomics</i> , 2019, 2019, 1-19.	0.8	17
7628	Secondary contact between diverged host lineages entails ecological speciation in a European hantavirus. <i>PLoS Biology</i> , 2019, 17, e3000142.	2.6	26
7629	Use of Genomics to Investigate Historical Importation of Shiga Toxin-Producing <i>Escherichia coli</i> Serogroup O26 and Nontoxic Variants into New Zealand. <i>Emerging Infectious Diseases</i> , 2019, 25, 489-500.	2.0	9
7630	Biosynthetic Gene Content of the "Perfume Lichens" <i>Evernia prunastri</i> and <i>Pseudevernia furfuracea</i> . <i>Molecules</i> , 2019, 24, 203.	1.7	34
7631	Estimating the biodiversity of terrestrial invertebrates on a forested island using DNA barcodes and metabarcoding data. <i>Ecological Applications</i> , 2019, 29, e01877.	1.8	37
7632	Hitchhiking the high seas: Global genomics of rafting crabs. <i>Ecology and Evolution</i> , 2019, 9, 957-974.	0.8	11
7633	<i>Acinetobacter chinensis</i> , a novel <i>Acinetobacter</i> species, carrying blaNDM-1, recovered from hospital sewage. <i>Journal of Microbiology</i> , 2019, 57, 350-355.	1.3	13
7634	The complete mitochondrial genome of <i>Tetraphleps aterrimus</i> (Hemiptera: Anthocoridae): Genomic comparisons and phylogenetic analysis of Cimicomorpha. <i>International Journal of Biological Macromolecules</i> , 2019, 130, 369-377.	3.6	12
7635	Emergence of the East-Central-South-African genotype of Chikungunya virus in Brazil and the city of Rio de Janeiro may have occurred years before surveillance detection. <i>Scientific Reports</i> , 2019, 9, 2760.	1.6	38
7636	Phylogeographic structuring of the amphidromous shrimp <i>Atya scabra</i> (Crustacea, Decapoda, Atyidae) unveiled by range-wide mitochondrial DNA sampling. <i>Marine and Freshwater Research</i> , 2019, 70, 1078.	0.7	11

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7637	Ancestral remnants or peripheral segregates? Phylogenetic relationships of two narrowly endemic Euphrasia species (Orobanchaceae) from the eastern European Alps. <i>AoB PLANTS</i> , 2019, 11, plz007.	1.2	2
7638	The Genome of the Fungal Pathogen <i>Verticillium dahliae</i> Reveals Extensive Bacterial to Fungal Gene Transfer. <i>Genome Biology and Evolution</i> , 2019, 11, 855-868.	1.1	18
7639	Two new species of Heptapterus (Siluriformes: Heptapteridae) from the Uruguay River basin, Brazil. <i>Journal of Fish Biology</i> , 2019, 94, 352-373.	0.7	7
7640	Invasive invertebrates associated with highly duplicated gene content. <i>Molecular Ecology</i> , 2019, 28, 1652-1663.	2.0	14
7641	<i>Aquella oligotrophica</i> gen. nov. sp. nov.: A new member of the family Neisseriaceae isolated from laboratory tap water. <i>MicrobiologyOpen</i> , 2019, 8, e793.	1.2	12
7642	Computational Intelligence Methods for Bioinformatics and Biostatistics. <i>Lecture Notes in Computer Science</i> , 2019, , .	1.0	0
7643	The <i>Galleria mellonella</i> Hologenome Supports Microbiota-Independent Metabolism of Long-Chain Hydrocarbon Beeswax. <i>Cell Reports</i> , 2019, 26, 2451-2464.e5.	2.9	103
7644	Phylogenomics and Morphological Reconstruction of Arcellinida Testate Amoebae Highlight Diversity of Microbial Eukaryotes in the Neoproterozoic. <i>Current Biology</i> , 2019, 29, 991-1001.e3.	1.8	49
7645	Chloroplast genomic data provide new and robust insights into the phylogeny and evolution of the Ranunculaceae. <i>Molecular Phylogenetics and Evolution</i> , 2019, 135, 12-21.	1.2	123
7646	Impacts of microbial assemblage and environmental conditions on the distribution of anatoxin-a producing cyanobacteria within a river network. <i>ISME Journal</i> , 2019, 13, 1618-1634.	4.4	60
7647	Prevalence of isomeric plastomes and effectiveness of plastome super-barcodes in yews (<i>Taxus</i>) worldwide. <i>Scientific Reports</i> , 2019, 9, 2773.	1.6	54
7648	Diversity of cytosine methylation across the fungal tree of life. <i>Nature Ecology and Evolution</i> , 2019, 3, 479-490.	3.4	98
7649	Phylogeography and species delimitation of <i>Cherax destructor</i> (Decapoda: Parastacidae) using genome-wide SNPs. <i>Marine and Freshwater Research</i> , 2019, 70, 857.	0.7	8
7650	Next-generation sequencing yields the complete chloroplast genome of <i>Abies Alba</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 575-576.	0.2	1
7651	Genome Sequencing of <i>Cladobotryum protrusum</i> Provides Insights into the Evolution and Pathogenic Mechanisms of the Cobweb Disease Pathogen on Cultivated Mushroom. <i>Genes</i> , 2019, 10, 124.	1.0	25
7652	Repeated evolution of a morphological novelty: a phylogenetic analysis of the inflated fruiting calyx in the Physalideae tribe (Solanaceae). <i>American Journal of Botany</i> , 2019, 106, 270-279.	0.8	30
7653	<i>Amnimonas aquatica</i> gen. nov., sp. nov., Isolated from a Freshwater River. <i>Current Microbiology</i> , 2019, 76, 478-484.	1.0	10
7654	Carbohydrate catabolic capability of a Flavobacteriia bacterium isolated from hadal water. <i>Systematic and Applied Microbiology</i> , 2019, 42, 263-274.	1.2	25

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7655	Systematic study of the Australian plant bug genus <i>Xasmasoma</i> , gen. nov. (Insecta : Heteroptera : Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 new species. <i>Invertebrate Systematics</i> , 2019, , .	0.5	1
7656	White shark genome reveals ancient elasmobranch adaptations associated with wound healing and the maintenance of genome stability. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 4446-4455.	3.3	92
7657	Unraveling the complex genome of <i>Saccharum spontaneum</i> using Polyploid Gene Assembler. <i>DNA Research</i> , 2019, 26, 205-216.	1.5	8
7658	Variation and inheritance of the <i>Xanthomonas</i> gene cluster required for activation of XA21-mediated immunity. <i>Molecular Plant Pathology</i> , 2019, 20, 656-672.	2.0	17
7659	Expansion of Vancomycin-Resistant <i>Enterococcus faecium</i> in an Academic Tertiary Hospital in Southwest Germany: a Large-Scale Whole-Genome-Based Outbreak Investigation. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	1.4	37
7660	A new leafhopper genus <i>Discolopeus</i> and nine new species (Hemiptera, Cicadellidae, Deltocephalinae) associated with shrubs, trees and poisonous plants in South Africa. <i>Zootaxa</i> , 2019, 4559, 201.	0.2	3
7661	Identification and profiling of narrow-leafed lupin (<i>Lupinus angustifolius</i>) microRNAs during seed development. <i>BMC Genomics</i> , 2019, 20, 135.	1.2	22
7662	Parental legacy, demography, and admixture influenced the evolution of the two subgenomes of the tetraploid <i>Capsella bursa-pastoris</i> (Brassicaceae). <i>PLoS Genetics</i> , 2019, 15, e1007949.	1.5	42
7663	A 28-Year History of HIV-1 Drug Resistance and Transmission in Washington, DC. <i>Frontiers in Microbiology</i> , 2019, 10, 369.	1.5	7
7664	Concurrent Proteomic Fingerprinting and Molecular Analysis of Cyathostomins. <i>Proteomics</i> , 2019, 19, 1800290.	1.3	16
7665	New species reveal unexpected interspecific microhabitat diversity in the genus <i>Uthina</i> Simon, 1893 (Araneae : Pholcidae). <i>Invertebrate Systematics</i> , 2019, , .	0.5	2
7666	Analysis of mitochondrial and chloroplast genomes in two volvocine algae: <i>Eudorina elegans</i> and <i>Eudorina cylindrica</i> (Volvocaceae, Chlorophyta). <i>European Journal of Phycology</i> , 2019, 54, 193-205.	0.9	12
7667	The complete chloroplast genome of a hemiparasitic plant <i>Tolypanthus maclurei</i> (Loranthaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 207-208.	0.2	5
7668	Genomic analysis of <i>Klebsiella pneumoniae</i> isolates from Malawi reveals acquisition of multiple ESBL determinants across diverse lineages. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 1223-1232.	1.3	36
7669	Evolutionary Rate Correlation between Mitochondrial-Encoded and Mitochondria-Associated Nuclear-Encoded Proteins in Insects. <i>Molecular Biology and Evolution</i> , 2019, 36, 1022-1036.	3.5	46
7670	Avian mitochondrial genomes retrieved from museum eggshell. <i>Molecular Ecology Resources</i> , 2019, 19, 1052-1062.	2.2	14
7671	Evolutionary Model of Cluster Divergence of the Emergent Marine Pathogen <i>Vibrio vulnificus</i> : From Genotype to Ecotype. <i>MBio</i> , 2019, 10, .	1.8	41
7672	Phylogenomic Analyses of <i>Bradyrhizobium</i> Reveal Uneven Distribution of the Lateral and Subpolar Flagellar Systems, Which Extends to Rhizobiales. <i>Microorganisms</i> , 2019, 7, 50.	1.6	16

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7673	Genome Mining and Comparative Analysis of <i>Streptococcus intermedius</i> Causing Brain Abscess in a Child. <i>Pathogens</i> , 2019, 8, 22.	1.2	13
7674	Eukaryotic Acquisition of a Bacterial Operon. <i>Cell</i> , 2019, 176, 1356-1366.e10.	13.5	74
7675	Prevalent weeds collected from cucurbit fields in Northeastern Brazil reveal new species diversity in the genus <i>Monosporascus</i> . <i>Annals of Applied Biology</i> , 2019, 174, 349-363.	1.3	7
7676	Leapfrog dispersal and mitochondrial introgression: Phylogenomics and biogeography of <i>Limnonectes fanged</i> frogs in the Lesser Sundas Archipelago of Wallacea. <i>Journal of Biogeography</i> , 2019, 46, 757-769.	1.4	19
7677	A new <i>Nucras</i> Gray, 1838 (Squamata: Lacertidae) from the Strandveld of the Western Cape, South Africa. <i>Zootaxa</i> , 2019, 4560, 149.	0.2	1
7678	Mitochondrial divergence suggests unexpected high species diversity in the opsariichthine fishes (Teleostei: Cyprinidae) and the revalidation of <i>Opsariichthys macrolepis</i> . <i>Ecology and Evolution</i> , 2019, 9, 2664-2677.	0.8	7
7679	Virome Diversity Correlates with Intestinal Microbiome Diversity in Adult Monozygotic Twins. <i>Cell Host and Microbe</i> , 2019, 25, 261-272.e5.	5.1	159
7680	Mixing of meteoric and geothermal fluids supports hyperdiverse chemosynthetic hydrothermal communities. <i>Nature Communications</i> , 2019, 10, 681.	5.8	57
7681	Mechanistic insights into the evolution of DUF26-containing proteins in land plants. <i>Communications Biology</i> , 2019, 2, 56.	2.0	75
7682	The <i>Cedrus</i> -associated truffle <i>Trappeindia himalayensis</i> is a morphologically unique and phylogenetically divergent species of <i>Rhizopogon</i> . <i>Mycologia</i> , 2019, 111, 225-234.	0.8	3
7683	Vegetative reproduction and phylogeny of a new subtidal alga from Korea: <i>Dipterocladia yongdeokkoi</i> sp. nov. (Ceramiales, Rhodophyta). <i>Phycologia</i> , 2019, 58, 26-35.	0.6	3
7684	Changing Trends in International Versus Domestic HCV Transmission in HIV-Positive Men Who Have Sex With Men: A Perspective for the Direct-Acting Antiviral Scale-Up Era. <i>Journal of Infectious Diseases</i> , 2019, 220, 91-99.	1.9	24
7685	Multilocus phylogeny, species delimitation and biogeography of Iberian valvatiform springsnails (Caenogastropoda: Hydrobiidae), with the description of a new genus. <i>Zoological Journal of the Linnean Society</i> , 2019, 186, 892-914.	1.0	29
7686	Evolutionary Origins of Pseudogenes and Their Association with Regulatory Sequences in Plants. <i>Plant Cell</i> , 2019, 31, 563-578.	3.1	47
7687	Medusavirus, a Novel Large DNA Virus Discovered from Hot Spring Water. <i>Journal of Virology</i> , 2019, 93, .	1.5	113
7688	Chromosome rearrangements shape the diversification of secondary metabolism in the cyclosporin producing fungus <i>Tolyposcladium inflatum</i> . <i>BMC Genomics</i> , 2019, 20, 120.	1.2	22
7689	Diversity of zoantharian species and their symbionts from the Macaronesian and Cape Verde ecoregions demonstrates their widespread distribution in the Atlantic Ocean. <i>Coral Reefs</i> , 2019, 38, 269-283.	0.9	14
7690	Discovery of endogenous retroviruses with mammalian envelopes in avian genomes uncovers long-term bird-mammal interaction. <i>Virology</i> , 2019, 530, 27-31.	1.1	6

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7691	Cryptic diversity and dynamic chromosome evolution in Alpine scorpions (Euscorpidae: Euscorpius). <i>Molecular Phylogenetics and Evolution</i> , 2019, 134, 152-163.	1.2	26
7692	Anaerobic degradation of hexadecane and phenanthrene coupled to sulfate reduction by enriched consortia from northern Gulf of Mexico seafloor sediment. <i>Scientific Reports</i> , 2019, 9, 1239.	1.6	31
7693	Unexpected population fragmentation in an endangered seabird: the case of the Peruvian diving-petrel. <i>Scientific Reports</i> , 2019, 9, 2021.	1.6	19
7694	Complete mitochondrial genome of a troglophile Cydnidae (Hemiptera). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 420-422.	0.2	0
7695	RNA Binding Motif Protein 48 Is Required for U12 Splicing and Maize Endosperm Differentiation. <i>Plant Cell</i> , 2019, 31, 715-733.	3.1	27
7696	Optimized DNA extraction and library preparation for minute arthropods: Application to target enrichment in chalcid wasps used for biocontrol. <i>Molecular Ecology Resources</i> , 2019, 19, 702-710.	2.2	48
7697	Molecular characterization, cellular localization, and light-enhanced expression of Beta-Na ⁺ /H ⁺ Exchanger-like in the whitish inner mantle of the giant clam, <i>Tridacna squamosa</i> , denote its role in light-enhanced shell formation. <i>Gene</i> , 2019, 695, 101-112.	1.0	10
7698	Molecular phylogenomics of the tribe Shoreeae (Dipterocarpaceae) using whole plastid genomes. <i>Annals of Botany</i> , 2019, 123, 857-865.	1.4	35
7699	A Critical Appraisal of the Placement of Xiphosura (Chelicerata) with Account of Known Sources of Phylogenetic Error. <i>Systematic Biology</i> , 2019, 68, 896-917.	2.7	138
7700	Divergent mitochondrial lineages arose within a large, panmictic population of the Savannah sparrow (<i>Passerculus sandwichensis</i>). <i>Molecular Ecology</i> , 2019, 28, 1765-1783.	2.0	21
7701	Uncovering Neotropical treefrog diversity: integrative taxonomy reveal paraphyly in <i>Boana atlantica</i> (Amphibia, Anura, Hylidae). <i>Amphibia - Reptilia</i> , 2019, 40, 511-521.	0.1	1
7702	Homothallism, morphology and phylogenetic position of a new species of <i>Sellaphora</i> (Bacillariophyta), <i>S. pausariae</i> . <i>Plant Ecology and Evolution</i> , 2019, 152, 203-218.	0.3	4
7703	Biodiversity genomics of North American <i>Dryobates</i> woodpeckers reveals little gene flow across the <i>D. nuttallii</i> x <i>D. scalaris</i> contact zone. <i>Auk</i> , 2019, 136, .	0.7	2
7704	Deceptive conservatism of claws: distinct phyletic lineages concealed within Isohypsibioidea (Eutardigrada) revealed by molecular and morphological evidence. <i>Contributions To Zoology</i> , 2019, 88, 78-132.	0.2	48
7705	The stoloniferous octocoral, <i>Hanabira yukibana</i> , gen. nov., sp. nov., of the southern Ryukyus has morphological and symbiont variation. <i>Contributions To Zoology</i> , 2019, 88, 54-77.	0.2	5
7706	Phylogeny and systematic revision of the helicarionid semislugs of eastern Queensland (Stylommatophora, Helicarionidae). <i>Contributions To Zoology</i> , 2019, 88, 351-451.	0.2	10
7707	Taxonomy of rock-wallabies, <i>Petrogale</i> (Marsupialia : Macropodidae). V. A description of two new subspecies of the black-footed rock-wallaby (<i>Petrogale lateralis</i>). <i>Australian Journal of Zoology</i> , 2019, 67, 19.	0.6	6
7708	<i>Inocybe caroticolor</i> from oak forests of Pakistan. <i>Mycotaxon</i> , 2019, 134, 241-251.	0.1	3

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7709	Draft Whole-Genome Sequences of <i>Xylella fastidiosa</i> subsp. <i>fastidiosa</i> Strains TPD3 and TPD4, Isolated from Grapevines in Hou-li, Taiwan. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	6
7710	A New Green Salamander in the Southern Appalachians: Evolutionary History of <i>Aneides aeneus</i> and Implications for Management and Conservation with the Description of a Cryptic Microendemic Species. <i>Copeia</i> , 2019, 107, 748.	1.4	10
7711	Taxonomic revision and molecular phylogeny of <i>Flemingia</i> subgenus <i>Rhynchosioides</i> (Leguminosae). <i>Blumea: Journal of Plant Taxonomy and Plant Geography</i> , 2019, 64, 253-271.	0.1	4
7712	A New Species of Damselfish (Teleostei: Pomacentridae: Pomacentrus) from Nosy Faho, Madagascar. <i>Copeia</i> , 2019, 107, 323.	1.4	1
7713	Back to the roots: a reappraisal of <i>Neocosmospora</i> . <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2019, 43, 90-185.	1.6	92
7714	Nucleic acid cleavage with a hyperthermophilic Cas9 from an uncultured Ignavibacterium. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 23100-23105.	3.3	17
7715	Conserved Patterns of Symmetric Inversion in the Genome Evolution of <i>Bordetella</i> Respiratory Pathogens. <i>MSystems</i> , 2019, 4, .	1.7	30
7716	Genome Assemblies of Two Rare Opportunistic Yeast Pathogens: <i>Diutina rugosa</i> (syn. <i>Candida</i>) Tj ETQq1 1 0.784314 rgBT /Ove Genetics, 2019, 9, 3921-3927.	0.8	6
7717	<i>Gomphonella olivacea</i> (Bacillariophyceae) â€™ a new phylogenetic position for a well-known taxon, its typification, new species and combinations. <i>Plant Ecology and Evolution</i> , 2019, 152, 219-247.	0.3	9
7718	Genome Sequences of Human Coronavirus OC43 and NL63, Associated with Respiratory Infections in Kilifi, Kenya. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	5
7719	Diversity in Natural Transformation Frequencies and Regulation across <i>Vibrio</i> Species. <i>MBio</i> , 2019, 10, .	1.8	29
7720	Epitypification of <i>Fusarium oxysporum</i> â€™ clearing the taxonomic chaos. <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2019, 43, 1-47.	1.6	131
7721	Maintenance of Sympatric and Allopatric Populations in Free-Living Terrestrial Bacteria. <i>MBio</i> , 2019, 10, .	1.8	19
7722	Disease Resistance Genetics and Genomics in Octoploid Strawberry. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3315-3332.	0.8	26
7723	The <i>de Novo</i> Reference Genome and Transcriptome Assemblies of the Wild Tomato Species <i>Solanum chilense</i> Highlights Birth and Death of NLR Genes Between Tomato Species. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3933-3941.	0.8	37
7724	Quality Analysis of Mobile Web Server. <i>IOP Conference Series: Materials Science and Engineering</i> , 2019, 662, 022043.	0.3	1
7725	The complete chloroplast genome sequence of the medicinal plant <i>Paris polyphylla</i> (Melanthiaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3971-3972.	0.2	1
7726	Mitogenomic phylogenetic analyses of <i>Leptogorgia virgulata</i> and <i>Leptogorgia hebes</i> (Anthozoa: Octocorallia) from the Gulf of Mexico provides insight on Gorgoniidae divergence between Pacific and Atlantic lineages. <i>Ecology and Evolution</i> , 2019, 9, 14114-14129.	0.8	3

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7727	Comparative Genomic Analysis of <i>Rhodococcus equi</i> : An Insight into Genomic Diversity and Genome Evolution. <i>International Journal of Genomics</i> , 2019, 2019, 1-14.	0.8	7
7728	Molecular and morphological data reveal hidden diversity in common North American <i>Frustulia</i> species (Amphipleuraceae). <i>Diatom Research</i> , 2019, 34, 205-223.	0.5	1
7729	5S Ribosomal DNA of Distantly Related <i>Quercus</i> Species: Molecular Organization and Taxonomic Application. <i>Cytology and Genetics</i> , 2019, 53, 459-466.	0.2	16
7730	New endemic <i>Fusarium</i> species hitch-hiking with pathogenic <i>Fusarium</i> strains causing Panama disease in small-holder banana plots in Indonesia. <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2019, 43, 48-69.	1.6	47
7731	Complete plastome sequences of two <i>Neottia</i> species and comparative analysis with other Neottieae species (Orchidaceae). <i>Folia Geobotanica</i> , 2019, 54, 257-266.	0.4	3
7732	The culturable mycobiota associated with the Mediterranean sponges <i>Aplysina cavernicola</i> , <i>Crambe crambe</i> and <i>Phorbas tenacior</i> . <i>FEMS Microbiology Letters</i> , 2019, 366, .	0.7	5
7733	Phylogenetic and Morphological Analyses Support the Resurrection of <i>Dendroconche</i> and the Recognition of Two New Genera in Polypodiaceae Subfamily Microsoroideae. <i>Systematic Botany</i> , 2019, 44, 737-752.	0.2	15
7734	Detailed Evaluation of Data Analysis Tools for Subtyping of Bacterial Isolates Based on Whole Genome Sequencing: <i>Neisseria meningitidis</i> as a Proof of Concept. <i>Frontiers in Microbiology</i> , 2019, 10, 2897.	1.5	8
7735	Target Capture Sequencing Unravels <i>Rubus</i> Evolution. <i>Frontiers in Plant Science</i> , 2019, 10, 1615.	1.7	73
7736	Greenlip Abalone (<i>Haliotis laevigata</i>) Genome and Protein Analysis Provides Insights into Maturation and Spawning. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3067-3078.	0.8	14
7737	Genomic analysis on broiler-associated <i>Clostridium perfringens</i> strains and exploratory caecal microbiome investigation reveals key factors linked to poultry necrotic enteritis. <i>Animal Microbiome</i> , 2019, 1, 12.	1.5	29
7738	Complete plastid genome of <i>Vanda concolor</i> (Orchidaceae, Aeridinae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3687-3688.	0.2	2
7739	The complete chloroplast genome of <i>Butomus umbellatus</i> L. and its phylogenetic position. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3700-3701.	0.2	1
7740	A review of <i>Austrocallerya</i> and <i>Pongamia</i> (Leguminosae subfamily Papilionoideae) in Australia, and the description of a new monotypic genus, <i>Ibatiria</i> . <i>Australian Systematic Botany</i> , 2019, , .	0.3	1
7741	A Coevolved EDS1-SAG101-NRG1 Module Mediates Cell Death Signaling by TIR-Domain Immune Receptors. <i>Plant Cell</i> , 2019, 31, 2430-2455.	3.1	198
7742	Metagenomic Nanopore Sequencing of Influenza Virus Direct from Clinical Respiratory Samples. <i>Journal of Clinical Microbiology</i> , 2019, 58, .	1.8	121
7743	Wnt Gene Expression During Early Embryogenesis in the Nymphalid Butterfly <i>Bicyclus anynana</i> . <i>Frontiers in Ecology and Evolution</i> , 2019, 7, .	1.1	18
7744	First record of tropical sea urchin <i>Echinometra</i> sp. C from Honshu, Japan. <i>Japanese Journal of Benthology</i> , 2019, 73, 109-117.	0.1	2

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7745	IMA Genome-F 11. IMA Fungus, 2019, 10, 13.	1.7	12
7746	The Emergence of Successful <i>Streptococcus pyogenes</i> Lineages through Convergent Pathways of Capsule Loss and Recombination Directing High Toxin Expression. <i>MBio</i> , 2019, 10, .	1.8	22
7747	Molecular Signatures Related to the Virulence of <i>Bacillus cereus</i> Sensu Lato, a Leading Cause of Devastating Endophthalmitis. <i>MSystems</i> , 2019, 4, .	1.7	4
7748	Unusual Metabolism and Hypervariation in the Genome of a <i>Gracilibacterium</i> (BD1-5) from an Oil-Degrading Community. <i>MBio</i> , 2019, 10, .	1.8	43
7749	Draft Genome Assembly and Annotation of the Gila Topminnow <i>Poeciliopsis occidentalis</i> . <i>Frontiers in Ecology and Evolution</i> , 2019, 7, .	1.1	3
7750	The Bacterial Symbionts of Closely Related Hydrothermal Vent Snails With Distinct Geochemical Habitats Show Broad Similarity in Chemoautotrophic Gene Content. <i>Frontiers in Microbiology</i> , 2019, 10, 1818.	1.5	21
7751	The complete chloroplast genome sequence of <i>Moringa oleifera</i> Lam. (Moringaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 4094-4095.	0.2	12
7752	Characterization of the complete chloroplast genome of <i>Epimedium brevicornu</i> (Berberidaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3681-3682.	0.2	2
7753	Characterization of the complete chloroplast genome of <i>Paederia scandens</i> (Rubiaceae): a Chinese folk medicinal plant. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 4075-4076.	0.2	1
7754	The complete chloroplast genome of <i>Eria corneri</i> (Orchidaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 4138-4139.	0.2	0
7755	The complete chloroplast genome sequence of <i>Cosmos bipinnatus</i> , the first of the genus <i>Cosmos</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 4204-4206.	0.2	1
7756	The complete plastid genome sequence of <i>Phyllodium pulchellum</i> (L.) Desv. (Leguminosae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 4207-4208.	0.2	0
7757	Complete mitogenome of the streptophyte green alga <i>Coleochaete scutata</i> (Coleochaetophyceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 4209-4210.	0.2	3
7758	Complete chloroplast genome sequence of <i>Swertia mileensis</i> (Gentianaceae): a medicinal species endemic to China. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 4166-4167.	0.2	2
7759	The complete plastid genome of <i>Iris domestica</i> : a traditional Chinese medicine. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 4214-4215.	0.2	2
7760	Characterization of the complete plastome of <i>Alopecurus aequalis</i> (Poaceae), a widespread weed. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 4216-4217.	0.2	4
7761	The complete chloroplast genome and phylogenetic analysis of <i>Veratrum mengtzeanum</i> Loes. F. (Liliaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 4170-4171.	0.2	4
7762	Semiautomatic Extraction of Morphological Characters from a Book about Insect Vectors of Chagas Disease. , 2019, , .		0

#	ARTICLE	IF	CITATIONS
7763	Characterization of the Complete Chloroplast Genome of <i>Acer truncatum</i> Bunge (Sapindales). <i>Trends in Plant Science</i> , 2019, 2019, 1-13.	0.9	12
7764	The Critical Importance of Rhodoliths in the Life Cycle Completion of Both Macro- and Microalgae, and as Holobionts for the Establishment and Maintenance of Marine Biodiversity. <i>Frontiers in Marine Science</i> , 2019, 5, .	1.2	42
7765	Dwarf minke whales from the South Pacific share a matrilineal lineage distinct from <i>Balaenoptera acutorostrata acutorostrata</i> and <i>B. a. scammoni</i> . <i>Australian Mammalogy</i> , 2019, 41, 231.	0.7	2
7766	Fungal Planet description sheets: 951–1041. <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2019, 43, 223-425.	1.6	126
7767	System OMICs analysis of <i>Mycobacterium tuberculosis</i> Beijing B0/W148 cluster. <i>Scientific Reports</i> , 2019, 9, 19255.	1.6	7
7768	Whole Plastome Sequencing Within <i>Silene</i> Section <i>Psammophilae</i> Reveals Mainland Hybridization and Divergence With the Balearic Island Populations. <i>Frontiers in Plant Science</i> , 2019, 10, 1466.	1.7	9
7770	Diverse, Abundant, and Novel Viruses Infecting the Marine <i>Roseobacter</i> RCA Lineage. <i>MSystems</i> , 2019, 4, .	1.7	27
7771	Taxonomy and Phylo Genetic Systematics. , 2019, , 17-52.		0
7772	Comparative Genomics Reveals a Well-Conserved Intrinsic Resistome in the Emerging Multidrug-Resistant Pathogen <i>Cupriavidus gilardii</i> . <i>MSphere</i> , 2019, 4, .	1.3	9
7773	Whole-Genome Sequence of a Unique <i>Eliaeroa</i> Species Strain Isolated from a Yellowstone National Park Hot Spring. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	2
7774	Phylogenetics of <i>Pinus</i> Subsection <i>Cembroides</i> Engelm. (Pinaceae) Inferred from Low-Copy Nuclear Gene Sequences. <i>Systematic Botany</i> , 2019, 44, 501-518.	0.2	14
7775	Transcriptional Regulation and Mechanism of SigN (ZpdN), a pBS32-Encoded Sigma Factor in <i>Bacillus subtilis</i> . <i>MBio</i> , 2019, 10, .	1.8	14
7776	Chloroplast primers for clade-wide phylogenetic studies of <i>Thalictrum</i> . <i>Applications in Plant Sciences</i> , 2019, 7, e11294.	0.8	6
7777	An empirical assessment of a single family-wide hybrid capture locus set at multiple evolutionary timescales in Asteraceae. <i>Applications in Plant Sciences</i> , 2019, 7, e11295.	0.8	28
7778	Multiple freshwater invasions of the tapertail anchovy (Clupeiformes: Engraulidae) of the Yangtze River. <i>Ecology and Evolution</i> , 2019, 9, 12202-12215.	0.8	10
7779	Vocal divergence is concordant with genomic evidence for strong reproductive isolation in grasshopper mice (<i>Onychomys</i>). <i>Ecology and Evolution</i> , 2019, 9, 12886-12896.	0.8	10
7780	From treetops to tabletops: a preliminary investigation of how plants are represented in popular modern board games. <i>Plants People Planet</i> , 2019, 1, 290-300.	1.6	3
7781	The genome of a subterrestrial nematode reveals adaptations to heat. <i>Nature Communications</i> , 2019, 10, 5268.	5.8	22

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7782	Evidence for adaptive introgression of exons across a hybrid swarm in deer. <i>BMC Evolutionary Biology</i> , 2019, 19, 199.	3.2	12
7783	Hooked on you: shape of attachment structures in cymothoid isopods reflects parasitic strategy. <i>BMC Evolutionary Biology</i> , 2019, 19, 207.	3.2	14
7784	OrthoFinder: phylogenetic orthology inference for comparative genomics. <i>Genome Biology</i> , 2019, 20, 238.	3.8	3,367
7785	Assessing the Diversity and Distribution of Apicomplexans in Host and Free-Living Environments Using High-Throughput Amplicon Data and a Phylogenetically Informed Reference Framework. <i>Frontiers in Microbiology</i> , 2019, 10, 2373.	1.5	33
7786	HPC: Hierarchical phylogeny construction. <i>PLoS ONE</i> , 2019, 14, e0221357.	1.1	1
7787	Evolution of <i>Streptococcus pneumoniae</i> Serotype 3 in England and Wales: A Major Vaccine Evader. <i>Genes</i> , 2019, 10, 845.	1.0	52
7788	Fungal Adaptation to the Advanced Stages of Wood Decomposition: Insights from the <i>Steccherinum ochraceum</i> . <i>Microorganisms</i> , 2019, 7, 527.	1.6	13
7789	A phylogenetic revision of the genus <i>Hypnum</i> : Towards completion. <i>Taxon</i> , 2019, 68, 628-660.	0.4	31
7790	A new species of <i>Clinostomum</i> Leidy, 1856 in East Asia based on genomic and morphological data. <i>Parasitology Research</i> , 2019, 118, 3253-3265.	0.6	13
7791	Mitogenome analysis of dwarf pufferfish (<i>Carinotetraodon travancoricus</i>) endemic to southwest India and its implications in the phylogeny of Tetraodontidae. <i>Journal of Genetics</i> , 2019, 98, 1.	0.4	0
7792	The Mitochondrial Genome of <i>Eleusine indica</i> and Characterization of Gene Content Within Poaceae. <i>Genome Biology and Evolution</i> , 2019, 12, 3684-3697.	1.1	3
7793	A High-quality Draft Genome Assembly of the Black-necked Crane (<i>Grus nigricollis</i>) Based on Nanopore Sequencing. <i>Genome Biology and Evolution</i> , 2019, 11, 3332-3340.	1.1	5
7794	Ancestral male recombination in <i>Drosophila albomicans</i> produced geographically restricted neo-Y chromosome haplotypes varying in age and onset of decay. <i>PLoS Genetics</i> , 2019, 15, e1008502.	1.5	30
7795	Demographic Histories and Genome-Wide Patterns of Divergence in Incipient Species of Shorebirds. <i>Frontiers in Genetics</i> , 2019, 10, 919.	1.1	14
7796	Multiple <i>Klebsiella pneumoniae</i> KPC Clones Contribute to an Extended Hospital Outbreak. <i>Frontiers in Microbiology</i> , 2019, 10, 2767.	1.5	27
7797	Group I alkenones and Isochrysidales in the world's largest maar lakes and their potential paleoclimate applications. <i>Organic Geochemistry</i> , 2019, 138, 103924.	0.9	7
7798	The evolution and genomic basis of beetle diversity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 24729-24737.	3.3	372
7799	<i>Arcobacter peruensis</i> sp. nov., a Chemolithoheterotroph Isolated from Sulfide- and Organic-Rich Coastal Waters off Peru. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	36

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7800	Complex Class 1 Integron in a Clinical <i>Escherichia coli</i> Strain From Vietnam Carrying Both <i>mcr-1</i> and <i>blaNDM-1</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 2472.	1.5	16
7801	Effective DNA extraction methods for mitochondrial phylogenomics of the sea urchins. <i>Zoosymposia</i> , 2019, 15, 192-202.	0.3	3
7802	Transcriptomic and evolutionary analysis of the mechanisms by which <i>P. argentatum</i> , a rubber producing perennial, responds to drought. <i>BMC Plant Biology</i> , 2019, 19, 494.	1.6	8
7803	Nuclear ITS and AFLPs provide surprising implications for the taxonomy of <i>Tephrosia longifolia</i> agg. and the endemic status of <i>T. longifolia</i> subsp. <i>moravica</i> . <i>Plant Systematics and Evolution</i> , 2019, 305, 865-884.	0.3	17
7804	Continuous and non-seasonal reproductive cycle of the alien species <i>Diopatra neapolitana</i> (Onuphidae, Annelida) in a tropical bay of SW Atlantic. <i>Estuarine, Coastal and Shelf Science</i> , 2019, 231, 106479.	0.9	9
7805	Taxonomy and phylogeny of <i>Pseudovorticella littoralis</i> sp. n. and <i>P. alani</i> sp. n. (Ciliophora:). <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 T</i>	0.5	4
7806	Characterization of the complete chloroplast genome of an annual halophyte, <i>Chenopodium glaucum</i> (Amaranthaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3898-3899.	0.2	7
7807	In silico definition of new ligninolytic peroxidase sub-classes in fungi and putative relation to fungal life style. <i>Scientific Reports</i> , 2019, 9, 20373.	1.6	13
7808	Draft genome sequences of five <i>Calonectria</i> species from Eucalyptus plantations in China, <i>Celoporthes dispersa</i> , <i>Sporothrix phasma</i> and <i>Alectoria sarmentosa</i> . <i>IMA Fungus</i> , 2019, 10, 22.	1.7	17
7809	Molecular phylogenetics of Black Cobra (<i>Naja naja</i>) in Pakistan. <i>Electronic Journal of Biotechnology</i> , 2019, 42, 23-29.	1.2	4
7810	Resolution of deep divergence of club fungi (phylum Basidiomycota). <i>Synthetic and Systems Biotechnology</i> , 2019, 4, 225-231.	1.8	6
7811	The complete chloroplast genome sequence of a Chinese endemic plant <i>Dendrobium hancockii</i> Rolfe (Orchidaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3860-3861.	0.2	0
7812	Population genomics of two congeneric Palaearctic shorebirds reveals differential impacts of Quaternary climate oscillations across habitats types. <i>Scientific Reports</i> , 2019, 9, 18172.	1.6	11
7813	A molecular phylogeny of carcinoecium-forming <i>Epizoanthus</i> (Hexacorallia: Zoantharia) from the Western Pacific Ocean with descriptions of three new species. <i>Systematics and Biodiversity</i> , 2019, 17, 773-786.	0.5	6
7814	Characterization of the complete chloroplast genome sequence of <i>Pennisetum glaucum</i> and its phylogenetic implications. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3764-3765.	0.2	2
7815	Complete chloroplast genome of <i>Erythropsis kwangsiensis</i> (Sterculiaceae), an endemic wild tree from South China. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3840-3841.	0.2	0
7816	The complete chloroplast genome sequence of <i>Brasenia schreberi</i> (Cabombaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3842-3843.	0.2	2
7817	The complete plastome of <i>Peucedanum praeruptorum</i> (Apiaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3612-3613.	0.2	7

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7818	The chloroplast genome of silk floss tree (<i>Ceiba speciosa</i>). Mitochondrial DNA Part B: Resources, 2019, 4, 3632-3633.	0.2	1
7819	The complete chloroplast genome of <i>Yunnanopilia longistaminea</i> (Opiliaceae), an endemic species in southwest China. Mitochondrial DNA Part B: Resources, 2019, 4, 3624-3625.	0.2	2
7820	The complete chloroplast genome of <i>Cymbidium floribundum</i> var. <i>pumilum</i> (Orchidaceae). Mitochondrial DNA Part B: Resources, 2019, 4, 3648-3649.	0.2	3
7821	Characterization of the complete chloroplast genome of <i>Magnolia wilsonii</i> (Magnoliaceae). Mitochondrial DNA Part B: Resources, 2019, 4, 3659-3660.	0.2	0
7822	The complete chloroplast genome sequence of <i>Ludisia discolor</i> from Hainan of China. Mitochondrial DNA Part B: Resources, 2019, 4, 3663-3664.	0.2	0
7823	Characterization of the complete chloroplast genome of <i>Buddleja alternifolia</i> (Buddleiaceae). Mitochondrial DNA Part B: Resources, 2019, 4, 3689-3690.	0.2	1
7824	The complete mitochondrial genome of <i>Amur ide</i> (<i>Leuciscus waleckii waleckii</i>). Mitochondrial DNA Part B: Resources, 2019, 4, 3702-3704.	0.2	0
7825	The complete chloroplast genome of <i>Swertia cordata</i> . Mitochondrial DNA Part B: Resources, 2019, 4, 3818-3819.	0.2	3
7826	Characterization of complete chloroplast genome of traditional Chinese medical plants <i>Paris Mairei</i> and its phylogenetic positions. Mitochondrial DNA Part B: Resources, 2019, 4, 3822-3823.	0.2	0
7827	The first complete chloroplast genome of <i>Liparis nervosa</i> and its phylogenetic position within Orchidaceae. Mitochondrial DNA Part B: Resources, 2019, 4, 3752-3753.	0.2	1
7828	The complete mitochondrial genome of <i>Mantis religiosa</i> (Mantodea: Mantidae) from Canada and its phylogeny. Mitochondrial DNA Part B: Resources, 2019, 4, 3797-3799.	0.2	7
7829	The complete chloroplast genome of <i>Cotoneaster schantungensis</i> . Mitochondrial DNA Part B: Resources, 2019, 4, 3760-3761.	0.2	0
7830	The complete chloroplast genome sequence of <i>Erigeron breviscapus</i> and <i>Erigeron multiradiatus</i> (Asteraceae). Mitochondrial DNA Part B: Resources, 2019, 4, 3826-3827.	0.2	3
7831	The complete chloroplast genome sequence of <i>Blastus pauciflorus</i> (Melastomataceae). Mitochondrial DNA Part B: Resources, 2019, 4, 3854-3855.	0.2	0
7832	The plastid genome of <i>Pentadiplandra brazzeana</i> Baillon (Pentadiplandraceae). Mitochondrial DNA Part B: Resources, 2019, 4, 4002-4003.	0.2	0
7833	The complete chloroplast genome sequence of <i>Paphiopedilum purpuratum</i> (Orchidaceae). Mitochondrial DNA Part B: Resources, 2019, 4, 3910-3911.	0.2	3
7834	The complete chloroplast genome of <i>Cymbidium changningense</i> (Orchidaceae). Mitochondrial DNA Part B: Resources, 2019, 4, 3991-3993.	0.2	1
7835	The complete chloroplast genome sequences of <i>Zanthoxylum nitidum</i> var. <i>nitidum</i> and <i>Z. nitidum</i> var. <i>tomentosum</i> . Mitochondrial DNA Part B: Resources, 2019, 4, 4019-4020.	0.2	1

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7836	Complete chloroplast genome sequence of <i>Mirabilis himalaica</i> (Nyctaginaceae). Mitochondrial DNA Part B: Resources, 2019, 4, 4021-4022.	0.2	0
7837	Complete mitochondrial genome of <i>Acropteris iphiata</i> (Lepidoptera: Uraniidae). Mitochondrial DNA Part B: Resources, 2019, 4, 4069-4070.	0.2	0
7838	The geography of evolutionary divergence in the highly endemic avifauna from the Sierra Madre del Sur, Mexico. BMC Evolutionary Biology, 2019, 19, 237.	3.2	19
7839	Systematics of <i>Tibouchina</i> and allies (Melastomataceae: Melastomateae): A new taxonomic classification. Taxon, 2019, 68, 937-1002.	0.4	29
7840	Convergent degeneration of olfactory receptor gene repertoires in marine mammals. BMC Genomics, 2019, 20, 977.	1.2	31
7841	Composite genome sequence of <i>Bacillus clausii</i> , a probiotic commercially available as Enterogermina®, and insights into its probiotic properties. BMC Microbiology, 2019, 19, 307.	1.3	41
7842	Integrating phylogeography and high-resolution X-ray CT reveals five new cryptic species and multiple hybrid zones among Australian earless dragons. Royal Society Open Science, 2019, 6, 191166.	1.1	12
7843	Cryptic intermediate snail host of the liver fluke <i>Fasciola hepatica</i> in Africa. Parasites and Vectors, 2019, 12, 573.	1.0	25
7844	Comprehensive analysis of chromosomal mobile genetic elements in the gut microbiome reveals phylum-level niche-adaptive gene pools. PLoS ONE, 2019, 14, e0223680.	1.1	59
7845	<i>Goniozus omanensis</i> (Hymenoptera: Bethyridae) an important parasitoid of the lesser date moth <i>Batrachedra amydraula</i> Meyrick (Lepidoptera: Batrachedridae) in Oman. PLoS ONE, 2019, 14, e0223761.	1.1	9
7846	Comparative Genomics Analysis of Ciliates Provides Insights on the Evolutionary History Within <i>Nassophorea</i> – <i>Synhymenia</i> – <i>Phyllopharyngea</i> Assemblage. Frontiers in Microbiology, 2019, 10, 2819.	1.5	31
7847	Natural Infection of <i>Aedes aegypti</i> by Chikungunya and Dengue type 2 Virus in a Transition Area of North-Northeast Brazil. Viruses, 2019, 11, 1126.	1.5	12
7848	Viral Diversity of Microbats within the South West Botanical Province of Western Australia. Viruses, 2019, 11, 1157.	1.5	23
7849	A bifunctional ATPase drives tad pilus extension and retraction. Science Advances, 2019, 5, eaay2591.	4.7	39
7850	Pathogenic <i>Leishmania</i> spp. detected in lizards from Northwest China using molecular methods. BMC Veterinary Research, 2019, 15, 446.	0.7	11
7851	Complete chloroplast genome sequences of two <i>Amomum</i> species (Zingiberaceae). Mitochondrial DNA Part B: Resources, 2019, 4, 3795-3796.	0.2	1
7852	Genetic and phylogenetic relationships analysis of the complete chloroplast genome <i>Cucumis sativus</i> to China. Mitochondrial DNA Part B: Resources, 2019, 4, 3900-3901.	0.2	1
7853	Characterization of the complete chloroplast genome of <i>Centaurea maculosa</i> (Asteraceae). Mitochondrial DNA Part B: Resources, 2019, 4, 3929-3930.	0.2	4

#	ARTICLE	IF	CITATIONS
7854	The complete plastid genome of <i>Vanda xichangensis</i> (Orchidaceae, Aeridinae). Mitochondrial DNA Part B: Resources, 2019, 4, 3985-3986.	0.2	5
7855	The complete chloroplast genome sequence of <i>Eranthis stellate</i> (Ranunculaceae). Mitochondrial DNA Part B: Resources, 2019, 4, 4025-4026.	0.2	1
7857	Emergence and Evolution of High-Level Cephalosporin-Resistant <i>Salmonella</i> Goldcoast in Northern Taiwan. Open Forum Infectious Diseases, 2019, 6, ofz447.	0.4	16
7858	LMAP_S: Lightweight Multigene Alignment and Phylogeny eStimation. BMC Bioinformatics, 2019, 20, 739.	1.2	1
7859	First report of <i>Klebsiella quasipneumoniae</i> harboring blaKPC-2 in Saudi Arabia. Antimicrobial Resistance and Infection Control, 2019, 8, 203.	1.5	15
7860	Characterization of the complete chloroplast genome sequence of <i>Dalbergia</i> species and its phylogenetic implications. Scientific Reports, 2019, 9, 20401.	1.6	46
7861	Whole genome sequencing, analyses of drug resistance-conferring mutations, and correlation with transmission of <i>Mycobacterium tuberculosis</i> carrying katG-S315T in Hanoi, Vietnam. Scientific Reports, 2019, 9, 15354.	1.6	20
7862	Extensive host-switching of avian feather lice following the Cretaceous-Paleogene mass extinction event. Communications Biology, 2019, 2, 445.	2.0	20
7863	Phylogenomics and mitochondrial genome evolution of the gall-associated doryctine wasp genera (Hymenoptera: Braconidae). Systematics and Biodiversity, 2019, 17, 731-744.	0.5	8
7864	Complete chloroplast genome of <i>Vincetoxicum hainanense</i> (Apocynaceae: Asclepiadoideae), an endangered liana endemic to China. Mitochondrial DNA Part B: Resources, 2019, 4, 3608-3609.	0.2	1
7865	Tripartite Symbiosis of an Anaerobic Scuticociliate with Two Hydrogenosome-Associated Endosymbionts, a <i>Holospira</i> -Related Alphaproteobacterium and a Methanogenic Archaeon. Applied and Environmental Microbiology, 2019, 85, .	1.4	26
7866	Whole-genome DNA similarity and population structure of <i>Plasmodiophora brassicae</i> strains from Canada. BMC Genomics, 2019, 20, 744.	1.2	28
7867	Exploring Actinobacteria Associated With Rhizosphere and Endosphere of the Native Alpine Medicinal Plant <i>Leontopodium nivale</i> Subspecies <i>alpinum</i> . Frontiers in Microbiology, 2019, 10, 2531.	1.5	28
7868	Delmarva (DMV/1639) Infectious Bronchitis Virus (IBV) Variants Isolated in Eastern Canada Show Evidence of Recombination. Viruses, 2019, 11, 1054.	1.5	34
7869	Annotated Draft Genomes of Two Caddisfly Species <i>Plectrocnemia conspersa</i> CURTIS and <i>Hydropsyche tenuis</i> NAVAS (Insecta: Trichoptera). Genome Biology and Evolution, 2019, 11, 3445-3451.	1.1	21
7870	Programmed DNA elimination of germline development genes in songbirds. Nature Communications, 2019, 10, 5468.	5.8	66
7871	Genome analyses of a placozoan rickettsial endosymbiont show a combination of mutualistic and parasitic traits. Scientific Reports, 2019, 9, 17561.	1.6	11
7872	Nanopore sequencing improves the draft genome of the human pathogenic amoeba <i>Naegleria fowleri</i> . Scientific Reports, 2019, 9, 16040.	1.6	24

#	ARTICLE	IF	CITATIONS
7873	An <i>Escherichia coli</i> ST131 pangenome atlas reveals population structure and evolution across 4,071 isolates. <i>Scientific Reports</i> , 2019, 9, 17394.	1.6	71
7874	The complete chloroplast genome sequence of <i>Bupleurum chinense</i> DC. (Apiaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3665-3666.	0.2	9
7875	Evolution of <i>Aspergillus oryzae</i> before and after domestication inferred by large-scale comparative genomic analysis. <i>DNA Research</i> , 2019, 26, 465-472.	1.5	26
7876	A Complete Genome Screening Program of Clinical Methicillin-Resistant <i>Staphylococcus aureus</i> Isolates Identifies the Origin and Progression of a Neonatal Intensive Care Unit Outbreak. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	1.8	16
7877	The complete mitochondrial genome and description of a new cryptic species of <i>Benedenia</i> Diesing, 1858 (Monogenea: Capsalidae), a major pathogen infecting the yellowtail kingfish <i>Seriola lalandi</i> Valenciennes in the South-East Pacific. <i>Parasites and Vectors</i> , 2019, 12, 490.	1.0	22
7878	The genetic basis of adaptive evolution in parasitic environment from the <i>Angiostrongylus cantonensis</i> genome. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007846.	1.3	9
7879	Extensive interlineage hybridization in the predominantly clonal <i>Hydrilla verticillata</i> . <i>American Journal of Botany</i> , 2019, 106, 1622-1637.	0.8	6
7880	Origin and evolution of <i>Atriplex</i> (Amaranthaceae s.l.) in the Americas: Unexpected insights from South American species. <i>Taxon</i> , 2019, 68, 1021-1036.	0.4	9
7881	First new species of Fulviformes (Hymenochaetales, Basidiomycota) from tropical Africa. <i>Mycological Progress</i> , 2019, 18, 1383-1393.	0.5	13
7882	Complete plastid genome of <i>Suriana maritima</i> L. (Surianaceae) and its implications in phylogenetic reconstruction of Fabales. <i>Journal of Genetics</i> , 2019, 98, 1.	0.4	1
7883	Complete chloroplast genome sequence of <i>Bougainvillea Spectabilis</i> (Nyctaginaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 4010-4011.	0.2	4
7884	A new forest dwelling button spider from South Africa (Araneae, Theridiidae, Latrodectus). <i>Zootaxa</i> , 2019, 4700, zootaxa.4700.4.12.	0.2	1
7885	Phylogenomics of 10,575 genomes reveals evolutionary proximity between domains Bacteria and Archaea. <i>Nature Communications</i> , 2019, 10, 5477.	5.8	197
7886	Size increase without genetic divergence in the Eurasian water shrew <i>Neomys fodiens</i> . <i>Scientific Reports</i> , 2019, 9, 17375.	1.6	3
7887	Natriuretic peptides appeared after their receptors in vertebrates. <i>BMC Evolutionary Biology</i> , 2019, 19, 215.	3.2	8
7888	VCGIDB: A Database and Web Resource for the Genomic Islands from <i>Vibrio cholerae</i> . <i>Pathogens</i> , 2019, 8, 261.	1.2	5
7889	Detection of Abrin-Like and Prepropulchellin-Like Toxin Genes and Transcripts Using Whole Genome Sequencing and Full-Length Transcript Sequencing of <i>Abrus precatorius</i> . <i>Toxins</i> , 2019, 11, 691.	1.5	7
7890	Inferring the mammal tree: Species-level sets of phylogenies for questions in ecology, evolution, and conservation. <i>PLoS Biology</i> , 2019, 17, e3000494.	2.6	659

#	ARTICLE	IF	CITATIONS
7891	Dactylonectria and Ilyonectria Species Causing Black Foot Disease of Andean Blackberry (Rubus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 7	0.7	13
7892	Characterization of the complete chloroplast genome sequence of <i>Impatiens pritzelii</i> (Balsaminaceae): an endemic species from China. Mitochondrial DNA Part B: Resources, 2019, 4, 4073-4074.	0.2	2
7893	Specialized sledge dogs accompanied Inuit dispersal across the North American Arctic. Proceedings of the Royal Society B: Biological Sciences, 2019, 286, 20191929.	1.2	38
7894	PacBio Long-Read Sequencing Reveals the Transcriptomic Complexity and Aux/IAA Gene Evolution in Gnetum (Gnetales). Forests, 2019, 10, 1043.	0.9	6
7895	Molecular evidence for the existence of five cryptic species within the Japanese species of <i>Marphysa</i> (Annelida: Eunicidae) known as "œlwa-mushi". Plankton and Benthos Research, 2019, 14, 303-314.	0.2	9
7896	Mode and tempo of human hepatitis virus evolution. Computational and Structural Biotechnology Journal, 2019, 17, 1384-1395.	1.9	7
7897	Trochodendron aralioides, the first chromosome-level draft genome in Trochodendrales and a valuable resource for basal eudicot research. GigaScience, 2019, 8, .	3.3	20
7898	Modification of the genome topology network and its application to the comparison of group B Streptococcus genomes. BMC Genomics, 2019, 20, 886.	1.2	0
7899	Impact of a single round of mass drug administration with azithromycin on active trachoma and ocular Chlamydia trachomatis prevalence and circulating strains in The Gambia and Senegal. Parasites and Vectors, 2019, 12, 497.	1.0	10
7900	Whole-genome sequencing of ocular Chlamydia trachomatis isolates from Gadarif State, Sudan. Parasites and Vectors, 2019, 12, 518.	1.0	11
7901	Bagaza Virus in Himalayan Monal Pheasants, South Africa, 2016–2017. Emerging Infectious Diseases, 2019, 25, 2299-2302.	2.0	10
7902	Annual Protist Community Dynamics in a Freshwater Ecosystem Undergoing Contrasted Climatic Conditions: The Saint-Charles River (Canada). Frontiers in Microbiology, 2019, 10, 2359.	1.5	36
7903	Characterization of the Mycobiome of the Seagrass, Zostera marina, Reveals Putative Associations With Marine Chytrids. Frontiers in Microbiology, 2019, 10, 2476.	1.5	34
7904	Ancient mitogenomics clarifies radiation of extinct Mascarene giant tortoises (Cylindraspis spp.). Scientific Reports, 2019, 9, 17487.	1.6	25
7905	Phylogeography, Population Structure, and Species Delimitation in Rockhopper Penguins (Eudyptes) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.0	3
7906	Analyses of Plastome Sequences Improve Phylogenetic Resolution and Provide New Insight Into the Evolutionary History of Asian Sonerileae/Dissochaeteae. Frontiers in Plant Science, 2019, 10, 1477.	1.7	26
7907	Species Identification of Oaks (Quercus L., Fagaceae) from Gene to Genome. International Journal of Molecular Sciences, 2019, 20, 5940.	1.8	35
7908	Gut uropathogen abundance is a risk factor for development of bacteriuria and urinary tract infection. Nature Communications, 2019, 10, 5521.	5.8	123

#	ARTICLE	IF	CITATIONS
7909	A taxonomic monograph of <i>Ipomoea</i> integrated across phylogenetic scales. <i>Nature Plants</i> , 2019, 5, 1136-1144.	4.7	67
7910	Bacteriophage targeting of gut bacterium attenuates alcoholic liver disease. <i>Nature</i> , 2019, 575, 505-511.	13.7	493
7911	Repeated long-distance dispersal and convergent evolution in hazel. <i>Scientific Reports</i> , 2019, 9, 16016.	1.6	8
7912	Phylogenetic surveillance of travel-related Zika virus infections through whole-genome sequencing methods. <i>Scientific Reports</i> , 2019, 9, 16433.	1.6	4
7913	Deciphering phylogenetic relationships and delimiting species boundaries using a Bayesian coalescent approach in protists: A case study of the ciliate genus <i>Spirostomum</i> (Ciliophora, Heterotrichea). <i>Scientific Reports</i> , 2019, 9, 16360.	1.6	26
7914	The $\hat{\mu}$ -oxidation pathway is downregulated during diapause termination in <i>Calanus</i> copepods. <i>Scientific Reports</i> , 2019, 9, 16686.	1.6	13
7915	Highly divergent lineage of narrow-headed vole from the Late Pleistocene Europe. <i>Scientific Reports</i> , 2019, 9, 17799.	1.6	25
7916	The complete mitochondrial genome of <i>Harpago chiragra</i> and <i>Lambis lambis</i> (Gastropoda: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf.50 57 Td	1.6	8
7917	RSH enzyme diversity for (p)ppGpp metabolism in <i>Phaeodactylum tricornutum</i> and other diatoms. <i>Scientific Reports</i> , 2019, 9, 17682.	1.6	15
7918	Isolation and comparative genomics of <i>Mycobacterium tuberculosis</i> isolates from cattle and their attendants in South India. <i>Scientific Reports</i> , 2019, 9, 17892.	1.6	14
7919	<i>Serratia liquefaciens</i> FG3 isolated from a metallophyte plant sheds light on the evolution and mechanisms of adaptive traits in extreme environments. <i>Scientific Reports</i> , 2019, 9, 18006.	1.6	10
7920	Phylogenomics investigation of sparids (Teleostei: Spariformes) using high-quality proteomes highlights the importance of taxon sampling. <i>Communications Biology</i> , 2019, 2, 400.	2.0	7
7921	Genetic variation associated with infection and the environment in the accidental pathogen <i>Burkholderia pseudomallei</i> . <i>Communications Biology</i> , 2019, 2, 428.	2.0	19
7922	Rapid, large-scale species discovery in hyperdiverse taxa using 1D MinION sequencing. <i>BMC Biology</i> , 2019, 17, 96.	1.7	91
7923	Root-Colonizing Endophytic Fungi of the Dominant Grass <i>Stipa krylovii</i> From a Mongolian Steppe Grassland. <i>Frontiers in Microbiology</i> , 2019, 10, 2565.	1.5	28
7924	Genetic and morphological diversity of mouse lemurs (<i>Microcebus</i> spp.) in northern Madagascar: The discovery of a putative new species?. <i>American Journal of Primatology</i> , 2019, 81, e23070.	0.8	12
7925	<i>Ophiobolus hydei</i> sp. nov. (Phaeosphaeriaceae, Ascomycota) from <i>Cirsium</i> and <i>Phlomis</i> in Uzbekistan. <i>Botany</i> , 2019, 97, 671-680.	0.5	14
7926	<p>A morpho-molecular re-appraisal of Polystigma fulvum and P. rubrum (Polystigma,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf.50 57 Td (Polyst		

#	ARTICLE	IF	CITATIONS
7927	<i>Tubeufia sahyadriensis</i> (Tubeufiaceae), a new dictyosporous anamorph from the Western Ghats, India. <i>Phytotaxa</i> , 2019, 423, 171-181.	0.1	3
7928	<i>Collastoma esotericum</i> (Neodalyellida: Umagillidae), a new species of sipunculan-inhabiting rhabdocoel from Queensland, Australia. <i>Zootaxa</i> , 2019, 4701, 563-573.	0.2	0
7929	A Glyphosate Pulse to Brackish Long-Term Microcosms Has a Greater Impact on the Microbial Diversity and Abundance of Planktonic Than of Biofilm Assemblages. <i>Frontiers in Marine Science</i> , 2019, 6, .	1.2	8
7930	Residual Variation Intolerance Score Detects Loci Under Selection in Neuroinvasive <i>Listeria monocytogenes</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 2702.	1.5	1
7931	The Transformation of Reference Microbiology Methods and Surveillance for <i>Salmonella</i> With the Use of Whole Genome Sequencing in England and Wales. <i>Frontiers in Public Health</i> , 2019, 7, 317.	1.3	66
7932	Rearrangement analysis of multiple bacterial genomes. <i>BMC Bioinformatics</i> , 2019, 20, 631.	1.2	7
7933	The ability of single genes vs full genomes to resolve time and space in outbreak analysis. <i>BMC Evolutionary Biology</i> , 2019, 19, 232.	3.2	35
7934	RNA-seq, de novo transcriptome assembly and flavonoid gene analysis in 13 wild and cultivated berry fruit species with high content of phenolics. <i>BMC Genomics</i> , 2019, 20, 995.	1.2	27
7935	Archaic mitochondrial DNA inserts in modern day nuclear genomes. <i>BMC Genomics</i> , 2019, 20, 1017.	1.2	8
7936	Genome sequencing of <i>Mycobacterium pinnipedii</i> strains: genetic characterization and evidence of superinfection in a South American sea lion (<i>Otaria flavescens</i>). <i>BMC Genomics</i> , 2019, 20, 1030.	1.2	21
7937	Variation in plastid genomes in the gynodioecious species <i>Silene vulgaris</i> . <i>BMC Plant Biology</i> , 2019, 19, 568.	1.6	8
7938	Microbial genomes from non-human primate gut metagenomes expand the primate-associated bacterial tree of life with over 1000 novel species. <i>Genome Biology</i> , 2019, 20, 299.	3.8	58
7939	Genetic determinants of genus-level glycan diversity in a bacterial protein glycosylation system. <i>PLoS Genetics</i> , 2019, 15, e1008532.	1.5	16
7940	Rapid loss of flight in the Aldabra white-throated rail. <i>PLoS ONE</i> , 2019, 14, e0226064.	1.1	5
7941	Molecular and morphological evidence for a new species of <i>Siphocranion</i> (Lamiaceae) from the Sino-Vietnamese border. <i>Phytotaxa</i> , 2019, 425, 1-18.	0.1	3
7942	<i>Leptolejeunea nigra</i> (Lejeuneaceae), a new species with brownish black ocelli based upon morphology and DNA sequences. <i>Phytotaxa</i> , 2019, 427, 31-42.	0.1	3
7943	Computational historical linguistics. <i>Theoretical Linguistics</i> , 2019, 45, 151-182.	0.1	12
7944	Agricultural systems as potential sources of emerging human mycoses caused by <i>Trichoderma</i> : a successful, common phylotype of <i>Trichoderma longibrachiatum</i> in the frontline. <i>FEMS Microbiology Letters</i> , 2019, 366, .	0.7	28

#	ARTICLE	IF	CITATIONS
7945	SureSelect targeted enrichment, a new cost effective method for the whole genome sequencing of <i>Candidatus Liberibacter asiaticus</i> . <i>Scientific Reports</i> , 2019, 9, 18962.	1.6	10
7946	A new Indo-Malayan family of Grassatores (Arachnida: Opiliones: Laniatores). <i>Invertebrate Systematics</i> , 2019, 33, 892-906.	0.5	8
7947	Overestimation of an Outbreak of <i>Enterobacter cloacae</i> in a Neonatal Intensive Care Unit in Germany, 2015. <i>Pediatric Infectious Disease Journal</i> , 2019, 38, 631-637.	1.1	3
7948	Phenotypic and Molecular Epidemiology of ESBL-, AmpC-, and Carbapenemase-Producing <i>Escherichia coli</i> in Northern and Eastern Europe. <i>Frontiers in Microbiology</i> , 2019, 10, 2465.	1.5	25
7949	Co-Isolation and Characterization of Two Pandoraviruses and a Mimivirus from a Riverbank in Japan. <i>Viruses</i> , 2019, 11, 1123.	1.5	19
7950	<i>Hygrocybe aurantiomagnifica</i> : a new species of section <i>Firmae</i> (Hygrophoraceae, Basidiomycota) from Brazil. <i>Kew Bulletin</i> , 2019, 74, 1.	0.4	1
7951	Mitochondrial genome characterization of the family Trigonidiidae (Orthoptera) reveals novel structural features and nad1 transcript ends. <i>Scientific Reports</i> , 2019, 9, 19092.	1.6	5
7952	Metatranscriptomic reconstruction reveals RNA viruses with the potential to shape carbon cycling in soil. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 25900-25908.	3.3	165
7953	Comparative Mitogenomic Analysis of the <i>Eurydema</i> Genus in the Context of Representative Pentatomidae (Hemiptera: Heteroptera) Taxa. <i>Journal of Insect Science</i> , 2019, 19, .	0.6	11
7954	Phylogeography and taxonomic revision of Nelson's pocket mouse (<i>Chaetodipus nelsoni</i>). <i>Journal of Mammalogy</i> , 2019, 100, 1847-1864.	0.6	3
7955	Changes in Microbiota Across Developmental Stages of <i>Aedes koreicus</i> , an Invasive Mosquito Vector in Europe: Indications for Microbiota-Based Control Strategies. <i>Frontiers in Microbiology</i> , 2019, 10, 2832.	1.5	38
7956	Limited DNA repair gene repertoire in Ascomycete yeast revealed by comparative genomics. <i>Genome Biology and Evolution</i> , 2019, 11, 3409-3423.	1.1	15
7957	Evolution and rapid spread of a reassortant A(H3N2) virus that predominated the 2017-2018 influenza season. <i>Virus Evolution</i> , 2019, 5, vez046.	2.2	19
7958	The C-Fern (<i>Ceratopteris richardii</i>) genome: insights into plant genome evolution with the first partial homosporous fern genome assembly. <i>Scientific Reports</i> , 2019, 9, 18181.	1.6	79
7959	Comparative morpho-anatomy and mitochondrial phylogeny of Semisulcospiridae in Yunnan, south-western China, with description of four new species (Gastropoda: Cerithioidea). <i>Invertebrate Systematics</i> , 2019, 33, 825-848.	0.5	6
7960	Receding ice drove parallel expansions in Southern Ocean penguins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 26690-26696.	3.3	35
7961	Phylogenetic and morphological infrageneric classification of the genus <i>Dendroceros</i> (Dendrocerotaceae; Anthocerotophyta), with the addition of two new subgenera. <i>Systematics and Biodiversity</i> , 2019, 17, 712-727.	0.5	4
7962	PhySpeTree: an automated pipeline for reconstructing phylogenetic species trees. <i>BMC Evolutionary Biology</i> , 2019, 19, 219.	3.2	3

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7963	Glacial Runoff Promotes Deep Burial of Sulfur Cycling-Associated Microorganisms in Marine Sediments. <i>Frontiers in Microbiology</i> , 2019, 10, 2558.	1.5	16
7964	Interspecific hybridization facilitates niche adaptation in beer yeast. <i>Nature Ecology and Evolution</i> , 2019, 3, 1562-1575.	3.4	83
7965	Fermentation innovation through complex hybridization of wild and domesticated yeasts. <i>Nature Ecology and Evolution</i> , 2019, 3, 1576-1586.	3.4	76
7966	Massive gene amplification on a recently formed <i>Drosophila</i> Y chromosome. <i>Nature Ecology and Evolution</i> , 2019, 3, 1587-1597.	3.4	55
7967	Stunted microbiota and opportunistic pathogen colonization in caesarean-section birth. <i>Nature</i> , 2019, 574, 117-121.	13.7	617
7968	One thousand plant transcriptomes and the phylogenomics of green plants. <i>Nature</i> , 2019, 574, 679-685.	13.7	1,162
7969	Higher-order epistasis shapes the fitness landscape of a xenobiotic-degrading enzyme. <i>Nature Chemical Biology</i> , 2019, 15, 1120-1128.	3.9	71
7970	Taxonomic notes on the <i>Ectoedemia suberis</i> and <i>angulifasciella</i> species groups in Japan (Lepidoptera: Nepticulidae). <i>Zootaxa</i> , 2019, 4706, 201-230.	0.2	0
7971	Morphological and phylogenetic analyses reveal a new species of <i>Fistulina</i> (Fistulinaceae, Agaricales) from Australia. <i>Phytotaxa</i> , 2019, 420, 233-240.	0.1	3
7972	<i>Ganoderma weixiensis</i> (Polyporaceae, Basidiomycota), a new member of the <i>G. lucidum</i> complex from Yunnan Province, China. <i>Phytotaxa</i> , 2019, 423, 75-86.	0.1	7
7973	<i>Bredia malipoensis</i> (Melastomataceae), a new species from Yunnan, China. <i>Phytotaxa</i> , 2019, 425, 127-136.	0.1	3
7974	Rock star flowers: <i>Conchocarpus hendrixii</i> (Galipeinae, Tj ETQq1 1 0.784314 rgBT /Ove genus. <i>Phytotaxa</i> , 2019, 422, 75-92.	0.1	6
7975	Stratified reconstruction of ancestral <i>Escherichia coli</i> diversification. <i>BMC Genomics</i> , 2019, 20, 936.	1.2	23
7976	Programmed Cell Death in <i>Neurospora crassa</i> Is Controlled by the Allorecognition Determinant <i>rcd-1</i> . <i>Genetics</i> , 2019, 213, 1387-1400.	1.2	32
7977	Phylogenetic Relationships Within and Delimitation of the Cosmopolitan Flowering Plant Genus <i>Stellaria</i> L. (Caryophyllaceae): Core Stars and Fallen Stars. <i>Systematic Botany</i> , 2019, 44, 857-876.	0.2	15
7978	Marine Bacteria from Rocas Atoll as a Rich Source of Pharmacologically Active Compounds. <i>Marine Drugs</i> , 2019, 17, 671.	2.2	10
7979	Volvate <i>Macrolepiota</i> from Brazil: <i>M. dunensis</i> sp. nov., <i>M. sabulosa</i> var. <i>velistellaris</i> var. nov., and observations on <i>M. pulchella</i> . <i>Mycotaxon</i> , 2019, 134, 223-239.	0.1	0
7980	Phylogeny of the Neotropical tribe Jacarandae (Bignoniaceae). <i>American Journal of Botany</i> , 2019, 106, 1589-1601.	0.8	8

#	ARTICLE	IF	CITATIONS
7981	The CENP-B box, a nucleotide motif involved in centromere formation, has multiple origins in New World monkeys. <i>Genes and Genetic Systems</i> , 2019, 94, 301-306.	0.2	7
7982	Morphology and Multi-Gene Phylogeny Reveal <i>Pestalotiopsis pinicola</i> sp. nov. and a New Host Record of <i>Cladosporium anthropophilum</i> from Edible Pine (<i>Pinus armandii</i>) Seeds in Yunnan Province, China. <i>Pathogens</i> , 2019, 8, 285.	1.2	14
7983	Phagocytosis-like cell engulfment by a planctomycete bacterium. <i>Nature Communications</i> , 2019, 10, 5529.	5.8	62
7984	Transcriptomic Evidence of Adaptive Evolution of the Epiphytic Fern <i>Asplenium nidus</i> . <i>International Journal of Genomics</i> , 2019, 2019, 1-9.	0.8	15
7985	Emergence of NDM-1- and CTX-M-3-Producing <i>Raoultella ornithinolytica</i> in Human Gut Microbiota. <i>Frontiers in Microbiology</i> , 2019, 10, 2678.	1.5	11
7987	Phylogeny of spiny frogs <i>Nanorana</i> (Anura: Dicroglossidae) supports a Tibetan origin of a Himalayan species group. <i>Ecology and Evolution</i> , 2019, 9, 14498-14511.	0.8	15
7988	Charting the Complexity of the Marine Microbiome through Single-Cell Genomics. <i>Cell</i> , 2019, 179, 1623-1635.e11.	13.5	158
7989	Sensory coding mechanisms revealed by optical tagging of physiologically defined neuronal types. <i>Science</i> , 2019, 366, 1384-1389.	6.0	21
7990	Genomic insights into mite phylogeny, fitness, development, and reproduction. <i>BMC Genomics</i> , 2019, 20, 954.	1.2	25
7991	Biofilm Formation of <i>Listeria monocytogenes</i> Strains Under Food Processing Environments and Pan-Genome-Wide Association Study. <i>Frontiers in Microbiology</i> , 2019, 10, 2698.	1.5	83
7992	Intraspecific Variation within the <i>Utricularia amethystina</i> Species Morphotypes Based on Chloroplast Genomes. <i>International Journal of Molecular Sciences</i> , 2019, 20, 6130.	1.8	23
7993	Clonal expansion of a virulent <i>Streptococcus suis</i> serotype 9 lineage distinguishable from carriage subpopulations. <i>Scientific Reports</i> , 2019, 9, 15429.	1.6	11
7994	Novel redox-active enzymes for ligninolytic applications revealed from multiomics analyses of <i>Peniophora</i> sp. CBMAI 1063, a laccase hyper-producer strain. <i>Scientific Reports</i> , 2019, 9, 17564.	1.6	24
7995	Multiple evolutionary origins of high mountain bellflowers with solitary flowers and calyx scales render a core Caucasian clade of the Scapiflorae group (Campanulaceae). <i>Systematics and Biodiversity</i> , 2019, 17, 690-711.	0.5	4
7996	Isolation and Characterization of Akhmeta Virus from Wild-Caught Rodents (<i>Apodemus</i> spp.) in Georgia. <i>Journal of Virology</i> , 2019, 93, .	1.5	9
7997	Evolution and Global Transmission of a Multidrug-Resistant, Community-Associated Methicillin-Resistant <i>Staphylococcus aureus</i> Lineage from the Indian Subcontinent. <i>MBio</i> , 2019, 10, .	1.8	50
7998	New Insights on <i>Lilium</i> Phylogeny Based on a Comparative Phylogenomic Study Using Complete Plastome Sequences. <i>Plants</i> , 2019, 8, 547.	1.6	13
7999	Zooxanthellate, Sclerite-Free, and Pseudopinnuled Octocoral <i>Hadaka nudidomus</i> gen. nov. et sp. nov. (Anthozoa, Octocorallia) from Mesophotic Reefs of the Southern Ryukyus Islands. <i>Diversity</i> , 2019, 11, 176.	0.7	2

#	ARTICLE	IF	CITATIONS
8000	A revision of the African genus <i>Mesanthemum</i> (Eriocaulaceae). <i>Kew Bulletin</i> , 2019, 74, 1.	0.4	4
8001	Tempo and mode of allopatric divergence in the weakly electric fish <i>Sternopygus dariensis</i> in the Isthmus of Panama. <i>Scientific Reports</i> , 2019, 9, 18828.	1.6	15
8002	A new species of <i>Ischnocnema</i> Reinhardt and Ltken, 1862 (Anura): Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 66 <i>Zootaxa</i> , 2019, 4706, 531-545.	0.2	2
8003	The sprightly little sphaerodactyl: Systematics and biogeography of
the Puerto Rican dwarf geckos <i>Sphaerodactylus</i> (Gekkota, Sphaerodactylidae). <i>Zootaxa</i> , 2019, 4712, zootaxa.4712.2.1.	0.2	10
8004	Regulatory context drives conservation of glycine riboswitch aptamers. <i>PLoS Computational Biology</i> , 2019, 15, e1007564.	1.5	6
8005	<i>Hemiboea guangdongensis</i> comb. & stat. nov., a cryptic species segregated from <i>H. subcapitata</i> (Gesneriaceae) based on morphological and molecular data. <i>Nordic Journal of Botany</i> , 2019, 37, .	0.2	3
8006	Persistence of Nasopharyngeal Pneumococcal Vaccine Serotypes and Increase of Nonvaccine Serotypes Among Vaccinated Infants and Their Mothers 5 Years After Introduction of Pneumococcal Conjugate Vaccine 13 in The Gambia. <i>Clinical Infectious Diseases</i> , 2019, 68, 1512-1521.	2.9	41
8007	Impacts of Inference Method and Data set Filtering on Phylogenomic Resolution in a Rapid Radiation of Ground Squirrels (Xerinae: Marmotini). <i>Systematic Biology</i> , 2019, 68, 298-316.	2.7	33
8008	Evidence from Australian mesic zone dung beetles supports their Gondwanan origin and Mesozoic diversification of the Scarabaeinae. <i>Insect Systematics and Evolution</i> , 2019, 50, 162-188.	0.2	12
8009	Detection and genotyping of enteric viruses in hospitalized children with acute gastroenteritis in Belm, Brazil: Occurrence of adenovirus viremia by species F, types 40/41. <i>Journal of Medical Virology</i> , 2019, 91, 378-384.	2.5	25
8010	Dynamic genomic architecture of mutualistic cooperation in a wild population of <i>Mesorhizobium</i> . <i>ISME Journal</i> , 2019, 13, 301-315.	4.4	34
8011	Characterization of a New HIV-1 CRF01_AE/B Recombinant Virus Form Among Men Who Have Sex with Men in Shanghai, China. <i>AIDS Research and Human Retroviruses</i> , 2019, 35, 414-418.	0.5	6
8012	Comparative analysis of five <i>Mucor</i> species transcriptomes. <i>Genomics</i> , 2019, 111, 1306-1314.	1.3	14
8013	Reassessment of the classification of Bryopsidales (Chlorophyta) based on chloroplast phylogenomic analyses. <i>Molecular Phylogenetics and Evolution</i> , 2019, 130, 397-405.	1.2	27
8014	Identification of a New Haplotype of <i>Candidatus Liberibacter solanacearum</i> ™ in <i>Solanum tuberosum</i> . <i>Plant Disease</i> , 2019, 103, 468-474.	0.7	54
8015	Exploring the generic delimitation of <i>Phyllagathis</i> and <i>Bredia</i> (Melastomataceae): A combined nuclear and chloroplast DNA analysis. <i>Journal of Systematics and Evolution</i> , 2019, 57, 256-267.	1.6	35
8016	Detection of <i>Pythium porphyrae</i> infecting Philippine <i>Pyropia acanthophora</i> based on morphology and nuclear rRNA internal transcribed spacer sequences. <i>Journal of General Plant Pathology</i> , 2019, 85, 72-78.	0.6	5
8017	A new pelagic predatory pike cichlid (Teleostei: Cichlidae: Crenicichla) from the <i>C. mandelburgeri</i> species complex with parallel and reticulate evolution. <i>Hydrobiologia</i> , 2019, 832, 377-395.	1.0	10

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8018	Molecular markers for phylogenetic applications derived from comparative plastome analysis of <i>Prunus</i> species. <i>Journal of Systematics and Evolution</i> , 2019, 57, 15-22.	1.6	7
8019	A new symbiotic nanoarchaeote (<i>Candidatus Nanoclepta minutus</i>) and its host (<i>Zestosphaera</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 2019, 42, 94-106.	1.2	76
8020	Is molecular evolution faster in the tropics?. <i>Heredity</i> , 2019, 122, 513-524.	1.2	25
8021	Estimating divergence times and ancestral breeding systems in <i>Ficus</i> and Moraceae. <i>Annals of Botany</i> , 2019, 123, 191-204.	1.4	30
8022	<i>Candidatus Prosilicoccus vernus</i> , a spring phytoplankton bloom associated member of the Flavobacteriaceae. <i>Systematic and Applied Microbiology</i> , 2019, 42, 41-53.	1.2	39
8023	Draft genome of the cotton aphid <i>Aphis gossypii</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2019, 105, 25-32.	1.2	55
8024	The complete mitochondrial genome of <i>Bactrocera biguttula</i> (Bezzi) (Diptera: Tephritidae) and phylogenetic relationships with other Dacini. <i>International Journal of Biological Macromolecules</i> , 2019, 126, 130-140.	3.6	13
8025	High cryptic diversity of bitterling fish in the southern West Palearctic. <i>Molecular Phylogenetics and Evolution</i> , 2019, 133, 1-11.	1.2	18
8026	Population genetic structure and species delimitation of a widespread, Neotropical dwarf gecko. <i>Molecular Phylogenetics and Evolution</i> , 2019, 133, 54-66.	1.2	29
8027	Time-course analysis of nuclear events during conjugation in the marine ciliate <i>Euplotes vannus</i> and comparison with other ciliates (Protozoa, Ciliophora). <i>Cell Cycle</i> , 2019, 18, 288-298.	1.3	31
8028	Historical demography of four gecko species specializing in boulder cave habitat: Implications in the evolutionary dead end hypothesis and conservation. <i>Molecular Ecology</i> , 2019, 28, 772-784.	2.0	8
8029	<i>OsACL2</i> negatively regulates cell death and disease resistance in rice. <i>Plant Biotechnology Journal</i> , 2019, 17, 1344-1356.	4.1	46
8030	Genome-Wide Identification and Comparative Analysis for OPT Family Genes in <i>Panax ginseng</i> and Eleven Flowering Plants. <i>Molecules</i> , 2019, 24, 15.	1.7	20
8031	<i>Sporocadaceae</i> , a family of coelomycetous fungi with appendage-bearing conidia. <i>Studies in Mycology</i> , 2019, 92, 287-415.	4.5	94
8032	Contrasting patterns of diversification between Amazonian and Atlantic forest clades of Neotropical lianas (<i>Amphilophium</i> , Bignoniaceae) inferred from plastid genomic data. <i>Molecular Phylogenetics and Evolution</i> , 2019, 133, 92-106.	1.2	43
8033	One Hundred Mitochondrial Genomes of Cicadas. <i>Journal of Heredity</i> , 2019, 110, 247-256.	1.0	27
8034	MobiSeq: De novo SNP discovery in model and non-model species through sequencing the flanking region of transposable elements. <i>Molecular Ecology Resources</i> , 2019, 19, 512-525.	2.2	4
8035	Molecular phylogeny and hemipenial diversity of South American species of <i>Amerotyphlops</i> (Typhlopidae, Scolecophidia). <i>Zoologica Scripta</i> , 2019, 48, 139-156.	0.7	13

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8036	Iridoid glucosides in the genus <i>Sutera</i> (Scrophulariaceae) as chemotaxonomic markers in tribe Limoselleae. <i>Phytochemistry</i> , 2019, 158, 149-155.	1.4	3
8037	Multiple evolutionary routes of the single polar capsule in <i>Thelohanellus</i> species (Myxozoa); Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.6	15
8038	Molecular phylogeny and evolution of world Tachinidae (Diptera). <i>Molecular Phylogenetics and Evolution</i> , 2019, 139, 106358.	1.2	60
8039	Phylogenetic relationships and divergence dating in the Glass Lizards (Anguinae). <i>Molecular Phylogenetics and Evolution</i> , 2019, 133, 128-140.	1.2	12
8040	Fish diversification at the pace of geomorphological changes: evolutionary history of western Iberian Leuciscinae (Teleostei: Leuciscidae) inferred from multilocus sequence data. <i>Molecular Phylogenetics and Evolution</i> , 2019, 133, 263-285.	1.2	19
8041	Molecular epidemiology of hepatitis B virus mutants associated with vaccine escape, drug resistance and diagnosis failure. <i>Journal of Viral Hepatitis</i> , 2019, 26, 552-560.	1.0	23
8042	A reciprocal translocation radically reshapes sex-linked inheritance in the common frog. <i>Molecular Ecology</i> , 2019, 28, 1877-1889.	2.0	30
8043	Low genetic divergence but many names in the endemic Patagonian frogs of the genus <i>Atelognathus</i> (Anura, Batrachylidae): A molecular genetic and morphological perspective. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2019, 57, 383-399.	0.6	6
8044	Evolution of green lacewings (Neuroptera: Chrysopidae): a molecular supermatrix approach. <i>Systematic Entomology</i> , 2019, 44, 499-513.	1.7	11
8045	A new surface gliding species of Chironomidae: An independent invasion of marine environments and its evolutionary implications. <i>Zoologica Scripta</i> , 2019, 48, 81-92.	0.7	9
8046	Co-carrying of KPC-2, NDM-5, CTX-M-3 and CTX-M-65 in three plasmids with serotype O89: H10 <i>Escherichia coli</i> strain belonging to the ST2 clone in China. <i>Microbial Pathogenesis</i> , 2019, 128, 1-6.	1.3	14
8047	A member of the CONSTANS-Like protein family is a putative regulator of reactive oxygen species homeostasis and spaceflight physiological adaptation. <i>AoB PLANTS</i> , 2019, 11, ply075.	1.2	8
8048	Computational Design of Stable and Soluble Biocatalysts. <i>ACS Catalysis</i> , 2019, 9, 1033-1054.	5.5	87
8049	Two new species of <i>Landouria</i> Godwin-Austen, 1918 from Timor-Leste (Stylommatophora); Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.2	4
8050	Regeneration of the acorn worm pygochord with the implication for its convergent evolution with the notochord. <i>Development Growth and Differentiation</i> , 2019, 61, 158-165.	0.6	4
8051	Mitochondrial genome of the entomophthoroid fungus <i>Conidiobolus heterosporus</i> provides insights into evolution of basal fungi. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 1379-1391.	1.7	31
8052	The mating system of the Eucalyptus canker pathogen <i>Chrysosporthe austroafricana</i> and closely related species. <i>Fungal Genetics and Biology</i> , 2019, 123, 41-52.	0.9	13
8053	Repeated evolutionary transitions of flavobacteria from marine to non-marine habitats. <i>Environmental Microbiology</i> , 2019, 21, 648-666.	1.8	43

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8054	Exploring gene tree incongruence at the origin of ants and bees (Hymenoptera). <i>Zoologica Scripta</i> , 2019, 48, 215-225.	0.7	3
8055	Sustainable use of mangroves as sources of valuable medicinal compounds: Species identification, propagation and secondary metabolite composition. <i>South African Journal of Botany</i> , 2019, 121, 317-328.	1.2	19
8056	Complex patterns of hybridization and introgression across evolutionary timescales in Mexican whiptail lizards (<i>Aspidoscelis</i>). <i>Molecular Phylogenetics and Evolution</i> , 2019, 132, 284-295.	1.2	25
8057	Molecular analysis of <i>Ulva compressa</i> (Chlorophyta, Ulvales) reveals its morphological plasticity, distribution and potential invasiveness on German North Sea and Baltic Sea coasts. <i>European Journal of Phycology</i> , 2019, 54, 102-114.	0.9	34
8058	Molecular systematics of the <i>Triplophysa robusta</i> (Cobitoidea) complex: Extensive gene flow in a depauperate lineage. <i>Molecular Phylogenetics and Evolution</i> , 2019, 132, 275-283.	1.2	14
8059	New patellogastropod mitogenomes help counteracting long-branch attraction in the deep phylogeny of gastropod mollusks. <i>Molecular Phylogenetics and Evolution</i> , 2019, 133, 12-23.	1.2	50
8060	Genomic sequence capture of haemosporidian parasites: Methods and prospects for enhanced study of host-parasite evolution. <i>Molecular Ecology Resources</i> , 2019, 19, 400-410.	2.2	16
8061	<i>Pleurotus opuntiae</i> revisited – An insight to the phylogeny of dimitic <i>Pleurotus</i> species with emphasis on the P. <i>Adjamor</i> complex. <i>Fungal Biology</i> , 2019, 123, 188-199.	1.1	11
8062	ABCF ATPases Involved in Protein Synthesis, Ribosome Assembly and Antibiotic Resistance: Structural and Functional Diversification across the Tree of Life. <i>Journal of Molecular Biology</i> , 2019, 431, 3568-3590.	2.0	90
8063	Widespread positive selection on cetacean TLR extracellular domain. <i>Molecular Immunology</i> , 2019, 106, 135-142.	1.0	31
8064	Phylogeny, historical biogeography and diversification rates in an economically important group of Neotropical palms: Tribe Euterpeae. <i>Molecular Phylogenetics and Evolution</i> , 2019, 133, 67-81.	1.2	14
8065	Genomic insights into the 2016-2017 cholera epidemic in Yemen. <i>Nature</i> , 2019, 565, 230-233.	13.7	129
8066	Novel genetic code and record-setting AT-richness in the highly reduced plastid genome of the holoparasitic plant <i>Balanophora</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 934-943.	3.3	66
8067	Interspecies Transmission, Genetic Diversity, and Evolutionary Dynamics of Pseudorabies Virus. <i>Journal of Infectious Diseases</i> , 2019, 219, 1705-1715.	1.9	101
8068	Phylogenetic Methods Inconsistently Predict the Direction of HIV Transmission Among Heterosexual Pairs in the HPTN 052 Cohort. <i>Journal of Infectious Diseases</i> , 2019, 220, 1406-1413.	1.9	18
8069	The Expansion of Inosine at the Wobble Position of tRNAs, and Its Role in the Evolution of Proteomes. <i>Molecular Biology and Evolution</i> , 2019, 36, 650-662.	3.5	34
8070	Genetic complexity in the replication-competent latent HIV reservoir increases with untreated infection duration in infected youth. <i>Aids</i> , 2019, 33, 211-218.	1.0	18
8071	Chromosomal level reference genome of <i>Tachypleus tridentatus</i> provides insights into evolution and adaptation of horseshoe crabs. <i>Molecular Ecology Resources</i> , 2019, 19, 744-756.	2.2	25

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8072	Divergent host use among cryptic species in the fungivorous ciid beetle <i>Octotemnus laminifrons</i> (Motschulsky, 1860), with descriptions of three new species from Japan. <i>Systematic Entomology</i> , 2019, 44, 179-191.	1.7	6
8073	Has past climate change affected cold-specialized species differentially through space and time?. <i>Systematic Entomology</i> , 2019, 44, 571-587.	1.7	4
8074	Metagenomic sequencing at the epicenter of the Nigeria 2018 Lassa fever outbreak. <i>Science</i> , 2019, 363, 74-77.	6.0	201
8075	Proposal of a new subfamily of Sciaridae (Diptera: Sciaridae), with description of one new species from South Korea. <i>Zootaxa</i> , 2019, 4543, 127-136.	0.2	5
8076	Convergent Evolution of the Army Ant Syndrome and Congruence in Big-Data Phylogenetics. <i>Systematic Biology</i> , 2019, 68, 642-656.	2.7	47
8077	Y Chromosome Sequences Reveal a Short Beringian Standstill, Rapid Expansion, and early Population structure of Native American Founders. <i>Current Biology</i> , 2019, 29, 149-157.e3.	1.8	94
8078	Insights from genome-wide approaches to identify variants associated to phenotypes at pan-genome scale: Application to <i>L. monocytogenes</i> ' ability to grow in cold conditions. <i>International Journal of Food Microbiology</i> , 2019, 291, 181-188.	2.1	38
8079	Deep mitochondrial lineage divergence among populations of the southern stingray (<i>Hypanus</i>) in the Caribbean. <i>Marine Biodiversity</i> , 2019, 49, 1627-1634.	0.3	6
8080	The complete chloroplast genome of <i>Chusquea culeou</i> (Poaceae: Bambusoideae: Bambuseae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 91-92.	0.2	3
8081	Inferring the biogeography and demographic history of an endangered butterfly in Europe from multilocus markers. <i>Biological Journal of the Linnean Society</i> , 2019, 126, 95-113.	0.7	10
8082	Competition among Nasal Bacteria Suggests a Role for Siderophore-Mediated Interactions in Shaping the Human Nasal Microbiota. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	57
8083	Comparative genomics of the major parasitic worms. <i>Nature Genetics</i> , 2019, 51, 163-174.	9.4	377
8084	Phylogenetic placement of the Peruvian-endemic genus <i>Machaerophorus</i> (Brassicaceae) based on molecular data and implication for its systematics. <i>Plant Systematics and Evolution</i> , 2019, 305, 77-87.	0.3	3
8085	Morphology, geographic distribution, and host preferences are poor predictors of phylogenetic relatedness in the mistletoe genus <i>Viscum</i> L.. <i>Molecular Phylogenetics and Evolution</i> , 2019, 131, 106-115.	1.2	20
8086	Phylogeny, Distribution, and Pathogenicity of <i>Lasiodiplodia</i> Species Associated With Cankers and Dieback Symptoms of Persian Lime in Mexico. <i>Plant Disease</i> , 2019, 103, 1156-1165.	0.7	23
8087	The population genomics of multiple tsetse fly (<i>Glossina fuscipes fuscipes</i>) admixture zones in Uganda. <i>Molecular Ecology</i> , 2019, 28, 66-85.	2.0	11
8088	Owlflyies are derived antlions: anchored phylogenomics supports a new phylogeny and classification of Myrmeleontidae (Neuroptera). <i>Systematic Entomology</i> , 2019, 44, 418-450.	1.7	59
8089	The introduced terrestrial slugs <i>Ambigolimax nyctelius</i> (Bourguignat, 1861) and <i>Ambigolimax valentianus</i> (Férussac, 1821) (Gastropoda: Limacidae) in California, with a discussion of taxonomy, systematics, and discovery by citizen science. <i>Journal of Natural History</i> , 2019, 53, 1607-1632.	0.2	15

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8090	The complete chloroplast genome of the lipstick tree, <i>Bixa Orellana</i> (Bixaceae). Mitochondrial DNA Part B: Resources, 2019, 4, 17-18.	0.2	2
8091	The Origin and Population History of the Endangered Golden Snub-Nosed Monkey (<i>Rhinopithecus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 20	3.5	20
8092	Pelagiphages in the <i>Podoviridae</i> family integrate into host genomes. Environmental Microbiology, 2019, 21, 1989-2001.	1.8	50
8093	Cryptic diversity in the Mexican highlands: Thousands of UCE loci help illuminate phylogenetic relationships, species limits and divergence times of montane rattlesnakes (<i>Viperidae</i> : <i>Crotalus</i>). Molecular Ecology Resources, 2019, 19, 349-365.	2.2	37
8094	A Malvaceae mystery: A mallow maelstrom of genome multiplications and maybe misleading methods?. Journal of Integrative Plant Biology, 2019, 61, 12-31.	4.1	25
8095	Identification and antifungal sensitivity of two new species of <i>Diaporthe</i> isolated. Journal of Infection and Chemotherapy, 2019, 25, 96-103.	0.8	11
8096	Heterologous expression and biochemical characterization of a novel cold-active α -amylase from the Antarctic bacteria <i>Pseudoalteromonas</i> sp. 2-3. Protein Expression and Purification, 2019, 155, 78-85.	0.6	22
8097	Pleistocene glaciation explains the disjunct distribution of the Chestnut-evented Nuthatch (<i>Aves</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 12	0.7	12
8098	The first two mitochondrial genomes of wood wasps (Hymenoptera: Symphyta): Novel gene rearrangements and higher-level phylogeny of the basal hymenopterans. International Journal of Biological Macromolecules, 2019, 123, 1189-1196.	3.6	17
8099	Four hundred shades of brown: Higher level phylogeny of the problematic <i>Euptychiina</i> (Lepidoptera.) Tj ETQq1 1 0.784314 rgBT /Overlock 36	1.2	36
8100	Resurrection of the East Asian genus <i>Eremotropa</i> (Monotropoideae, Ericaceae), based on molecular and morphological data. Journal of Systematics and Evolution, 2019, 57, 75-80.	1.6	1
8101	Nuclear protein phylogenies support the monophyly of the three bryophyte groups (Bryophyta) Tj ETQq1 1 0.784314 rgBT /Overlock 84	3.5	84
8102	Protist Diversity and Seasonal Dynamics in Skagerrak Plankton Communities as Revealed by Metabarcoding and Microscopy. Journal of Eukaryotic Microbiology, 2019, 66, 494-513.	0.8	60
8103	Complete nitrification: insights into the ecophysiology of comammox <i>Nitrospira</i> . Applied Microbiology and Biotechnology, 2019, 103, 177-189.	1.7	224
8104	Phylogenomic Signatures of Ancient Introgression in a Rogue Lineage of Darters (Teleostei: Percidae). Systematic Biology, 2019, 68, 329-346.	2.7	42
8105	Translineage polymorphism and nonbifurcating diversification of the genus <i>Picea</i> . New Phytologist, 2019, 222, 576-587.	3.5	29
8106	Mitogenomics of Central American weakly-electric fishes. Gene, 2019, 686, 164-170.	1.0	4
8107	Increased evolutionary rates and conserved transcriptional response following allopolyploidization in brown algae. Evolution; International Journal of Organic Evolution, 2019, 73, 59-72.	1.1	11

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8108	The use of next generation sequencing for improving food safety: Translation into practice. <i>Food Microbiology</i> , 2019, 79, 96-115.	2.1	225
8109	DNA barcoding the ichthyofauna of the Yangtze River: Insights from the molecular inventory of a mega-diverse temperate fauna. <i>Molecular Ecology Resources</i> , 2019, 19, 1278-1291.	2.2	34
8110	Genome-wide analysis reveals the evolution and structural features of WRINKLED1 in plants. <i>Molecular Genetics and Genomics</i> , 2019, 294, 329-341.	1.0	16
8111	Implications of introgression for wildlife translocations: the case of North American martens. <i>Conservation Genetics</i> , 2019, 20, 153-166.	0.8	16
8112	The genome of the medicinal plant <i>Andrographis paniculata</i> provides insight into the biosynthesis of the bioactive diterpenoid neoandrographolide. <i>Plant Journal</i> , 2019, 97, 841-857.	2.8	75
8113	Phylogeny of Mesoamerican freshwater mussels and a revised tribe-level classification of the Amblyminae. <i>Zoologica Scripta</i> , 2019, 48, 106-117.	0.7	15
8114	Genome sequencing of oomycete isolates from Chile supports the New Zealand origin of <i>Phytophthora kernoviae</i> and makes available the first <i>Nothophytophthora</i> sp. genome. <i>Molecular Plant Pathology</i> , 2019, 20, 423-431.	2.0	16
8115	The complete mitochondrial genome of <i>Parasesarma pictum</i> (Brachyura: Grapsoidea: Sesarmidae) and comparison with other Brachyuran crabs. <i>Genomics</i> , 2019, 111, 799-807.	1.3	24
8116	The complex study of complexes: The first well-supported phylogeny of two species complexes within genus <i>Caridina</i> (Decapoda: Caridea: Atyidae) sheds light on evolution, biogeography, and habitat. <i>Molecular Phylogenetics and Evolution</i> , 2019, 131, 164-180.	1.2	12
8117	Advancing mite phylogenomics: Designing ultraconserved elements for Acari phylogeny. <i>Molecular Ecology Resources</i> , 2019, 19, 465-475.	2.2	30
8118	Beyond buzz-pollination – departures from an adaptive plateau lead to new pollination syndromes. <i>New Phytologist</i> , 2019, 221, 1136-1149.	3.5	61
8119	An analysis of characterized plant sesquiterpene synthases. <i>Phytochemistry</i> , 2019, 158, 157-165.	1.4	67
8120	Rare and phylogenetically distinct plant species exhibit less diverse root-associated pathogen communities. <i>Journal of Ecology</i> , 2019, 107, 1226-1237.	1.9	11
8121	Noteworthy record of the Ethiopian genet, <i>Genetta abyssinica</i> , (Carnivora, Viverridae) from Djibouti informs its phylogenetic position within <i>Genetta</i> . <i>Mammalia</i> , 2019, 83, 180-189.	0.3	6
8122	Deep genomic analysis of <i>Coelastrella saipanensis</i> (Scenedesmaceae, Chlorophyta): comparative chloroplast genomics of Scenedesmaceae. <i>European Journal of Phycology</i> , 2019, 54, 52-65.	0.9	12
8123	CoevDB: a database of intramolecular coevolution among protein-coding genes of the bony vertebrates. <i>Nucleic Acids Research</i> , 2019, 47, D50-D54.	6.5	1
8124	Phylogeny of the beetle supertribe Trechitae (Coleoptera: Carabidae): Unexpected clades, isolated lineages, and morphological convergence. <i>Molecular Phylogenetics and Evolution</i> , 2019, 132, 151-176.	1.2	33
8125	Complete genome sequence of <i>Pelolinea submarina</i> MO-CFX1T within the phylum Chloroflexi, isolated from subseafloor sediment. <i>Marine Genomics</i> , 2019, 46, 49-53.	0.4	5

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8126	Changes in long chain alkenone distributions and Isochrysidales groups along the Baltic Sea salinity gradient. <i>Organic Geochemistry</i> , 2019, 127, 92-103.	0.9	31
8127	On a new species of titi monkey (Primates: <i>Plecturocebus</i> Byrne et al., 2016), from Alta Floresta, southern Amazon, Brazil. <i>Molecular Phylogenetics and Evolution</i> , 2019, 132, 117-137.	1.2	32
8128	Evolution and extinction of the giant rhinoceros <i>Elasmotherium sibiricum</i> sheds light on late Quaternary megafaunal extinctions. <i>Nature Ecology and Evolution</i> , 2019, 3, 31-38.	3.4	50
8129	Reef fish functional traits evolve fastest at trophic extremes. <i>Nature Ecology and Evolution</i> , 2019, 3, 191-199.	3.4	23
8130	Genome sequence of the opportunistic human pathogen <i>Magnusiomyces capitatus</i> . <i>Current Genetics</i> , 2019, 65, 539-560.	0.8	14
8131	Bronchoscope-associated clusters of multidrug-resistant <i>Pseudomonas aeruginosa</i> and carbapenem-resistant <i>Klebsiella pneumoniae</i> . <i>Infection Control and Hospital Epidemiology</i> , 2019, 40, 40-46.	1.0	36
8132	The Changing Epidemiological Profile of HIV-1 Subtype B Epidemic in Ukraine. <i>AIDS Research and Human Retroviruses</i> , 2019, 35, 155-163.	0.5	7
8133	Specimen-based analysis of morphology and the environment in ecologically dominant grasses: the power of the herbarium. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20170403.	1.8	25
8134	Genomic and transcriptomic insights into the survival of the subaerial cyanobacterium <i>Nostoc flagelliforme</i> in arid and exposed habitats. <i>Environmental Microbiology</i> , 2019, 21, 845-863.	1.8	32
8135	Mechanisms of cnidocyte development in the moon jellyfish <i>Aurelia</i> . <i>Evolution & Development</i> , 2019, 21, 72-81.	1.1	10
8136	Patterns of cross-resistance and collateral sensitivity between clinical antibiotics and natural antimicrobials. <i>Evolutionary Applications</i> , 2019, 12, 878-887.	1.5	20
8137	Accelerated pseudogenization of trace amine-associated receptor genes in primates. <i>Genes, Brain and Behavior</i> , 2019, 18, e12543.	1.1	9
8138	Collections from the mesophytic zone off Bermuda reveal three species of Kallymeniaceae (Gigartinales, Rhodophyta) in genera with transoceanic distributions. <i>Journal of Phycology</i> , 2019, 55, 415-424.	1.0	9
8139	Disentangling structural genomic and behavioural barriers in a sea of connectivity. <i>Molecular Ecology</i> , 2019, 28, 1394-1411.	2.0	68
8140	Comparative genomics of <i>Rhizophagus irregularis</i> , <i>R. Æcerebriforme</i> , <i>R. Ædiaphanus</i> and <i>Gigaspora rosea</i> highlights specific genetic features in Glomeromycotina. <i>New Phytologist</i> , 2019, 222, 1584-1598.	3.5	133
8141	Metagenomic profiling of ticks: Identification of novel rickettsial genomes and detection of tick-borne canine parvovirus. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0006805.	1.3	27
8142	A Phylogenetic Study of the ANT Family Points to a preANT Gene as the Ancestor of Basal and euANT Transcription Factors in Land Plants. <i>Frontiers in Plant Science</i> , 2019, 10, 17.	1.7	21
8143	Extensive Unexplored Human Microbiome Diversity Revealed by Over 150,000 Genomes from Metagenomes Spanning Age, Geography, and Lifestyle. <i>Cell</i> , 2019, 176, 649-662.e20.	13.5	1,087

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8144	Community of dark-spored myxomycetes in ground litter and soil of taiga forest (Nizhne-Svirskiy) Tj ETQq0 0 0 rgBT, /Overlock 10 Tf 50 7	0.7	24
8145	Complete mitochondrial genome of <i>Japalura flaviceps</i> : Deep insights into the phylogeny and gene rearrangements of Agamidae species. <i>International Journal of Biological Macromolecules</i> , 2019, 125, 423-431.	3.6	23
8146	Phylogeny and species delimitation of near Eastern <i>Neurergus</i> newts (Salamandridae) based on genome-wide RADseq data analysis. <i>Molecular Phylogenetics and Evolution</i> , 2019, 133, 189-197.	1.2	24
8147	The complete chloroplast genome of <i>Aphelandra knappiae</i> (Acanthaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 273-274.	0.2	5
8148	The Evolutionary Traceability of a Protein. <i>Genome Biology and Evolution</i> , 2019, 11, 531-545.	1.1	23
8149	Diversity and distribution of the <i>bmp</i> gene cluster and its Polybrominated products in the genus <i>Pseudoalteromonas</i> . <i>Environmental Microbiology</i> , 2019, 21, 1575-1585.	1.8	15
8150	Evolution of the latitudinal diversity gradient in the hyperdiverse ant genus <i>Pheidole</i> . <i>Global Ecology and Biogeography</i> , 2019, 28, 456-470.	2.7	29
8151	Growth and Chloroplast Replacement of the Benthic Mixotrophic Ciliate <i>Mesodinium coatsi</i> . <i>Journal of Eukaryotic Microbiology</i> , 2019, 66, 625-636.	0.8	5
8152	Molecular and morphological evidence for a new species of liverwort, <i>Lejeunea heinrichsii</i> (Marchantiophyta: Lejeuneaceae) from Taveuni, Fiji. <i>Journal of Systematics and Evolution</i> , 2019, 57, 361-370.	1.6	6
8153	Cystic Fibrosis-Associated <i>Stenotrophomonas maltophilia</i> Strain-Specific Adaptations and Responses to pH. <i>Journal of Bacteriology</i> , 2019, 201, .	1.0	11
8154	First description of an euryoecious acanthoecid choanoflagellate species, <i>Enibas tolerabilis</i> gen. et sp. nov. from a salar in the Chilean Andes based on morphological and transcriptomic data. <i>European Journal of Protistology</i> , 2019, 67, 106-113.	0.5	18
8155	The complete chloroplast genome of <i>Populus xiangchengensis</i> , an endemic species in Southwest China. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 70-71.	0.2	8
8156	Chromids Aid Genome Expansion and Functional Diversification in the Family <i>Burkholderiaceae</i> . <i>Molecular Biology and Evolution</i> , 2019, 36, 562-574.	3.5	34
8157	The phylogeny of Ryocalanoidea (Copepoda, Calanoida) based on morphology and a multi-gene analysis with a description of new ryocalanoidean species. <i>Zoological Journal of the Linnean Society</i> , 2019, 185, 925-957.	1.0	7
8158	Mitochondrial complex <i>II</i> of plants: subunit composition, assembly, and function in respiration and signaling. <i>Plant Journal</i> , 2019, 98, 405-417.	2.8	52
8159	Young colonization history of a widespread sand dollar (Echinodermata; Clypeasteroidea) in western Taiwan. <i>Quaternary International</i> , 2019, 528, 120-129.	0.7	3
8160	Cox1 barcoding versus multilocus species delimitation: validation of two mite species with contrasting effective population sizes. <i>Parasites and Vectors</i> , 2019, 12, 8.	1.0	25
8161	Utility of Whole Genome Sequencing To Describe the Persistence and Evolution of <i>Listeria monocytogenes</i> Strains within Crabmeat Processing Environments Linked to Two Outbreaks of Listeriosis. <i>Journal of Food Protection</i> , 2019, 82, 30-38.	0.8	24

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8162	Genome of the candidate phylum Aminicenantes bacterium from a deep subsurface thermal aquifer revealed its fermentative saccharolytic lifestyle. <i>Extremophiles</i> , 2019, 23, 189-200.	0.9	74
8163	<i>Jiangella anatolica</i> sp. nov. isolated from coastal lake soil. <i>Antonie Van Leeuwenhoek</i> , 2019, 112, 887-895.	0.7	6
8164	Morphology, morphogenesis and molecular phylogeny of a freshwater ciliate, <i>Monomicrocaryon euglenivorum euglenivorum</i> (Ciliophora, Oxytrichidae). <i>European Journal of Protistology</i> , 2019, 68, 25-36.	0.5	31
8165	Birth of an order: Comprehensive molecular phylogenetic study excludes <i>Herpomyces</i> (Fungi). <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50</i>	1.2	27
8166	Phylogeny and biogeography of the narrowly endemic <i>Doronicum cataractarum</i> (Asteraceae) from the eastern European Alps: Pleistocene origin from Alpine ancestors rather than Tertiary relic with southwest Asian affinity. <i>Plant Systematics and Evolution</i> , 2019, 305, 139-149.	0.3	3
8167	Unmasking Antarctic mollusc lineages: novel evidence from philinoid snails (Gastropoda:). <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50</i>	1.5	12
8168	Toward a multigene phylogeny of the Cymatosiraceae (Bacillariophyta, Mediophyceae) II: morphological and molecular insights into the taxonomy of the forgotten species <i>Campylosira africana</i> and of <i>Extubocellulus</i> , with a description of two new taxa. <i>Journal of Phycology</i> , 2019, 55, 425-441.	1.0	8
8169	Sexual morph of <i>Phaeoacremonium aureum</i> from <i>Rhizophora mucronata</i> collected in southern Thailand. <i>Phytotaxa</i> , 2019, 387, 21.	0.1	1
8170	<i>Lecanicillium coprophilum</i> (Cordycipitaceae, Hypocreales), a new species of fungus from the feces of <i>Marmota monax</i> in China. <i>Phytotaxa</i> , 2019, 387, 55.	0.1	25
8171	Revalidation of <i>Caridina natalensis</i> De Man, 1908 (Crustacea: Decapoda: Atyidae) in the South Western Indian Ocean. <i>Zootaxa</i> , 2019, 4543, 375-387.	0.2	1
8172	Two new genera of Podostemaceae from northern Central Laos: saltational evolution and enigmatic morphology. <i>Journal of Plant Research</i> , 2019, 132, 19-31.	1.2	3
8173	Phylogenomics of an extra-Antarctic notothenioid radiation reveals a previously unrecognized lineage and diffuse species boundaries. <i>BMC Evolutionary Biology</i> , 2019, 19, 13.	3.2	18
8174	HIV-1 molecular transmission clusters in nine European countries and Canada: association with demographic and clinical factors. <i>BMC Medicine</i> , 2019, 17, 4.	2.3	43
8175	Draft Genome Assembly and Population Genetics of an Agricultural Pollinator, the Solitary Alkali Bee (<i>Halictidae</i> : <i>Nomia melanderi</i>). <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 625-634.	0.8	19
8176	Spatial Phylogenetics of Florida Vascular Plants: The Effects of Calibration and Uncertainty on Diversity Estimates. <i>IScience</i> , 2019, 11, 57-70.	1.9	41
8177	Molecular Hydrogen, a Neglected Key Driver of Soil Biogeochemical Processes. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	48
8178	A Real-Time Multiplex PCR Assay for Detection of <i>Elizabethkingia</i> Species and Differentiation between <i>Elizabethkingia anophelis</i> and <i>E. meningoseptica</i> . <i>Journal of Clinical Microbiology</i> , 2019, 57, .	1.8	6
8179	The complete plastid genomes of two Fabaceae orphan crops from Africa. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 93-94.	0.2	5

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8180	Phylogenetic inference in section <i>Archerythroxyllum</i> informs taxonomy, biogeography, and the domestication of coca (<i>Erythroxyllum</i> species). <i>American Journal of Botany</i> , 2019, 106, 154-165.	0.8	18
8181	Diversity and Composition of Pelagic Prokaryotic and Protist Communities in a Thin Arctic Sea-Ice Regime. <i>Microbial Ecology</i> , 2019, 78, 388-408.	1.4	26
8182	The origin and diversification of the Entorrhizales: deep evolutionary roots but recent speciation with a phylogenetic and phenotypic split between associates of the Cyperaceae and Juncaceae. <i>Organisms Diversity and Evolution</i> , 2019, 19, 13-30.	0.7	9
8183	Commensal Enterobacteriaceae Protect against Salmonella Colonization through Oxygen Competition. <i>Cell Host and Microbe</i> , 2019, 25, 128-139.e5.	5.1	159
8184	A New Spiralian Phylogeny Places the Enigmatic Arrow Worms among Gnathiferans. <i>Current Biology</i> , 2019, 29, 312-318.e3.	1.8	201
8185	Phylogenomics of the adaptive radiation of <i>Triturus</i> newts supports gradual ecological niche expansion towards an incrementally aquatic lifestyle. <i>Molecular Phylogenetics and Evolution</i> , 2019, 133, 120-127.	1.2	38
8186	Species delimitation and interspecific relationships of the endangered herb genus <i>Notopterygium</i> inferred from multilocus variations. <i>Molecular Phylogenetics and Evolution</i> , 2019, 133, 142-151.	1.2	13
8187	Functional annotation of orthologs in metagenomes: a case study of genes for the transformation of oceanic dimethylsulfoniopropionate. <i>ISME Journal</i> , 2019, 13, 1183-1197.	4.4	24
8188	Species delimitation in endangered groundwater salamanders: Implications for aquifer management and biodiversity conservation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 2624-2633.	3.3	74
8189	The complete mitochondrial genome of <i>Salinator takii</i> (Gastropoda: Amphibolinae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 355-356.	0.2	0
8190	The complete chloroplast genome of a true mangrove <i>Sonneratia apetala</i> and its phylogenetic implications. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 160-161.	0.2	2
8191	Illumina midi-barcodes: quality proof and applications. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2019, 30, 490-499.	0.7	10
8192	Remote tropical island colonization does not preclude symbiotic specialists: new evidence of mycorrhizal specificity across the geographic distribution of the Hawaiian endemic orchid <i>Anoectochilus sandvicensis</i> . <i>Annals of Botany</i> , 2019, 123, 657-666.	1.4	6
8193	Comparative genome analysis of <i>Aspergillus flavus</i> clinically isolated in Japan. <i>DNA Research</i> , 2019, 26, 95-103.	1.5	11
8194	Repeated Evolution Versus Common Ancestry: Sex Chromosome Evolution in the Haplochromine Cichlid <i>Pseudocrenilabrus philander</i> . <i>Genome Biology and Evolution</i> , 2019, 11, 439-458.	1.1	26
8195	Plastome-Wide Rearrangements and Gene Losses in Carnivorous Droseraceae. <i>Genome Biology and Evolution</i> , 2019, 11, 472-485.	1.1	40
8196	Detection and characterization of ESBL-producing <i>Escherichia coli</i> expressing <i>mcr-1</i> from dairy cows in China. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 321-325.	1.3	41
8197	Identification of Cuticular Protein Genes in the Colorado Potato Beetle <i>Leptinotarsa decemlineata</i> (Coleoptera: Chrysomelidae). <i>Journal of Economic Entomology</i> , 2019, 112, 912-923.	0.8	12

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8198	The species of the genus <i>Platycheirus</i> Lepeletier & Serville, 1828 (Diptera, Syrphidae) from Taiwan, with a discussion on intersex specimens. <i>Journal of Asia-Pacific Entomology</i> , 2019, 22, 281-295.	0.4	2
8199	Cross-species hybridization and the origin of North African date palms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 1651-1658.	3.3	95
8200	Complete mitochondrial genome of a rare diatom (Bacillariophyta) <i>Proschkinia</i> and its phylogenetic and taxonomic implications. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 25-26.	0.2	11
8201	Characterization of the complete chloroplast genome of <i>Scurrula parasitica</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 247-248.	0.2	2
8202	Plastid Genomes and Proteins Illuminate the Evolution of Eustigmatophyte Algae and Their Bacterial Endosymbionts. <i>Genome Biology and Evolution</i> , 2019, 11, 362-379.	1.1	29
8203	Identification of Phycocyanin Gene Family in Legume Plants and their Involvement in Nodulation of <i>Medicago truncatula</i> . <i>Plant and Cell Physiology</i> , 2019, 60, 900-915.	1.5	12
8204	Morphological and Molecular Identification of a New Ciliate, <i>Zoothamnium palmplatum</i> nov. spec. (Ciliophora, Peritrichia) from North China. <i>Journal of Eukaryotic Microbiology</i> , 2019, 66, 670-679.	0.8	4
8205	Discovery of a Thermostable GH10 Xylanase with Broad Substrate Specificity from the Arctic Mid-Ocean Ridge Vent System. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	38
8206	Examination and Reconstruction of Three Ancient Endogenous Parvovirus Capsid Protein Gene Remnants Found in Rodent Genomes. <i>Journal of Virology</i> , 2019, 93, .	1.5	13
8207	Cluster expansion of apolipoprotein D (ApoD) genes in teleost fishes. <i>BMC Evolutionary Biology</i> , 2019, 19, 9.	3.2	5
8208	Evaluating the usefulness of alignment filtering methods to reduce the impact of errors on evolutionary inferences. <i>BMC Evolutionary Biology</i> , 2019, 19, 21.	3.2	96
8209	Co-option of the PRDM14-CBFA2T complex from motor neurons to pluripotent cells during vertebrate evolution. <i>Development (Cambridge)</i> , 2019, 146, .	1.2	9
8210	Molecular epidemiology of 16S rRNA methyltransferase in Brazil: RmtG in <i>Klebsiella aerogenes</i> ST93 (CC4). <i>Anais Da Academia Brasileira De Ciencias</i> , 2019, 91, e20180762.	0.3	11
8211	Multiple connections between Amazonia and Atlantic Forest shaped the phylogenetic and morphological diversity of <i>Chiasmocleis</i> Mehely, 1904 (Anura: Microhylidae: Gastrophryninae). <i>Molecular Phylogenetics and Evolution</i> , 2019, 130, 198-210.	1.2	33
8212	Phylogenomics and multigene phylogenies decipher two new cryptic marine algae from California, <i>Gelidium gabrielsonii</i> and <i>G. Akathyanniae</i> (Gelidiales, Rhodophyta). <i>Journal of Phycology</i> , 2019, 55, 160-172.	1.0	22
8213	Phylogeny, diversity and biogeography of Neotropical sipo snakes (Serpentes: Colubrinae: Chironius). <i>Molecular Phylogenetics and Evolution</i> , 2019, 130, 315-329.	1.2	9
8214	Insight from an ultraconserved element bait set designed for hemipteran phylogenetics integrated with genomic resources. <i>Molecular Phylogenetics and Evolution</i> , 2019, 130, 297-303.	1.2	51
8215	Phylogenetic imprint of woody plants on the soil mycobiome in natural mountain forests of eastern China. <i>ISME Journal</i> , 2019, 13, 686-697.	4.4	76

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8216	Analyses of genome-scale variation reveal divergence of two <i>Sinallaria</i> species (Brassicaceae) with continuous but limited gene flow. <i>Journal of Systematics and Evolution</i> , 2019, 57, 268-277.	1.6	9
8217	The evolutionary history of the goby <i>Elacatinus puncticulatus</i> in the tropical eastern pacific: Effects of habitat discontinuities and local environmental variability. <i>Molecular Phylogenetics and Evolution</i> , 2019, 130, 269-285.	1.2	17
8218	A phylogenetic examination of host use evolution in the quinaia and testacea groups of <i>Drosophila</i> . <i>Molecular Phylogenetics and Evolution</i> , 2019, 130, 233-243.	1.2	33
8219	Phylotranscriptomic Insights into the Diversification of Endothermic <i>Thunnus</i> Tunas. <i>Molecular Biology and Evolution</i> , 2019, 36, 84-96.	3.5	15
8220	Sex-Biased Dispersal Obscures Species Boundaries in Integrative Species Delimitation Approaches. <i>Systematic Biology</i> , 2019, 68, 441-459.	2.7	21
8221	Comparative genomics of the <i>Komagataeibacter</i> strains—Efficient bionanocellulose producers. <i>MicrobiologyOpen</i> , 2019, 8, e00731.	1.2	51
8222	Extreme Lewontin's Paradox in Ubiquitous Marine Phytoplankton Species. <i>Molecular Biology and Evolution</i> , 2019, 36, 4-14.	3.5	37
8223	Diversification and historical demography of the rapid racerunner (<i>Eremias velox</i>) in relation to geological history and Pleistocene climatic oscillations in arid Central Asia. <i>Molecular Phylogenetics and Evolution</i> , 2019, 130, 244-258.	1.2	18
8224	Whole-Genome Alignment and Comparative Annotation. <i>Annual Review of Animal Biosciences</i> , 2019, 7, 41-64.	3.6	62
8225	Revising the taxonomy of the <i>Acinetobacter lwoffii</i> group: The description of <i>Acinetobacter pseudolwoffii</i> sp. nov. and emended description of <i>Acinetobacter lwoffii</i> . <i>Systematic and Applied Microbiology</i> , 2019, 42, 159-167.	1.2	45
8226	Insights into the Evolution of Shells and Love Darts of Land Snails Revealed from Their Matrix Proteins. <i>Genome Biology and Evolution</i> , 2019, 11, 380-397.	1.1	25
8227	Epidemiology of tick-borne pathogens in the semi-arid and the arid agro-ecological zones of Punjab province, Pakistan. <i>Transboundary and Emerging Diseases</i> , 2019, 66, 526-536.	1.3	49
8228	The mitochondrial genome of <i>Greenidea psidii</i> van der Goot (Hemiptera: Aphididae: Greenideinae) and comparisons with other Aphididae aphids. <i>International Journal of Biological Macromolecules</i> , 2019, 122, 824-832.	3.6	20
8229	Mitochondrial phylogenomics of the Hymenoptera. <i>Molecular Phylogenetics and Evolution</i> , 2019, 131, 8-18.	1.2	104
8230	A phylogenomic and molecular markers based taxonomic framework for members of the order Entomoplasmatales: proposal for an emended order Mycoplasmatales containing the family Spiroplasmataceae and emended family Mycoplasmataceae comprised of six genera. <i>Antonie Van Leeuwenhoek</i> , 2019, 112, 561-588.	0.7	81
8231	<i>Gelidium brasiliense</i> sp. nov. (Gelidiales, Rhodophyta): a diminutive agarophyte from Brazil. <i>Journal of Applied Phycology</i> , 2019, 31, 951-958.	1.5	5
8232	PER extended-spectrum β -lactamases originate from <i>Pararheinheimera</i> spp. <i>International Journal of Antimicrobial Agents</i> , 2019, 53, 158-164.	1.1	12
8233	Gene-wise resampling outperforms site-wise resampling in phylogenetic coalescence analyses. <i>Molecular Phylogenetics and Evolution</i> , 2019, 131, 80-92.	1.2	33

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8234	Tip-dating and the origin of Telluraves. <i>Molecular Phylogenetics and Evolution</i> , 2019, 131, 55-63.	1.2	10
8235	Ancestral Genomes: a resource for reconstructed ancestral genes and genomes across the tree of life. <i>Nucleic Acids Research</i> , 2019, 47, D271-D279.	6.5	17
8236	Barcoding of parasitoid wasps (Braconidae and Chalcidoidea) associated with wild and cultivated olives in the Western Cape of South Africa. <i>Genome</i> , 2019, 62, 183-199.	0.9	15
8237	Group A Rotavirus VP1 Polymerase and VP2 Core Shell Proteins: Intergenotypic Sequence Variation and <i>In Vitro</i> Functional Compatibility. <i>Journal of Virology</i> , 2019, 93, .	1.5	17
8238	Hybrid capture data unravel a rapid radiation of pimpliform parasitoid wasps (Hymenoptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 582 T	1.7	43
8239	Isolation and Characterization of a Distinct Influenza A Virus from Egyptian Bats. <i>Journal of Virology</i> , 2019, 93, .	1.5	42
8240	Geospatial variation in co-occurrence networks of nitrifying microbial guilds. <i>Molecular Ecology</i> , 2019, 28, 293-306.	2.0	50
8241	Characterization of a strain representing a new <i>Enterobacter</i> species, <i>Enterobacter chengduensis</i> sp. nov.. <i>Antonie Van Leeuwenhoek</i> , 2019, 112, 491-500.	0.7	26
8242	Characterization and comparison of the mitochondrial genomes from two <i>Lyophyllum</i> fungal species and insights into phylogeny of Agaricomycetes. <i>International Journal of Biological Macromolecules</i> , 2019, 121, 364-372.	3.6	42
8243	<i>Albugo candida</i> race diversity, ploidy and host-associated microbes revealed using DNA sequence capture on diseased plants in the field. <i>New Phytologist</i> , 2019, 221, 1529-1543.	3.5	41
8244	Unraveling the intricate biodiversity of the benthic harpacticoid genus <i>Nannopus</i> (Copepoda,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 347 366-379.	1.2	12
8245	Parasitoid Jewel Wasp Mounts Multipronged Neurochemical Attack to Hijack a Host Brain. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 99-114.	2.5	27
8246	ParGenes: a tool for massively parallel model selection and phylogenetic tree inference on thousands of genes. <i>Bioinformatics</i> , 2019, 35, 1771-1773.	1.8	51
8247	The mitochondrial genomes of <i>Statilia maculata</i> and <i>S. nemoralis</i> (Mantidae: Mantinae) with different duplications of trnR genes. <i>International Journal of Biological Macromolecules</i> , 2019, 121, 839-845.	3.6	15
8248	Phylogeny of <i>Schinus</i> L. (Anacardiaceae) with a new infrageneric classification and insights into evolution of spinescence and floral traits. <i>Molecular Phylogenetics and Evolution</i> , 2019, 133, 302-351.	1.2	18
8249	Unveiling patterns of genetic variation in parasite-host associations: an example with pinworms and Neotropical primates. <i>Parasitology</i> , 2019, 146, 356-362.	0.7	9
8250	High genetic diversity in the <i>Dirofilaria repens</i> species complex revealed by mitochondrial genomes of feline microfilaria samples from Narathiwat, Thailand. <i>Transboundary and Emerging Diseases</i> , 2019, 66, 389-399.	1.3	22
8252	Evolutionary and ecological patterns within the South African Bathyergidae: Implications for taxonomy. <i>Molecular Phylogenetics and Evolution</i> , 2019, 130, 181-197.	1.2	8

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8253	How Well Does Your Phylogenetic Model Fit Your Data?. <i>Systematic Biology</i> , 2019, 68, 157-167.	2.7	15
8254	Chitin synthesis and degradation in <i>Lepeophtheirus salmonis</i> : Molecular characterization and gene expression profile during synthesis of a new exoskeleton. <i>Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology</i> , 2019, 227, 123-133.	0.8	13
8255	A Non-Flagellated Member of the Myxogastria and Expansion of the Echinosteliida. <i>Journal of Eukaryotic Microbiology</i> , 2019, 66, 538-544.	0.8	19
8256	GABA-modulating bacteria of the human gut microbiota. <i>Nature Microbiology</i> , 2019, 4, 396-403.	5.9	590
8257	The soil organic matter decomposition mechanisms in ectomycorrhizal fungi are tuned for liberating soil organic nitrogen. <i>ISME Journal</i> , 2019, 13, 977-988.	4.4	128
8258	<i>Coccinectria pachysandricola</i> , Causal Agent of a New Foliar Blight Disease of <i>Sarcococca hookeriana</i> . <i>Plant Disease</i> , 2019, 103, 1337-1346.	0.7	8
8259	Recent lake expansion triggered the adaptive radiation of freshwater snails in the ancient Lake Biwa. <i>Evolution Letters</i> , 2019, 3, 43-54.	1.6	23
8260	Restriction-Site-Associated DNA Sequencing Reveals a Cryptic <i>Viburnum</i> Species on the North American Coastal Plain. <i>Systematic Biology</i> , 2019, 68, 187-203.	2.7	36
8261	Phylogeography of a widespread lizard complex reflects patterns of both geographic and ecological isolation. <i>Molecular Ecology</i> , 2019, 28, 644-657.	2.0	23
8262	Emergence and adaptation of H3N2 canine influenza virus from avian influenza virus: An overlooked role of dogs in interspecies transmission. <i>Transboundary and Emerging Diseases</i> , 2019, 66, 842-851.	1.3	9
8263	Comparative mitogenome analysis of three species and monophyletic inference of Catantopinae (Orthoptera: Acridoidea). <i>Genomics</i> , 2019, 111, 1728-1735.	1.3	21
8264	Geographic distributions, phenotypes, and phylogenetic relationships of <i>Phalloceros</i> (Cyprinodontiformes: Poeciliidae): Insights about diversification among sympatric species pools. <i>Molecular Phylogenetics and Evolution</i> , 2019, 132, 265-274.	1.2	20
8265	Molecular phylogenetics supports a clade of red algal parasites retaining native plastids: taxonomy and terminology revised. <i>Journal of Phycology</i> , 2019, 55, 279-288.	1.0	8
8266	Enlarged and highly repetitive plastome of <i>Lagarostrobos</i> and plastid phylogenomics of Podocarpaceae. <i>Molecular Phylogenetics and Evolution</i> , 2019, 133, 24-32.	1.2	8
8267	<i>Lichinodium</i> is a new lichenized lineage in the Leotiomycetes. <i>Fungal Diversity</i> , 2019, 94, 23-39.	4.7	20
8268	A heterodimeric glutathione S-transferase that stereospecifically breaks lignin's β^2 (R)-aryl ether bond reveals the diversity of bacterial β^2 -etherases. <i>Journal of Biological Chemistry</i> , 2019, 294, 1877-1890.	1.6	32
8269	Molecular phylogenetics and biogeography provide insights into the subgeneric classification of <i>Wiedemannia</i> Zetterstedt (Diptera: Empididae: Clinocerinae). <i>Systematic Entomology</i> , 2019, 44, 559-570.	1.7	8
8270	Emergence and Spread of Basal Lineages of <i>Yersinia</i> <i>pestis</i> during the Neolithic Decline. <i>Cell</i> , 2019, 176, 295-305.e10.	13.5	168

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8271	Resolving Deep Nodes in an Ancient Radiation of Neotropical Fishes in the Presence of Conflicting Signals from Incomplete Lineage Sorting. <i>Systematic Biology</i> , 2019, 68, 573-593.	2.7	54
8272	Whole Genome Sequencing detects Inter-Facility Transmission of Carbapenem-resistant <i>Klebsiella pneumoniae</i> . <i>Journal of Infection</i> , 2019, 78, 187-199.	1.7	26
8273	Genome-scale transfer of mitochondrial DNA from legume hosts to the holoparasite <i>Lophophytum mirabile</i> (Balanophoraceae). <i>Molecular Phylogenetics and Evolution</i> , 2019, 132, 243-250.	1.2	44
8274	Genomic comparisons reveal biogeographic and anthropogenic impacts in the koala (<i>Phascolarctos</i>) Tj ETQq1 1 0.784314 rgBT /Over bo 122, 525-544.	1.2	29
8275	Individual immune selection pressure has limited impact on seasonal influenza virus evolution. <i>Nature Ecology and Evolution</i> , 2019, 3, 302-311.	3.4	25
8276	Genome-wide discovery of epistatic loci affecting antibiotic resistance in <i>Neisseria gonorrhoeae</i> using evolutionary couplings. <i>Nature Microbiology</i> , 2019, 4, 328-338.	5.9	41
8277	The complete chloroplast genome of the endangered Pinaceae species <i>Abies ziyuanensis</i> and its phylogenetic implications. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 137-138.	0.2	3
8278	The first complete chloroplast genomes of two Alismataceae species, and the phylogenetic relationship under order Alismatales. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 122-123.	0.2	4
8279	The <i>Suhomyces</i> clade: from single isolate to multiple species to disintegrating sex loci. <i>FEMS Yeast Research</i> , 2019, 19, .	1.1	10
8280	Mitogenomics Reveals a Novel Genetic Code in Hemichordata. <i>Genome Biology and Evolution</i> , 2019, 11, 29-40.	1.1	20
8281	Outbreak of viral haemorrhagic septicaemia (<sc>VHS</sc>) in lumpfish (<i>Cyclopterus lumpus</i>) in Iceland caused by <sc>VHS</sc> virus genotype <sc>IV</sc>. <i>Journal of Fish Diseases</i> , 2019, 42, 47-62.	0.9	28
8282	Light capture and pigment diversity in marine and freshwater cryptophytes. <i>Journal of Phycology</i> , 2019, 55, 552-564.	1.0	28
8283	Historical biogeography of the termite clade Rhinotermitinae (Blattodea: Isoptera). <i>Molecular Phylogenetics and Evolution</i> , 2019, 132, 100-104.	1.2	21
8284	Remedial Treatment of Corroded Iron Objects by Environmental <i>Aeromonas</i> Isolates. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	10
8285	<i>Emydomyces testavorans</i> , a New Genus and Species of Onygenalean Fungus Isolated from Shell Lesions of Freshwater Aquatic Turtles. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	1.8	33
8286	Land bridges in the Pleistocene contributed to flora assembly on the continental islands of South China: Insights from the evolutionary history of <i>Quercus championii</i> . <i>Molecular Phylogenetics and Evolution</i> , 2019, 132, 36-45.	1.2	33
8287	Balancing Specificity and Promiscuity in Enzyme Evolution: Multidimensional Activity Transitions in the Alkaline Phosphatase Superfamily. <i>Journal of the American Chemical Society</i> , 2019, 141, 370-387.	6.6	35
8288	A database-driven approach identifies additional diterpene synthase activities in the mint family (Lamiaceae). <i>Journal of Biological Chemistry</i> , 2019, 294, 1349-1362.	1.6	53

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8289	<i>Nephromyces</i> Encodes a Urate Metabolism Pathway and Predicted Peroxisomes, Demonstrating That These Are Not Ancient Losses of Apicomplexans. <i>Genome Biology and Evolution</i> , 2019, 11, 41-53.	1.1	20
8290	Phylogenomics of Endogonaceae and evolution of mycorrhizas within Mucoromycota. <i>New Phytologist</i> , 2019, 222, 511-525.	3.5	81
8291	Considerations on the Taxonomy of the Genus <i>Arhuaco</i> Adams and Bernard 1977, and its Relationships with the Genus <i>Pronophila</i> Doubleday [1849] (Nymphalidae, Satyrinae). <i>Neotropical Entomology</i> , 2019, 48, 302-313.	0.5	4
8292	Morphology and SSU rDNA-based phylogeny of two <i>Euplotes</i> species from China: <i>E. wuhanensis</i> sp. n. and <i>E. muscicola</i> Kahl, 1932 (Ciliophora, Euplotida). <i>European Journal of Protistology</i> , 2019, 67, 1-14.	0.5	20
8293	Next-generation sequencing yields the complete chloroplast genome of <i>Abies kawakamii</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 29-30.	0.2	4
8294	Insights into the Evolution of the New World Diploid Cottons (<i>Gossypium</i>), Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 547 53-71.	1.1	45
8295	Inferring introgression using RADseq and <i>DFOIL</i> : Power and pitfalls revealed in a case study of spiny lizards (<i>Sceloporus</i>). <i>Molecular Ecology Resources</i> , 2019, 19, 818-837.	2.2	23
8296	<i>Nephrocystidium pickii</i> Weissenberg, 1921 belongs to Myxozoa (Cnidaria) but is not conspecific with <i>Myxidium lieberkuehni</i> BÄ¼tschli, 1882 (Myxozoa: Bivalvulida: Variisporina: Myxidiidae): molecular-genetic evidence. <i>Systematic Parasitology</i> , 2019, 96, 15-22.	0.5	1
8297	Two major clades of blind mole rats (<i>Nannospalax</i> sp.) revealed by mtDNA and microsatellite genotyping in Western and Central Turkey. <i>Mammalian Biology</i> , 2019, 94, 38-47.	0.8	3
8298	Continued reassortment of avian H6 influenza viruses from Southern China, 2014â€“2016. <i>Transboundary and Emerging Diseases</i> , 2019, 66, 592-598.	1.3	19
8299	Species delimitation in Neotropical fishes of the genus <i>Characidium</i> (Teleostei, Characiformes). <i>Zoologica Scripta</i> , 2019, 48, 69-80.	0.7	22
8300	Community structure and fibrolytic activities of anaerobic rumen fungi in dromedary camels. <i>Journal of Basic Microbiology</i> , 2019, 59, 101-110.	1.8	22
8301	Mitochondrial DNA and their nuclear copies in the parasitic wasp <i>Pteromalus puparum</i> : A comparative analysis in Chalcidoidea. <i>International Journal of Biological Macromolecules</i> , 2019, 121, 572-579.	3.6	15
8302	Systematics, genetics, and biogeography of intertidal mites (Acari, Oribatida) from the Andaman Sea and Strait of Malacca. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2019, 57, 91-112.	0.6	17
8303	Detecting Amino Acid Coevolution with Bayesian Graphical Models. <i>Methods in Molecular Biology</i> , 2019, 1851, 105-122.	0.4	5
8304	Multilocus phylogeny and revised classification for mountain dragons of the genus <i>Japalura</i> s.l. (Reptilia: Agamidae: Draconinae) from Asia. <i>Zoological Journal of the Linnean Society</i> , 2019, 185, 246-267.	1.0	21
8305	Near-complete phylogeny and taxonomic revision of the world's babblers (Aves: Passeriformes). <i>Molecular Phylogenetics and Evolution</i> , 2019, 130, 346-356.	1.2	72
8306	Allopatric diversification and evolutionary melting pot in a North African Palearctic relict: The biogeographic history of <i>Salamandra algira</i> . <i>Molecular Phylogenetics and Evolution</i> , 2019, 130, 81-91.	1.2	25

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8307	Discovery of several novel, widespread, and ecologically distinct marine <i>Thaumarchaeota</i> viruses that encode <i>amoC</i> nitrification genes. <i>ISME Journal</i> , 2019, 13, 618-631.	4.4	103
8308	Birth and death of Mx genes and the presence/absence of genes regulating Mx transcription are correlated with the diversity of anti-pathogenicity in vertebrate species. <i>Molecular Genetics and Genomics</i> , 2019, 294, 121-133.	1.0	5
8309	A dedicated target capture approach reveals variable genetic markers across micro- and macro-evolutionary time scales in palms. <i>Molecular Ecology Resources</i> , 2019, 19, 221-234.	2.2	42
8310	Comparative Mitogenomic Analysis of Forensically Important Sarcophagid Flies (Diptera: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 392-407.	0.9	16
8311	How rivers and historical climate oscillations impact on genetic structure in Chinese Muntjac (<i>Muntiacus reevesi</i>)?. <i>Diversity and Distributions</i> , 2019, 25, 116-128.	1.9	4
8312	Genotyping-by-sequencing (GBS), ITS and cpDNA phylogenies reveal the existence of a distinct Pyrenean/Cantabrian lineage in the European high mountain genus <i>Homogyne</i> (Asteraceae) and imply dual westward migration of the genus. <i>Alpine Botany</i> , 2019, 129, 21-31.	1.1	3
8313	Towards a global phylogeny of freshwater mussels (Bivalvia: Unionida): Species delimitation of Chinese taxa, mitochondrial phylogenomics, and diversification patterns. <i>Molecular Phylogenetics and Evolution</i> , 2019, 130, 45-59.	1.2	48
8314	Microbial communities associated with phosphogenic sediments and phosphoclast-associated <i>scp</i> DNA of the Benguela upwelling system. <i>Geobiology</i> , 2019, 17, 76-90.	1.1	9
8315	Of puzzles and pavements: a quantitative exploration of leaf epidermal cell shape. <i>New Phytologist</i> , 2019, 221, 540-552.	3.5	66
8316	Forensic human identification with targeted microbiome markers using nearest neighbor classification. <i>Forensic Science International: Genetics</i> , 2019, 38, 130-139.	1.6	45
8317	Phylogenomics, life history and morphological evolution of ophiocomid brittlestars. <i>Molecular Phylogenetics and Evolution</i> , 2019, 130, 67-80.	1.2	22
8318	High-Throughput Reconstruction of Ancestral Protein Sequence, Structure, and Molecular Function. <i>Methods in Molecular Biology</i> , 2019, 1851, 135-170.	0.4	15
8319	The Bear Giant-Skipper genome suggests genetic adaptations to living inside yucca roots. <i>Molecular Genetics and Genomics</i> , 2019, 294, 211-226.	1.0	10
8320	The complete mitochondrial genome of <i>Budorcas taxicolor tibetana</i> (Artiodactyla: Bovidae) and comparison with other Caprinae species: Insight into the phylogeny of the genus <i>Budorcas</i> . <i>International Journal of Biological Macromolecules</i> , 2019, 121, 223-232.	3.6	18
8321	Discovery of swimming larvae in Elmidae (Coleoptera: Byrrhoidea). <i>Entomological Science</i> , 2019, 22, 3-5.	0.3	2
8322	Molecular phylogeny of <i>Chondrocyclus</i> (Gastropoda: Cyclophoridae), a widespread genus of sedentary, restricted-range snails. <i>Molecular Phylogenetics and Evolution</i> , 2019, 131, 193-210.	1.2	7
8323	Py _{scp} PHLAWD: A python tool for phylogenetic dataset construction. <i>Methods in Ecology and Evolution</i> , 2019, 10, 104-108.	2.2	37
8324	Comparative Phylogeography of Forest-Dependent Mammals Reveals Paleo-Forest Corridors throughout Sundaland. <i>Journal of Heredity</i> , 2019, 110, 158-172.	1.0	40

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8325	Novel <i>Cardinium</i> strains in non-marine ostracod (Crustacea) hosts from natural populations. <i>Molecular Phylogenetics and Evolution</i> , 2019, 130, 406-415.	1.2	14
8326	Emerging evolutionary paradigms in antibiotic discovery. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2019, 46, 257-271.	1.4	76
8327	TreeGrafter: phylogenetic tree-based annotation of proteins with Gene Ontology terms and other annotations. <i>Bioinformatics</i> , 2019, 35, 518-520.	1.8	22
8328	The Origin of a New Sex Chromosome by Introgression between Two Stickleback Fishes. <i>Molecular Biology and Evolution</i> , 2019, 36, 28-38.	3.5	57
8329	Phylogeny, biogeography and divergence times of <i>Astragalus</i> section <i>Incarni</i> DC. (Fabaceae) inferred from nrDNA ITS and plastid <i>rpl32</i> L _(UAG) sequences. <i>Nordic Journal of Botany</i> , 2019, 37, .	0.2	9
8330	Cryptic diversity in the smooth snake (<i>Coronella austriaca</i>). <i>Amphibia - Reptilia</i> , 2019, 40, 179-192.	0.1	15
8331	Cobweb disease on oyster culinary-medicinal mushroom (<i>Pleurotus ostreatus</i>) caused by the mycoparasite <i>Cladobotryum mycophilum</i> . <i>Journal of Plant Pathology</i> , 2019, 101, 349-354.	0.6	14
8332	Improved taxon sampling and multigene phylogeny of unicellular chlamydomonads closely related to the colonial volvocalean lineage Tetrabaenaceae-Goniaceae-Volvocaceae (Volvocales, Chlorophyceae). <i>Molecular Phylogenetics and Evolution</i> , 2019, 130, 1-8.	1.2	11
8333	Comparative analysis of spleen transcriptome detects differences in evolutionary adaptation of immune defense functions in bighead carp and silver carp. <i>Fish and Shellfish Immunology</i> , 2019, 84, 148-157.	1.6	12
8334	Phenotypic and life-history diversification in Amazonian frogs despite past introgressions. <i>Molecular Phylogenetics and Evolution</i> , 2019, 130, 169-180.	1.2	9
8335	Phylogenetic placement and redescription of <i>Aleochara blackburni</i> Bernhauer & Scheerpeltz, 1926 (Coleoptera: Staphylinidae) from coastal Australia. <i>Austral Entomology</i> , 2019, 58, 76-84.	0.8	4
8336	Genome-Wide Analysis of MDR and XDR Tuberculosis from Belarus: Machine-Learning Approach. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 1398-1408.	1.9	8
8337	A new phylogeny of ichthyosaurs (Reptilia: Diapsida). <i>Journal of Systematic Palaeontology</i> , 2019, 17, 129-155.	0.6	56
8338	Molecular phylogeny of Entomobrya (Collembola: Entomobryidae) from China: Color pattern groups and multiple origins. <i>Insect Science</i> , 2019, 26, 587-597.	1.5	15
8339	Complete chloroplast genome of <i>Cinnamomum japonicum</i> (Laurales: Lauraceae), an endangered tree species. <i>Conservation Genetics Resources</i> , 2019, 11, 267-269.	0.4	2
8340	Complete mitochondrial genome sequence of the Przewalski's gazelle (<i>Procapra przewalskii</i>). <i>Conservation Genetics Resources</i> , 2019, 11, 369-371.	0.4	2
8341	Description and phylogeny of the mitochondrial genome of <i>Sabethes chloropterus</i> , <i>Sabethes glaucodaemon</i> and <i>Sabethes belisarioi</i> (Diptera: Culicidae). <i>Genomics</i> , 2019, 111, 607-611.	1.3	24
8342	The complete mitochondrial genome of <i>Panthera pardus</i> (Felidae: Pantheriinae), a first-class national-protected wild animal from China. <i>Conservation Genetics Resources</i> , 2019, 11, 389-392.	0.4	3

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8343	Characterization of the chloroplast genome of <i>Erythrophleum fordii</i> (Fabaceae). Conservation Genetics Resources, 2019, 11, 165-167.	0.4	4
8344	Characterization of the complete mitochondrial genome of <i>Rusa unicolor hainana</i> (Artiodactyla: Tj ETQq1 1 0.784314 rgBT /Overlock 11	0.4	2
8345	Systematic survey of non-retroviral virus-like elements in eukaryotic genomes. Virus Research, 2019, 262, 30-36.	1.1	27
8346	The complete mitochondrial genome of the sea star <i>Echinaster (Othilia) brasiliensis</i> (Asteroidea: Tj ETQq1 1 0.784314 rgBT /Overlock 11	0.4	3
8347	The complete mitochondrial genome of the southern two-lined salamander, <i>Eurycea cirrigera</i> (Caudata: Plethodontidae). Conservation Genetics Resources, 2019, 11, 177-179.	0.4	0
8348	The complete chloroplast genome of <i>Corylopsis coreana</i> (Hamamelidaceae). Conservation Genetics Resources, 2019, 11, 291-293.	0.4	2
8349	Complete chloroplast genome of the threatened <i>Rhoiptelea chiliantha</i> (Juglandaceae s.l.). Conservation Genetics Resources, 2019, 11, 317-319.	0.4	2
8350	Characterization of the complete chloroplast genome of <i>Juniperus microsperma</i> (Cupressaceae), a rare endemic from the Qinghai-Tibet Plateau. Conservation Genetics Resources, 2019, 11, 325-328.	0.4	3
8351	Tracing the maternal origin of the common wall lizard (<i>Podarcis muralis</i>) on the northern range margin in Central Europe. Mitochondrion, 2019, 46, 149-157.	1.6	10
8352	Characterization of the complete chloroplast genome of an endemic species of pea family in China, <i>Ormosia hosiei</i> (Fabaceae). Conservation Genetics Resources, 2019, 11, 443-446.	0.4	3
8353	Intraspecific mitochondrial genome comparison identified CYTB as a high-resolution population marker in a new pest <i>Athetis lepigone</i> . Genomics, 2019, 111, 744-752.	1.3	15
8354	Evidence for panmixia despite barriers to gene flow in the hooked mussel, <i>Ischadium recurvum</i> (Mytilidae; Brachidontinae) along the North American coastline. Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2019, 30, 75-81.	0.7	0
8355	The chloroplast genome of <i>Chunia bucklandioides</i> (Hamamelidaceae): a rare tree endemic to Hainan, China. Conservation Genetics Resources, 2019, 11, 427-429.	0.4	3
8356	Species integrity and origin of <i>Oreochromis hunteri</i> (Pisces: Cichlidae), endemic to crater Lake Chala (Kenyaâ€”Tanzania). Hydrobiologia, 2019, 832, 269-282.	1.0	7
8357	Genomic sequence investigation <i>Streptococcus pyogenes</i> clusters in England (2010â€”2015). Clinical Microbiology and Infection, 2019, 25, 96-101.	2.8	9
8358	The complete chloroplast genome sequence of <i>Ostrya chisosensis</i> . Conservation Genetics Resources, 2019, 11, 93-95.	0.4	0
8359	The complete chloroplast genome of <i>Cupressus jiangeensis</i> (cupressaceae), a critically endangered conifer species in China. Conservation Genetics Resources, 2019, 11, 67-69.	0.4	2
8360	Complete mitochondrial genome of <i>Chrysolophus pictus</i> (Galliformes: Phasianidae), a protected and endangered pheasant species of China. Conservation Genetics Resources, 2019, 11, 121-124.	0.4	0

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8361	Characterization of the complete plastome of western red cedar, <i>Thuja plicata</i> (Cupressaceae). Conservation Genetics Resources, 2019, 11, 79-81.	0.4	3
8362	The complete chloroplast genome of a critically endangered tree species in China, <i>Cyclobalanopsis obovatifolia</i> (Fagaceae). Conservation Genetics Resources, 2019, 11, 31-33.	0.4	3
8363	When did the ancestor of true bugs become stinky? Disentangling the phylogenomics of Hemipteraâ€“Heteroptera. Cladistics, 2019, 35, 42-66.	1.5	53
8364	The complete maternal mitochondrial genome of <i>Acuticosta chinensis</i> (Bivalvia: Unionoidea). Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 57	0.4	1
8365	Two new species of <i>Cardicola</i> (Trematoda: Aporocotylidae) from the damselfish <i>Abudefduf whitleyi</i> (Perciformes: Pomacentridae) and the triggerfish <i>Sufflamen chrysopterum</i> (Tetraodontiformes). Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 57	0.4	1
8366	Population genetic structure and phylogeography of sterlet (<i>Acipenser ruthenus</i>), Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 57 and Analysis, 2019, 30, 156-164.	0.7	5
8367	<i>Leptographium wushanense</i> sp. nov., associated with <i>Tomicus armandii</i> on <i>Pinus armandii</i> in Southwestern China. Mycoscience, 2020, 61, 43-48.	0.3	3
8368	Morphological and molecular characterization of two new species of the genus <i>Aporcelinus</i> Andr�ssy, 2009 (Nematoda, Dorylaimida, Aporcelaimidae) from the USA, with new insights on the phylogeny of the genus. Journal of Helminthology, 2020, 94, e22.	0.4	4
8369	Rapid Laurasian diversification of a pantropical bird family during the Oligoceneâ€“Miocene transition. Ibis, 2020, 162, 137-152.	1.0	10
8370	Biochar soil amendments in prairie restorations do not interfere with benefits from inoculation with native arbuscular mycorrhizal fungi. Restoration Ecology, 2020, 28, 785-795.	1.4	13
8371	Diversity of <i>Rhabdochona mexicana</i> (Nematoda: Rhabdochonidae), a parasite of <i>Astyanax</i> spp. (Characidae) in Mexico and Guatemala, using mitochondrial and nuclear genes, with the description of a new species. Journal of Helminthology, 2020, 94, e34.	0.4	4
8372	Complete mitochondrial genomes of three <i>Oxya</i> grasshoppers (Orthoptera) and their implications for phylogenetic reconstruction. Genomics, 2020, 112, 289-296.	1.3	14
8373	Integrated transcriptome provides resources and insights into the adaptive evolution of colonized brown trout (<i>Salmo trutta fario</i>) in the Tibetan Plateau. Journal of the World Aquaculture Society, 2020, 51, 763-774.	1.2	7
8374	Understand the genomic diversity and evolution of fungal pathogen <i>Candida glabrata</i> by genome-wide analysis of genetic variations. Methods, 2020, 176, 82-90.	1.9	17
8375	Model Choice, Missing Data, and Taxon Sampling Impact Phylogenomic Inference of Deep Basidiomycota Relationships. Systematic Biology, 2020, 69, 17-37.	2.7	34
8376	Accounting for Uncertainty in the Evolutionary Timescale of Green Plants Through Clock-Partitioning and Fossil Calibration Strategies. Systematic Biology, 2020, 69, 1-16.	2.7	55
8377	Dates and rates in grapeâ€™s plastomes: evolution in slow motion. Current Genetics, 2020, 66, 123-140.	0.8	10
8378	Mesozoic mitogenome rearrangements and freshwater mussel (Bivalvia: Unionoidea) macroevolution. Heredity, 2020, 124, 182-196.	1.2	27

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8379	Cross-transmission Is Not the Source of New Mycobacterium abscessus Infections in a Multicenter Cohort of Cystic Fibrosis Patients. <i>Clinical Infectious Diseases</i> , 2020, 70, 1855-1864.	2.9	48
8380	Phylogenomics Uncovers Confidence and Conflict in the Rapid Radiation of Australo-Papuan Rodents. <i>Systematic Biology</i> , 2020, 69, 431-444.	2.7	44
8381	Molecular phylogenetic analysis resolves <i>Trisetum</i> (Poaceae: Pooideae: Koeleriinae) polyphyletic: Evidence for a new genus, <i>Sibirotrisetum</i> and resurrection of <i>Acrospelion</i> . <i>Journal of Systematics and Evolution</i> , 2020, 58, 517-526.	1.6	17
8382	Genetic analysis reveals strong phylogeographical divergences within the Scarlet Macaw <i>Ara macao</i> . <i>Ibis</i> , 2020, 162, 735-748.	1.0	6
8383	A reevaluation of the Andean Genus <i>Petroravenia</i> (Brassicaceae: Thelypodieae) based on morphological and molecular data. <i>Journal of Systematics and Evolution</i> , 2020, 58, 43-58.	1.6	2
8384	Characterization of the complete mitochondrial genome of <i>Uca lacteus</i> and comparison with other Brachyuran crabs. <i>Genomics</i> , 2020, 112, 10-19.	1.3	30
8385	Mean and Variance of Phylogenetic Trees. <i>Systematic Biology</i> , 2020, 69, 139-154.	2.7	12
8386	Inverse dispersal patterns in a group of ant parasitoids (Hymenoptera: Eucharitidae: Oraseminae) and their ant hosts. <i>Systematic Entomology</i> , 2020, 45, 1-19.	1.7	14
8387	Taxonomic status of seven nominal species of the anchovy genus <i>Stolephorus</i> described by Delsman (1931), Hardenberg (1933), and Dutt and Babu Rao (1959), with redescrptions of <i>Stolephorus tri</i> (Bleeker) <i>Tj ETQq0,0 0 rgBTj/Overlock Research</i> , 2020, 67, 7-38.	0.5	15
8388	Phylogenomic Relationships of Diploids and the Origins of Allotetraploids in <i>Dactylorhiza</i> (Orchidaceae). <i>Systematic Biology</i> , 2020, 69, 91-109.	2.7	89
8389	Characterization of the unarmored dinoflagellate <i>Pselodinium pirum</i> (Cerato-peridiniaceae) from Jiaozhou Bay, China. <i>Phycological Research</i> , 2020, 68, 3-13.	0.8	7
8390	Uncovering the genomic signature of ancient introgression between white oak lineages (<i>Quercus</i>). <i>New Phytologist</i> , 2020, 226, 1158-1170.	3.5	63
8391	Species delimitation and phylogeography of <i>Abies delavayi</i> complex: Inferred from morphological, molecular, and climatic data. <i>Journal of Systematics and Evolution</i> , 2020, 58, 234-246.	1.6	9
8392	Phylogeny of the orb-weaving spider family Araneidae (Araneae: Araneoidea). <i>Cladistics</i> , 2020, 36, 1-21.	1.5	66
8393	Decoding and analysis of organelle genomes of Indian tea (<i>Camellia assamica</i>) for phylogenetic confirmation. <i>Genomics</i> , 2020, 112, 659-668.	1.3	19
8394	Zebrafish Model for Nonsyndromic X-Linked Sensorineural Deafness, <i>DFNX1</i> . <i>Anatomical Record</i> , 2020, 303, 544-555.	0.8	16
8395	The mitochondrial genomes of three skippers: Insights into the evolution of the family Hesperiiidae (Lepidoptera). <i>Genomics</i> , 2020, 112, 432-441.	1.3	22
8396	Unraveling Deep Branches of the Sigmodontinae Tree (Rodentia: Cricetidae) in Eastern South America. <i>Journal of Mammalian Evolution</i> , 2020, 27, 139-160.	1.0	24

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8397	Interrogating Genomic-Scale Data for Squamata (Lizards, Snakes, and Amphisbaenians) Shows no Support for Key Traditional Morphological Relationships. <i>Systematic Biology</i> , 2020, 69, 502-520.	2.7	191
8398	APPLES: Scalable Distance-Based Phylogenetic Placement with or without Alignments. <i>Systematic Biology</i> , 2020, 69, 566-578.	2.7	51
8399	The many faced symbiotic snakelocks anemone (<i>Anemonia viridis</i> , Anthozoa): host and symbiont genetic differentiation among colour morphs. <i>Heredity</i> , 2020, 124, 351-366.	1.2	7
8400	The recent emergence of a highly related virulent <i>Clostridium difficile</i> clade with unique characteristics. <i>Clinical Microbiology and Infection</i> , 2020, 26, 492-498.	2.8	36
8401	Learning from Dynamic Traits: Seasonal Shifts Yield Insights into Ecophysiological Trade-Offs across Scales from Macroevolutionary to Intraindividual. <i>International Journal of Plant Sciences</i> , 2020, 181, 88-102.	0.6	10
8402	Detection of Nonhematologic Neoplasms by Routine Flow Cytometry Analysis. <i>American Journal of Clinical Pathology</i> , 2020, 153, 99-104.	0.4	10
8403	Horizontal acquisition of a patchwork Calvin cycle by symbiotic and free-living <i>Campylobacterota</i> (formerly <i>Epsilonproteobacteria</i>). <i>ISME Journal</i> , 2020, 14, 104-122.	4.4	55
8404	Investigating Transfusion-related Sepsis Using Culture-Independent Metagenomic Sequencing. <i>Clinical Infectious Diseases</i> , 2020, 71, 1179-1185.	2.9	21
8405	Comparative Genomic Analysis of the Pheromone Receptor Class 1 Family (V1R) Reveals Extreme Complexity in Mouse Lemurs (Genus, <i>Microcebus</i>) and a Chromosomal Hotspot across Mammals. <i>Genome Biology and Evolution</i> , 2020, 12, 3562-3579.	1.1	12
8406	Patterns of Genomic Differentiation in the <i>Drosophila nasuta</i> Species Complex. <i>Molecular Biology and Evolution</i> , 2020, 37, 208-220.	3.5	26
8407	Sympatric western lowland gorillas, central chimpanzees and humans are infected with different trichomonads. <i>Parasitology</i> , 2020, 147, 225-230.	0.7	1
8408	Reassessment of the genus <i>Lophurella</i> (<i>Rhodomelaceae</i> , <i>Rhodophyta</i>) from Australia and New Zealand reveals four cryptic species. <i>European Journal of Phycology</i> , 2020, 55, 113-128.	0.9	17
8409	Characterisation of the β -lactam resistance enzyme in <i>Acanthamoeba castellanii</i> . <i>International Journal of Antimicrobial Agents</i> , 2020, 55, 105823.	1.1	4
8410	Plastid phylogenomic insights into the evolution of the <i>Caprifoliaceae</i> s.l. (<i>Dipsacales</i>). <i>Molecular Phylogenetics and Evolution</i> , 2020, 142, 106641.	1.2	52
8411	<i>Planctopirus ephydatiae</i> , a novel Planctomycete isolated from a freshwater sponge. <i>Systematic and Applied Microbiology</i> , 2020, 43, 126022.	1.2	52
8412	Marked changes in diversity and relative activity of picoeukaryotes with depth in the world ocean. <i>ISME Journal</i> , 2020, 14, 437-449.	4.4	80
8413	Integrative approach untangles the misconceptions about the range and identity of two stingless bees from the Brazilian semiarid region. <i>Journal of Apicultural Research</i> , 2020, 59, 592-598.	0.7	0
8414	Retrospective investigation of listeriosis outbreaks in small ruminants using different analytical approaches for whole genome sequencing-based typing of <i>Listeria monocytogenes</i> . <i>Infection, Genetics and Evolution</i> , 2020, 77, 104047.	1.0	15

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8415	Continued Adaptation of C4 Photosynthesis After an Initial Burst of Changes in the Andropogoneae Grasses. <i>Systematic Biology</i> , 2020, 69, 445-461.	2.7	27
8416	Ophiostomatales (Ascomycota) associated with <i>Tomicus</i> species in southwestern China with an emphasis on <i>Ophiostoma canum</i> . <i>Journal of Forestry Research</i> , 2020, 31, 2549-2562.	1.7	1
8417	Accelerated diversification correlated with functional traits shapes extant diversity of the early divergent angiosperm family Annonaceae. <i>Molecular Phylogenetics and Evolution</i> , 2020, 142, 106659.	1.2	29
8418	Phylogenomic Resolution of the Cetacean Tree of Life Using Target Sequence Capture. <i>Systematic Biology</i> , 2020, 69, 479-501.	2.7	160
8419	A chromosome-level genome assembly of <i>Pyropia haitanensis</i> (Bangiales, Rhodophyta). <i>Molecular Ecology Resources</i> , 2020, 20, 216-227.	2.2	37
8420	Comparative genome/transcriptome analysis probes Boraginales' phylogenetic position, WGDs in Boraginales, and key enzyme genes in the alkannin/shikonin core pathway. <i>Molecular Ecology Resources</i> , 2020, 20, 228-241.	2.2	24
8421	Genomic landscape of the global oak phylogeny. <i>New Phytologist</i> , 2020, 226, 1198-1212.	3.5	186
8422	Novel H5N6 avian influenza virus reassortants with European H5N8 isolated in migratory birds, China. <i>Transboundary and Emerging Diseases</i> , 2020, 67, 648-660.	1.3	10
8423	Expansin gene loss is a common occurrence during adaptation to an aquatic environment. <i>Plant Journal</i> , 2020, 101, 666-680.	2.8	12
8424	Genome-wide identification and analysis of genes encoding cuticular proteins in the endoparasitoid wasp <i>Pteromalus puparum</i> (Hymenoptera: Pteromalidae). <i>Archives of Insect Biochemistry and Physiology</i> , 2020, 103, e21628.	0.6	8
8425	Overexpression of an alternative allele of carboxyl/choline esterase 4 (CCE04) of <i>Tetranychus urticae</i> is associated with high levels of resistance to the keto-enol acaricide spiroticlofen. <i>Pest Management Science</i> , 2020, 76, 1142-1153.	1.7	29
8426	Controlling oxygen vacancies and enhanced visible light photocatalysis of CeO ₂ /ZnO nanocomposites. <i>Journal of Photochemistry and Photobiology A: Chemistry</i> , 2020, 392, 112156.	2.0	90
8427	Evolution of endemic and sylvatic lineages of dengue virus. <i>Cladistics</i> , 2020, 36, 115-128.	1.5	2
8428	Substrate-specificity of cytochrome P450-mediated detoxification as an evolutionary strategy for specialization on furanocoumarin-containing hostplants: CYP6AE89 in parsnip webworms. <i>Insect Molecular Biology</i> , 2020, 29, 112-123.	1.0	19
8429	Phylogeography of the bitterling <i>Tanakia lanceolata</i> (Teleostei: Cyprinidae) in Japan inferred from mitochondrial cytochrome b gene sequences. <i>Ichthyological Research</i> , 2020, 67, 105-116.	0.5	18
8430	<i>Metschnikowia miensis</i> f.a., sp. nov., isolated from flowers in Mie prefecture, Japan. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 321-329.	0.7	3
8431	A critical review on exploiting the pharmaceutical potential of plant endophytic fungi. <i>Biotechnology Advances</i> , 2020, 39, 107462.	6.0	206
8432	Phylogenetic divergence within the Arcellinida (Amoebozoa) is congruent with test size and metabolism type. <i>European Journal of Protistology</i> , 2020, 72, 125645.	0.5	9

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8433	Fine-Scale Haplotype Structure Reveals Strong Signatures of Positive Selection in a Recombining Bacterial Pathogen. <i>Molecular Biology and Evolution</i> , 2020, 37, 417-428.	3.5	27
8434	One hundred years later, resurrection of <i>Tydemania gardineri</i> A. Gepp & E. Gepp (Udoteaceae.) <i>Tj ETQq1 1 0.784314 rgBT / Overlock</i> 0.9 3	0.9	3
8435	Species delimitation and systematics of the green pythons (<i>Morelia viridis</i> complex) of melanesia and Australia. <i>Molecular Phylogenetics and Evolution</i> , 2020, 142, 106640.	1.2	18
8436	Advances in the phylogeny of the South American cool-season grass genus <i>Chascolytrum</i> (Poaceae.) <i>Tj ETQq1 1 0.784314 rgBT / Overlock</i> 0.8 8	0.8	8
8437	Plastome phylogenomics of Poaceae: alternate topologies depend on alignment gaps. <i>Botanical Journal of the Linnean Society</i> , 2020, 192, 9-20.	0.8	29
8438	The first complete mitochondrial genome of the sand dollar <i>Sinaechinocyamus mai</i> (Echinoidea.) <i>Tj ETQq1 1 0.784314 rgBT / Overlock</i> 1.3 16	1.3	16
8439	The late blooming amphipods: Global change promoted post-Jurassic ecological radiation despite Palaeozoic origin. <i>Molecular Phylogenetics and Evolution</i> , 2020, 143, 106664.	1.2	62
8440	MicroRNA528, a hub regulator modulating ROS homeostasis via targeting of a diverse set of genes encoding copper-containing proteins in monocots. <i>New Phytologist</i> , 2020, 225, 385-399.	3.5	56
8441	Evolutionary history of water voles revisited: confronting a new phylogenetic model from molecular data with the fossil record. <i>Mammalia</i> , 2020, 84, 171-184.	0.3	19
8442	Whole-genome sequencing and analysis of the Chinese herbal plant <i>Gelsemium elegans</i> . <i>Acta Pharmaceutica Sinica B</i> , 2020, 10, 374-382.	5.7	29
8443	Multilocus phylogeny defines a new classification of Staphylininae (Coleoptera, Staphylinidae), a rove beetle group with high lineage diversity. <i>Systematic Entomology</i> , 2020, 45, 114-127.	1.7	31
8444	High prevalence of <i>Wolbachia</i> infection does not explain unidirectional cytoplasmic incompatibility of <i>Altica</i> flea beetles. <i>Ecological Entomology</i> , 2020, 45, 67-78.	1.1	4
8445	The diversity and evolution of odorant receptors in beetles (Coleoptera). <i>Insect Molecular Biology</i> , 2020, 29, 77-91.	1.0	68
8446	Emergence and adaptive evolution of Nipah virus. <i>Transboundary and Emerging Diseases</i> , 2020, 67, 121-132.	1.3	15
8447	Snakehead (Teleostei: Channidae) diversity and the Eastern Himalaya biodiversity hotspot. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2020, 58, 356-386.	0.6	21
8448	Genome-wide analysis sheds light on the high-altitude adaptation of the buff-throated partridge (<i>Tetraophasis szechenyii</i>). <i>Molecular Genetics and Genomics</i> , 2020, 295, 31-46.	1.0	11
8449	Morphology, Morphogenesis, and Phylogeny of <i>Urosoma caudata</i> (Ehrenberg, 1833) Berger, 1999 (Ciliophora, Hypotrichia) based on a Chinese Population. <i>Journal of Eukaryotic Microbiology</i> , 2020, 67, 76-85.	0.8	9
8450	The desert hamster <i>Phodopus roborovskii</i> (Satunin, 1903) (Rodentia, Cricetidae) from north-western Tibetan plateau, Ladakh, India: an addition to the mammalian fauna of the Indian subcontinent. <i>Mammalia</i> , 2020, 84, 253-258.	0.3	0

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8469	Redescription of <i>Acanthogyrus</i> (<i>Acanthosentis</i>) <i>maroccanus</i> (Dollfus, 1951) (<i>Acanthocephala</i>): Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 74 Algeria, and first molecular data. <i>Journal of Helminthology</i> , 2020, 94, e82.	0.4	4
8470	ModelTest-NG: A New and Scalable Tool for the Selection of DNA and Protein Evolutionary Models. <i>Molecular Biology and Evolution</i> , 2020, 37, 291-294.	3.5	1,021
8471	Phylogenetic Estimation of Community Composition and Novel Eukaryotic Lineages in Base Mine Lake: An Oil Sands Tailings Reclamation Site in Northern Alberta. <i>Journal of Eukaryotic Microbiology</i> , 2020, 67, 86-99.	0.8	14
8472	Plastid phylogenomics improve phylogenetic resolution in the Lauraceae. <i>Journal of Systematics and Evolution</i> , 2020, 58, 423-439.	1.6	56
8473	A molecular phylogeny of <i>Cochylina</i> , with confirmation of its relationship to <i>Euliina</i> (<i>Lepidoptera</i>): Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 13	1.7	13
8474	Macroevolutionary Analyses Suggest That Environmental Factors, Not Venom Apparatus, Play Key Role in Terebridae Marine Snail Diversification. <i>Systematic Biology</i> , 2020, 69, 413-430.	2.7	11
8475	Early Colonization of Weathered Polyethylene by Distinct Bacteria in Marine Coastal Seawater. <i>Microbial Ecology</i> , 2020, 79, 517-526.	1.4	96
8476	Mitochondrial genomes and 28S rDNA contradict the proposed obsolescence of the order Tetraonchidea (<i>Platyhelminthes</i> : <i>Monogenea</i>). <i>International Journal of Biological Macromolecules</i> , 2020, 143, 891-901.	3.6	5
8477	Genomic evidence sheds light on the genetic mechanisms of musk secretion in muskrats. <i>International Journal of Biological Macromolecules</i> , 2020, 145, 1189-1198.	3.6	3
8478	Phylotranscriptomics confirms <i>Alveopora</i> is sister to <i>Montipora</i> within the family <i>Acroporidae</i> . <i>Marine Genomics</i> , 2020, 50, 100703.	0.4	9
8479	Early diversification and permeable species boundaries in the Mediterranean firs. <i>Annals of Botany</i> , 2020, 125, 495-507.	1.4	24
8480	Species of <i>Cryphonectriaceae</i> occupy an endophytic niche in the <i>Melastomataceae</i> and are putative latent pathogens of <i>Eucalyptus</i> . <i>European Journal of Plant Pathology</i> , 2020, 156, 273-283.	0.8	9
8481	Genomic Epidemiology as a Public Health Tool to Combat Mosquito-Borne Virus Outbreaks. <i>Journal of Infectious Diseases</i> , 2020, 221, S308-S318.	1.9	15
8482	Dur3 and nrt2 genes in the bloom-forming dinoflagellate <i>Prorocentrum minimum</i> : Transcriptional responses to available nitrogen sources. <i>Chemosphere</i> , 2020, 241, 125083.	4.2	9
8483	Morphology and molecular phylogeny of a new hypotrich ciliate, <i>Anteholosticha songi</i> nov. spec., and an American population of <i>Holosticha pullaster</i> (Müller, 1773) Foissner et al., 1991 (<i>Ciliophora</i>): Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 13	1.5	13
8484	Phylogenetic implications of mitogenome rearrangements in East Asian potamiscine freshwater crabs (<i>Brachyura</i> : <i>Potamidae</i>). <i>Molecular Phylogenetics and Evolution</i> , 2020, 143, 106669.	1.2	26
8485	Cross-contamination and strong mitonuclear discordance in <i>Empria</i> sawflies (<i>Hymenoptera</i>): Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 107 T 106670.	1.2	10
8486	Evidences of aromatic degradation dominantly via the phenylacetic acid pathway in marine benthic <i>Thermopfundales</i> . <i>Environmental Microbiology</i> , 2020, 22, 329-342.	1.8	12

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8487	Fusaric acid instigates the invasion of banana by <i>Fusarium oxysporum</i> f. sp. <i>cubense</i> <sc>4. <i>New Phytologist</i> , 2020, 225, 913-929.	3.5	49
8488	New clade of silicified bolidophytes that belong to <i>Triparma</i> (Bolidophyceae, Stramenopiles). <i>Phycological Research</i> , 2020, 68, 178-182.	0.8	4
8489	Genomic evidence suggests <i>Mesapamea remmi</i> is an imaginary species (Lepidoptera: Noctuidae). <i>Systematic Entomology</i> , 2020, 45, 302-311.	1.7	1
8490	Enigmatic Phytomyxid Parasite of the Alien Seagrass <i>Halophila stipulacea</i> : New Insights into Its Ecology, Phylogeny, and Distribution in the Mediterranean Sea. <i>Microbial Ecology</i> , 2020, 79, 631-643.	1.4	9
8491	Genetic Contribution of Paleopolyploidy to Adaptive Evolution in Angiosperms. <i>Molecular Plant</i> , 2020, 13, 59-71.	3.9	178
8492	The Green Revolution shaped the population structure of the rice pathogen <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> . <i>ISME Journal</i> , 2020, 14, 492-505.	4.4	29
8493	Molecular survey of the red algal family Rhodomelaceae (Ceramiales, Rhodophyta) in Australia reveals new introduced species. <i>Journal of Applied Phycology</i> , 2020, 32, 2535-2547.	1.5	11
8494	Population genomics of <i>Tillandsia landbeckii</i> reveals unbalanced genetic diversity and founder effects in the Atacama Desert. <i>Global and Planetary Change</i> , 2020, 184, 103076.	1.6	14
8495	<i>Plasmodium vivax</i> Malaria Viewed through the Lens of an Eradicated European Strain. <i>Molecular Biology and Evolution</i> , 2020, 37, 773-785.	3.5	38
8496	Long-read metabarcoding of the eukaryotic rDNA operon to phylogenetically and taxonomically resolve environmental diversity. <i>Molecular Ecology Resources</i> , 2020, 20, 429-443.	2.2	68
8497	Genotyping of <i>Mycobacterium tuberculosis</i> spreading in Hanoi, Vietnam using conventional and whole genome sequencing methods. <i>Infection, Genetics and Evolution</i> , 2020, 78, 104107.	1.0	11
8498	Vegetative desiccation tolerance in the resurrection plant <i>Xerophyta humilis</i> has not evolved through reactivation of the seed canonical LAFL regulatory network. <i>Plant Journal</i> , 2020, 101, 1349-1367.	2.8	19
8499	Linking evolutionary mode to palaeoclimate change reveals rapid radiations of staphylinoid beetles in low-energy conditions. <i>Environmental Epigenetics</i> , 2020, 66, 435-444.	0.9	28
8500	Identification of the pathogen responsible for tea white scab disease. <i>Journal of Phytopathology</i> , 2020, 168, 28-35.	0.5	1
8501	Long solids retention times and attached growth phase favor prevalence of comammox bacteria in nitrogen removal systems. <i>Water Research</i> , 2020, 169, 115268.	5.3	98
8502	Reticulate Evolution Helps Explain Apparent Homoplasy in Floral Biology and Pollination in Baobabs (<i>Adansonia</i> ; <i>Bombacoideae</i> ; <i>Malvaceae</i>). <i>Systematic Biology</i> , 2020, 69, 462-478.	2.7	32
8503	<i>Mesostigma viride</i> Genome and Transcriptome Provide Insights into the Origin and Evolution of Streptophyta. <i>Advanced Science</i> , 2020, 7, 1901850.	5.6	40
8504	Mitochondrial Metagenomics Reveals the Ancient Origin and Phylodiversity of Soil Mites and Provides a Phylogeny of the Acari. <i>Molecular Biology and Evolution</i> , 2020, 37, 683-694.	3.5	42

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8505	Molecular insights into the phylogeny of Blapstinina (Coleoptera: Tenebrionidae: Opatrini). Systematic Entomology, 2020, 45, 337-348.	1.7	11
8506	Molecular confirmation and morphological reassessment of <i>Udotea geppiorum</i> (Bryopsidales) European Journal of Phycology, 2020, 55, 186-196.	0.9	6
8507	Large-scale genomic sequence data resolve the deepest divergences in the legume phylogeny and support a near-simultaneous evolutionary origin of all six subfamilies. New Phytologist, 2020, 225, 1355-1369.	3.5	94
8508	Anchored hybrid enrichment challenges the traditional classification of flesh flies (Diptera: Tephritidae) Molecular Biology and Evolution, 2020, 37, 730-756.	1.7	32
8509	A novel reassortant clade 2.3.4.4 highly pathogenic avian influenza H5N6 virus identified in South Korea in 2018. Infection, Genetics and Evolution, 2020, 78, 104056.	1.0	13
8510	Two novel cricetine mitogenomes: Insight into the mitogenomic characteristics and phylogeny in Cricetinae (Rodentia: Cricetidae). Genomics, 2020, 112, 1716-1725.	1.3	9
8511	Multi-SpaM: a maximum-likelihood approach to phylogeny reconstruction using multiple spaced-word matches and quartet trees. NAR Genomics and Bioinformatics, 2020, 2, lqz013.	1.5	12
8512	High Phenotypic and Genotypic Diversity of <i>Enterococcus faecium</i> from Clinical and Commensal Isolates in Third Level Hospital. Microbial Drug Resistance, 2020, 26, 227-237.	0.9	1
8513	Phylogenomics Identifies an Ancestral Burst of Gene Duplications Predating the Diversification of Aphidomorpha. Molecular Biology and Evolution, 2020, 37, 730-756.	3.5	29
8514	Male-male competition and repeated evolution of terrestrial breeding in Atlantic Coastal Forest frogs*. Evolution; International Journal of Organic Evolution, 2020, 74, 459-475.	1.1	9
8515	Optimizing Phylogenomics with Rapidly Evolving Long Exons: Comparison with Anchored Hybrid Enrichment and Ultraconserved Elements. Molecular Biology and Evolution, 2020, 37, 904-922.	3.5	39
8516	The mitochondrial genome of the dung beetle, <i>Copris tripartitus</i> , with mitogenomic comparisons within Scarabaeidae (Coleoptera). International Journal of Biological Macromolecules, 2020, 144, 874-891.	3.6	12
8517	Hepatitis B Virus: Alternative phylogenetic hypotheses and its impact on molecular evolution inferences. Virus Research, 2020, 276, 197776.	1.1	3
8518	The power of neuropeptide precursor sequences to reveal phylogenetic relationships in insects: A case study on Blattodea. Molecular Phylogenetics and Evolution, 2020, 143, 106686.	1.2	12
8519	Metatranscriptomics yields new genomic resources and sensitive detection of infections for diverse blood parasites. Molecular Ecology Resources, 2020, 20, 14-28.	2.2	25
8520	A novel taxon selection method, aimed at minimizing recombination, clarifies the discovery of a new sub-population of <i>Helicobacter pylori</i> from Australia. Evolutionary Applications, 2020, 13, 278-289.	1.5	6
8521	Between an ocean and a high place: coastal drainage isolation generates endemic cryptic species in the Cape kurper <i>Sandelia capensis</i> (Anabantiformes: Anabantidae), Cape Region, South Africa. Journal of Fish Biology, 2020, 96, 1087-1099.	0.7	12
8522	Contrasting Mixotrophic Lifestyles Reveal Different Ecological Niches in Two Closely Related Marine Protists. Journal of Phycology, 2020, 56, 52-67.	1.0	41

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8523	The Arctic <i>Cylindrocystis</i> (Zygnematophyceae, Streptophyta) Green Algae are Genetically and Morphologically Diverse and Exhibit Effective Accumulation of Polyphosphate. <i>Journal of Phycology</i> , 2020, 56, 217-232.	1.0	21
8524	The Pseudoplagioporinae, a new subfamily in the Opecoelidae Ozaki, 1925 (Trematoda) for a small clade parasitizing mainly lehrinid fishes, with three new species. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2020, 58, 79-113.	0.6	8
8525	The enigmatic Crimean green lizard (<i>Lacerta viridis magnifica</i>) is extinct but not valid: Mitogenomics of a 120-year-old museum specimen reveals historical introduction. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2020, 58, 303-307.	0.6	12
8526	Repeated evolution of queen parthenogenesis and social hybridogenesis in <i>Cataglyphis</i> desert ants. <i>Molecular Ecology</i> , 2020, 29, 549-564.	2.0	26
8527	Genetic diversity of respiratory enteroviruses and rhinoviruses in febrile adults, Singapore, 2007-2013. <i>Influenza and Other Respiratory Viruses</i> , 2020, 14, 67-71.	1.5	9
8528	Molecular Phylogenetic Position of <i>Hoplonympha natator</i> (Trichonympha, Parabasalia): Horizontal Symbiont Transfer or Differential Loss?. <i>Journal of Eukaryotic Microbiology</i> , 2020, 67, 268-272.	0.8	4
8529	Geophytism in monocots leads to higher rates of diversification. <i>New Phytologist</i> , 2020, 225, 1023-1032.	3.5	22
8530	Cyanobacterial carboxysomes contain an unique rubisco-activase-like protein. <i>New Phytologist</i> , 2020, 225, 793-806.	3.5	29
8531	Genetic variation and temperature affects hybrid barriers during interspecific hybridization. <i>Plant Journal</i> , 2020, 101, 122-140.	2.8	20
8532	Inhibition of histone acetylation and deacetylation enzymes affects longevity, development, and fecundity in the pea aphid (<i>Acyrtosiphon pisum</i>). <i>Archives of Insect Biochemistry and Physiology</i> , 2020, 103, e21614.	0.6	9
8533	Direct oxidation esterification of methacrolein with methanol: Oxygen vacancy promotion of Zr-doped Au/CeO ₂ nanorods. <i>Canadian Journal of Chemical Engineering</i> , 2020, 98, 767-774.	0.9	15
8534	The complete mitochondrial genomes of two model ectomycorrhizal fungi (<i>Laccaria</i>): features, intron dynamics and phylogenetic implications. <i>International Journal of Biological Macromolecules</i> , 2020, 145, 974-984.	3.6	52
8535	Asymmetric Distribution of Gene Trees Can Arise under Purifying Selection If Differences in Population Size Exist. <i>Molecular Biology and Evolution</i> , 2020, 37, 881-892.	3.5	12
8536	Computational Framework for High-Quality Production and Large-Scale Evolutionary Analysis of Metagenome Assembled Genomes. <i>Molecular Biology and Evolution</i> , 2020, 37, 593-598.	3.5	11
8537	Structural diversity in the Mycobacteria DUF3349 superfamily. <i>Protein Science</i> , 2020, 29, 670-685.	3.1	1
8538	Adaptive Radiation of the Flukes of the Family Fasciolidae Inferred from Genome-Wide Comparisons of Key Species. <i>Molecular Biology and Evolution</i> , 2020, 37, 84-99.	3.5	28
8539	Treeio: An R Package for Phylogenetic Tree Input and Output with Richly Annotated and Associated Data. <i>Molecular Biology and Evolution</i> , 2020, 37, 599-603.	3.5	348
8540	Living Trees: High-Quality Reproducible and Reusable Construction of Bacterial Phylogenetic Trees. <i>Molecular Biology and Evolution</i> , 2020, 37, 563-575.	3.5	17

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8541	The Effect of Older Age on the Perioperative Outcomes of Spinal Fusion Surgery in Patients With Lumbar Degenerative Disc Disease With Spondylolisthesis: A Propensity Score-Matched Analysis. <i>Neurosurgery</i> , 2020, 87, 672-678.	0.6	10
8542	Transitions between the Terrestrial and Epiphytic Habit Drove the Evolution of Seed-Aerodynamic Traits in Orchids. <i>American Naturalist</i> , 2020, 195, 275-283.	1.0	11
8543	Molecular epidemiology of <i>Sporothrix schenckii</i> isolates in Malaysia. <i>Medical Mycology</i> , 2020, 58, 617-625.	0.3	12
8544	Assessing the status of critically endangered Kondana soft-furred rat (<i>Millardia kondana</i>) using integrative taxonomy: combining evidence from morphological, molecular and environmental niche modeling. <i>Mammalia</i> , 2020, 84, 392-406.	0.3	0
8545	Developmental gene expression as a phylogenetic data class: support for the monophyly of Arachnoplumonata. <i>Development Genes and Evolution</i> , 2020, 230, 137-153.	0.4	27
8546	Newly discovered coralline algae in Southeast Brazil: <i>Tectolithon fluminense</i> gen. et sp. nov. and <i>Crustaphyllum atlanticum</i> sp. nov. (Hapalidiales, Rhodophyta). <i>Phycologia</i> , 2020, 59, 101-115.	0.6	13
8547	Transcriptome-Wide Patterns of the Genetic and Expression Variations in Two Sympatric Schizothoracine Fishes in a Tibetan Plateau Glacier Lake. <i>Genome Biology and Evolution</i> , 2020, 12, 3725-3737.	1.1	6
8548	Comparative genomics reveal shared genomic changes in syngnathid fishes and signatures of genetic convergence with placental mammals. <i>National Science Review</i> , 2020, 7, 964-977.	4.6	32
8549	Characterizing the ribosomal tandem repeat and its utility as a DNA barcode in lichen-forming fungi. <i>BMC Evolutionary Biology</i> , 2020, 20, 2.	3.2	16
8550	Evolutionary relationships among bifidobacteria and their hosts and environments. <i>BMC Genomics</i> , 2020, 21, 26.	1.2	26
8551	Identification of a novel anthocyanin synthesis pathway in the fungus <i>Aspergillus sydowii</i> H-1. <i>BMC Genomics</i> , 2020, 21, 29.	1.2	26
8552	Long live the king: chromosome-level assembly of the lion (<i>Panthera leo</i>) using linked-read, Hi-C, and long-read data. <i>BMC Biology</i> , 2020, 18, 3.	1.7	34
8553	Non-parametric correction of estimated gene trees using TRACTION. <i>Algorithms for Molecular Biology</i> , 2020, 15, 1.	0.3	11
8554	Global evaluation of taxonomic relationships and admixture within the <i>Culex pipiens</i> complex of mosquitoes. <i>Parasites and Vectors</i> , 2020, 13, 8.	1.0	25
8555	CSO – A sequence optimization software for engineering chloroplast expression in <i>Chlamydomonas reinhardtii</i> . <i>Algal Research</i> , 2020, 46, 101788.	2.4	6
8556	<i>Euplotes octocarinatus</i> Carter, 1972 (Ciliophora, Spirotrichea, Euplotidae): Considerations on its morphology, phylogeny, and biogeography. <i>European Journal of Protistology</i> , 2020, 74, 125667.	0.5	7
8557	Phenotype and genomic background of <i>Arcobacter butzleri</i> strains and taxogenomic assessment of the species. <i>Food Microbiology</i> , 2020, 89, 103416.	2.1	19
8558	Eight high-quality genomes reveal pan-genome architecture and ecotype differentiation of <i>Brassica napus</i> . <i>Nature Plants</i> , 2020, 6, 34-45.	4.7	449

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8559	ipyrad: Interactive assembly and analysis of RADseq datasets. <i>Bioinformatics</i> , 2020, 36, 2592-2594.	1.8	479
8560	Disentangling Population History and Character Evolution among Hybridizing Lineages. <i>Molecular Biology and Evolution</i> , 2020, 37, 1295-1305.	3.5	5
8561	Morphological and molecular description of <i>Armillifer moniliformis</i> larvae isolated from Sri Lankan brown palm civet (<i>Paradoxurus montanus</i>). <i>Parasitology Research</i> , 2020, 119, 773-781.	0.6	0
8562	Three marine strains constitute the novel genus and species <i>Crateriforma conspicua</i> in the phylum Planctomycetes. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 1797-1809.	0.7	35
8563	<i>Blastopirellula retiformator</i> sp. nov. isolated from the shallow-sea hydrothermal vent system close to Panarea Island. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 1811-1822.	0.7	29
8564	Description of the novel planctomycetal genus <i>Bremerella</i> , containing <i>Bremerella volcania</i> sp. nov., isolated from an active volcanic site, and reclassification of <i>Blastopirellula crema</i> as <i>Bremerella crema</i> comb. nov.. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 1823-1837.	0.7	36
8565	Phylogenetic placement of <i>Leptosphaeria polylepidis</i> , a pathogen of Andean endemic <i>Polylepis tarapacana</i> , and its newly discovered mycoparasite <i>Sajamaea mycophila</i> gen. et sp. nov.. <i>Mycological Progress</i> , 2020, 19, 1-14.	0.5	7
8566	In vitro inferred interactions of selected entomopathogenic fungi from Taiwan and eggs of <i>Meloidogyne graminicola</i> . <i>Mycological Progress</i> , 2020, 19, 97-109.	0.5	9
8567	A comprehensive phylogeographic study of <i>Arion vulgaris</i> Moquin-Tandon, 1855 (Gastropoda: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 42).	0.7	11
8568	<i>Colletotrichum truncatum</i> causing anthracnose on papaya fruit (<i>Carica papaya</i>) in Brazil. <i>Australasian Plant Disease Notes</i> , 2020, 15, 1.	0.4	7
8569	Bioprecipitation of As4S4 polymorphs in an abandoned mine adit. <i>Applied Geochemistry</i> , 2020, 113, 104511.	1.4	13
8570	Prevalence and molecular epidemiology of bovine leukemia virus in Colombian cattle. <i>Infection, Genetics and Evolution</i> , 2020, 80, 104171.	1.0	16
8571	Evidence for phylogenetically and catabolically diverse active diazotrophs in deep-sea sediment. <i>ISME Journal</i> , 2020, 14, 971-983.	4.4	43
8572	A shared genetic basis of mimicry across swallowtail butterflies points to ancestral co-option of doublesex. <i>Nature Communications</i> , 2020, 11, 6.	5.8	55
8573	Long-read sequencing reveals genomic structural variations that underlie creation of quality protein maize. <i>Nature Communications</i> , 2020, 11, 17.	5.8	45
8574	Phylogeny and taxonomy of <i>Ceriporia</i> and other related taxa and description of three new species. <i>Mycologia</i> , 2020, 112, 64-82.	0.8	17
8575	Chromosome-level genome assembly reveals the unique genome evolution of the swimming crab (<i>Portunus trituberculatus</i>). <i>GigaScience</i> , 2020, 9, .	3.3	44
8576	<i>Gymnopilus dunensis</i> , a new species from Punjab province, Pakistan. <i>Phytotaxa</i> , 2020, 428, 51-59.	0.1	4

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8577	Cortinarius section Thaumasti in South American Nothofagaceae forests. Mycologia, 2020, 112, 329-341.	0.8	5
8578	Evolutionary rates are correlated between cockroach symbionts and mitochondrial genomes. Biology Letters, 2020, 16, 20190702.	1.0	17
8579	Genome size variation in butterflies (Insecta, Lepidoptera, Papilionoidea): a thorough phylogenetic comparison. Systematic Entomology, 2020, 45, 571-582.	1.7	22
8580	<i>Sida sivarajanii</i> (Malvaceae): a new species from India. Phytotaxa, 2020, 428, 104-112.	0.1	4
8581	Identification of some Egyptian leafhopper species (Hemiptera: Cicadellidae) using DNA barcoding. Biologia (Poland), 2020, 75, 1337-1346.	0.8	2
8582	Hemotropic mycoplasmas (hemoplasmas) in free-ranging bats from Southern Brazil. Comparative Immunology, Microbiology and Infectious Diseases, 2020, 69, 101416.	0.7	9
8583	The transferability and evolution of NDM-1 and KPC-2 co-producing <i>Klebsiella pneumoniae</i> from clinical settings. EBioMedicine, 2020, 51, 102599.	2.7	87
8584	Meta-analysis of Pandemic <i>Escherichia coli</i> ST131 Plasmidome Proves Restricted Plasmid-clade Associations. Scientific Reports, 2020, 10, 36.	1.6	41
8585	Defining the core group of the genus <i>Gomphonema</i> Ehrenberg with molecular and morphological methods. Botany Letters, 2020, 167, 114-159.	0.7	17
8586	Gene fragmentation and RNA editing without borders: eccentric mitochondrial genomes of diplomids. Nucleic Acids Research, 2020, 48, 2694-2708.	6.5	31
8587	Analysis of MADS-box genes revealed modified flowering gene network and diurnal expression in pineapple. BMC Genomics, 2020, 21, 8.	1.2	21
8588	Hierarchical Hybrid Enrichment: Multitiered Genomic Data Collection Across Evolutionary Scales, With Application to Chorus Frogs (<i>Pseudacris</i>). Systematic Biology, 2020, 69, 756-773.	2.7	16
8589	Phylogeny of European Anodontini (Bivalvia: Unionidae) with a redescription of <i>Anodonta exulcerata</i> . Zoological Journal of the Linnean Society, 2020, 189, 745-761.	1.0	13
8590	A new Southern Ocean species in the remarkable and rare amphipod family Podosiridae (Crustacea): <i>Tj ETQq1</i> . <i>Over</i> 190, 613-631.	1.0	3
8591	Eight in one: morphological and molecular analyses reveal cryptic diversity in Amazonian alopoglossid lizards (Squamata: Gymnophthalmoidea). Zoological Journal of the Linnean Society, 2020, 190, 227-270.	1.0	9
8592	Genome analysis of the marine bacterium <i>Kiloniella laminariae</i> and first insights into comparative genomics with related <i>Kiloniella</i> species. Archives of Microbiology, 2020, 202, 815-824.	1.0	9
8593	Description of three bacterial strains belonging to the new genus <i>Novipirellula</i> gen. nov., reclassification of <i>Rhodopirellula rosea</i> and <i>Rhodopirellula caenicola</i> and readjustment of the genus threshold of the phylogenetic marker <i>rpoB</i> for Planctomycetaceae. Antonie Van Leeuwenhoek, 2020, 113, 1779-1795.	0.7	56
8594	Diversity and Expression Patterns of MADS-Box Genes in <i>Gnetum luofuense</i> —Implications for Functional Diversity and Evolution. Tropical Plant Biology, 2020, 13, 36-49.	1.0	8

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8596	Comparative genomic analysis of <i>Streptococcus dysgalactiae</i> subspecies <i>dysgalactiae</i> , an occasional cause of zoonotic infection. <i>Pathology</i> , 2020, 52, 262-266.	0.3	12
8597	<i>Modestobacter excelsi</i> sp. nov., a novel actinobacterium isolated from a high altitude Atacama Desert soil. <i>Systematic and Applied Microbiology</i> , 2020, 43, 126051.	1.2	21
8598	Protection of White Leghorn chickens by recombinant fowlpox vector vaccine with an updated H5 insert against Mexican H5N2 avian influenza viruses. <i>Vaccine</i> , 2020, 38, 1526-1534.	1.7	6
8599	Comparing PFGE, MLST, and WGS in monitoring the spread of macrolide and rifampin resistant <i>Rhodococcus equi</i> in horse production. <i>Veterinary Microbiology</i> , 2020, 242, 108571.	0.8	3
8600	Genetic variation and admixture of red-eared sliders (<i>Trachemys scripta elegans</i>) in the USA. <i>Molecular Phylogenetics and Evolution</i> , 2020, 145, 106722.	1.2	16
8601	The roles of vicariance and dispersal in the differentiation of two species of the <i>Rhinella marina</i> species complex. <i>Molecular Phylogenetics and Evolution</i> , 2020, 145, 106723.	1.2	12
8602	An integrative phylogenomic approach illuminates the evolutionary history of Old World tree frogs (Anura: Rhacophoridae). <i>Molecular Phylogenetics and Evolution</i> , 2020, 145, 106724.	1.2	23
8603	The enigmatic Leiosaurae clade: Phylogeography, species delimitation, phylogeny and historical biogeography of its southernmost species. <i>Molecular Phylogenetics and Evolution</i> , 2020, 144, 106725.	1.2	10
8604	Phylogenomics, co-evolution of ecological niche and morphology, and historical biogeography of buckeyes, horsechestnuts, and their relatives (Hippocastaneae, Sapindaceae) and the value of RAD-Seq for deep evolutionary inferences back to the Late Cretaceous. <i>Molecular Phylogenetics and Evolution</i> , 2020, 145, 106726.	1.2	24
8605	Metabolic activity analyses demonstrate that Lokiarchaeon exhibits homoacetogenesis in sulfidic marine sediments. <i>Nature Microbiology</i> , 2020, 5, 248-255.	5.9	48
8606	Marine diatom assemblages of the Nosy Be Island coasts, NW Madagascar: species composition and biodiversity using molecular and morphological taxonomy. <i>Systematics and Biodiversity</i> , 2020, 18, 161-180.	0.5	8
8607	Clarifying the taxonomy of <i>Gymnodinium fuscum</i> var. <i>rubrum</i> from Bavaria (Germany) and placing it in a molecular phylogeny of the Gymnodiniaceae (Dinophyceae). <i>Systematics and Biodiversity</i> , 2020, 18, 102-115.	0.5	7
8608	First record of <i>Caulerpa lentillifera</i> J. Agardh (Bryopsidales, Chlorophyta) from China. <i>Marine Biology Research</i> , 2020, 16, 44-49.	0.3	3
8609	Cultivable marine fungi from the Arctic Archipelago of Svalbard and their antibacterial activity. <i>Mycology</i> , 2020, 11, 230-242.	2.0	19
8610	The complete chloroplast genome sequence of <i>Tainia cordifolia</i> (Orchidaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1-2.	0.2	2
8611	A comprehensive, genus-level time-calibrated phylogeny of the tree flora of Mediterranean Europe and an assessment of its vulnerability. <i>Botany Letters</i> , 2020, 167, 276-289.	0.7	6
8612	Reinterpreting the phylogenetic position, systematics and distribution of the <i>Raddia-Sucrea</i> lineage (Poaceae, Olyrinae), with a new monotypic and endangered herbaceous bamboo genus from Brazil. <i>Botanical Journal of the Linnean Society</i> , 2020, 192, 34-60.	0.8	8
8613	Deep Residual Neural Networks Resolve Quartet Molecular Phylogenies. <i>Molecular Biology and Evolution</i> , 2020, 37, 1495-1507.	3.5	32

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8614	RAD sequencing resolves the phylogeny, taxonomy and biogeography of Trichophoreae despite a recent rapid radiation (Cyperaceae). <i>Molecular Phylogenetics and Evolution</i> , 2020, 145, 106727.	1.2	18
8615	The life aquatic with spiders (Araneae): repeated evolution of aquatic habitat association in Dictynidae and allied taxa. <i>Zoological Journal of the Linnean Society</i> , 2020, 189, 862-920.	1.0	18
8616	Analyses of environmental sequences and two regions of chloroplast genomes revealed the presence of new clades of photosynthetic euglenids in marine environments. <i>Environmental Microbiology Reports</i> , 2020, 12, 78-91.	1.0	5
8617	Morphology and Phylogeny of Two Novel Pleurostomatids (Ciliophora, Litostomatea), Establishing a New Genus. <i>Journal of Eukaryotic Microbiology</i> , 2020, 67, 252-262.	0.8	10
8618	Phylogenomics â€” principles, opportunities and pitfalls of bigâ€”data phylogenetics. <i>Systematic Entomology</i> , 2020, 45, 225-247.	1.7	118
8619	Phylogenomic analysis of the beetle suborder Adephaga with comparison of tailored and generalized ultraconserved element probe performance. <i>Systematic Entomology</i> , 2020, 45, 552-570.	1.7	35
8620	The phylogeny of insects in the dataâ€”driven era. <i>Systematic Entomology</i> , 2020, 45, 540-551.	1.7	18
8621	The out-of-India hypothesis: evidence from an ancient centipede genus, <i>Rhysida</i> (Chilopoda). <i>Zoological Journal of the Linnean Society</i> , 2020, 189, 828-861.	1.0	17
8622	Core genome multi-locus sequence typing as an essential tool in a high-cost livestock-associated methicillin-resistant <i>Staphylococcus aureus</i> CC398 hospital outbreak. <i>Journal of Hospital Infection</i> , 2020, 104, 574-581.	1.4	14
8623	No support for the emergence of lichens prior to the evolution of vascular plants. <i>Geobiology</i> , 2020, 18, 3-13.	1.1	48
8624	Exploring community assembly among Javanese and Balinese freshwater shrimps (Atyidae). <i>Zoological Journal of the Linnean Society</i> , 2020, 189, 342-354.	1.0	4
8625	Oxidative stress and the early coevolution of life and biospheric oxygen. , 2020, , 67-85.		6
8626	Resolving relationships in an exceedingly young Neotropical orchid lineage using Genotyping-by-sequencing data. <i>Molecular Phylogenetics and Evolution</i> , 2020, 144, 106672.	1.2	23
8627	Detection of haplosporidian protistan parasites supports an increase to their known diversity, geographic range and bivalve host specificity. <i>Parasitology</i> , 2020, 147, 584-592.	0.7	7
8628	The other side of the Sahulian coin: biogeography and evolution of Melanesian forest dragons (Agamidae). <i>Biological Journal of the Linnean Society</i> , 2020, 129, 99-113.	0.7	13
8629	Cophylogenetic relationships between <i>Dactylogyrus</i> (Monogenea) ectoparasites and endemic cyprinoids of the northâ€”eastern European periâ€”Mediterranean region. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2020, 58, 1-21.	0.6	16
8630	Floral fragrances in two closely related fruit fly orchids, <i>Bulbophyllum hortorum</i> and <i>B. macranthoides</i> (Orchidaceae): assortments of phenylbutanoids to attract tephritid fruit fly males. <i>Applied Entomology and Zoology</i> , 2020, 55, 55-64.	0.6	14
8631	Automatic standardized processing and identification of tropical bat calls using deep learning approaches. <i>Biological Conservation</i> , 2020, 241, 108269.	1.9	29

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8632	Diamantina: An endemic new genus of Neotropical Atalophlebiinae (Ephemeroptera: Leptophlebiidae) evidenced by morphological and molecular data. <i>Zoologischer Anzeiger</i> , 2020, 284, 30-42.	0.4	4
8633	MRSA dynamic circulation between the community and the hospital setting: New insights from a cohort study. <i>Journal of Infection</i> , 2020, 80, 24-37.	1.7	17
8634	<i>Ortholinea scatophagi</i> (Myxosporaea: Ortholineidae), a novel myxosporaeon infecting the spotted scat, <i>Scatophagus argus</i> (Linnaeus 1766) from southwest coast of India. <i>Parasitology International</i> , 2020, 75, 102020.	0.6	6
8635	Ciliary force-responsive striated fibers promote basal body connections and cortical interactions. <i>Journal of Cell Biology</i> , 2020, 219, .	2.3	23
8636	Genomic identification and characterization of co-occurring <i>Harveyi</i> clade species following a vibriosis outbreak in Pacific white shrimp, <i>Penaeus (Litopenaeus) vannamei</i> . <i>Aquaculture</i> , 2020, 518, 734628.	1.7	8
8637	Molecular and Morphological Delimitation of Species in the Group of <i>Lepocinclis Ovum</i> -like taxa (Euglenida). <i>Journal of Phycology</i> , 2020, 56, 283-299.	1.0	11
8638	First case of parthenogenesis in ladybirds (Coleoptera: Coccinellidae) suggests new mechanisms for the evolution of asexual reproduction. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2020, 58, 194-208.	0.6	12
8639	A group of species <i>Psychropotes longicauda</i> (Psychropotidae, Elaspodida, Holothuroidea) from the Kuril-Kamchatka Trench area (North-West Pacific). <i>Progress in Oceanography</i> , 2020, 180, 102222.	1.5	12
8640	Molecular phylogenetics and floral evolution of the <i>Cirrhoptalum</i> alliance (Bulbophyllum,) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 427 Td</i> and Evolution, 2020, 143, 106689.	1.2	20
8641	Phylogenetic Conflicts, Combinability, and Deep Phylogenomics in Plants. <i>Systematic Biology</i> , 2020, 69, 579-592.	2.7	53
8642	Divergence and support among slightly suboptimal likelihood gene trees. <i>Cladistics</i> , 2020, 36, 322-340.	1.5	20
8643	The nervous and circulatory systems of a Cretaceous crinoid: preservation, palaeobiology and evolutionary significance. <i>Palaeontology</i> , 2020, 63, 243-253.	1.0	5
8644	Species delimitation based on integrative approach suggests reallocation of genus in Hypostomini catfish (Siluriformes, Loricariidae). <i>Hydrobiologia</i> , 2020, 847, 563-578.	1.0	16
8645	Mitogenome evolution in ladybirds: Potential association with dietary adaptation. <i>Ecology and Evolution</i> , 2020, 10, 1042-1053.	0.8	12
8646	<i>Sarocladium</i> species associated with rice in Taiwan. <i>Mycological Progress</i> , 2020, 19, 67-80.	0.5	12
8647	Transcriptomic signature of rapidly evolving immune genes in a highland fish. <i>Fish and Shellfish Immunology</i> , 2020, 97, 587-592.	1.6	5
8648	High-resolution mycobiota analysis reveals dynamic intestinal translocation preceding invasive candidiasis. <i>Nature Medicine</i> , 2020, 26, 59-64.	15.2	193
8649	Phylogenetic placement of environmental sequences using taxonomically reliable databases helps to rigorously assess dinophyte biodiversity in Bavarian lakes (Germany). <i>Freshwater Biology</i> , 2020, 65, 193-208.	1.2	19

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8650	Conflicting phylogenetic signals in genomic data of the coffee family (Rubiaceae). <i>Journal of Systematics and Evolution</i> , 2020, 58, 440-460.	1.6	36
8651	Human Blastomycosis in South Africa Caused by <i>Blastomyces percursus</i> and <i>Blastomyces emzantsi</i> sp. nov., 1967 to 2014. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	1.8	35
8652	Evolutionary superscaffolding and chromosome anchoring to improve <i>Anopheles</i> genome assemblies. <i>BMC Biology</i> , 2020, 18, 1.	1.7	177
8653	New ophiostomatoid fungi from wounds on storm-damaged trees in Afromontane forests of the Cape Floristic Region. <i>Mycological Progress</i> , 2020, 19, 81-95.	0.5	4
8654	Molecular evidence for adaptive evolution of olfactory-related genes in cervids. <i>Genes and Genomics</i> , 2020, 42, 355-360.	0.5	2
8655	Phylogenetic evidence revealed <i>Cantharocybe virosa</i> (Agaricales, Hygrophoraceae) as a new clinical record for gastrointestinal mushroom poisoning in Thailand. <i>Toxicological Research</i> , 2020, 36, 239-248.	1.1	9
8656	Nodal paralogues underlie distinct mechanisms for visceral left-right asymmetry in reptiles and mammals. <i>Nature Ecology and Evolution</i> , 2020, 4, 261-269.	3.4	20
8657	The complete chloroplast genome sequence of <i>Aconitum austroyunnanense</i> W. T. Wang (Ranunculaceae): a medicinal plant endemic to China. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 248-249.	0.2	1
8658	An enigmatic population of <i>Alsodes</i> (Anura, Alsodidae) from the Andes of central Chile with three species-level mitochondrial lineages. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2020, 31, 25-34.	0.7	1
8659	Ascidian caveolin induces membrane curvature and protects tissue integrity and morphology during embryogenesis. <i>FASEB Journal</i> , 2020, 34, 1345-1361.	0.2	23
8660	Global biogeographic synthesis and priority conservation regions of the relict tree family Juglandaceae. <i>Journal of Biogeography</i> , 2020, 47, 643-657.	1.4	28
8661	Phylogeny of Physarida (Amoebozoa, Myxogastria) Based on the Small Subunit Ribosomal RNA Gene, Redefinition of <i>Physarum pusillum</i> s. str. and Reinstatement of <i>P.Âgravidum</i> Morgan. <i>Journal of Eukaryotic Microbiology</i> , 2020, 67, 327-336.	0.8	10
8662	A mitochondrial phylogeny uncovers taxonomic ambiguity and complex phylogeographic patterns in the eastern Australian land snail <i>Austrochloritis</i> (Stylommatophora, Camaenidae). <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2020, 58, 1005-1020.	0.6	4
8663	Paraphyletic species no more – genomic data resolve a Pleistocene radiation and validate morphological species of the <i>Melanoplus scudderi</i> complex (Insecta: Orthoptera). <i>Systematic Entomology</i> , 2020, 45, 594-605.	1.7	28
8664	Phylogeny of the superfamily Gelechioidea (Lepidoptera: Obtectomera), with an exploratory application on geometric morphometrics. <i>Zoologica Scripta</i> , 2020, 49, 307-328.	0.7	24
8665	<i>Stolephorus babarani</i> , a new species of anchovy (Teleostei: Tj ETQq1 1 0.784314 rgBT /Overloc 509-520.	0.2	9
8666	Global comparison of bicosoecid Cafeteria-like flagellates from the deep ocean and surface waters, with reorganization of the family Cafeteriaceae. <i>European Journal of Protistology</i> , 2020, 73, 125665.	0.5	30
8667	An overview of the Dactylosomatidae (Apicomplexa: Adeleorina: Dactylosomatidae), with the description of <i>Dactylosoma kermi</i> n. sp. parasitising <i>Ptychadena anchietae</i> and <i>Sclerophrys gutturalis</i> from South Africa. <i>International Journal for Parasitology: Parasites and Wildlife</i> , 2020, 11, 246-260.	0.6	15

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8668	Phylogeny and trait variation of Japanese <i>Rubus</i> subgenus <i>Ideaobatus</i> . <i>Scientia Horticulturae</i> , 2020, 264, 109150.	1.7	5
8669	DNA sequence repeats identify numerous Type I restriction modification systems that are potential epigenetic regulators controlling phase-variable regulons; phasevarions. <i>FASEB Journal</i> , 2020, 34, 1038-1051.	0.2	29
8670	The Enterobase user's guide, with case studies on <i>Salmonella</i> transmissions, <i>Yersinia pestis</i> phylogeny, and <i>Escherichia</i> core genomic diversity. <i>Genome Research</i> , 2020, 30, 138-152.	2.4	577
8671	Ancestral and neo-sex chromosomes contribute to population divergence in a dioecious plant. <i>Evolution; International Journal of Organic Evolution</i> , 2020, 74, 256-269.	1.1	17
8672	<i>Rhodopirellula heiligendammensis</i> sp. nov., <i>Rhodopirellula pilleata</i> sp. nov., and <i>Rhodopirellula solitaria</i> sp. nov. isolated from natural or artificial marine surfaces in Northern Germany and California, USA, and emended description of the genus <i>Rhodopirellula</i> . <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 1737-1750.	0.7	35
8673	<i>Alienimonas californiensis</i> gen. nov. sp. nov., a novel Planctomycete isolated from the kelp forest in Monterey Bay. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 1751-1766.	0.7	40
8674	Three novel <i>Rubripirellula</i> species isolated from plastic particles submerged in the Baltic Sea and the estuary of the river Warnow in northern Germany. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 1767-1778.	0.7	41
8675	<i>Zulustylis</i> (<i>Abildgaardieae</i> , <i>Cyperaceae</i>) – a new genus from sub-Saharan Africa. <i>South African Journal of Botany</i> , 2020, 128, 326-332.	1.2	5
8676	Origin and evolution of the CYP4G subfamily in insects, cytochrome P450 enzymes involved in cuticular hydrocarbon synthesis. <i>Molecular Phylogenetics and Evolution</i> , 2020, 143, 106695.	1.2	62
8677	Recombination of B- and T-cell epitope-rich loci from <i>Aedes</i> - and <i>Culex</i> -borne flaviviruses shapes Zika virus epidemiology. <i>Antiviral Research</i> , 2020, 174, 104676.	1.9	11
8678	Reply to: Revisiting the origin of octoploid strawberry. <i>Nature Genetics</i> , 2020, 52, 5-7.	9.4	44
8679	The complete chloroplast genome sequence of horticultural plant, <i>Impatiens hawkeri</i> (Sect.) Tj ETQq1 1 0.784314 rgBJ /Overlock	0.2	3
8680	Phylogenetic Systematics and Evolution of the Spider Infraorder Mygalomorphae Using Genomic Scale Data. <i>Systematic Biology</i> , 2020, 69, 671-707.	2.7	83
8681	The complete chloroplast genome sequence of a <i>Castanea henryi</i> cultivar. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 180-181.	0.2	0
8682	Organellomic data sets confirm a cryptic consensus on (unrooted) land-plant relationships and provide new insights into bryophyte molecular evolution. <i>American Journal of Botany</i> , 2020, 107, 91-115.	0.8	38
8683	Insights into reproductive isolation within the pelagic copepod <i>Pleuromamma abdominalis</i> with high genetic diversity using genome-wide SNP data. <i>Marine Biology</i> , 2020, 167, 1.	0.7	15
8684	<i>Rubinisphaera italica</i> sp. nov. isolated from a hydrothermal area in the Tyrrhenian Sea close to the volcanic island Panarea. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 1727-1736.	0.7	38
8685	The complete chloroplast genome of Chinese medicine (<i>Psoralea corylifolia</i>): Molecular structures, barcoding and phylogenetic analysis. <i>Plant Gene</i> , 2020, 21, 100216.	1.4	10

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8686	Phylogenomics provides robust support for a two-domains tree of life. <i>Nature Ecology and Evolution</i> , 2020, 4, 138-147.	3.4	159
8687	A jumbo phage that forms a nucleus-like structure evades CRISPR-Cas DNA targeting but is vulnerable to type III RNA-based immunity. <i>Nature Microbiology</i> , 2020, 5, 48-55.	5.9	123
8688	A High-Quality Reference Genome Assembly of the Saltwater Crocodile, <i>Crocodylus porosus</i> , Reveals Patterns of Selection in Crocodylidae. <i>Genome Biology and Evolution</i> , 2020, 12, 3635-3646.	1.1	15
8689	The Laboratory Domestication of Zebrafish: From Diverse Populations to Inbred Substrains. <i>Molecular Biology and Evolution</i> , 2020, 37, 1056-1069.	3.5	30
8690	Failure to diverge in African Great Lakes: The case of <i>Dolicirroplectanum lacustre</i> gen. nov. comb. nov. (Monogenea, Diplectanidae) infecting latid hosts. <i>Journal of Great Lakes Research</i> , 2020, 46, 1113-1130.	0.8	16
8691	Multigene phylogeny uncovers oviposition-related evolutionary history of Cerambycinae (Coleoptera: Tj ETQq1 1 0,784314 rgBT /Over	1.2	18
8692	The water lily genome and the early evolution of flowering plants. <i>Nature</i> , 2020, 577, 79-84.	13.7	238
8693	<i>Lobophora</i> (Dictyotales) Species Richness, Ecology and Biogeography Across the North Eastern Atlantic Archipelagos and Description of Two New Species. <i>Journal of Phycology</i> , 2020, 56, 346-357.	1.0	12
8694	Locally Acquired Human Infection with Swine-Origin Influenza A(H3N2) Variant Virus, Australia, 2018. <i>Emerging Infectious Diseases</i> , 2020, 26, 143-147.	2.0	14
8695	Protist Interactions and Community Structure During Early Autumn in the Kerguelen Region (Southern Ocean). <i>Protist</i> , 2020, 171, 125709.	0.6	25
8696	Comparative mitochondrial genomic analysis of <i>Macrophthalmus pacificus</i> and insights into the phylogeny of the Ocyropoidea & Grapsoidea. <i>Genomics</i> , 2020, 112, 82-91.	1.3	24
8697	Phylogeny and biogeography of the <i>Cavernicola</i> (Platyhelminthes: Tricladida): Relicts of an epigeal group sheltering in caves?. <i>Molecular Phylogenetics and Evolution</i> , 2020, 145, 106709.	1.2	9
8698	Revisiting the origin of octoploid strawberry. <i>Nature Genetics</i> , 2020, 52, 2-4.	9.4	58
8699	Genera of Inocybaceae: New skin for the old ceremony. <i>Mycologia</i> , 2020, 112, 83-120.	0.8	48
8700	Molecular data reveals a new holomorphic marine fungus, <i>Halobyssothecium estuariae</i> , and the asexual morph of <i>Keissleriella phragmiticola</i> . <i>Mycology</i> , 2020, 11, 167-183.	2.0	9
8701	Emergence and Evolution of ERM Proteins and Merlin in Metazoans. <i>Genome Biology and Evolution</i> , 2020, 12, 3710-3724.	1.1	9
8702	Genomic Mechanisms of Physiological and Morphological Adaptations of Limestone Langurs to Karst Habitats. <i>Molecular Biology and Evolution</i> , 2020, 37, 952-968.	3.5	27
8703	Molecular characterization of feline paramyxovirus in Japanese cat populations. <i>Archives of Virology</i> , 2020, 165, 413-418.	0.9	19

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8704	Pan-Genomic Analysis of African Swine Fever Virus. <i>Virologica Sinica</i> , 2020, 35, 662-665.	1.2	12
8705	Cryptic ecological and geographic diversification in coral-associated nudibranchs. <i>Molecular Phylogenetics and Evolution</i> , 2020, 144, 106698.	1.2	31
8706	Extensive paraphyly in the typical owl family (Strigidae). <i>Auk</i> , 2020, 137, .	0.7	31
8707	Microsporidia with Vertical Transmission Were Likely Shaped by Nonadaptive Processes. <i>Genome Biology and Evolution</i> , 2020, 12, 3599-3614.	1.1	27
8708	Linking Branch Lengths across Sets of Loci Provides the Highest Statistical Support for Phylogenetic Inference. <i>Molecular Biology and Evolution</i> , 2020, 37, 1202-1210.	3.5	42
8709	Marine species formation along the rise of Central America: The anomuran crab <i>Megalobrachium</i> . <i>Molecular Ecology</i> , 2020, 29, 413-428.	2.0	7
8710	Assessment of <i>Polygala paniculata</i> (Polygalaceae) characteristics for evolutionary studies of legume-rhizobia symbiosis. <i>Journal of Plant Research</i> , 2020, 133, 109-122.	1.2	3
8711	Extremophilic nitrite-oxidizing <i>Chloroflexi</i> from Yellowstone hot springs. <i>ISME Journal</i> , 2020, 14, 364-379.	4.4	93
8712	HIV drug resistance in a cohort of HIV-infected MSM in the United States. <i>Aids</i> , 2020, 34, 91-101.	1.0	16
8713	Transfer of the Thecate Amoeba <i>Lecythium mutabilis</i> to a Novel Genus <i>Omnivora</i> (Fiscullidae.) <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 100</i>	0.8	1
8714	Molecular phylogeny of the family Coccidae (Hemiptera, Coccoomorpha), with a discussion of their waxy ovisacs. <i>Systematic Entomology</i> , 2020, 45, 396-414.	1.7	13
8715	Species delimitation and evolutionary relationships among <i>Phoebis</i> New World sulphur butterflies (Lepidoptera, Pieridae, Coliadinae). <i>Systematic Entomology</i> , 2020, 45, 481-492.	1.7	7
8716	TARGETED RESEQUENCING OF WETLAND SEDIMENT AS A TOOL FOR AVIAN INFLUENZA VIRUS SURVEILLANCE. <i>Journal of Wildlife Diseases</i> , 2020, 56, 397.	0.3	17
8717	Biodiversity of protists and nematodes in the wild nonhuman primate gut. <i>ISME Journal</i> , 2020, 14, 609-622.	4.4	32
8718	Characterization of the complete chloroplast genome of sugar maple (<i>Acer saccharum</i>). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 21-22.	0.2	2
8719	Genetic consequences of plant edaphic specialization to solfatara fields: Phylogenetic and population genetic analysis of <i>Carex angustisquama</i> (Cyperaceae). <i>Molecular Ecology</i> , 2020, 29, 3234-3247.	2.0	6
8720	Mitochondrial genomes and genetic structure of the Kemp's ridley sea turtle (<i>Lepidochelys</i>) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 100</i>	0.8	12
8721	Morphology and phylogeny of four marine or brackish water spirotrich ciliates (Protozoa.) <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 100</i>	0.5	19

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8722	The mitochondrial genome of <i>Morchella importuna</i> (272.2Åkb) is the largest among fungi and contains numerous introns, mitochondrial non-conserved open reading frames and repetitive sequences. <i>International Journal of Biological Macromolecules</i> , 2020, 143, 373-381.	3.6	63
8723	Spatio-temporal formation of the genetic diversity in the Mediterranean dwelling lichen during the Neogene and Quaternary epochs. <i>Molecular Phylogenetics and Evolution</i> , 2020, 144, 106704.	1.2	7
8724	Molecular phylogeny of Ceriantharia (Cnidaria: Anthozoa) reveals non-monophyly of traditionally accepted families. <i>Zoological Journal of the Linnean Society</i> , 2020, 190, 397-416.	1.0	6
8725	Genomic and phenomic analysis of island ant community assembly. <i>Molecular Ecology</i> , 2020, 29, 1611-1627.	2.0	7
8726	Combined molecular and morphological data provide insights into the evolution and classification of Chilocorini ladybirds (Coleoptera: Coccinellidae). <i>Systematic Entomology</i> , 2020, 45, 447-463.	1.7	10
8727	Novel sexual dimorphism in a new genus of Bathynellidae from Russia, with a revision of phylogenetic relationships. <i>Zoologica Scripta</i> , 2020, 49, 47-63.	0.7	8
8728	Endophytic Microbiome of Biofuel Plant <i>Miscanthus sinensis</i> (Poaceae) Interacts with Environmental Gradients. <i>Microbial Ecology</i> , 2020, 80, 133-144.	1.4	9
8729	Insights into the symbiotic relationship between scale worms and carnivorous sponges (Cladorhizidae, Chondrocladia). <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2020, 156, 103191.	0.6	9
8730	Quite an oddity: new worldwide records of <i>Renouxia</i> (Rhodogorgonales, Rhodophyta), including <i>R. marerubra</i> sp. nov.. <i>European Journal of Phycology</i> , 2020, 55, 197-206.	0.9	3
8731	Genome-wide sequence information reveals recurrent hybridization among diploid wheat wild relatives. <i>Plant Journal</i> , 2020, 102, 493-506.	2.8	40
8732	Cultivation and functional characterization of 79 planctomycetes uncovers their unique biology. <i>Nature Microbiology</i> , 2020, 5, 126-140.	5.9	164
8733	Unexpected mitochondrial genome diversity revealed by targeted single-cell genomics of heterotrophic flagellated protists. <i>Nature Microbiology</i> , 2020, 5, 154-165.	5.9	44
8734	Epigenomic characterization of <i>Clostridioides difficile</i> finds a conserved DNA methyltransferase that mediates sporulation and pathogenesis. <i>Nature Microbiology</i> , 2020, 5, 166-180.	5.9	75
8735	Is <i>Pteropyrum</i> a pathway to C4 evolution in Polygonaceae? An integrative approach to the taxonomy and anatomy of <i>Pteropyrum</i> (C3), an immediate relative of <i>Calligonum</i> (C4). <i>Botanical Journal of the Linnean Society</i> , 2020, 192, 369-400.	0.8	11
8736	Exploring the impact of morphology, multiple sequence alignment and choice of optimality criteria in phylogenetic inference: a case study with the Neotropical orb-weaving spider genus <i>Wagneriana</i> (Araneae: Araneidae). <i>Zoological Journal of the Linnean Society</i> , 2020, 188, 976-1151.	1.0	14
8737	Multiple Euryhaline Lineages of Centrohelids (Haptista: Centroplasthelida) in Inland Saline Waters Revealed with Metabarcoding. <i>Journal of Eukaryotic Microbiology</i> , 2020, 67, 223-231.	0.8	10
8738	Unraveling the diversification and systematic puzzle of the highly polymorphic <i>Psammobates tentorius</i> (Bell, 1828) complex (Reptilia: Testudinidae) through phylogenetic analyses and species delimitation approaches. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2020, 58, 308-326.	0.6	7
8739	Deciphering the high-quality genome sequence of coriander that causes controversial feelings. <i>Plant Biotechnology Journal</i> , 2020, 18, 1444-1456.	4.1	56

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8740	The phylogeny of the African wood mice (Muridae, Hylomyscus) based on complete mitochondrial genomes and five nuclear genes reveals their evolutionary history and undescribed diversity. <i>Molecular Phylogenetics and Evolution</i> , 2020, 144, 106703.	1.2	35
8741	Phylogenetic Analysis of Human Immunodeficiency Virus from People Who Inject Drugs in Indonesia, Ukraine, and Vietnam: HPTN 074. <i>Clinical Infectious Diseases</i> , 2020, 71, 1836-1846.	2.9	6
8742	Morphological and molecular characterization of two Trichodina (Ciliophora, Peritrichia) species from freshwater fishes in China. <i>European Journal of Protistology</i> , 2020, 72, 125647.	0.5	14
8743	Comparison of colonial volvocine algae based on phylotranscriptomic analysis of gene family evolution and natural selection. <i>European Journal of Phycology</i> , 2020, 55, 100-112.	0.9	10
8744	Genetic Diversity of <i>Listeria monocytogenes</i> Isolates from Invasive Listeriosis in China. <i>Foodborne Pathogens and Disease</i> , 2020, 17, 215-227.	0.8	12
8745	Phylogeny of the <i>Eisenia nordenskioldi</i> complex based on mitochondrial genomes. <i>European Journal of Soil Biology</i> , 2020, 96, 103137.	1.4	17
8746	Genetic variation, pseudocryptic diversity, and phylogeny of <i>Erpobdella</i> (Annelida: Hirudinida: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 507 143, 106688.	1.2	5
8747	Genome size and endopolyploidy evolution across the moss phylogeny. <i>Annals of Botany</i> , 2020, 125, 543-555.	1.4	21
8748	The Genome of the Blind Soil-Dwelling and Ancestrally Wingless Dipluran <i>Campodea augens</i> : A Key Reference Hexapod for Studying the Emergence of Insect Innovations. <i>Genome Biology and Evolution</i> , 2020, 12, 3534-3549.	1.1	3
8749	Metabolic relationships of uncultured bacteria associated with the microalgae <i>Gambierdiscus</i> . <i>Environmental Microbiology</i> , 2020, 22, 1764-1783.	1.8	28
8750	Surface resistance to SSVs and SIRVs in pilin deletions of <i>Sulfolobus islandicus</i> . <i>Molecular Microbiology</i> , 2020, 113, 718-727.	1.2	22
8751	First insights into circulating XDR and pre-XDR <i>Mycobacterium tuberculosis</i> in Southern Brazil. <i>Infection, Genetics and Evolution</i> , 2020, 78, 104127.	1.0	7
8752	Phylogeographic pattern and population structure of the Persian stone loach, <i>Oxynoemacheilus persa</i> (Heckel 1847) (family: Nemacheilidae) in southern Iran with implications for conservation. <i>Environmental Biology of Fishes</i> , 2020, 103, 77-88.	0.4	4
8753	Population Genomic Analyses Reveal Connectivity via Human-Mediated Transport across <i>Populus</i> Plantations in North America and an Undescribed Subpopulation of <i>Sphaerulina musiva</i> . <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 189-199.	1.4	14
8754	A new contribution to the taxonomy and molecular phylogeny of three, well-known freshwater species of the ciliate genus <i>Spirostomum</i> (Protozoa: Ciliophora: Heterotrichea). <i>Zoological Journal of the Linnean Society</i> , 2020, 189, 158-177.	1.0	27
8755	Parallel loss of sweet and umami taste receptor function from phocids and otarioids suggests multiple colonizations of the marine realm by pinnipeds. <i>Journal of Biogeography</i> , 2020, 47, 235-249.	1.4	10
8756	Genomic landscape and genetic manipulation of the black soldier fly <i>Hermetia illucens</i> , a natural waste recycler. <i>Cell Research</i> , 2020, 30, 50-60.	5.7	136
8757	Defining the eco-enzymological role of the fungal strain <i>Coniochaeta</i> sp. 2T2.1 in a tripartite lignocellulolytic microbial consortium. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	12

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8758	Giant protists (xenophyophores) function as fish nurseries. <i>Ecology</i> , 2020, 101, e02933.	1.5	10
8759	Characterization and expression analysis of P5CS (Pyrroline-5-carboxylate synthase) gene in two distinct populations of the Atlantic Forest native species <i>Eugenia uniflora</i> L.. <i>Molecular Biology Reports</i> , 2020, 47, 1033-1043.	1.0	7
8760	Environmental factors determining distribution and activity of anammox bacteria in minerotrophic fen soils. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	5
8761	The Mitogenome of Norway Spruce and a Reappraisal of Mitochondrial Recombination in Plants. <i>Genome Biology and Evolution</i> , 2020, 12, 3586-3598.	1.1	35
8762	Tackling Rapid Radiations With Targeted Sequencing. <i>Frontiers in Plant Science</i> , 2019, 10, 1655.	1.7	106
8763	<i>Stygamoeba cauta</i> n. sp. (Amoebozoa, Discosea) – a new brackish-water species from NivÅ¥ Bay (Baltic Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	0.5	1
8764	Redescriptions of three tintinnine ciliates (Ciliophora: Tintinnina) from coastal waters in China based on lorica features, cell morphology, and rDNA sequence data. <i>European Journal of Protistology</i> , 2020, 72, 125659.	0.5	17
8765	High diversity and multiple invasions to North America by fungi grown by the northern-most <i>Trachymyrmex</i> and <i>Mycetomoellerius</i> ant species. <i>Fungal Ecology</i> , 2020, 44, 100878.	0.7	11
8766	Optimal markers for the identification of <i>Colletotrichum</i> species. <i>Molecular Phylogenetics and Evolution</i> , 2020, 143, 106694.	1.2	51
8767	Microbial risk factors for treatment failure of pivmecillinam in community-acquired urinary tract infections caused by ESBL-producing <i>Escherichia coli</i> . <i>Apmis</i> , 2020, 128, 232-241.	0.9	3
8768	Ancient DNA from an extinct Mediterranean micromammal – <i>Hypnomys morpheus</i> (Rodentia): Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 Systematics and Evolutionary Research, 2020, 58, 427-438.	0.6	6
8769	Short communication: Whole-genome sequence analysis of 4 fecal blaCMY-2-producing <i>Escherichia coli</i> isolates from Holstein dairy calves. <i>Journal of Dairy Science</i> , 2020, 103, 877-883.	1.4	9
8770	A new species of <i>Atriophallophorus</i> Deblock & RosÅ©, 1964 (Trematoda: Microphallidae) described from in vitro-grown adults and metacercariae from <i>Potamopyrgus antipodarum</i> (Gray, 1843) (Mollusca): Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.4	1
8771	The case of an arctic wild ass highlights the utility of ancient DNA for validating problematic identifications in museum collections. <i>Molecular Ecology Resources</i> , 2020, 20, 1182-1190.	2.2	8
8772	Chromosomal-level assembly of <i>Takifugu obscurus</i> (Abe, 1949) genome using third-generation DNA sequencing and Hi-C analysis. <i>Molecular Ecology Resources</i> , 2020, 20, 520-530.	2.2	46
8773	Hidden in the DNA: How multiple historical processes and natural history traits shaped patterns of cryptic diversity in an Amazon leaf-litter lizard <i>Loxopholis osvaldoi</i> (Squamata): Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	1.0	1
8774	Evolutionary trajectories of tooth histology patterns in modern sharks (Chondrichthyes.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 102 Td (E	0.9	30
8775	Plastome phylogenomic insights into the Sino-Japanese biogeography of <i>Diabelia</i> (Caprifoliaceae). <i>Journal of Systematics and Evolution</i> , 2020, 58, 972-987.	1.6	18

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8776	Cell wall-anchored 5'-nucleotidases in Gram-positive cocci. <i>Molecular Microbiology</i> , 2020, 113, 691-698.	1.2	12
8777	<i>Helicobacter pylori</i> Infections in the Bronx, New York: Surveying Antibiotic Susceptibility and Strain Lineage by Whole-Genome Sequencing. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	1.8	20
8778	Retinoic Acid Signaling Regulates the Metamorphosis of Feather Stars (Crinoidea, Echinodermata): Insight into the Evolution of the Animal Life Cycle. <i>Biomolecules</i> , 2020, 10, 37.	1.8	6
8779	The Terrestrial Carnivorous Plant <i>Utricularia reniformis</i> Sheds Light on Environmental and Life-Form Genome Plasticity. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3.	1.8	30
8780	Comparative Pangenomics of the Mammalian Gut Commensal <i>Bifidobacterium longum</i> . <i>Microorganisms</i> , 2020, 8, 7.	1.6	23
8781	Resolving the taxonomy of the <i>Merodon dobrogensis</i> species subgroup (Diptera: Syrphidae), with the description of a new species. <i>Canadian Entomologist</i> , 2020, 152, 36-59.	0.4	6
8782	Molecular analysis of the invasive populations of <i>Urochloa</i> (Poaceae) in a large Neotropical reservoir. <i>Aquatic Botany</i> , 2020, 161, 103183.	0.8	4
8783	An Ancient and Eroded Social Supergene Is Widespread across Formica Ants. <i>Current Biology</i> , 2020, 30, 304-311.e4.	1.8	57
8784	A barotolerant ciliate isolated from the abyssal deep sea of the North Atlantic: <i>Euplotes dominicanus</i> sp. n. (Ciliophora, Euplotia). <i>European Journal of Protistology</i> , 2020, 73, 125664.	0.5	12
8785	Pteropods from the Kuril-Kamchatka Trench and the sea of Okhotsk (Euopisthobranchia; Gastropoda). <i>Progress in Oceanography</i> , 2020, 181, 102259.	1.5	4
8786	Characterization of <i>Dermosteca</i> sp. Infection in a midwestern state-endangered salamander (<i>Ambystoma platineum</i>) and a co-occurring common species (<i>Ambystoma texanum</i>). <i>Parasitology</i> , 2020, 147, 360-370.	0.7	1
8787	Adventurous cuisine in Laos: <i>Hebeloma parvisporum</i> , a new species in <i>Hebeloma</i> section <i>Porphyrospora</i> . <i>Mycologia</i> , 2020, 112, 172-184.	0.8	11
8788	<i>Psiloboletinus</i> is an independent genus sister to <i>Suillus</i> . <i>Mycologia</i> , 2020, 112, 185-196.	0.8	3
8789	Revision of leccinoid fungi, with emphasis on North American taxa, based on molecular and morphological data. <i>Mycologia</i> , 2020, 112, 197-211.	0.8	26
8790	Phylogenomic insights into the <i>Fascicularia-Ochagavia</i> group (Bromelioideae, Bromeliaceae). <i>Botanical Journal of the Linnean Society</i> , 2020, 192, 642-655.	0.8	9
8791	Systematics of <i>Vriesea</i> (Bromeliaceae): phylogenetic relationships based on nuclear gene and partial plastome sequences. <i>Botanical Journal of the Linnean Society</i> , 2020, 192, 656-674.	0.8	23
8792	Evidence of linked selection on the Z chromosome of hybridizing hummingbirds*. <i>Evolution; International Journal of Organic Evolution</i> , 2020, 74, 725-739.	1.1	18
8793	Epidemiological and evolutionary dynamics of influenza B virus in coastal Kenya as revealed by genomic analysis of strains sampled over a single season. <i>Virus Evolution</i> , 2020, 6, veaa045.	2.2	4

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8794	Towards a unified classification for human respiratory syncytial virus genotypes. <i>Virus Evolution</i> , 2020, 6, veaa052.	2.2	31
8795	Preadaptation of pandemic GII.4 Noroviruses in unsampled virus reservoirs years before emergence. <i>Virus Evolution</i> , 2020, 6, veaa067.	2.2	22
8796	Investigating the demographic history of Japan using ancient oral microbiota. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190578.	1.8	19
8797	Paleogenomic insights into the red complex bacteria <i>Tannerella forsythia</i> in Pre-Hispanic and Colonial individuals from Mexico. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190580.	1.8	18
8798	The impact of rainforest area reduction in the Guineo-Congolian region on the tempo of diversification and habitat shifts in the <i>Berlinia</i> clade (Leguminosae). <i>Journal of Biogeography</i> , 2020, 47, 2728-2740.	1.4	4
8799	Evolutionary history and eco-climatic diversification in southern African dung beetle <i>Sisyphus</i> . <i>Journal of Biogeography</i> , 2020, 47, 2698-2713.	1.4	4
8800	A chromosome-scale reference genome of trifoliate orange (<i>Poncirus trifoliata</i>) provides insights into disease resistance, cold tolerance and genome evolution in <i>Citrus</i> . <i>Plant Journal</i> , 2020, 104, 1215-1232.	2.8	56
8801	New contributions to two ciliate genera (Ciliophora, Heterotrichea) based on morphological and molecular analyses, with description of a new <i>Gruberia</i> species. <i>BMC Microbiology</i> , 2020, 20, 297.	1.3	8
8802	Companion Animals Are Spillover Hosts of the Multidrug-Resistant Human Extraintestinal <i>Escherichia coli</i> Pandemic Clones ST131 and ST1193. <i>Frontiers in Microbiology</i> , 2020, 11, 1968.	1.5	38
8803	VHSV Single Amino Acid Polymorphisms (SAPs) Associated With Virulence in Rainbow Trout. <i>Frontiers in Microbiology</i> , 2020, 11, 1984.	1.5	14
8804	Seasonal and Geographical Transitions in Eukaryotic Phytoplankton Community Structure in the Atlantic and Pacific Oceans. <i>Frontiers in Microbiology</i> , 2020, 11, 542372.	1.5	22
8805	Diversity of Light Sensing Molecules and Their Expression During the Embryogenesis of the Cuttlefish (<i>Sepia officinalis</i>). <i>Frontiers in Physiology</i> , 2020, 11, 521989.	1.3	8
8806	Unraveling the Spiraling Radiation: A Phylogenomic Analysis of Neotropical <i>Costus</i> L. <i>Frontiers in Plant Science</i> , 2020, 11, 1195.	1.7	10
8807	Analysis of the Codon Usage Pattern of HA and NA Genes of H7N9 Influenza A Virus. <i>International Journal of Molecular Sciences</i> , 2020, 21, 7129.	1.8	12
8808	Three new <i>Ophiocordyceps</i> species in the <i>Ophiocordyceps pseudoacicularis</i> species complex on Lepidoptera larvae in Southeast Asia. <i>Mycological Progress</i> , 2020, 19, 1043-1056.	0.5	7
8809	Rhodocybe-Clitopilus clade (Entolomataceae, Basidiomycota) in the Dominican Republic: new taxa and first reports of <i>Clitocella</i> , <i>Clitopilus</i> , and <i>Rhodocybe</i> for Hispaniola. <i>Mycological Progress</i> , 2020, 19, 1083-1099.	0.5	9
8810	<i>Fusarium massalimae</i> sp. nov. (<i>F. lateritium</i> species complex) occurs endophytically in leaves of <i>Handroanthus chrysotrichus</i> . <i>Mycological Progress</i> , 2020, 19, 1133-1142.	0.5	3
8811	Growth response of <i>Dinophysis</i> , <i>Mesodinium</i> , and <i>Teleaulax</i> cultures to temperature, irradiance, and salinity. <i>Harmful Algae</i> , 2020, 98, 101896.	2.2	17

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8812	Phylogeny, Evolution, and Biogeography of the North American Trapdoor Spider Family Euctenizidae (Araneae: Mygalomorphae) and the Discovery of a New "Endangered Living Fossil"™ Along California's Central Coast. <i>Insect Systematics and Diversity</i> , 2020, 4, .	0.7	9
8813	Cryptic species in White Cloud Mountain minnow, <i>Tanichthys albonubes</i> : Taxonomic and conservation implications. <i>Molecular Phylogenetics and Evolution</i> , 2020, 153, 106950.	1.2	8
8814	Transit From Autotrophism to Heterotrophism: Sequence Variation and Evolution of Chloroplast Genomes in Orobanchaceae Species. <i>Frontiers in Genetics</i> , 2020, 11, 542017.	1.1	6
8815	An Improved hgcAB Primer Set and Direct High-Throughput Sequencing Expand Hg-Methylator Diversity in Nature. <i>Frontiers in Microbiology</i> , 2020, 11, 541554.	1.5	33
8816	Genomic Analysis of two NDM-1 <i>Providencia stuartii</i> Strains Recovered from a Single Patient. <i>Current Microbiology</i> , 2020, 77, 4029-4036.	1.0	5
8817	Diversity, prevalence and phylogenetic positioning of <i>Botrytis</i> species in Brazil. <i>Fungal Biology</i> , 2020, 124, 940-957.	1.1	6
8818	The Draft Genome of <i>Coelastrum proboscideum</i> (Sphaeropleales, Chlorophyta). <i>Protist</i> , 2020, 171, 125758.	0.6	2
8819	The wide distribution and horizontal transfers of beta satellite DNA in eukaryotes. <i>Genomics</i> , 2020, 112, 5295-5304.	1.3	2
8820	Understanding and predicting ciprofloxacin minimum inhibitory concentration in <i>Escherichia coli</i> with machine learning. <i>Scientific Reports</i> , 2020, 10, 15026.	1.6	24
8822	Morphometry and colony structure of ants of the genus <i>Cardiocondyla</i> (Hymenoptera: Formicidae) from Georgia. <i>Zoology in the Middle East</i> , 2020, 66, 347-356.	0.2	0
8823	Ancestral gene duplications in mosses characterized by integrated phylogenomic analyses. <i>Journal of Systematics and Evolution</i> , 2022, 60, 144-159.	1.6	19
8824	Phylogenomics enables biogeographic analysis and a new subtribal classification of Andropogoneae (Poaceae "Panicoideae). <i>Journal of Systematics and Evolution</i> , 2020, 58, 1003-1030.	1.6	31
8825	Phylogeny and taxonomy of <i>Afrocyratia</i> , a new genus of Vitaceae from continental Africa and Madagascar. <i>Journal of Systematics and Evolution</i> , 2020, 58, 1090-1107.	1.6	5
8826	Phylogenomics of the hyperdiverse daisy tribes: Anthemideae, Astereae, Calenduleae, Gnaphalieae, and Senecioneae. <i>Journal of Systematics and Evolution</i> , 2020, 58, 841-852.	1.6	26
8827	Sequence analysis of the <i>Petunia inflata</i> S-locus region containing 17 S-Locus Box genes and the S-RNase gene involved in self-incompatibility. <i>Plant Journal</i> , 2020, 104, 1348-1368.	2.8	14
8828	Fibrillar evolution through the Tree of Life: Comparative genomics and microsynteny network analyses provide new insights into the evolutionary history of Fibrillar. <i>PLoS Computational Biology</i> , 2020, 16, e1008318.	1.5	8
8829	Role of BgaA as a Pneumococcal Virulence Factor Elucidated by Molecular Evolutionary Analysis. <i>Frontiers in Microbiology</i> , 2020, 11, 582437.	1.5	5
8830	New Parasite Records for the Sunfish <i>Mola mola</i> in the Mediterranean Sea and Their Potential Use as Biological Tags for Long-Distance Host Migration. <i>Frontiers in Veterinary Science</i> , 2020, 7, 579728.	0.9	12

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8831	Newly Explored Faecalibacterium Diversity Is Connected to Age, Lifestyle, Geography, and Disease. <i>Current Biology</i> , 2020, 30, 4932-4943.e4.	1.8	72
8832	Evolutionary trade-offs in the chemical defense of floral and fruit tissues across genus <i>Cornus</i> . <i>American Journal of Botany</i> , 2020, 107, 1260-1273.	0.8	3
8833	New Lineage of Microbial Predators Adds Complexity to Reconstructing the Evolutionary Origin of Animals. <i>Current Biology</i> , 2020, 30, 4500-4509.e5.	1.8	24
8834	Phylogenetic relationships amongst the African genera of subtribe Orchidinae s.l. (Orchidaceae); Tj ETQq1 1 0.784314 rgBT /Overlock 10 T Evolution, 2020, 153, 106946.	1.2	9
8835	The complete chloroplast genome sequences of two <i>Chaenomeles</i> species (<i>Chaenomeles cathayensis</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T	0.2	2
8836	Phylogenomics of Parasitic and Nonparasitic Lice (Insecta: Psocodea): Combining Sequence Data and Exploring Compositional Bias Solutions in Next Generation Data Sets. <i>Systematic Biology</i> , 2021, 70, 719-738.	2.7	43
8837	The evolution of coloration and opsins in tarantulas. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20201688.	1.2	5
8838	Cyanophage host-derived genes reflect contrasting selective pressures with depth in the oxic and anoxic water column of the Eastern Tropical North Pacific. <i>Environmental Microbiology</i> , 2021, 23, 2782-2800.	1.8	13
8839	The evolution of autotomy in leaf-footed bugs. <i>Evolution; International Journal of Organic Evolution</i> , 2020, 74, 897-910.	1.1	31
8840	Dynamics of <i>bla</i> KPC-2 Dissemination from Non-CG258 <i>Klebsiella pneumoniae</i> to Other <i>Enterobacteriales</i> via IncN Plasmids in an Area of High Endemicity. <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	1.4	27
8841	<i>Emesis planeca</i> n. comb. (Lepidoptera: Riodinidae): a new combination revealed by molecular evidence with a description of its morphological variation	0.2	0
8842	Spatio-Temporal Mutational Profile Appearances of Swedish SARS-CoV-2 during the Early Pandemic. <i>Viruses</i> , 2020, 12, 1026.	1.5	12
8843	Morphological and molecular separation between <i>Macrocamptoptera grangeri</i> Soyka and <i>M. metotarsa</i> (Girault) (Hymenoptera: Mymaridae). <i>Journal of Natural History</i> , 2020, 54, 585-596.	0.2	1
8844	Genetic Diversity Analysis of Coxsackievirus A8 Circulating in China and Worldwide Reveals a Highly Divergent Genotype. <i>Viruses</i> , 2020, 12, 1061.	1.5	4
8845	Epidemiology of <i>Burkholderia</i> Infections in People with Cystic Fibrosis in Canada between 2000 and 2017. <i>Annals of the American Thoracic Society</i> , 2020, 17, 1549-1557.	1.5	9
8846	<i>Moniliophthora perniciosa</i> , the mushroom causing witches' broom disease of cacao: Insights into its taxonomy, ecology and host range in Brazil. <i>Fungal Biology</i> , 2020, 124, 983-1003.	1.1	13
8847	Genomic and experimental data provide new insights into luciferin biosynthesis and bioluminescence evolution in fireflies. <i>Scientific Reports</i> , 2020, 10, 15882.	1.6	14
8848	Aenigmachannidae, a new family of snakehead fishes (Teleostei: Channoidei) from subterranean waters of South India. <i>Scientific Reports</i> , 2020, 10, 16081.	1.6	8

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8849	Strain-Level Analysis of <i>Bifidobacterium</i> spp. from Gut Microbiomes of Adults with Differing Lactase Persistence Genotypes. <i>MSystems</i> , 2020, 5, .	1.7	12
8850	The complete chloroplast genome sequence of <i>Hemerocallis fulva</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 3543-3544.	0.2	1
8851	Genetic diversity, phylogeography, and evolutionary dynamics of highly pathogenic avian influenza A (H5N6) viruses. <i>Virus Evolution</i> , 2020, 6, veaa079.	2.2	23
8852	Adaptive evolution shapes the present-day distribution of the thermal sensitivity of population growth rate. <i>PLoS Biology</i> , 2020, 18, e3000894.	2.6	21
8853	Phylogeography and potential glacial refugia of terrestrial gastropod <i>Faustina faustina</i> (Rossmässler). <i>Journal of Biogeography</i> , 2020, 47, 1071-1083.	0.7	8
8854	Loop 1 of APOBEC3C Regulates its Antiviral Activity against HIV-1. <i>Journal of Molecular Biology</i> , 2020, 432, 6200-6227.	2.0	11
8855	Large scale genome reconstructions illuminate <i>Wolbachia</i> evolution. <i>Nature Communications</i> , 2020, 11, 5235.	5.8	71
8856	Reference transcriptomes and comparative analyses of six species in the threatened rosewood genus <i>Dalbergia</i> . <i>Scientific Reports</i> , 2020, 10, 17749.	1.6	20
8857	Ancient genomes reveal tropical bovid species in the Tibetan Plateau contributed to the prevalence of hunting game until the late Neolithic. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 28150-28159.	3.3	28
8858	Methanogenic archaea in peatlands. <i>FEMS Microbiology Letters</i> , 2020, 367, .	0.7	35
8859	IMA Genome - F13. <i>IMA Fungus</i> , 2020, 11, 19.	1.7	13
8860	Fast Recognition of <i>Lecanicillium</i> spp., and Its Virulence Against <i>Frankliniella occidentalis</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 561381.	1.5	15
8861	Comparative Plastid Genomics of Non-Photosynthetic Chrysophytes: Genome Reduction and Compaction. <i>Frontiers in Plant Science</i> , 2020, 11, 572703.	1.7	8
8862	The New <i>Klebsiella pneumoniae</i> ST152 Variants with Hypermucoviscous Phenotype Isolated from Renal Transplant Recipients with Asymptomatic Bacteriuria: Genetic Characteristics by WGS. <i>Genes</i> , 2020, 11, 1189.	1.0	10
8863	Complete Chloroplast Genome of <i>Argania spinosa</i> : Structural Organization and Phylogenetic Relationships in Sapotaceae. <i>Plants</i> , 2020, 9, 1354.	1.6	21
8864	Phylogenetics and Systematics in a Nutshell. <i>Systematic Botany</i> , 2020, 45, 81-112.		4
8865	A unique clade of light-driven proton-pumping rhodopsins evolved in the cyanobacterial lineage. <i>Scientific Reports</i> , 2020, 10, 16752.	1.6	17
8866	Phylogeographical analysis of character displacement in feeding phenotypes of snail-feeding <i>Acoptolabrus</i> ground beetles. <i>Biological Journal of the Linnean Society</i> , 2020, 131, 936-951.	0.7	2

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8867	Genomic differentiation in an endemic Philippine genus (<i>Aves: Sarcophanops</i>) owing to geographical isolation on recently disassociated islands. <i>Biological Journal of the Linnean Society</i> , 2020, 131, 814-821.	0.7	2
8868	The SoNAP gene from sugarcane (<i>Saccharum officinarum</i>) encodes a senescence-associated NAC transcription factor involved in response to osmotic and salt stress. <i>Journal of Plant Research</i> , 2020, 133, 897-909.	1.2	5
8869	Molecular and epidemiological surveillance of polymyxin-resistant <i>Klebsiella pneumoniae</i> strains isolated from Brazil with multiple mgrB gene mutations. <i>International Journal of Medical Microbiology</i> , 2020, 310, 151448.	1.5	17
8870	<i>Entamoeba</i> and <i>Giardia</i> parasites implicated as hosts of CRESS viruses. <i>Nature Communications</i> , 2020, 11, 4620.	5.8	34
8871	<i>Trigonotis motuoensis</i> (Boraginaceae), a new species from Xizang, China. <i>Phytotaxa</i> , 2020, 461, 233-242.	0.1	1
8872	The chloroplast genome of <i>Adiantum reniforme</i> var. <i>sinense</i> , an endangered fern endemic to China. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 3286-3287.	0.2	0
8873	The mole genome reveals regulatory rearrangements associated with adaptive intersexuality. <i>Science</i> , 2020, 370, 208-214.	6.0	41
8874	Cross-Protection by Inactivated H5 Prepandemic Vaccine Seed Strains against Diverse Goose/Guangdong Lineage H5N1 Highly Pathogenic Avian Influenza Viruses. <i>Journal of Virology</i> , 2020, 94, .	1.5	11
8875	Distinctive gene and protein characteristics of extremely piezophilic <i>Colwellia</i> . <i>BMC Genomics</i> , 2020, 21, 692.	1.2	27
8876	Two new species of the <i>Peronospora belbahrii</i> species complex, <i>Pe. choii</i> sp. nov. and <i>Pe. salviae-pratensis</i> sp. nov., and a new host for <i>Pe. salviae-officinalis</i> . <i>Fungal Systematics and Evolution</i> , 2020, 6, 38-52.	0.9	6
8877	A Novel RNA Virus, <i>Macrobrachium rosenbergii</i> Golda Virus (MrGV), Linked to Mass Mortalities of the Larval Giant Freshwater Prawn in Bangladesh. <i>Viruses</i> , 2020, 12, 1120.	1.5	11
8878	Multilocus phylogeny- and fruiting feature-assisted delimitation of European <i>Cyclocybe aegerita</i> from a new Asian species complex and related species. <i>Mycological Progress</i> , 2020, 19, 1001-1016.	0.5	15
8879	<i>Mycoenterolobium aquadictyosporium</i> sp. nov. (Pleosporomycetidae, Dothideomycetes) from a freshwater habitat in Thailand. <i>Mycological Progress</i> , 2020, 19, 1031-1042.	0.5	5
8880	Genomes of the Banyan Tree and Pollinator Wasp Provide Insights into Fig-Wasp Coevolution. <i>Cell</i> , 2020, 183, 875-889.e17.	13.5	71
8881	The Guaymas Basin Subseafloor Sedimentary Archaeome Reflects Complex Environmental Histories. <i>IScience</i> , 2020, 23, 101459.	1.9	22
8882	Phylogenomics of the Neotropical fish family Serrasalminidae with a novel intrafamilial classification (Teleostei: Characiformes). <i>Molecular Phylogenetics and Evolution</i> , 2020, 153, 106945.	1.2	15
8883	The complete chloroplast genome sequence of a popular ornamental plant <i>Calibrachoa hybrida</i> (Solanaceae: Petunioideae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 3374-3375.	0.2	2
8884	New Environment, New Invaders—Repeated Horizontal Transfer of LINEs to Sea Snakes. <i>Genome Biology and Evolution</i> , 2020, 12, 2370-2383.	1.1	11

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8885	Escherichia coli Sequence Type 457 Is an Emerging Extended-Spectrum-β ² -Lactam-Resistant Lineage with Reservoirs in Wildlife and Food-Producing Animals. <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 65, .	1.4	30
8886	Experimental Infection and Genetic Characterization of Two Different Capripox Virus Isolates in Small Ruminants. <i>Viruses</i> , 2020, 12, 1098.	1.5	19
8887	Molecular diversity and coalescent species delimitation of avian haemosporidian parasites in an endemic bird species of South America. <i>Parasitology Research</i> , 2020, 119, 4033-4047.	0.6	4
8888	Clinical and molecular characteristics of carbapenem non-susceptible Escherichia coli: A nationwide survey from Oman. <i>PLoS ONE</i> , 2020, 15, e0239924.	1.1	18
8889	Influence of silver nanoparticles on a common contaminant isolated during the establishment of <i>Stevia rebaudiana</i> Bertoni culture. <i>Plant Cell, Tissue and Organ Culture</i> , 2020, 143, 609-618.	1.2	7
8890	Diversification of DNA-Binding Specificity by Permissive and Specificity-Switching Mutations in the ParB/Noc Protein Family. <i>Cell Reports</i> , 2020, 32, 107928.	2.9	21
8891	Spirotrichonympha (Parabasalia) symbionts of the termite <i>Paraneotermes simplicicornis</i> . <i>European Journal of Protistology</i> , 2020, 76, 125742.	0.5	5
8892	The complete mitochondrial genome of medicinal fungus <i>Taiwanofungus camphoratus</i> reveals gene rearrangements and intron dynamics of Polyporales. <i>Scientific Reports</i> , 2020, 10, 16500.	1.6	18
8893	A phylogeny for the plant pathogen <i>Piptoporellus baudonii</i> using a multigene data set. <i>Mycologia</i> , 2020, 112, 1017-1025.	0.8	7
8894	Additional new species suggest high dictyostelid diversity on Madagascar. <i>Mycologia</i> , 2020, 112, 1026-1042.	0.8	2
8895	World Travelers: DNA Barcoding Unmasks the Origin of Cloning Asteroid Larvae from the Caribbean. <i>Biological Bulletin</i> , 2020, 239, 73-79.	0.7	6
8896	Comparative genomic analyses illuminate the distinct evolution of megabats within Chiroptera. <i>DNA Research</i> , 2020, 27, .	1.5	10
8897	Efficient inference, potential, and limitations of site-specific substitution models. <i>Virus Evolution</i> , 2020, 6, veaa066.	2.2	3
8898	Global and regional dispersal patterns of hepatitis B virus genotype E from and in Africa: A full-genome molecular analysis. <i>PLoS ONE</i> , 2020, 15, e0240375.	1.1	21
8899	<i>Bolbea parasitica</i> gen. et sp. nov., a cultivable holocarpic parasitoid of the early-diverging Saprolegniomycetes. <i>Fungal Systematics and Evolution</i> , 2020, 6, 129-137.	0.9	1
8900	Generic boundaries in subtribe Saussureinae (Compositae: Cardueae): Insights from HybSeq data. <i>Taxon</i> , 2020, 69, 694-714.	0.4	8
8901	The complete chloroplast genome sequence of <i>Hippeastrum rutilum</i> (Amaryllidoideae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 3387-3388.	0.2	4
8902	Learning the heterogeneous hypermutation landscape of immunoglobulins from high-throughput repertoire data. <i>Nucleic Acids Research</i> , 2020, 48, 10702-10712.	6.5	20

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8903	Multiobjective Formulation of Multiple Sequence Alignment for Phylogeny Inference. IEEE Transactions on Cybernetics, 2022, 52, 2775-2786.	6.2	5
8904	Inter-Algorithm Multiobjective Cooperation for Phylogenetic Reconstruction on Amino Acid Data. IEEE Transactions on Cybernetics, 2022, 52, 3577-3591.	6.2	1
8905	Molecular phylogeny reveals high diversity and endemism in the limestone karst-restricted land snail genus <i>Sophina</i> Benson, 1859 from Myanmar (Eupulmonata: Helicarionidae), with description of four new species. Journal of Zoological Systematics and Evolutionary Research, 2020, 58, 957-981.	0.6	11
8906	Real-time tracking of Tomato brown rugose fruit virus (ToBRFV) outbreaks in the Netherlands using Nextstrain. PLoS ONE, 2020, 15, e0234671.	1.1	33
8907	Precise Species Identification and Taxonomy Update for the Genus <i>Kluyvera</i> With Reporting <i>Kluyvera sichuanensis</i> sp. nov.. Frontiers in Microbiology, 2020, 11, 579306.	1.5	13
8908	Large-scale genome sequencing of mycorrhizal fungi provides insights into the early evolution of symbiotic traits. Nature Communications, 2020, 11, 5125.	5.8	258
8909	Investigations on the phylogenetic position of the ditypic genus <i>Froriepia</i> reveal <i>Yildirimlia</i> , a new genus of Apiaceae. Taxon, 2020, 69, 1259-1272.	0.4	4
8910	Evolution and biogeography of the <i>Zanclaea-Scleractinia</i> symbiosis. Coral Reefs, 2022, 41, 779-795.	0.9	18
8911	Integrative systematics approaches revealed that the rare red alga <i>Schimmelmannia</i> (Schimmelmanniaceae, Acrosymphytales) from Japan is a new species: The description of <i>S. benzaiteniana</i> sp. nov.. Phycological Research, 2020, 68, 290-297.	0.8	4
8912	Chicken Astrovirus (CAstV) Molecular Studies Reveal Evidence of Multiple Past Recombination Events in Sequences Originated from Clinical Samples of White Chick Syndrome (WCS) in Western Canada. Viruses, 2020, 12, 1096.	1.5	21
8913	Kinetid in larval cells of Spongillida (Porifera: Demospongiae): tracing the ancestral traits. Organisms Diversity and Evolution, 2020, 20, 669-680.	0.7	1
8914	Metagenomic profiling of ammonia- and methane-oxidizing microorganisms in two sequential rapid sand filters. Water Research, 2020, 185, 116288.	5.3	52
8915	Dynamics in Secondary Metabolite Gene Clusters in Otherwise Highly Syntenic and Stable Genomes in the Fungal Genus <i>Botrytis</i> . Genome Biology and Evolution, 2020, 12, 2491-2507.	1.1	22
8916	Phylogenomic analysis clarifies the evolutionary origin of <i>Coffea arabica</i> . Journal of Systematics and Evolution, 2021, 59, 953-963.	1.6	16
8917	Genomic analyses reveal evolutionary and geologic context for the plateau fungus <i>Ophiocordyceps sinensis</i> . Chinese Medicine, 2020, 15, 107.	1.6	8
8918	Contrasting population structure and demographic history of cereal aphids in different environmental and agricultural landscapes. Ecology and Evolution, 2020, 10, 9647-9662.	0.8	15
8919	Evolutionary conservation of opsin gene expression patterns in the compound eyes of darkling beetles. Development Genes and Evolution, 2020, 230, 339-345.	0.4	3
8920	Genomic Adaptations and Evolutionary History of the Extinct Scimitar-Toothed Cat, <i>Homotherium latidens</i> . Current Biology, 2020, 30, 5018-5025.e5.	1.8	34

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8921	Ultraconserved element bait set for trypanosomatida target enrichment and phylogenetics. <i>Experimental Parasitology</i> , 2020, 219, 108015.	0.5	1
8922	Mitochondrial genome sequencing and phylogeny of <i>Haemagogus albomaculatus</i> , <i>Haemagogus leucocelaenus</i> , <i>Haemagogus spegazzinii</i> , and <i>Haemagogus tropicalis</i> (Diptera: Culicidae). <i>Scientific Reports</i> , 2020, 10, 16948.	1.6	12
8923	Probable long-term prevalence for a predominant <i>Mycobacterium tuberculosis</i> clone of a Beijing genotype in Colon, Panama. <i>Transboundary and Emerging Diseases</i> , 2021, 68, 2229-2238.	1.3	2
8924	Contributions to <i>Disholcaspis</i> Dalla Torre And Kieffer (Hymenoptera: Cynipidae: Cynipini). <i>Zootaxa</i> , 2020, 4859, 355-382.	0.2	0
8925	Phylogeny and Structure of Fatty Acid Photodecarboxylases and Glucose-Methanol-Choline Oxidoreductases. <i>Catalysts</i> , 2020, 10, 1072.	1.6	16
8926	Genome-wide identification and transcriptional modulation of histone variants and modification related genes in the low pH-exposed marine rotifer <i>Brachionus koreanus</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2020, 36, 100748.	0.4	3
8927	The Radiation of Darwin's Giant Daisies in the Galápagos Islands. <i>Current Biology</i> , 2020, 30, 4989-4998.e7.	1.8	35
8928	Occurrence of <i>Listeria</i> and <i>Escherichia coli</i> in frozen fruit and vegetables collected from retail and catering premises in England 2018-2019. <i>International Journal of Food Microbiology</i> , 2020, 334, 108849.	2.1	30
8929	Taxonomy and Molecular Phylogenetics of <i>Ensiculiferaceae</i> , fam. nov. (Peridinales, Dinophyceae), with Consideration of their Life-history. <i>Protist</i> , 2020, 171, 125759.	0.6	11
8930	Antimicrobial resistance and genomic insights into bovine mastitis-associated <i>Staphylococcus aureus</i> in Australia. <i>Veterinary Microbiology</i> , 2020, 250, 108850.	0.8	11
8931	Microbiota Supplementation with <i>Bifidobacterium</i> and <i>Lactobacillus</i> Modifies the Preterm Infant Gut Microbiota and Metabolome: An Observational Study. <i>Cell Reports Medicine</i> , 2020, 1, 100077.	3.3	119
8932	A genome resource for green millet <i>Setaria viridis</i> enables discovery of agronomically valuable loci. <i>Nature Biotechnology</i> , 2020, 38, 1203-1210.	9.4	103
8933	Whitefly genomes contain ribotoxin coding genes acquired from plants. <i>Scientific Reports</i> , 2020, 10, 15503.	1.6	24
8934	Myanmar <i>Burkholderia pseudomallei</i> strains are genetically diverse and originate from Asia with phylogenetic evidence of reintroductions from neighbouring countries. <i>Scientific Reports</i> , 2020, 10, 16260.	1.6	11
8935	Continental-scale patterns of hyper-cryptic diversity within the freshwater model taxon <i>Gammarus fossarum</i> (Crustacea, Amphipoda). <i>Scientific Reports</i> , 2020, 10, 16536.	1.6	51
8936	Biased Gene Retention in the Face of Introgression Obscures Species Relationships. <i>Genome Biology and Evolution</i> , 2020, 12, 1646-1663.	1.1	24
8937	Positive Selection and Gene Expression Analyses from Salivary Glands Reveal Discrete Adaptations within the Ecologically Diverse Bat Family Phyllostomidae. <i>Genome Biology and Evolution</i> , 2020, 12, 1419-1428.	1.1	7
8938	Alignment-Integrated Reconstruction of Ancestral Sequences Improves Accuracy. <i>Genome Biology and Evolution</i> , 2020, 12, 1549-1565.	1.1	15

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8939	Convergent Evolution and Structural Adaptation to the Deep Ocean in the Protein-Folding Chaperonin CCT1±. <i>Genome Biology and Evolution</i> , 2020, 12, 1929-1942.	1.1	9
8940	Species Diversity in the Braconid Wasp Genus <i>Allorhogas</i> (Doryctinae) Associated With Cynipid Galls on Live Oaks (<i>Quercus</i> : Fagaceae) Using Natural History, Phylogenetics, and Morphology. <i>Insect Systematics and Diversity</i> , 2020, 4, .	0.7	7
8941	Morphological, Phylogenetic and Ecophysiological Characterization of a New Ciliate, <i>Platynematum rossellomorai</i> n. sp. (Oligohymenophorea, Scuticociliatia), Detected in a Hypersaline Pond on Mallorca, Spain. <i>Protist</i> , 2020, 171, 125751.	0.6	6
8942	<i>Cladosterigma</i>: an enigmatic fungus, previously considered a basidiomycete, now revealed as an ascomycete member of the Gomphillaceae. <i>Mycologia</i> , 2020, 112, 829-846.	0.8	1
8943	Assessing biodiversity within the range of <i>Heleobia chimbaensis</i> (Caenogastropoda:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 582 T	0.5	4
8944	<i>Falsigemmobacter faecalis</i> gen. nov. sp. nov., isolated from faeces of <i>Rhinopithecus roxellanae</i> , and reclassification of <i>Gemmobacter intermedius</i> as <i>Falsigemmobacter intermedius</i> comb. nov. <i>Archives of Microbiology</i> , 2020, 202, 2599-2606.	1.0	1
8945	Chromosome number evolution in dalbergioid legumes (Papilionoideae, Leguminosae). <i>Revista Brasileira De Botanica</i> , 2020, 43, 575-587.	0.5	5
8946	Extensive cryptic diversity in the widely distributed <i>Polysiphonia scopulorum</i> (Rhodomelaceae,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 582 T and <i>Evolution</i> , 2020, 152, 106909.	1.2	24
8947	<i>Escherichia coli</i> ST8196 is a novel, locally evolved, and extensively drug resistant pathogenic lineage within the ST131 clonal complex. <i>Emerging Microbes and Infections</i> , 2020, 9, 1780-1792.	3.0	3
8948	First description of antimicrobial resistance in carbapenem-susceptible <i>Klebsiella pneumoniae</i> after imipenem treatment, driven by outer membrane remodeling. <i>BMC Microbiology</i> , 2020, 20, 218.	1.3	14
8949	Plastome phylogenomic study of Gentianeae (Gentianaceae): widespread gene tree discordance and its association with evolutionary rate heterogeneity of plastid genes. <i>BMC Plant Biology</i> , 2020, 20, 340.	1.6	35
8950	Antimicrobial Resistance in Wildlife in Guadeloupe (French West Indies): Distribution of a Single blaCTXâ€“1/Incl1/ST3 Plasmid Among Humans and Wild Animals. <i>Frontiers in Microbiology</i> , 2020, 11, 1524.	1.5	25
8951	Characterization of a new subgroup of <i>Rhizoctonia solani</i> anastomosis group 3 (AG-3 TM) associated with tomato leaf blight. <i>Journal of General Plant Pathology</i> , 2020, 86, 457-467.	0.6	8
8952	Extreme plastid RNA editing may confound phylogenetic reconstruction: A case study of <i>Selaginella</i> (lycophytes). <i>Plant Diversity</i> , 2020, 42, 356-361.	1.8	13
8953	Diatom DNA metabarcoding for ecological assessment: Comparison among bioinformatics pipelines used in six European countries reveals the need for standardization. <i>Science of the Total Environment</i> , 2020, 745, 140948.	3.9	53
8954	Six reference-quality genomes reveal evolution of bat adaptations. <i>Nature</i> , 2020, 583, 578-584.	13.7	210
8955	Evolutionary and phylogenetic aspects of the chloroplast genome of <i>Chaenomeles</i> species. <i>Scientific Reports</i> , 2020, 10, 11466.	1.6	41
8956	Genomic insights of body plan transitions from bilateral to pentameral symmetry in Echinoderms. <i>Communications Biology</i> , 2020, 3, 371.	2.0	34

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8957	Rediscovery, range extension, habitat and phylogenetic relation of the endemic Scaled Sandveld Lizard <i>Nucras scalaris</i> Laurent, 1964 (Sauria: Lacertidae) in the central Angolan plateau. <i>African Journal of Herpetology</i> , 2020, 69, 12-28.	0.3	6
8958	FastMulRFS: fast and accurate species tree estimation under generic gene duplication and loss models. <i>Bioinformatics</i> , 2020, 36, i57-i65.	1.8	28
8959	Excessive Parallelism in Protein Evolution of Lake Baikal Amphipod Species Flock. <i>Genome Biology and Evolution</i> , 2020, 12, 1493-1503.	1.1	1
8960	Chromosome-level de novo assembly of the pig-tailed macaque genome using linked-read sequencing and HiC proximity scaffolding. <i>GigaScience</i> , 2020, 9, .	3.3	6
8961	Asterid Phylogenomics/Phylotranscriptomics Uncover Morphological Evolutionary Histories and Support Phylogenetic Placement for Numerous Whole-Genome Duplications. <i>Molecular Biology and Evolution</i> , 2020, 37, 3188-3210.	3.5	82
8962	Is Phylotranscriptomics as Reliable as Phylogenomics?. <i>Molecular Biology and Evolution</i> , 2020, 37, 3672-3683.	3.5	52
8963	Modifying Plant Photosynthesis and Growth via Simultaneous Chloroplast Transformation of Rubisco Large and Small Subunits. <i>Plant Cell</i> , 2020, 32, 2898-2916.	3.1	79
8964	Comparative phylogenomics reveal complex evolution of life history strategies in a clade of bivalves with parasitic larvae (Bivalvia: Unionoida: Ambleminae). <i>Cladistics</i> , 2020, 36, 505-520.	1.5	21
8965	Animal-mediated long-distance dispersals and migrations shaping the intercontinental disjunctions of <i>Celastrus</i> (Celastraceae) among five continents. <i>Journal of Systematics and Evolution</i> , 2020, 58, 945-957.	1.6	7
8966	Genomic insights on the contribution of balancing selection and local adaptation to the long-term survival of a widespread living fossil tree, <i>Cercidiphyllum japonicum</i> . <i>New Phytologist</i> , 2020, 228, 1674-1689.	3.5	22
8967	The complete mitochondrial genome of the Eurasian wryneck <i>Jynx torquilla</i> (Aves: Piciformes: Picidae) and its phylogenetic inference. <i>Zootaxa</i> , 2020, 4810, 351-360.	0.2	3
8968	Pseudohyphal growth in <i>Saccharomyces cerevisiae</i> involves protein kinase-regulated lipid flippases. <i>Journal of Cell Science</i> , 2020, 133, .	1.2	18
8969	Analysis of p67 allelic sequences reveals a subtype of allele type 1 unique to buffalo-derived <i>Theileria parva</i> parasites from southern Africa. <i>PLoS ONE</i> , 2020, 15, e0231434.	1.1	7
8970	Taxonomic novelties in Magnolia-associated pleosporalean fungi in the Kunming Botanical Gardens (Yunnan, China). <i>PLoS ONE</i> , 2020, 15, e0235855.	1.1	35
8971	Genomic Analysis of Diverse Members of the Fungal Genus <i>Monosporascus</i> Reveals Novel Lineages, Unique Genome Content and a Potential Bacterial Associate. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2573-2583.	0.8	5
8972	Systematic Humanization of the Yeast Cytoskeleton Discerns Functionally Replaceable from Divergent Human Genes. <i>Genetics</i> , 2020, 215, 1153-1169.	1.2	14
8973	First elucidation of the life cycle in the family Brachycladiidae (Digenea), parasites of marine mammals. <i>International Journal for Parasitology</i> , 2020, 50, 997-1009.	1.3	9
8974	Evolving sequence mutations in the Middle East Respiratory Syndrome Coronavirus (MERS-CoV). <i>Journal of Infection and Public Health</i> , 2020, 13, 1544-1550.	1.9	11

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8975	Parablepharisma (Ciliophora) is not a Heterotrich: A Phylogenetic and Morphological Study with the Proposal of New Taxa. <i>Protist</i> , 2020, 171, 125716.	0.6	13
8976	Bacterial chemolithoautotrophy via manganese oxidation. <i>Nature</i> , 2020, 583, 453-458.	13.7	152
8977	Mystery unveiled: Diacanthodes Singer a lineage within the core polyporoid clade. <i>Systematics and Biodiversity</i> , 2020, 18, 538-556.	0.5	6
8978	Co-circulation of both low and highly pathogenic avian influenza H5 viruses in current poultry epidemics in Taiwan. <i>Virus Evolution</i> , 2020, 6, veaa037.	2.2	16
8979	Conserved ZZ/ZW sex chromosomes in Caribbean croaking geckos (<i>Aristelliger</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50,582 Td (Sp	0.8	13
8980	Bioinformatic, genomic and evolutionary analysis of genes: A case study in dipteran CSPs. <i>Methods in Enzymology</i> , 2020, 642, 35-79.	0.4	0
8981	Genomic Blueprint of Glycine Betaine Metabolism in Coral Metaorganisms and Their Contribution to Reef Nitrogen Budgets. <i>IScience</i> , 2020, 23, 101120.	1.9	30
8982	Secrets from the deep: Pseudotanaididae (Crustacea: Tanaidacea) diversity from the Kuril-Kamchatka Trench. <i>Progress in Oceanography</i> , 2020, 183, 102288.	1.5	10
8983	Spanning the depths or depth-restricted: Three new species of Bathymodiolus (Bivalvia, Mytilidae) and a new record for the hydrothermal vent Bathymodiolus thermophilus at methane seeps along the Costa Rica margin. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2020, 164, 103322.	0.6	10
8984	Intraspecific variation within Castor bean (<i>Ricinus communis</i> L.) based on chloroplast genomes. <i>Industrial Crops and Products</i> , 2020, 155, 112779.	2.5	29
8985	GBA3: a polymorphic pseudogene in humans that experienced repeated gene loss during mammalian evolution. <i>Scientific Reports</i> , 2020, 10, 11565.	1.6	2
8986	Divergent evolutionary trajectories of influenza B viruses underlie their contemporaneous epidemic activity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 619-628.	3.3	80
8987	Phylogenetic relationships of the carnivorous terrestrial snail family Streptaxidae (Stylommatophora: Achatinina) in Thailand and surrounding areas of Southeast Asia. <i>Systematics and Biodiversity</i> , 2020, 18, 720-738.	0.5	7
8988	Selection for Reducing Energy Cost of Protein Production Drives the GC Content and Amino Acid Composition Bias in Gene Transfer Agents. <i>MBio</i> , 2020, 11, .	1.8	12
8989	Australia: A Continent Without Native Powdery Mildews? The First Comprehensive Catalog Indicates Recent Introductions and Multiple Host Range Expansion Events, and Leads to the Re-discovery of Salmonomyces as a New Lineage of the Erysiphales. <i>Frontiers in Microbiology</i> , 2020, 11, 1571.	1.5	26
8990	Fungal pathogens occurring on <i>Orthopterida</i> in Thailand. <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2020, 44, 140-160.	1.6	18
8991	Longitudinal Isolation of Potent Near-Germline SARS-CoV-2-Neutralizing Antibodies from COVID-19 Patients. <i>Cell</i> , 2020, 182, 843-854.e12.	13.5	310
8992	Phylogeography and population dynamics of the Eastern Mediterranean whiting (<i>Merlangius</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50,582 Td (Sp Research, 2020, 229, 105614.	0.9	5

#	ARTICLE	IF	CITATIONS
8993	characterization of d-LA homo-oligomer degradation by the isolated strains. <i>Polymer Degradation and Stability</i> , 2020, 179, 109231.	2.7	11
8994	Groundwater <i>Elusimicrobia</i> are metabolically diverse compared to gut microbiome <i>Elusimicrobia</i> and some have a novel nitrogenase paralog. <i>ISME Journal</i> , 2020, 14, 2907-2922.	4.4	51
8995	Delimiting boundaries between species: excavating sponges close to <i>Cliona mucronata</i> (Demospongiae). <i>Systematics and Biodiversity</i> , 2020, 18, 573-591.	0.5	0
8996	Genomic Determination of Relative Risks for <i>Clostridioides difficile</i> Infection From Asymptomatic Carriage in Intensive Care Unit Patients. <i>Clinical Infectious Diseases</i> , 2021, 73, e1727-e1736.	2.9	20
8997	Using Constrained-INC for Large-scale Gene Tree and Species Tree Estimation. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, 18, 1-1.	1.9	2
8998	Sustainable Management of Invasive Pests in Africa. <i>Sustainability in Plant and Crop Protection</i> , 2020, , .	0.2	3
8999	Dawn of the dinophytes: A first attempt to date origin and diversification of harmful algae. <i>Harmful Algae</i> , 2020, 97, 101871.	2.2	9
9000	Structure and evolution of polysporangiate anthers in Melastomataceae. <i>Perspectives in Plant Ecology, Evolution and Systematics</i> , 2020, 46, 125556.	1.1	9
9001	The Identification and Evolutionary Trends of the Solute Carrier Superfamily in Arthropods. <i>Genome Biology and Evolution</i> , 2020, 12, 1429-1439.	1.1	12
9002	Speciation through chromosomal fusion and fission in Lepidoptera. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190539.	1.8	76
9003	A Species delimitation approach to uncover cryptic species in the South American fire ant decapitating flies (Diptera: Phoridae: Pseudacteon). <i>PLoS ONE</i> , 2020, 15, e0236086.	1.1	8
9004	Identification of tick-borne pathogens in ticks collected from wild animals in Turkey. <i>Parasitology Research</i> , 2020, 119, 3083-3091.	0.6	24
9005	CD4+ T Cells Recognize Conserved Influenza A Epitopes through Shared Patterns of V-Gene Usage and Complementary Biochemical Features. <i>Cell Reports</i> , 2020, 32, 107885.	2.9	11
9006	A novel interspecies recombinant enterovirus (Enterovirus A120) isolated from a case of acute flaccid paralysis in China. <i>Emerging Microbes and Infections</i> , 2020, 9, 1733-1743.	3.0	6
9007	AbGRI4, a novel antibiotic resistance island in multiply antibiotic-resistant <i>Acinetobacter baumannii</i> clinical isolates. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 2760-2768.	1.3	18
9008	Long-term isolation of European steppe outposts boosts the biome's conservation value. <i>Nature Communications</i> , 2020, 11, 1968.	5.8	34
9009	Genomic differentiation and intercontinental population structure of mosquito vectors <i>Culex pipiens pipiens</i> and <i>Culex pipiens molestus</i> . <i>Scientific Reports</i> , 2020, 10, 7504.	1.6	24
9010	Full genome sequencing of archived wild type and vaccine rinderpest virus isolates prior to their destruction. <i>Scientific Reports</i> , 2020, 10, 6563.	1.6	10

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9011	Synergism between the Black Queen effect and the proteomic constraint on genome size reduction in the photosynthetic picoeukaryotes. <i>Scientific Reports</i> , 2020, 10, 8918.	1.6	2
9012	Patterns and Rates of Plastid <i>rps12</i> Gene Evolution Inferred in a Phylogenetic Context using Plastomic Data of Ferns. <i>Scientific Reports</i> , 2020, 10, 9394.	1.6	17
9013	Phylogeny and taxonomic revision of <i>Kernia</i> and <i>Acaulium</i> . <i>Scientific Reports</i> , 2020, 10, 10302.	1.6	7
9014	Using larval barcoding to estimate stomatopod species richness at Lizard Island, Australia for conservation monitoring. <i>Scientific Reports</i> , 2020, 10, 10990.	1.6	11
9015	Subtyping analysis reveals new variants and accelerated evolution of <i>Clostridioides difficile</i> toxin B. <i>Communications Biology</i> , 2020, 3, 347.	2.0	42
9016	Mitochondrial genome characterization and phylogenetic analysis of bird schistosome <i>Trichobilharzia szidati</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2592-2594.	0.2	1
9017	The complete chloroplast genome sequence of <i>Ajania pacifica</i> (Nakai) Bremer & Humphries. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2399-2400.	0.2	2
9018	Characterization of the complete chloroplast genome of <i>Apocynum venetum</i> L. (Apocynaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2475-2476.	0.2	1
9019	Characterization of the complete chloroplast genome of <i>Zingiber zerumbet</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2629-2630.	0.2	1
9020	The complete chloroplast genome of <i>Scutellaria tsinyunensis</i> (Lamiaceae), an endemic species from China. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2568-2570.	0.2	4
9021	The complete chloroplast genome of <i>Rosa cymosa</i> (Rosaceae), a traditional medicinal plant in South China. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2571-2572.	0.2	3
9022	The complete chloroplast genome sequence of <i>Tapiscia sinensis</i> (Staphyleaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2658-2660.	0.2	1
9023	Complete chloroplast genome sequence of <i>Bambusa subtruncata</i> (Bambusodae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2609-2610.	0.2	0
9024	Complete mitogenome of the entomopathogenic fungus <i>Orbiocrella patchii</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2695-2696.	0.2	0
9025	Extensive gene loss in the plastome of holoparasitic plant <i>Cistanche tubulosa</i> (Orobanchaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2679-2681.	0.2	2
9026	Phylogeography of the European brook lamprey (<scp><i>Lampetra planeri</i></scp>) and the European river lamprey (<scp><i>Lampetra fluviatilis</i></scp>) species pair based on mitochondrial data. <i>Journal of Fish Biology</i> , 2020, 96, 905-912.	0.7	8
9027	Phylogenetic and spatial distribution of evolutionary diversification, isolation, and threat in turtles and crocodylians (non-avian archosauromorphs). <i>BMC Evolutionary Biology</i> , 2020, 20, 81.	3.2	38
9028	Genomic Comparison of Insect Gut Symbionts from Divergent Burkholderia Subclades. <i>Genes</i> , 2020, 11, 744.	1.0	14

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9029	Phylogenetic relationships in the genus <i>Cheracebus</i> (Callicebinae, Pitheciidae). <i>American Journal of Primatology</i> , 2020, 82, e23167.	0.8	3
9030	Land masses and oceanic currents drive population structure of <i>Heritiera littoralis</i> , a widespread mangrove in the Indo-West Pacific. <i>Ecology and Evolution</i> , 2020, 10, 7349-7363.	0.8	14
9031	Lingering Taxonomic Challenges Hinder Conservation and Management of Global Bonefishes. <i>Fisheries</i> , 2020, 45, 347-358.	0.6	15
9032	Early evolution of Coriariaceae (Cucurbitales) in light of a new early Campanian (ca. 82 Mya) pollen record from Antarctica. <i>Taxon</i> , 2020, 69, 87-99.	0.4	7
9033	<i>Caulifigura coniformis</i> gen. nov., sp. nov., a novel member of the family Planctomycetaceae isolated from a red biofilm sampled in a hydrothermal area. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 1927-1937.	0.7	15
9034	<i>Rosistilla oblonga</i> gen. nov., sp. nov. and <i>Rosistilla carotiformis</i> sp. nov., isolated from biotic or abiotic surfaces in Northern Germany, Mallorca, Spain and California, USA. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 1939-1952.	0.7	20
9035	PARMAP: A Pan-Genome-Based Computational Framework for Predicting Antimicrobial Resistance. <i>Frontiers in Microbiology</i> , 2020, 11, 578795.	1.5	10
9036	Origin and Evolution of Studiervirinae Bacteriophages Infecting <i>Pectobacterium</i> : Horizontal Transfer Assists Adaptation to New Niches. <i>Microorganisms</i> , 2020, 8, 1707.	1.6	20
9037	Molecular markers reveal diversity in composition of <i>Megastigmus</i> (Hymenoptera: Megastigmidae) from eucalypt galls. <i>Ecology and Evolution</i> , 2020, 10, 11565-11578.	0.8	1
9038	Expression of four new ferritins from grooved carpet shell clam <i>Ruditapes decussatus</i> challenged with <i>Perkinsus olseni</i> and metals (Cd, Cu and Zn). <i>Aquatic Toxicology</i> , 2020, 229, 105675.	1.9	3
9039	The importance of the Mexican taxa of Asteraceae in the family phylogeny. <i>Journal of Systematics and Evolution</i> , 2020, 59, 935.	1.6	4
9040	Directional divergence of Ep300 duplicates in teleosts and its implications. <i>BMC Evolutionary Biology</i> , 2020, 20, 140.	3.2	2
9041	Genomic and phylogenetic characterization of ChPV2, a novel goat PV closely related to the Xi-PV1 species infecting bovines. <i>Virology Journal</i> , 2020, 17, 167.	1.4	4
9042	Phylogenomic Analysis of <i>Campylobacter fetus</i> Reveals a Clonal Structure of Insertion Element ISCfe1 Positive Genomes. <i>Frontiers in Microbiology</i> , 2020, 11, 585374.	1.5	4
9043	Transcriptome Analysis and Knockdown of the Juvenile Hormone Esterase Gene Reveal Abnormal Feeding Behavior in the Sugarcane Giant Borer. <i>Frontiers in Physiology</i> , 2020, 11, 588450.	1.3	5
9044	Plant Broth- (Not Bovine-) Based Culture Media Provide the Most Compatible Vegan Nutrition for In Vitro Culturing and In Situ Probing of Plant Microbiota. <i>Diversity</i> , 2020, 12, 418.	0.7	5
9045	SURF1 related Leigh syndrome: Clinical and molecular findings of 16 patients from Turkey. <i>Molecular Genetics and Metabolism Reports</i> , 2020, 25, 100657.	0.4	10
9046	Genomic evidence supporting the clonal expansion of extensively drug-resistant tuberculosis bacteria belonging to a rare proto-Beijing genotype. <i>Emerging Microbes and Infections</i> , 2020, 9, 2632-2641.	3.0	5

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9047	A targeted sequence capture array for phylogenetics and population genomics in the Salicaceae. Applications in Plant Sciences, 2020, 8, e11394.	0.8	9
9048	<i>Stolephorus acinaces</i> , a new anchovy from northern Borneo, and redescription of <i>Stolephorus andhraensis</i> Babu Rao, 1966 (Clupeiformes: Engraulidae). Marine Biodiversity, 2020, 50, 1.	0.3	8
9049	The complete chloroplast genome sequence of medicinal plant: <i>Astragalus laxmannii</i> (Fabaceae). Mitochondrial DNA Part B: Resources, 2020, 5, 3643-3644.	0.2	5
9050	The complete mitochondrial genome of <i>Eutrichosiphum pasaniae</i> (Okajima, 1908) (Hemiptera: Tj ETQq1 1 0.784314 4gBT /Over	0.2	4
9051	Phylogenomic Analysis of a 55.1-kb 19-Gene Dataset Resolves a Monophyletic <i>Fusarium</i> that Includes the <i>Fusarium solani</i> Species Complex. Phytopathology, 2021, 111, 1064-1079.	1.1	107
9052	Dispersal ability correlates with range size in Amazonian habitat-restricted birds. Proceedings of the Royal Society B: Biological Sciences, 2020, 287, 20201450.	1.2	15
9053	Structural and functional characterization of the deep-sea thermophilic bacteriophage GVE2 tailspike protein. International Journal of Biological Macromolecules, 2020, 164, 4415-4422.	3.6	3
9054	Thermogenic hydrocarbon biodegradation by diverse depth-stratified microbial populations at a Scotian Basin cold seep. Nature Communications, 2020, 11, 5825.	5.8	72
9055	A Malagasy element in Continental Africa: a new subspecies of the rare <i>Amauris nossima</i> (Nymphalidae, Danaeinae) from the Kenyan coast. African Zoology, 2020, 55, 337-350.	0.2	1
9056	The complete chloroplast genome of the monotypic genus of <i>Bulleyia</i> Schltr. (Orchidaceae). Mitochondrial DNA Part B: Resources, 2020, 5, 3645-3646.	0.2	1
9057	Chloroplast characterizations of a <i>Phalaenopsis</i> native to China, <i>Phalaenopsis mannii</i> (Orchidaceae). Mitochondrial DNA Part B: Resources, 2020, 5, 3707-3708.	0.2	3
9058	Effects of geographical location on potentially valuable components in <i>Ulva intestinalis</i> sampled along the Swedish coast. Applied Phycology, 2020, 1, 80-92.	0.6	8
9059	Highly Pathogenic Avian Influenza A(H7N3) Virus in Poultry, United States, 2020. Emerging Infectious Diseases, 2020, 26, 2966-2969.	2.0	13
9060	Comparative Analysis of the Fecal Microbiota of Wild and Captive Beal™s Eyed Turtle (<i>Sacalia bealei</i>) by 16S rRNA Gene Sequencing. Frontiers in Microbiology, 2020, 11, 570890.	1.5	12
9061	Morphological, Genetic and Biological Evidences to Understand <i>Meromacrus Rondani</i> Diversity: New Species and Early Stages (Diptera: Syrphidae). Insects, 2020, 11, 791.	1.0	1
9062	The complete chloroplast genome of the <i>Euphorbia maculata</i> L. (Euphorbiaceae): characterization and phylogeny. Mitochondrial DNA Part B: Resources, 2020, 5, 3695-3696.	0.2	0
9063	Diversity, Host Ranges, and Potential Drivers of Speciation Among the Inquiline Enemies of Oak Gall Wasps (Hymenoptera: Cynipidae). Insect Systematics and Diversity, 2020, 4, .	0.7	14
9064	RAD-sequencing reveals patterns of diversification and hybridization, and the accumulation of reproductive isolation in a clade of partially sympatric, tropical island trees. Molecular Ecology, 2021, 30, 4520-4537.	2.0	12

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9065	Equine-Like H3 Avian Influenza Viruses in Wild Birds, Chile. <i>Emerging Infectious Diseases</i> , 2020, 26, 2887-2898.	2.0	2
9066	Evolutionary Convergence of C4 Photosynthesis: A Case Study in the Nyctaginaceae. <i>Frontiers in Plant Science</i> , 2020, 11, 578739.	1.7	10
9067	Diversity and Distribution of a Novel Genus of Hyperthermophilic Aquificae Viruses Encoding a Proof-Reading Family-A DNA Polymerase. <i>Frontiers in Microbiology</i> , 2020, 11, 583361.	1.5	7
9068	Comparative Genomics Analyses of Lifestyle Transitions at the Origin of an Invasive Fungal Pathogen in the Genus <i>Cryphonectria</i> . <i>MSphere</i> , 2020, 5, .	1.3	17
9069	Deep Convergence, Shared Ancestry, and Evolutionary Novelty in the Genetic Architecture of <i>Heliconius</i> Mimicry. <i>Genetics</i> , 2020, 216, 765-780.	1.2	13
9070	<i>Entoloma sequestratum</i> , a new species from northern Thailand, and a worldwide key to sequester taxa of <i>Entoloma</i> (<i>Entolomataceae</i>). <i>Fungal Systematics and Evolution</i> , 2020, 6, 253-263.	0.9	4
9071	The First Pycnogonid Draft Genome of <i>Nymphon striatum</i> . <i>Frontiers in Ecology and Evolution</i> , 2020, 8, .	1.1	2
9072	Wooden Stepping Stones: Diversity and Biogeography of Deep-Sea Wood Boring Xylophagidae (Mollusca: Bivalvia) in the North-East Atlantic Ocean, With the Description of a New Genus. <i>Frontiers in Marine Science</i> , 2020, 7, .	1.2	9
9073	DNA-Based Authentication and Metabolomics Analysis of Medicinal Plants Samples by DNA Barcoding and Ultra-High-Performance Liquid Chromatography/Triple Quadrupole Mass Spectrometry (UHPLC-MS). <i>Plants</i> , 2020, 9, 1601.	1.6	14
9074	Evolution of Biomineralization Genes in the Prismatic Layer of the Pen Shell <i>Atrina pectinata</i> . <i>Journal of Molecular Evolution</i> , 2020, 88, 742-758.	0.8	5
9075	Mercury Methylation Genes Identified across Diverse Anaerobic Microbial Guilds in a Eutrophic Sulfate-Enriched Lake. <i>Environmental Science & Technology</i> , 2020, 54, 15840-15851.	4.6	50
9076	The earliest diverging extant scleractinian corals recovered by mitochondrial genomes. <i>Scientific Reports</i> , 2020, 10, 20714.	1.6	16
9077	The complete chloroplast genome of <i>Zanthoxylum acanthopodium</i> DC. (Rutaceae) and its phylogenetic analysis. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 3618-3619.	0.2	2
9078	Characterization of the complete chloroplast genome of <i>Populus deltoides</i> Zhonglin 2025. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 3705-3706.	0.2	3
9079	CAPRIB: a user-friendly tool to study amino acid changes and selection for the exploration of intra-genus evolution. <i>BMC Genomics</i> , 2020, 21, 832.	1.2	2
9080	The Mosaic Architecture of NRPS-PKS in the Arbuscular Mycorrhizal Fungus <i>Gigaspora margarita</i> Shows a Domain With Bacterial Signature. <i>Frontiers in Microbiology</i> , 2020, 11, 581313.	1.5	8
9081	Plastid genomes of <i>Elaeagnus mollis</i> : comparative and phylogenetic analyses. <i>Journal of Genetics</i> , 2020, 99, 1.	0.4	5
9082	Conserved epitopes with high HLA-I population coverage are targets of CD8+ T cells associated with high IFN- γ responses against all dengue virus serotypes. <i>Scientific Reports</i> , 2020, 10, 20497.	1.6	5

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9083	The complete chloroplast genome sequences of five pinnate-leaved <i>Primula</i> species and phylogenetic analyses. <i>Scientific Reports</i> , 2020, 10, 20782.	1.6	13
9084	Analysis of <i>Drosophila</i> Atg8 proteins reveals multiple lipidation-independent roles. <i>Autophagy</i> , 2021, 17, 2565-2575.	4.3	27
9085	Hybrid capture of 964 nuclear genes resolves evolutionary relationships in the mimosoid legumes and reveals the polytomous origins of a large pantropical radiation. <i>American Journal of Botany</i> , 2020, 107, 1710-1735.	0.8	51
9086	Phylogenetic relationships and sectional delineation within <i>Gentiana</i> (Gentianaceae). <i>Taxon</i> , 2020, 69, 1221-1238.	0.4	23
9087	New insights into the taxonomic status, distribution and natural history of De Witte's Clicking Frog (<i>Kassinula wittei</i> Laurent, 1940). <i>African Zoology</i> , 2020, 55, 311-322.	0.2	7
9088	Mitochondrial genome of the mason bee, <i>Osmia pedicornis</i> (Hymenoptera: Megachilidae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 3746-3748.	0.2	0
9089	Comparative Genomic Analyses Reveal a Specific Mutation Pattern Between Human Coronavirus SARS-CoV-2 and Bat-CoV RaTG13. <i>Frontiers in Microbiology</i> , 2020, 11, 584717.	1.5	23
9090	Genome skimming and exploration of DNA barcodes for Taiwan endemic cypresses. <i>Scientific Reports</i> , 2020, 10, 20650.	1.6	2
9091	Updates to the recently introduced family Lacipirellulaceae in the phylum Planctomycetes: isolation of strains belonging to the novel genera <i>Aeoliella</i> , <i>Botrimarina</i> , <i>Pirellulimonas</i> and <i>Pseudobythopirellula</i> and the novel species <i>Bythopirellula polymerisocia</i> and <i>Posidoniimonas corsicana</i> . <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 1979-1997.	0.7	47
9092	Phylogenetic analysis of cell-cycle regulatory proteins within the Symbiodiniaceae. <i>Scientific Reports</i> , 2020, 10, 20473.	1.6	1
9093	PhaeoNet: A Holistic RNAseq-Based Portrait of Transcriptional Coordination in the Model Diatom <i>Phaeodactylum tricornutum</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 590949.	1.7	26
9094	Feral populations of <i>Brassica oleracea</i> along Atlantic coasts in western Europe. <i>Ecology and Evolution</i> , 2020, 10, 11810-11825.	0.8	11
9095	A revision of species of the <i>Parmelia saxatilis</i> complex in the Iberian Peninsula with the description of <i>P. rojoi</i> , a new potentially relict species. <i>Lichenologist</i> , 2020, 52, 365-376.	0.5	5
9096	Whole-genome single nucleotide polymorphism and mating compatibility studies reveal the presence of distinct species in sub-Saharan Africa <i>Bemisia tabaci</i> whiteflies. <i>Insect Science</i> , 2021, 28, 1553-1566.	1.5	19
9097	A new species of glass sponge (Hexactinellida: Sceptrulophora: Uncinateridae) from the Weijia Seamount in the northwestern Pacific Ocean. <i>Zootaxa</i> , 2020, 4878, 322-334.	0.2	2
9098	Discovery and characterisation of circular bacteriocin plantacyclin B21AG from <i>Lactiplantibacillus plantarum</i> B21. <i>Heliyon</i> , 2020, 6, e04715.	1.4	35
9099	A molecular study of the lichen genus <i>Byssoloma</i> Trevisan (Pilocarpaceae) with descriptions of three new species from China. <i>Lichenologist</i> , 2020, 52, 387-396.	0.5	2
9100	Critical Factors Facilitating <i>Candidatus</i> Nitrotoga To Be Prevalent Nitrite-Oxidizing Bacteria in Activated Sludge. <i>Environmental Science & Technology</i> , 2020, 54, 15414-15423.	4.6	43

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9101	Microbiota-directed fibre activates both targeted and secondary metabolic shifts in the distal gut. <i>Nature Communications</i> , 2020, 11, 5773.	5.8	55
9102	Atypical chemoreceptor arrays accommodate high membrane curvature. <i>Nature Communications</i> , 2020, 11, 5763.	5.8	20
9103	Repeated gain and loss of a single gene modulates the evolution of vascular plant pathogen lifestyles. <i>Science Advances</i> , 2020, 6, .	4.7	58
9104	The complete chloroplast genome of <i>Edgeworthia chrysantha</i> (Thymelaeaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 3639-3640.	0.2	4
9105	Real-Time Investigation of a Large Nosocomial Influenza A Outbreak Informed by Genomic Epidemiology. <i>Clinical Infectious Diseases</i> , 2021, 73, e4375-e4383.	2.9	13
9106	Carlgren's hesitation allayed: redescription and systematics of <i>Heteranthus verruculatus</i> Klunzinger, 1877 (Cnidaria, Actiniaria), with a redefinition of Heteranthidae Carlgren, 1900. <i>Contributions To Zoology</i> , 2020, 90, 155-182.	0.2	0
9107	The 256-kb mitochondrial genome of <i>Clavaria fumosa</i> is the largest among phylum Basidiomycota and is rich in introns and intronic ORFs. <i>IMA Fungus</i> , 2020, 11, 26.	1.7	27
9108	A Single Cysteine Residue in the Translocation Pathway of the Mitosomal ADP/ATP Carrier from <i>Cryptosporidium parvum</i> Confers a Broad Nucleotide Specificity. <i>International Journal of Molecular Sciences</i> , 2020, 21, 8971.	1.8	5
9109	An investigation of irreproducibility in maximum likelihood phylogenetic inference. <i>Nature Communications</i> , 2020, 11, 6096.	5.8	32
9110	The complete chloroplast genome sequence of <i>Laplacea alpestris</i> and its phylogenetic position. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 3789-3791.	0.2	1
9111	Pattern blending enriches the diversity of animal colorations. <i>Science Advances</i> , 2020, 6, .	4.7	12
9112	Genomic patterns and characterizations of chromosomally-encoded <i>mcr-1</i> in <i>Escherichia coli</i> populations. <i>Gut Pathogens</i> , 2020, 12, 55.	1.6	10
9113	Comparative Analysis of Complete Chloroplast Genome Sequences of Wild and Cultivated <i>Bougainvillea</i> (Nyctaginaceae). <i>Plants</i> , 2020, 9, 1671.	1.6	8
9114	Complete chloroplast genome sequence of <i>Amomum villosum</i> and comparative analysis with other Zingiberaceae plants. <i>Chinese Herbal Medicines</i> , 2020, 12, 375-383.	1.2	9
9115	Morphology, ultrastructure, genomics, and phylogeny of <i>Euplotes vanleeuwenhoekii</i> sp. nov. and its ultra-reduced endosymbiont <i>Candidatus Pinguicoccus supinus</i> sp. nov.. <i>Scientific Reports</i> , 2020, 10, 20311.	1.6	37
9116	Evolution of H9N2 avian influenza viruses in Iran, 2017–2019. <i>Transboundary and Emerging Diseases</i> , 2021, 68, 3405-3414.	1.3	3
9117	Genome Sequence of the Unusual Purple Photosynthetic Bacterium <i>Phaeovibrio sulfidiphilus</i> , Only Distantly Related to Rhodospirillaceae, Reveals Unique Genes for Respiratory Nitrate Reduction and Glycerol Metabolism. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	1
9118	Genetic Determinants of Resistance to Extended-Spectrum Cephalosporin and Fluoroquinolone in <i>Escherichia coli</i> Isolated from Diseased Pigs in the United States. <i>MSphere</i> , 2020, 5, .	1.3	23

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9119	Impact of homologous recombination on core genome phylogenies. BMC Genomics, 2020, 21, 829.	1.2	17
9120	Molecular convergent and parallel evolution among four high-elevation anuran species from the Tibetan region. BMC Genomics, 2020, 21, 839.	1.2	9
9121	Crystal structure of the yeast heterodimeric ADAT2/3 deaminase. BMC Biology, 2020, 18, 189.	1.7	20
9122	Ontogeny and Phylogeny of a New Hypotrichous Ciliate (Protista, Ciliophora), <i>Metaurostylopsis alrasheidi</i> n. sp., With Establishment of a New Genus <i>Monourostylopsis</i> n. gen.. Frontiers in Marine Science, 2020, 7, .	1.2	5
9123	Description of <i>Allocanariomyces</i> and <i>Parachaetomium</i> , two new genera, and <i>Achaetomium aegilopsis</i> sp. nov. in the Chaetomiaceae. Mycological Progress, 2020, 19, 1415-1427.	0.5	3
9124	Three new cryptic Caribbean species in the <i>Leucocoprinus heinemannii</i> complex (Agaricaceae.) Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.5	0
9125	Studies in <i>Gyromitra</i> I: the <i>Gyromitra gigas</i> species complex. Mycological Progress, 2020, 19, 1459-1473.	0.5	7
9126	Genomics of Population Differentiation in Humpback Dolphins, <i>Sousa</i> spp. in the Indo-Pacific Ocean. Journal of Heredity, 2020, 111, 652-660.	1.0	3
9127	Phylogenomics of Perityleae (Compositae) provides new insights into morphological and chromosomal evolution of the rock daisies. Journal of Systematics and Evolution, 2020, 58, 853-880.	1.6	13
9128	Single-Cell Genomic Sequencing of Three Peritrichs (Protista, Ciliophora) Reveals Less Biased Stop Codon Usage and More Prevalent Programmed Ribosomal Frameshifting Than in Other Ciliates. Frontiers in Marine Science, 2020, 7, .	1.2	14
9129	The complete plastome of <i>Nannoglottis ravida</i> , an extremely endangered species in the Qinghai-Tibet Plateau. Mitochondrial DNA Part B: Resources, 2020, 5, 3709-3711.	0.2	0
9130	Emergence of a Clinical <i>Escherichia coli</i> Sequence Type 131 Strain Carrying a Chromosomal blaKPC ² Gene. Frontiers in Microbiology, 2020, 11, 586764.	1.5	4
9131	Testing spore amyloidity in Agaricales under light microscope: the case study of <i>Tricholoma</i> . IMA Fungus, 2020, 11, 24.	1.7	3
9132	New Light on Historical Specimens Reveals a New Species of Ladybird (Coleoptera: Coccinellidae): Morphological, Museomic, and Phylogenetic Analyses. Insects, 2020, 11, 766.	1.0	2
9133	Comparative transcriptome analysis reveals evolutionary divergence and shared network of cold and salt stress response in diploid D-genome cotton. BMC Plant Biology, 2020, 20, 518.	1.6	6
9134	An Investigation into the Genetic History of Japanese Populations of Three Starfish, <i>Acanthaster planci</i> , <i>Linckia laevigata</i> , and <i>Asterias amurensis</i> , Based on Complete Mitochondrial DNA Sequences. G3: Genes, Genomes, Genetics, 2020, 10, 2519-2528.	0.8	5
9135	The assessment of leading traits in the taxonomy of the <i>Bacillus cereus</i> group. Antonie Van Leeuwenhoek, 2020, 113, 2223-2242.	0.7	9
9136	Two new species of <i>Hygroaster</i> from Madagascar. Mycological Progress, 2020, 19, 1293-1300.	0.5	3

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9137	Mitochondrial and plastid genome variability of <i>Corallina officinalis</i> (Corallinales). <i>Trends in Ecology and Evolution</i> , 2020, 35, 1074-1082.	10.6	742
9138	Phylogenomics and species delimitation for effective conservation of manta and devil rays. <i>Molecular Ecology</i> , 2020, 29, 4783-4796.	2.0	45
9139	Expanded Phylogenetic Diversity and Metabolic Flexibility of Mercury-Methylating Microorganisms. <i>Microbial Systems</i> , 2020, 5, .	1.7	56
9140	Factors associated with phylogenetic clustering of hepatitis C among people who inject drugs in Baltimore. <i>BMC Infectious Diseases</i> , 2020, 20, 815.	1.3	9
9141	Molecular phylogeny of the tribe Philodryadini Cope, 1886 (Dipsadidae: Xenodontinae): Rediscovering the diversity of the South American Racers. <i>Papeis Avulsos De Zoologia</i> , 0, 60, e20206053.	0.4	5
9142	Plastomes of eight <i>Ligusticum</i> species: characterization, genome evolution, and phylogenetic relationships. <i>BMC Plant Biology</i> , 2020, 20, 519.	1.6	42
9143	Genome-wide survey of soybean papain-like cysteine proteases and their expression analysis in root nodule symbiosis. <i>BMC Plant Biology</i> , 2020, 20, 517.	1.6	9
9144	Metagenomic Association Analysis of Gut Symbiont <i>Limosilactobacillus reuteri</i> Without Host-Specific Genome Isolation. <i>Frontiers in Microbiology</i> , 2020, 11, 585622.	1.5	4
9145	Biological soil crusts: new genera and species of Cyanobacteria from Brazilian semi-arid regions. <i>Phytotaxa</i> , 2020, 470, 263-281.	0.1	9
9146	Mitochondrial genomes of Late Pleistocene caballine horses from China belong to a separate clade. <i>Quaternary Science Reviews</i> , 2020, 250, 106691.	1.4	9
9147	A molecular phylogeny of Pilocarpaceae Zahlbr., including a new species of <i>Tapellaria</i> All. Arg. and new records of foliicolous lichenized fungi from Thailand. <i>Lichenologist</i> , 2020, 52, 377-385.	0.5	4
9148	" <i>Umbilicaria orientalis</i> " a new species of <i>Umbilicaria</i> subg. <i>Papillophora</i> with an East Asian distribution: morphological delimitation and molecular evidence. <i>Lichenologist</i> , 2020, 52, 353-364.	0.5	3
9149	A cellulose synthase-derived enzyme catalyses 3-O-glucuronosylation in saponin biosynthesis. <i>Nature Communications</i> , 2020, 11, 5664.	5.8	58
9150	Chloroplast genomes elucidate diversity, phylogeny, and taxonomy of <i>Pulsatilla</i> (Ranunculaceae). <i>Scientific Reports</i> , 2020, 10, 19781.	1.6	20
9151	Biophysical analysis of the structural evolution of substrate specificity in RuBisCO. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 30451-30457.	3.3	14
9152	Three new species of Synergini wasps from same galls on <i>Lithocarpus glaber</i> (Thunb.) in Hunan, China (Hymenoptera, Cynipidae). <i>Insect Systematics and Evolution</i> , 2020, 51, 551-583.	0.2	5
9153	Genome- and Proteome-Wide Analysis of Lysine Acetylation in <i>Vibrio vulnificus</i> Vv180806 Reveals Its Regulatory Roles in Virulence and Antibiotic Resistance. <i>Frontiers in Microbiology</i> , 2020, 11, 591287.	1.5	11
9154	Genome-Wide Association Studies Detect Multiple QTLs for Productivity in Mesoamerican Diversity Panel of Common Bean Under Drought Stress. <i>Frontiers in Plant Science</i> , 2020, 11, 574674.	1.7	24

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9155	In Silico Characterization and Phylogenetic Distribution of Extracellular Matrix Components in the Model Rhizobacteria <i>Pseudomonas fluorescens</i> F113 and Other Pseudomonads. <i>Microorganisms</i> , 2020, 8, 1740.	1.6	20
9156	Further Advance of <i>Gambierdiscus</i> Species in the Canary Islands, with the First Report of <i>Gambierdiscus belizeanus</i> . <i>Toxins</i> , 2020, 12, 692.	1.5	26
9157	Climatic and topographic changes since the Miocene influenced the diversification and biogeography of the tent tortoise (<i>Psammobates tentorius</i>) species complex in Southern Africa. <i>BMC Evolutionary Biology</i> , 2020, 20, 153.	3.2	7
9158	Into and Out of the Qinghai-Tibet Plateau and the Himalayas: Centers of origin and diversification across five clades of Eurasian montane and alpine passerine birds. <i>Ecology and Evolution</i> , 2020, 10, 9283-9300.	0.8	25
9159	Genomic analyses of a livestock pest, the New World screwworm, find potential targets for genetic control programs. <i>Communications Biology</i> , 2020, 3, 424.	2.0	26
9160	Phylogeography of the "cosmopolitan" orb-weaver <i>Argiope trifasciata</i> (Araneae: Araneidae). <i>Biological Journal of the Linnean Society</i> , 2020, 131, 61-75.	0.7	6
9161	Blastomycosis in Africa and the Middle East: A Comprehensive Review of Reported Cases and Reanalysis of Historical Isolates Based on Molecular Data. <i>Clinical Infectious Diseases</i> , 2021, 73, e1560-e1569.	2.9	19
9162	Angels in disguise: sympatric hybridization in the marine angelfishes is widespread and occurs between deeply divergent lineages. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20201459.	1.2	18
9163	Precise Species Identification for <i>Enterobacter</i> : a Genome Sequence-Based Study with Reporting of Two Novel Species, <i>Enterobacter quasiroggenskampii</i> sp. nov. and <i>Enterobacter quasimori</i> sp. nov. <i>MSystems</i> , 2020, 5, .	1.7	95
9164	Genetic Diversity Among <i>Mycobacterium avium</i> Subspecies Revealed by Analysis of Complete Genome Sequences. <i>Frontiers in Microbiology</i> , 2020, 11, 1701.	1.5	21
9165	Composition and activity of nitrifier communities in soil are unresponsive to elevated temperature and CO ₂ , but strongly affected by drought. <i>ISME Journal</i> , 2020, 14, 3038-3053.	4.4	43
9166	Whole-exome sequencing and genome-wide evolutionary analyses identify novel candidate genes associated with infrared perception in pit vipers. <i>Scientific Reports</i> , 2020, 10, 13033.	1.6	3
9167	Comparative Genome Analysis of <i>Bacillus sporothermodurans</i> with Its Closest Phylogenetic Neighbor, <i>Bacillus oleronius</i> , and <i>Bacillus cereus</i> and <i>Bacillus subtilis</i> Groups. <i>Microorganisms</i> , 2020, 8, 1185.	1.6	2
9168	Improved <i>Brassica oleracea</i> JZS assembly reveals significant changing of LTR-RT dynamics in different morphotypes. <i>Theoretical and Applied Genetics</i> , 2020, 133, 3187-3199.	1.8	55
9169	<i>Retroporomonorchis pansho</i> n. g., n. sp., an unusual monorchiid trematode exploiting an atypical host. <i>Systematic Parasitology</i> , 2020, 97, 441-454.	0.5	6
9170	Increased Mutation Rate Is Linked to Genome Reduction in Prokaryotes. <i>Current Biology</i> , 2020, 30, 3848-3855.e4.	1.8	44
9171	Efflux pump activity potentiates the evolution of antibiotic resistance across <i>S. aureus</i> isolates. <i>Nature Communications</i> , 2020, 11, 3970.	5.8	79
9172	Genesis and spread of multiple reassortants during the 2016/2017 H5 avian influenza epidemic in Eurasia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 20814-20825.	3.3	63

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9173	The complete mitochondrial genome of <i>Nassarius graniferus</i> (Gastropoda: Nassariinae). Mitochondrial DNA Part B: Resources, 2020, 5, 2946-2947.	0.2	0
9174	Rapid diversification rates in Amazonian Chrysobalanaceae inferred from plastid genome phylogenetics. Botanical Journal of the Linnean Society, 2020, 194, 271-289.	0.8	7
9175	Revalidation of <i>Ogyrides occidentalis</i> (Ortmann, 1893) (Decapoda: Caridea: Ogyrididae) from Brazil based on morphological and mtDNA evidences. Journal of Crustacean Biology, 2020, 40, 627-633.	0.3	2
9176	The <i>Acer truncatum</i> genome provides insights into nervonic acid biosynthesis. Plant Journal, 2020, 104, 662-678.	2.8	52
9177	<i>Toxoplasma gondii</i> oocysts, <i>Giardia</i> cysts and <i>Cryptosporidium</i> oocysts in outdoor swimming pools in Brazil. Zoonoses and Public Health, 2020, 67, 785-795.	0.9	9
9178	Genetic and Phenotypic Factors Associated with Persistent Shedding of Shiga Toxin-Producing <i>Escherichia coli</i> by Beef Cattle. Applied and Environmental Microbiology, 2020, 86, .	1.4	7
9179	Genomic Surveillance of Yellow Fever Virus Epizootic in São Paulo, Brazil, 2016 – 2018. PLoS Pathogens, 2020, 16, e1008699.	2.1	39
9180	The Genome Sequence of Alpine <i>Megacarpaea delavayi</i> Identifies Species-Specific Whole-Genome Duplication. Frontiers in Genetics, 2020, 11, 812.	1.1	10
9181	<i>Micractinium tetrahymenae</i> (Trebouxiophyceae, Chlorophyta), a New Endosymbiont Isolated from Ciliates. Diversity, 2020, 12, 200.	0.7	15
9182	The biosynthesis of the anti-microbial diterpenoid leubethanol in <i>Leucophyllum frutescens</i> proceeds via an all-cis prenyl intermediate. Plant Journal, 2020, 104, 693-705.	2.8	15
9183	Taxonomy and phylogeny of polypores with ganodermatoid basidiospores (Ganodermataceae). Mycological Progress, 2020, 19, 725-741.	0.5	15
9184	Four new species of <i>Phylloporia</i> (Hymenochaetales, Basidiomycota) from southeastern Taiwan. Mycological Progress, 2020, 19, 743-752.	0.5	5
9185	The Neotropical <i>Fomitiporia</i> (Hymenochaetales, Basidiomycota): the redefinition of <i>F. apiahyna</i> s.s. allows revealing a high hidden species diversity. Mycological Progress, 2020, 19, 769-790.	0.5	5
9186	Cryptic diversity in the model fern genus <i>Ceratopteris</i> (Pteridaceae). Molecular Phylogenetics and Evolution, 2020, 152, 106938.	1.2	11
9187	A high-contiguity <i>Brassica nigra</i> genome localizes active centromeres and defines the ancestral <i>Brassica</i> genome. Nature Plants, 2020, 6, 929-941.	4.7	94
9188	Identifying Leafhopper Targets for Controlling Aster Yellows in Carrots and Celery. Insects, 2020, 11, 411.	1.0	7
9189	Phylogeny and biogeography of the <i>Daniellia</i> clade (Leguminosae: Detarioideae), a tropical tree lineage largely threatened in Africa and Madagascar. Molecular Phylogenetics and Evolution, 2020, 146, 106752.	1.2	6
9190	Genome assembly of wild tea tree DASZ reveals pedigree and selection history of tea varieties. Nature Communications, 2020, 11, 3719.	5.8	108

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9191	Phylogenomic analyses reveal a rare new genus of wasp (Hymenoptera, Ichneumonidae, Cryptinae) from the Brazilian Atlantic Forest. <i>Systematics and Biodiversity</i> , 2020, 18, 646-661.	0.5	6
9192	The Origin and Spread of Locally Adaptive Seasonal Camouflage in Snowshoe Hares. <i>American Naturalist</i> , 2020, 196, 316-332.	1.0	29
9193	Simultaneous Viral Whole-Genome Sequencing and Differential Expression Profiling in Respiratory Syncytial Virus Infection of Infants. <i>Journal of Infectious Diseases</i> , 2020, 222, S666-S671.	1.9	11
9194	Identification of Candidate Olfactory Genes in the Antennal Transcriptome of the Stink Bug <i>Halyomorpha halys</i> . <i>Frontiers in Physiology</i> , 2020, 11, 876.	1.3	23
9195	Socially Parasitic Ants Evolve a Mosaic of Host-Matching and Parasitic Morphological Traits. <i>Current Biology</i> , 2020, 30, 3639-3646.e4.	1.8	17
9196	Freshwater biogeography in Wallacea: The case of sphaeriid bivalves in the Malili lake system (Sulawesi, Indonesia). <i>Journal of Great Lakes Research</i> , 2020, 46, 1176-1186.	0.8	7
9197	Sampling and summarizing transmission trees with multi-strain infections. <i>Bioinformatics</i> , 2020, 36, i362-i370.	1.8	3
9198	Adding stars to the <i>Chromodoris</i> (Nudibranchia, Chromodorididae) galaxy with the description of four new species. <i>Zootaxa</i> , 2020, 4819, zootaxa.4819.3.1.	0.2	5
9199	The Genome of <i>Microthlaspi erraticum</i> (Brassicaceae) Provides Insights Into the Adaptation to Highly Calcareous Soils. <i>Frontiers in Plant Science</i> , 2020, 11, 943.	1.7	4
9200	Two New Benthic Diatoms of the Genus <i>Achnanthisidium</i> (Bacillariophyceae) from the Hangang River, Korea. <i>Diversity</i> , 2020, 12, 285.	0.7	6
9201	Fungal Planet description sheets: 1042–1111. <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2020, 44, 301-459.	1.6	91
9202	Evolutionary network genomics of wood formation in a phylogenetic survey of angiosperm forest trees. <i>New Phytologist</i> , 2020, 228, 1811-1823.	3.5	8
9203	Multi-gene phylogeny and taxonomy of <i>Amauroderma</i> s. lat. (Ganodermataceae). <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2020, 44, 206-239.	1.6	43
9204	Biogeographic diversification of <i>Mahonia</i> (Berberidaceae): Implications for the origin and evolution of East Asian subtropical evergreen broadleaved forests. <i>Molecular Phylogenetics and Evolution</i> , 2020, 151, 106910.	1.2	28
9205	Genomic footprints of repeated evolution of CAM photosynthesis in a Neotropical species radiation. <i>Plant, Cell and Environment</i> , 2020, 43, 2987-3001.	2.8	15
9206	Discovery and Genomic Characterization of a 382-Nucleotide Deletion in ORF7b and ORF8 during the Early Evolution of SARS-CoV-2. <i>MBio</i> , 2020, 11, .	1.8	245
9207	The genome sequence of the grape phylloxera provides insights into the evolution, adaptation, and invasion routes of an iconic pest. <i>BMC Biology</i> , 2020, 18, 90.	1.7	40
9208	Type I-F CRISPR-Cas Distribution and Array Dynamics in <i>Legionella pneumophila</i> . <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1039-1050.	0.8	12

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9209	Imported Monkeypox, Singapore. <i>Emerging Infectious Diseases</i> , 2020, 26, 1826-1830.	2.0	198
9210	A Hopeful Sea-Monster: A Very Large Homologous Recombination Event Impacting the Core Genome of the Marine Pathogen <i>Vibrio anguillarum</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 1430.	1.5	7
9211	Quantification of Cable Bacteria in Marine Sediments via qPCR. <i>Frontiers in Microbiology</i> , 2020, 11, 1506.	1.5	14
9212	<i>Burkholderia cepacia</i> Complex Taxon K: Where to Split?. <i>Frontiers in Microbiology</i> , 2020, 11, 1594.	1.5	35
9213	Phylogenomic Relationships and Evolution of Polyploid <i>Salix</i> Species Revealed by RAD Sequencing Data. <i>Frontiers in Plant Science</i> , 2020, 11, 1077.	1.7	54
9214	On the Risks of Phylogeny-Based Strain Prioritization for Drug Discovery: <i>Streptomyces lunaelactis</i> as a Case Study. <i>Biomolecules</i> , 2020, 10, 1027.	1.8	18
9215	Is the Distribution of Two Rare Orchid Sister Species Limited by Their Main Mycobiont?. <i>Diversity</i> , 2020, 12, 262.	0.7	10
9216	Building a Robust, Densely-Sampled Spider Tree of Life for Ecosystem Research. <i>Diversity</i> , 2020, 12, 288.	0.7	14
9217	What Drives the Diversity of the Most Abundant Terrestrial Cercozoan Family (Rhogostomidae,) Tj ETQqO 0 0 rgBT (Overlock 10 Tf 50 42	1.6	22
9218	A new species of <i>Synarthonia</i> from Luxembourg, and a new combination in the genus <i>Reichlingia</i> (Arthoniaceae). <i>Lichenologist</i> , 2020, 52, 261-266.	0.5	3
9219	Replacement and Parallel Simplification of Nonhomologous Proteinases Maintain Venom Phenotypes in Rear-Fanged Snakes. <i>Molecular Biology and Evolution</i> , 2020, 37, 3563-3575.	3.5	15
9220	Evolution of dependoparvoviruses across geological timescales—implications for design of AAV-based gene therapy vectors. <i>Virus Evolution</i> , 2020, 6, veaa043.	2.2	10
9221	The Frequency of Sex: Population Genomics Reveals Differences in Recombination and Population Structure of the Aflatoxin-Producing Fungus <i>Aspergillus flavus</i> . <i>MBio</i> , 2020, 11, .	1.8	27
9222	Concurrent Infection of Skunk Adenovirus-1, <i>Listeria monocytogenes</i> , and a Regionally Specific Clade of Canine Distemper Virus in One Gray Fox (<i>Urocyon cinereoargenteus</i>) and Concurrent Listeriosis and Canine Distemper in a Second Gray Fox. <i>Pathogens</i> , 2020, 9, 591.	1.2	11
9223	Marine water environmental DNA metabarcoding provides a comprehensive fish diversity assessment and reveals spatial patterns in a large oceanic area. <i>Ecology and Evolution</i> , 2020, 10, 7560-7584.	0.8	50
9224	Genomic analysis of phylogenetic group B2 extraintestinal pathogenic <i>E. coli</i> causing infections in dogs in Australia. <i>Veterinary Microbiology</i> , 2020, 248, 108783.	0.8	20
9225	Evolutionary origins of the SARS-CoV-2 sarbecovirus lineage responsible for the COVID-19 pandemic. <i>Nature Microbiology</i> , 2020, 5, 1408-1417.	5.9	772
9226	Transmission and evolutionary dynamics of human coronavirus OC43 strains in coastal Kenya investigated by partial spike sequence analysis, 2015–16. <i>Virus Evolution</i> , 2020, 6, veaa031.	2.2	4

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9227	Tol-Pal System and Rgs Proteins Interact to Promote Unipolar Growth and Cell Division in <i>Sinorhizobium meliloti</i> . <i>MBio</i> , 2020, 11, .	1.8	18
9228	New insights into the evolutionary history of <i>Megacodon</i> : Evidence from a newly discovered species. <i>Plant Diversity</i> , 2020, 42, 198-208.	1.8	7
9229	The identity of <i>Calicium corynellum</i> (Ach.) Ach.. <i>Lichenologist</i> , 2020, 52, 333-335.	0.5	1
9230	Origin and functional differentiation of (E)- β -ocimene synthases reflect the expansion of monoterpenes in angiosperms. <i>Journal of Experimental Botany</i> , 2020, 71, 6571-6586.	2.4	7
9231	A Diverse Panel of Clinical <i>Acinetobacter baumannii</i> for Research and Development. <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	1.4	39
9232	Community Structure of Arbuscular Mycorrhizal Fungi in Soils of Switchgrass Harvested for Bioenergy. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	9
9233	<i>Acinetobacter baumannii</i> NCIMB8209: a Rare Environmental Strain Displaying Extensive Insertion Sequence-Mediated Genome Remodeling Resulting in the Loss of Exposed Cell Structures and Defensive Mechanisms. <i>MSphere</i> , 2020, 5, .	1.3	12
9234	Plastome Phylogenomic and Biogeographical Study on <i>Thuja</i> (<i>Cupressaceae</i>). <i>BioMed Research International</i> , 2020, 2020, 1-13.	0.9	5
9235	Genomic architecture of endogenous ichnoviruses reveals distinct evolutionary pathways leading to virus domestication in parasitic wasps. <i>BMC Biology</i> , 2020, 18, 89.	1.7	24
9236	Mitochondrial metabolic genes provide phylogeographic relationships of global collections of <i>Aedes aegypti</i> (Diptera: Culicidae). <i>PLoS ONE</i> , 2020, 15, e0235430.	1.1	5
9237	Biogeography of the freshwater gastropod, <i>Planorbella trivolvis</i> , in the western United States. <i>PLoS ONE</i> , 2020, 15, e0235989.	1.1	11
9238	Prevalence and Implications of Contamination in Public Genomic Resources: A Case Study of 43 Reference Arthropod Assemblies. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 721-730.	0.8	25
9239	Expression of Multiple engrailed Family Genes in Eyespots of <i>Bicyclus anynana</i> Butterflies Does Not Implicate the Duplication Events in the Evolution of This Morphological Novelty. <i>Frontiers in Ecology and Evolution</i> , 2020, 8, .	1.1	7
9240	Genomic Insights of <i>Cryobacterium</i> Isolated From Ice Core Reveal Genome Dynamics for Adaptation in Glacier. <i>Frontiers in Microbiology</i> , 2020, 11, 1530.	1.5	12
9241	Diverse Microorganisms in Sediment and Groundwater Are Implicated in Extracellular Redox Processes Based on Genomic Analysis of Bioanode Communities. <i>Frontiers in Microbiology</i> , 2020, 11, 1694.	1.5	9
9242	<i>Pestalotiopsis pini</i> sp. nov., an Emerging Pathogen on Stone Pine (<i>Pinus pinea</i> L.). <i>Forests</i> , 2020, 11, 805.	0.9	14
9243	Identification of High Molecular Variation Loci in Complete Chloroplast Genomes of <i>Mammillaria</i> (Cactaceae, Caryophyllales). <i>Genes</i> , 2020, 11, 830.	1.0	8
9244	Genomic Characterization and Expression of Juvenile Hormone Esterase-Like Carboxylesterase Genes in Pacific White Shrimp, <i>Litopenaeus vannamei</i> . <i>International Journal of Molecular Sciences</i> , 2020, 21, 5444.	1.8	6

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9245	Phylogenetic and Timescale Analysis of Barmah Forest Virus as Inferred from Genome Sequence Analysis. <i>Viruses</i> , 2020, 12, 732.	1.5	9
9246	Molecular Tracing of SARS-CoV-2 in Italy in the First Three Months of the Epidemic. <i>Viruses</i> , 2020, 12, 798.	1.5	46
9247	Species diversity of Pleosporalean taxa associated with <i>Camellia sinensis</i> (L.) Kuntze in Taiwan. <i>Scientific Reports</i> , 2020, 10, 12762.	1.6	15
9248	Characterization of the complete mitochondrial genome of <i>Morchella eohespera</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 3048-3049.	0.2	4
9249	Something old, something new: Evolution of Colombian weedy rice (<i>Oryza</i> spp.) through de novo de-domestication, exotic gene flow, and hybridization. <i>Evolutionary Applications</i> , 2020, 13, 1968-1983.	1.5	16
9250	The evolution of sexually dimorphic cuticular hydrocarbons in blowflies (Diptera: Calliphoridae). <i>Journal of Evolutionary Biology</i> , 2020, 33, 1468-1486.	0.8	11
9251	Phylogenomic analyses reveal a Palaeozoic radiation and support a freshwater origin for clitellate annelids. <i>Zoologica Scripta</i> , 2020, 49, 614-640.	0.7	34
9252	The alcohol dehydrogenase gene family in sugarcane and its involvement in cold stress regulation. <i>BMC Genomics</i> , 2020, 21, 521.	1.2	57
9253	Characteristics of Extended-Spectrum Beta-Lactamase-Producing Enterobacteriaceae and Contact to Animals in Estonia. <i>Microorganisms</i> , 2020, 8, 1130.	1.6	2
9254	The genome of the marine monogonont rotifer <i>Brachionus rotundiformis</i> and insight into species-specific detoxification components in <i>Brachionus</i> spp.. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2020, 36, 100714.	0.4	7
9255	Acquisition and Adaptation of Ultra-small Parasitic Reduced Genome Bacteria to Mammalian Hosts. <i>Cell Reports</i> , 2020, 32, 107939.	2.9	152
9256	<i>Rhizobium indicum</i> sp. nov., isolated from root nodules of pea (<i>Pisum sativum</i>) cultivated in the Indian trans-Himalayas. <i>Systematic and Applied Microbiology</i> , 2020, 43, 126127.	1.2	21
9257	Analysis of ultraconserved elements supports African origins of narrow-mouthed frogs. <i>Molecular Phylogenetics and Evolution</i> , 2020, 146, 106771.	1.2	19
9258	A new classification of <i>Carex</i> (Cyperaceae) subgenera supported by a HybSeq backbone phylogenetic tree. <i>Botanical Journal of the Linnean Society</i> , 2020, 194, 141-163.	0.8	48
9259	<i>Salmonella enterica</i> Serovar Hvitvingfoss in Bar-Tailed Godwits (<i>Limosa lapponica</i>) from Roebuck Bay, Northwestern Australia. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	6
9260	Evidence Supporting an Antimicrobial Origin of Targeting Peptides to Endosymbiotic Organelles. <i>Cells</i> , 2020, 9, 1795.	1.8	19
9261	Complete chloroplast genome of <i>Salvia plebeia</i> : organization, specific barcode and phylogenetic analysis. <i>Chinese Journal of Natural Medicines</i> , 2020, 18, 563-572.	0.7	20
9262	<i>Tenuifilum thalassicum</i> gen. nov., sp. nov., a novel moderate thermophilic anaerobic bacterium from a Kunashir Island shallow hot spring representing a new family Tenuifilaceae fam. nov. in the class Bacteroidia. <i>Systematic and Applied Microbiology</i> , 2020, 43, 126126.	1.2	22

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9263	The whale shark genome reveals how genomic and physiological properties scale with body size. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 20662-20671.	3.3	32
9264	The complete chloroplast genome of <i>Araucaria cunninghamii</i> (Araucariaceae). Mitochondrial DNA Part B: Resources, 2020, 5, 2934-2935.	0.2	1
9265	The origin of the giant ground beetle <i>Aplothorax burchelli</i> on St Helena Island. Biological Journal of the Linnean Society, 2020, 131, 50-60.	0.7	4
9266	Between predators and parasitoids: Complex interactions among shelter traits, predation and parasitism in a shelter-building caterpillar community. Functional Ecology, 2020, 34, 2186-2198.	1.7	18
9267	Trehalose and (iso)floridoside production under desiccation stress in red alga <i>Porphyra umbilicalis</i> and the genes involved in their synthesis. Journal of Phycology, 2020, 56, 1468-1480.	1.0	6
9268	Phylogenomic approaches reveal how climate shapes patterns of genetic diversity in an African rain forest tree species. Molecular Ecology, 2020, 29, 3560-3573.	2.0	17
9269	Characterization and Comparative Analysis of Two Rheum Complete Chloroplast Genomes. BioMed Research International, 2020, 2020, 1-11.	0.9	5
9270	High relatedness of invasive multi-drug resistant non-typhoidal Salmonella genotypes among patients and asymptomatic carriers in endemic informal settlements in Kenya. PLoS Neglected Tropical Diseases, 2020, 14, e0008440.	1.3	40
9271	Population genomics identifies a distinct Plasmodium vivax population on the China-Myanmar border of Southeast Asia. PLoS Neglected Tropical Diseases, 2020, 14, e0008506.	1.3	18
9272	Comparative gut transcriptome analysis of <i>Diatraea saccharalis</i> in response to the dietary source. PLoS ONE, 2020, 15, e0235575.	1.1	7
9273	Phylogenomic Analyses of Non-Dikarya Fungi Supports Horizontal Gene Transfer Driving Diversification of Secondary Metabolism in the Amphibian Gastrointestinal Symbiont, <i>Basidiobolus</i> . G3: Genes, Genomes, Genetics, 2020, 10, 3417-3433.	0.8	27
9274	Molecular systematics of the genus <i>Musa</i> L. (Zingiberales: Musaceae) in Andaman and Nicobar Islands. Biologia (Poland), 2020, 75, 1825-1843.	0.8	7
9275	Cyanobacteria Phylogenetic Studies Reveal Evidence for Polyphyletic Genera from Thermal and Freshwater Habitats. Diversity, 2020, 12, 298.	0.7	17
9276	<i>Neofabraea kienholzii</i> , a novel causal agent of grapevine trunk diseases in Hungary. European Journal of Plant Pathology, 2020, 157, 975-984.	0.8	3
9277	Soil microbiome drives the recovery of ecosystem functions after fire. Soil Biology and Biochemistry, 2020, 149, 107948.	4.2	40
9278	<i>Fossombronina isaloensis</i> Cargill & D.A.Callaghan, a new liverwort from sandstone massifs in southern Madagascar. Journal of Bryology, 2020, 42, 213-222.	0.4	0
9279	<i>Pseudohurleytrema yolandae</i> n. sp., the first monorchiid trematode reported from the Triacanthidae (Tetraodontiformes). Systematic Parasitology, 2020, 97, 491-500.	0.5	6
9280	Investigation of sequential outbreaks of <i>Burkholderia cepacia</i> and multidrug-resistant extended spectrum β -lactamase producing <i>Klebsiella</i> species in a West African tertiary hospital neonatal unit: a retrospective genomic analysis. Lancet Microbe, The, 2020, 1, e119-e129.	3.4	26

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9281	The complete mitochondrial genome of <i>Xanthomantis bimaculata</i> (Mantodea: Iridopterygidae) and its phylogeny. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 3079-3081.	0.2	6
9282	Integrative taxonomy identifies a new stingray species of the genus <i>Hypanus</i> Rafinesque, 1818 (Dasyatidae, Myliobatiformes), from the Tropical Southwestern Atlantic. <i>Journal of Fish Biology</i> , 2020, 97, 1120-1142.	0.7	20
9283	Symbiodiniaceae Dinoflagellates Express Urease in Three Subcellular Compartments and Upregulate its Expression Levels <i>in Situ</i> in Three Organs of a Giant Clam (<i>Tridacna squamosa</i>) During Illumination. <i>Journal of Phycology</i> , 2020, 56, 1696-1711.	1.0	9
9284	RADseq resolves the phylogeny of Hawaiian Myrsine (Primulaceae) and provides evidence for hybridization. <i>Journal of Systematics and Evolution</i> , 2020, 58, 823-840.	1.6	12
9285	Lousy grouse: Comparing evolutionary patterns in Alaska galliform lice to understand host evolution and host-parasite interactions. <i>Ecology and Evolution</i> , 2020, 10, 8379-8393.	0.8	11
9286	Proposal of <i>Spinulacorpis biforme</i> (Smales, 2014) n. g., n. comb. and the Spinulacorpidae n. fam. to resolve paraphyly of the acanthocephalan family Rhadinorhynchidae. <i>Systematic Parasitology</i> , 2020, 97, 477-490.	0.5	5
9287	Reconsidering <i>Mycobacterium bovis</i> as a proxy for zoonotic tuberculosis: a molecular epidemiological surveillance study. <i>Lancet Microbe</i> , 2020, 1, e66-e73.	3.4	53
9288	<i>Thecamoeba foliovenanda</i> n. sp. (Amoebozoa, Discosea, Thecamoebida) – One more case of sibling species among amoebae of the genus <i>Thecamoeba</i> . <i>European Journal of Protistology</i> , 2020, 76, 125716.	0.5	6
9289	Genome-wide SNPs clarify lineage diversity confused by coloration in coral snakes of the <i>Micrurus diastema</i> species complex (Serpentes: Elapidae). <i>Molecular Phylogenetics and Evolution</i> , 2020, 147, 106770.	1.2	20
9290	Towards yeast taxogenomics: lessons from novel species descriptions based on complete genome sequences. <i>FEMS Yeast Research</i> , 2020, 20, .	1.1	38
9291	<i>Cenostigma tocaninum</i> , a new host of <i>Colletotrichum siamense</i> . <i>Forest Pathology</i> , 2020, 50, e12623.	0.5	1
9292	A Chromosome-Level Genome Assembly of Garlic (<i>Allium sativum</i>) Provides Insights into Genome Evolution and Allicin Biosynthesis. <i>Molecular Plant</i> , 2020, 13, 1328-1339.	3.9	89
9293	Miniaturization, Genome Size, and Biological Size in a Diverse Clade of Salamanders. <i>American Naturalist</i> , 2020, 196, 634-648.	1.0	25
9294	Systematics and Biogeography of the Red Algal Genus <i>Yonagunia</i> from the Indo-Pacific Including the Description of Two New Species from Taiwan. <i>Journal of Phycology</i> , 2020, 56, 1542-1556.	1.0	9
9295	A seventeenth-century <i>Mycobacterium tuberculosis</i> genome supports a Neolithic emergence of the <i>Mycobacterium tuberculosis</i> complex. <i>Genome Biology</i> , 2020, 21, 201.	3.8	44
9296	Ancient drainage networks mediated a large-scale genetic introgression in the East Asian freshwater snails. <i>Ecology and Evolution</i> , 2020, 10, 8186-8196.	0.8	14
9297	Deep Mutational Scanning of SARS-CoV-2 Receptor Binding Domain Reveals Constraints on Folding and ACE2 Binding. <i>Cell</i> , 2020, 182, 1295-1310.e20.	13.5	1,726
9298	Rapid detection of ciguatoxins in <i>Gambierdiscus</i> and <i>Fukuyoa</i> with immunosensing tools. <i>Ecotoxicology and Environmental Safety</i> , 2020, 204, 111004.	2.9	22

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9299	Coordinating Sulfur Pools under Sulfate Deprivation. <i>Trends in Plant Science</i> , 2020, 25, 1227-1239.	4.3	62
9300	Below the waterline: cryptic diversity of aquatic pipid frogs (<i>Pipa carvalhoi</i>) unveiled through an integrative taxonomy approach. <i>Systematics and Biodiversity</i> , 2020, 18, 771-783.	0.5	4
9301	The complete chloroplast genome sequence of <i>Acorus tatarinowii</i> (Araceae) from Fujian, China. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 3159-3160.	0.2	6
9302	Predicting functional effects of missense variants in voltage-gated sodium and calcium channels. <i>Science Translational Medicine</i> , 2020, 12, .	5.8	84
9303	A new plasmid carrying mphA causes prevalence of azithromycin resistance in enterotoxigenic <i>Escherichia coli</i> serogroup O6. <i>BMC Microbiology</i> , 2020, 20, 247.	1.3	22
9304	Skeletal and muscular pelvic morphology of hillstream loaches (Cypriniformes: Balitoridae). <i>Journal of Morphology</i> , 2020, 281, 1280-1295.	0.6	10
9305	Ancient Bacterial Genomes Reveal a High Diversity of <i>Treponema pallidum</i> Strains in Early Modern Europe. <i>Current Biology</i> , 2020, 30, 3788-3803.e10.	1.8	47
9306	Oral and vaginal microbiota in selected field mice of the genus <i>Apodemus</i> : a wild population study. <i>Scientific Reports</i> , 2020, 10, 13246.	1.6	8
9307	Fatal Outcome of Chikungunya Virus Infection in Brazil. <i>Clinical Infectious Diseases</i> , 2021, 73, e2436-e2443.	2.9	40
9308	Phylogeny and diversification of the gallopheasants (Aves: Galliformes): Testing roles of sexual selection and environmental niche divergence. <i>Zoologica Scripta</i> , 2020, 49, 549-562.	0.7	5
9309	Expression Profiles of ANGUSTIFOLIA3 and SHOOT MERISTEMLESS, Key Genes for Meristematic Activity in a One-Leaf Plant <i>Monophyllaea glabra</i> , Revealed by Whole-Mount In Situ Hybridization. <i>Frontiers in Plant Science</i> , 2020, 11, 1160.	1.7	9
9310	Transcriptomic Analysis of Four Cerianthid (Cnidaria, Ceriantharia) Venoms. <i>Marine Drugs</i> , 2020, 18, 413.	2.2	20
9311	Genomic Analysis of Three Cheese-Borne <i>Pseudomonas lactis</i> with Biofilm and Spoilage-Associated Behavior. <i>Microorganisms</i> , 2020, 8, 1208.	1.6	14
9312	Genetic Features of HIV-1 Integrase Sub-Subtype A6 Predominant in Russia and Predicted Susceptibility to INSTIs. <i>Viruses</i> , 2020, 12, 838.	1.5	22
9313	Phylogenomics of the Leaf-Footed Bug Subfamily Coreinae (Hemiptera: Coreidae). <i>Insect Systematics and Diversity</i> , 2020, 4, .	0.7	17
9314	A new genus of Bucephalidae Poche, 1907 (Trematoda: Digenea) for three new species infecting the yellowtail pike, <i>Sphyraena obtusata</i> Cuvier (Sphyraenidae), from Moreton Bay, Queensland, Australia. <i>Systematic Parasitology</i> , 2020, 97, 455-476.	0.5	9
9315	The Morphology and Phylogeny of Three Diophrys Ciliates Collected from the Subtropical Waters of China, Including a New Species (Ciliophora; Euplotia). <i>Journal of Ocean University of China</i> , 2020, 19, 975-987.	0.6	3
9316	First report of <i>Plasmopara sphagnetocolae</i> on the native Hawaiian plant <i>Lipochaeta integrifolia</i> . <i>Australasian Plant Disease Notes</i> , 2020, 15, 1.	0.4	1

#	ARTICLE	IF	CITATIONS
9317	Successful without sex – the enigmatic biology and evolutionary origin of coralroot bittercress (<i>Cardamine bulbifera</i> , Brassicaceae). <i>Perspectives in Plant Ecology, Evolution and Systematics</i> , 2020, 46, 125557.	1.1	3
9318	The Molecular Diversity of Phagotrophic Euglenids Examined Using Single-cell Methods. <i>Protist</i> , 2020, 171, 125757.	0.6	8
9319	Evolutionary Remodeling of the Cell Envelope in Bacteria of the Planctomycetes Phylum. <i>Genome Biology and Evolution</i> , 2020, 12, 1528-1548.	1.1	13
9320	Predicting the short-term success of human influenza virus variants with machine learning. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20200319.	1.2	13
9321	<i>Erythrina variegata</i> is a new host species to <i>Colletotrichum siamense</i> in Brazil. <i>Forest Pathology</i> , 2020, 50, e12625.	0.5	1
9322	The clearwing moths (Lepidoptera, Sesiidae) of Australia, New Guinea and the Pacific Islands. <i>Zootaxa</i> , 2020, 4833, zootaxa.4833.1.1.	0.2	1
9323	A new species of <i>Raffaelea</i> from beetle-infested <i>Leucaena leucocephala</i> . <i>Fungal Systematics and Evolution</i> , 2020, 6, 305-314.	0.9	5
9324	Strain-Level Metagenomic Data Analysis of Enriched In Vitro and In Silico Spiked Food Samples: Paving the Way towards a Culture-Free Foodborne Outbreak Investigation Using STEC as a Case Study. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5688.	1.8	14
9326	Ancient incomplete lineage sorting of Hyles and Rhodafra (Lepidoptera: Sphingidae). <i>Organisms Diversity and Evolution</i> , 2020, 20, 527-536.	0.7	5
9327	Implications of Foraging and Interspecies Interactions of Birds for Carriage of <i>Escherichia coli</i> Strains Resistant to Critically Important Antimicrobials. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	24
9328	Diverged and Active Partitiviruses in Lichen. <i>Frontiers in Microbiology</i> , 2020, 11, 561344.	1.5	9
9329	Three novel species and a new record of <i>Daldinia</i> (Hypoxyalaceae) from Thailand. <i>Mycological Progress</i> , 2020, 19, 1113-1132.	0.5	6
9330	Conservation analysis of core cell cycle regulators and their transcriptional behavior during limb regeneration in <i>Ambystoma mexicanum</i> . <i>Mechanisms of Development</i> , 2020, 164, 103651.	1.7	6
9331	Comparative Genome Sequence Analyses of Geographic Samples of <i>Aspergillus fumigatus</i> – Relevance for Amphotericin B Resistance. <i>Microorganisms</i> , 2020, 8, 1673.	1.6	11
9332	Recent genome duplications facilitate the phenotypic diversity of Hb repertoire in the Cyprinidae. <i>Science China Life Sciences</i> , 2020, 64, 1149-1164.	2.3	6
9333	A highly rifampicin resistant <i>Mycobacterium tuberculosis</i> strain emerging in Southern Brazil. <i>Tuberculosis</i> , 2020, 125, 102015.	0.8	7
9334	Neural architecture and regeneration in the acoel <i>Hofstenia miamia</i> . <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20201198.	1.2	16
9335	Lineage-specific patterns of chromosome evolution are the rule not the exception in Polyneoptera insects. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20201388.	1.2	19

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9336	KrÄ¼appel-like factor/specificity protein evolution in the Spiralia and the implications for cephalopod visual system novelties. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20202055.	1.2	8
9337	Variola virus genome sequenced from an eighteenth-century museum specimen supports the recent origin of smallpox. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190572.	1.8	24
9338	Metagenomics of the modern and historical human oral microbiome with phylogenetic studies on <i>Streptococcus mutans</i> and <i>Streptococcus sobrinus</i> . <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190573.	1.8	12
9339	Evolutionary history of <i>Mycobacterium leprae</i> in the Pacific Islands. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190582.	1.8	12
9340	Functional redundancy imparts process stability to acidic Fe(II)-oxidizing microbial reactors. <i>Environmental Microbiology</i> , 2021, 23, 3682-3694.	1.8	6
9341	A new species of frog in the <i>Litoria ewingii</i> species group (Anura: Pelodyadidae) from south-eastern Australia. <i>Zootaxa</i> , 2020, 4858, zootaxa.4858.2.3.	0.2	9
9342	Genome-enabled insights into the biology of thrips as crop pests. <i>BMC Biology</i> , 2020, 18, 142.	1.7	54
9343	Human pegivirus (HPgV, GBV-C) RNA in volunteer blood donors from a public hemotherapy service in Northern Brazil. <i>Virology Journal</i> , 2020, 17, 153.	1.4	10
9344	<i>Streptococcus pneumoniae</i> Serotype 12F-CC4846 and Invasive Pneumococcal Disease after Introduction of 13-Valent Pneumococcal Conjugate Vaccine, Japan, 2015–2017. <i>Emerging Infectious Diseases</i> , 2020, 26, 2660-2668.	2.0	5
9345	Complete Genomic Analysis of VRE From a Cattle Feedlot: Focus on 2 Antibiotic Resistance. <i>Frontiers in Microbiology</i> , 2020, 11, 571958.	1.5	2
9346	The Viral Hemorrhagic Septicemia Virus (VHSV) Markers of Virulence in Rainbow Trout (<i>Oncorhynchus mykiss</i>). <i>Frontiers in Microbiology</i> , 2020, 11, 574231.	1.5	21
9347	Genome Sequencing of <i>Paecilomyces Penicillatus</i> Provides Insights into Its Phylogenetic Placement and Mycoparasitism Mechanisms on Morel Mushrooms. <i>Pathogens</i> , 2020, 9, 834.	1.2	19
9348	The Effects of Ecological Traits on the Rate of Molecular Evolution in Ray-Finned Fishes: A Multivariable Approach. <i>Journal of Molecular Evolution</i> , 2020, 88, 689-702.	0.8	6
9349	An update on the indigenous vascular flora of sub-Antarctic Marion Island: taxonomic changes, sequences for DNA barcode loci, and genome size data. <i>Polar Biology</i> , 2020, 43, 1817-1828.	0.5	8
9350	Multidisciplinary approach to describe <i>Trebouxia</i> diversity within lichenized fungi <i>Buellia zoharyi</i> from the Canary Islands. <i>Symbiosis</i> , 2020, 82, 19-34.	1.2	11
9351	Ethylene-independent functions of the ethylene precursor ACC in <i>Marchantia polymorpha</i> . <i>Nature Plants</i> , 2020, 6, 1335-1344.	4.7	46
9352	Triticum population sequencing provides insights into wheat adaptation. <i>Nature Genetics</i> , 2020, 52, 1412-1422.	9.4	178
9353	A revision of the genus <i>Poconoma</i> Tams & Bowden (Lepidoptera: Noctuidae: Apameini: Sesamiina) with the description of a new genus and two new sesamiine species from the Afrotropical region. <i>Annales De La Societe Entomologique De France</i> , 2020, 56, 313-331.	0.4	1

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9354	The complete plastid genome of <i>Ficus erecta</i> (Moraceae). Mitochondrial DNA Part B: Resources, 2020, 5, 3335-3336.	0.2	2
9355	Characterization of the complete chloroplast genome of the <i>Phoebe bournei</i> . Mitochondrial DNA Part B: Resources, 2020, 5, 3291-3292.	0.2	3
9356	Complete mitochondrial genome of <i>Glomeridesmus spelaeus</i> (Diplopoda, Glomeridesmida), a troglitic species from iron-ore caves in Eastern Amazon. Mitochondrial DNA Part B: Resources, 2020, 5, 3272-3273.	0.2	5
9357	The complete chloroplast genome sequence of <i>Dendrobium densiflorum</i> and its phylogenetic implications. Mitochondrial DNA Part B: Resources, 2020, 5, 3316-3317.	0.2	1
9358	The complete chloroplast genome of <i>Akebia trifoliata</i> subsp. <i>australis</i> (Lardizabalaceae), a medicinal plant in China. Mitochondrial DNA Part B: Resources, 2020, 5, 3333-3334.	0.2	1
9359	The complete chloroplast genome sequence of <i>Leucanthemella linearis</i> (Matsum. ex Matsum.) Tzvelev (Asteraceae), endangered plant of Korea. Mitochondrial DNA Part B: Resources, 2020, 5, 3360-3362.	0.2	0
9360	The complete chloroplast genome sequence of <i>Turpinia montana</i> (Staphyleaceae). Mitochondrial DNA Part B: Resources, 2020, 5, 3354-3356.	0.2	0
9361	The complete nucleotide molecular sequence of plastid genome of <i>Zanthoxylum armatum</i> (Rutaceae). Mitochondrial DNA Part B: Resources, 2020, 5, 3400-3401.	0.2	0
9362	The complete chloroplast genome of <i>Hosta plantaginea</i> (Lam.) Aschers. Mitochondrial DNA Part B: Resources, 2020, 5, 3402-3403.	0.2	0
9363	The complete chloroplast genome sequence of <i>Catalpa fargesii</i> f. <i>duclouxii</i> (Bignoniaceae). Mitochondrial DNA Part B: Resources, 2020, 5, 3427-3429.	0.2	1
9364	The complete chloroplast genome sequence of <i>Bambusa beecheyana</i> var. <i>pubescens</i> (Bambusodae). Mitochondrial DNA Part B: Resources, 2020, 5, 3467-3468.	0.2	1
9365	The complete chloroplast genome sequence of <i>Acanthopanax trifoliatum</i> (Linn.) Merr.. Mitochondrial DNA Part B: Resources, 2020, 5, 3408-3409.	0.2	1
9366	Characterization of the plastome of <i>Camellia pingguoensis</i> (Theaceae), an endangered and endemic yellow camellia species in China. Mitochondrial DNA Part B: Resources, 2020, 5, 3527-3528.	0.2	0
9367	The complete chloroplast genome of <i>Hydrangea davidii</i> (Hydrangeaceae). Mitochondrial DNA Part B: Resources, 2020, 5, 3587-3589.	0.2	0
9368	Origins of cultivars of <i>Chrysanthemum</i> – Evidence from the chloroplast genome and nuclear LFY gene. <i>Journal of Systematics and Evolution</i> , 2020, 58, 925-944.	1.6	30
9369	Population Structure of <i>Listeria monocytogenes</i> in Emilia-Romagna (Italy) and Implications on Whole Genome Sequencing Surveillance of Listeriosis. <i>Frontiers in Public Health</i> , 2020, 8, 519293.	1.3	7
9370	Chloroplast Genome Analysis of Two Medicinal <i>Coelogyne</i> spp. (Orchidaceae) Shed Light on the Genetic Information, Comparative Genomics, and Species Identification. <i>Plants</i> , 2020, 9, 1332.	1.6	7
9371	Specialized cockroach pollination in the rare and endangered plant <i>Vincetoxicum hainanense</i> in China. <i>American Journal of Botany</i> , 2020, 107, 1355-1365.	0.8	11

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9372	Phylogeographic analysis of H5N1 highly pathogenic avian influenza virus isolated in Cambodia from 2018 to 2019. <i>Infection, Genetics and Evolution</i> , 2020, 86, 104599.	1.0	0
9373	Genomic profiling of bacterial and fungal communities and their predictive functionality during pulque fermentation by whole-genome shotgun sequencing. <i>Scientific Reports</i> , 2020, 10, 15115.	1.6	29
9374	Antennal Proteome of the <i>Solenopsis invicta</i> (Hymenoptera: Formicidae): Caste Differences in Olfactory Receptors and Chemosensory Support Proteins. <i>Journal of Insect Science</i> , 2020, 20, .	0.6	5
9375	Antimicrobial Susceptibility and Phylogenetic Relations in a German Cohort Infected with <i>Mycobacterium abscessus</i> . <i>Journal of Clinical Microbiology</i> , 2020, 58, .	1.8	18
9376	Tissue Tropisms of Avian Influenza A Viruses Affect Their Spillovers from Wild Birds to Pigs. <i>Journal of Virology</i> , 2020, 94, .	1.5	7
9377	From People to <i>Panthera</i> : Natural SARS-CoV-2 Infection in Tigers and Lions at the Bronx Zoo. <i>MBio</i> , 2020, 11, .	1.8	298
9378	The flattened and needlelike leaves of the pine family (Pinaceae) share a conserved genetic network for adaxial-abaxial polarity but have diverged for photosynthetic adaptation. <i>BMC Evolutionary Biology</i> , 2020, 20, 131.	3.2	7
9379	The global population of SARS-CoV-2 is composed of six major subtypes. <i>Scientific Reports</i> , 2020, 10, 18289.	1.6	45
9380	The complete chloroplast genome sequence of <i>Butea monosperma</i> (Fabaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 3255-3256.	0.2	0
9381	Characterization of the complete chloroplast genome of <i>Corydalis inopinata</i> Prain ex Fedde (Papaveraceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 3284-3285.	0.2	6
9382	The complete chloroplast genome of <i>Cryptomeria japonica</i> var. <i>sinensis</i> (Cupressaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 3392-3393.	0.2	1
9383	Pacific Biosciences assembly with Hi-C mapping generates an improved, chromosome-level goose genome. <i>GigaScience</i> , 2020, 9, .	3.3	20
9384	Novel gene rearrangement pattern in the mitochondrial genomes of <i>Torleya mikhaili</i> and <i>Cincticostella fusca</i> (Ephemeroptera: Ephemerellidae). <i>International Journal of Biological Macromolecules</i> , 2020, 165, 3106-3114.	3.6	17
9385	Strain-specific strategies of 2-fucosyllactose, 3-fucosyllactose, and difucosyllactose assimilation by <i>Bifidobacterium longum</i> subsp. <i>infantis</i> Bi-26 and ATCC 15697. <i>Scientific Reports</i> , 2020, 10, 15919.	1.6	38
9386	Characterization of the complete chloroplast genome of <i>Arisaema erubescens</i> (Wall.) Schott, a traditional Chinese medicinal herb. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 3149-3150.	0.2	3
9387	The complete chloroplast genome of <i>Lindera pulcherrima</i> var. <i>hemsleyana</i> (Lauraceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 3249-3250.	0.2	0
9388	The complete chloroplast genomes of two species of <i>Zygophyllum</i> (Zygophyllaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 3476-3477.	0.2	5
9389	Complete chloroplast genome of <i>Paphiopedilum emersonii</i> (Orchidaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 3500-3501.	0.2	1

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9390	Characterization of the complete mitochondrial genome of <i>Euw Wallacea fornicatus</i> (Eichhoff), Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 Part B: Resources, 2020, 5, 3502-3504.	0.2	4
9391	The complete chloroplast genome of <i>Fraxinus hupehensis</i> and phylogenetic analysis of Lamiales. Mitochondrial DNA Part B: Resources, 2020, 5, 3561-3562.	0.2	0
9392	Multidrug-Resistant CTX-M and CMY-2 Producing <i>Escherichia coli</i> Isolated from Healthy Household Dogs from the Great Metropolitan Area, Costa Rica. Microbial Drug Resistance, 2020, 26, 1421-1428.	0.9	7
9393	The Quaternary evolutionary history of Bristol rock cress (<i>Arabis scabra</i> , Brassicaceae), a Mediterranean element with an outpost in the north-western Atlantic region. Annals of Botany, 2020, 126, 103-118.	1.4	3
9394	Transmission Dynamics and Microevolution of <i>Neisseria meningitidis</i> During Carriage and Invasive Disease in High School Students in Georgia and Maryland, 2006–2007. Journal of Infectious Diseases, 2020, 223, 2038-2047.	1.9	6
9395	Origins and Molecular Evolution of the NusG Paralog RfaH. MBio, 2020, 11, .	1.8	15
9396	Genomic evidence for recurrent genetic admixture during the domestication of Mediterranean olive trees (<i>Olea europaea</i> L.). BMC Biology, 2020, 18, 148.	1.7	39
9397	Most Cephalaspidea have a shell, but transcriptomes can provide them with a backbone (Gastropoda: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 5	1.2	1
9398	Contrasting signatures of genomic divergence during sympatric speciation. Nature, 2020, 588, 106-111.	13.7	115
9399	Cultivated Tomato (<i>Solanum lycopersicum</i> L.) Suffered a Severe Cytoplasmic Bottleneck during Domestication: Implications from Chloroplast Genomes. Plants, 2020, 9, 1443.	1.6	11
9400	<i>Streptomyces alkaliterrae</i> sp. nov., isolated from an alkaline soil, and emended descriptions of <i>Streptomyces alkaliphilus</i> , <i>Streptomyces calidiresistens</i> and <i>Streptomyces durbertensis</i> . Systematic and Applied Microbiology, 2020, 43, 126153.	1.2	17
9401	An enhanced target-enrichment bait set for Hexacorallia provides phylogenomic resolution of the staghorn corals (Acroporidae) and close relatives. Molecular Phylogenetics and Evolution, 2020, 153, 106944.	1.2	59
9402	High prevalence of <i>mcr-1</i> -encoded colistin resistance in commensal <i>Escherichia coli</i> from broiler chicken in Bangladesh. Scientific Reports, 2020, 10, 18637.	1.6	28
9403	Phylogeny and systematics of the <i>Sesamia coniota</i> Hampson species group (Lepidoptera: Noctuidae: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 5 region. Annales De La Societe Entomologique De France, 2020, 56, 417-435.	0.4	1
9404	Ethylene signaling mediates host invasion by parasitic plants. Science Advances, 2020, 6, .	4.7	37
9405	All the Colors of the Rainbow: Diversification of Flower Color and Intraspecific Color Variation in the Genus <i>Iris</i> . Frontiers in Plant Science, 2020, 11, 569811.	1.7	15
9406	Pathogenic <i>Escherichia coli</i> Possess Elevated Growth Rates under Exposure to Sub-Inhibitory Concentrations of Azithromycin. Antibiotics, 2020, 9, 735.	1.5	5
9407	Genomic Characterization of Methicillin-Resistant <i>Staphylococcus aureus</i> (MRSA) by High-Throughput Sequencing in a Tertiary Care Hospital. Genes, 2020, 11, 1219.	1.0	10

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9408	Mitochondrial evolution in the entomopathogenic fungal genus <i>Beauveria</i> . Archives of Insect Biochemistry and Physiology, 2020, 105, e21754.	0.6	5
9409	Evolutionary Biology – A Transdisciplinary Approach. , 2020, , .		5
9410	High-throughput cultivation based on dilution-to-extinction with catalase supplementation and a case study of cultivating <i>acl</i> bacteria from Lake Soyang. Journal of Microbiology, 2020, 58, 893-905.	1.3	14
9411	Distinct Polysaccharide Utilization Determines Interspecies Competition between Intestinal <i>Prevotella</i> spp.. Cell Host and Microbe, 2020, 28, 838-852.e6.	5.1	86
9412	Genome based evolutionary lineage of SARS-CoV-2 towards the development of novel chimeric vaccine. Infection, Genetics and Evolution, 2020, 85, 104517.	1.0	17
9413	Strong oral plaque microbiome signatures for dental implant diseases identified by strain-resolution metagenomics. Npj Biofilms and Microbiomes, 2020, 6, 47.	2.9	54
9414	Fungal diversity notes 1277–1386: taxonomic and phylogenetic contributions to fungal taxa. Fungal Diversity, 2020, 104, 1-266.	4.7	60
9415	From landrace to modern hybrid broccoli: the genomic and morphological domestication syndrome within a diverse <i>B. oleracea</i> collection. Horticulture Research, 2020, 7, 159.	2.9	11
9416	CryoEM structure of the type IVa pilus secretin required for natural competence in <i>Vibrio cholerae</i> . Nature Communications, 2020, 11, 5080.	5.8	21
9417	Host-symbiont coevolution, cryptic structure, and bleaching susceptibility, in a coral species complex (<i>Scleractinia</i> ; <i>Poritidae</i>). Scientific Reports, 2020, 10, 16995.	1.6	33
9418	Spirochetes isolated from arthropods constitute a novel genus <i>Entomospira</i> genus novum within the order Spirochaetales. Scientific Reports, 2020, 10, 17053.	1.6	5
9419	Crystal structure and site-directed mutagenesis of circular bacteriocin plantacyclin B21AG reveals cationic and aromatic residues important for antimicrobial activity. Scientific Reports, 2020, 10, 17398.	1.6	10
9420	Current and historic HIV-1 molecular epidemiology in paediatric and adult population from Kinshasa in the Democratic Republic of Congo. Scientific Reports, 2020, 10, 18461.	1.6	11
9421	A step-down photophobic response in coral larvae: implications for the light-dependent distribution of the common reef coral, <i>Acropora tenuis</i> . Scientific Reports, 2020, 10, 17680.	1.6	18
9422	Carbapenems drive the collateral resistance to ceftaroline in cystic fibrosis patients with MRSA. Communications Biology, 2020, 3, 599.	2.0	9
9423	Comparative ACE2 variation and primate COVID-19 risk. Communications Biology, 2020, 3, 641.	2.0	121
9424	Global analysis of adenylate-forming enzymes reveals $\hat{1}^2$ -lactone biosynthesis pathway in pathogenic <i>Nocardia</i> . Journal of Biological Chemistry, 2020, 295, 14826-14839.	1.6	22
9425	Gene flow in the Antarctic bivalve <i>Aequiyoldia eightsii</i> (Jay, 1839) suggests a role for the Antarctic Peninsula Coastal Current in larval dispersal. Royal Society Open Science, 2020, 7, 200603.	1.1	11

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9426	Multi-omic detection of <i>Mycobacterium leprae</i> in archaeological human dental calculus. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190584.	1.8	31
9427	The entomophagous caterpillar fungus <i>Ophiocordyceps sinensis</i> is consumed by its lepidopteran host as a plant endophyte. <i>Fungal Ecology</i> , 2020, 47, 100989.	0.7	26
9428	The seventh pandemic of cholera in Europe revisited by microbial genomics. <i>Nature Communications</i> , 2020, 11, 5347.	5.8	13
9429	Circumscription of <i>Lithophyllum racemosum</i> (Corallinales, Rhodophyta) from the western Mediterranean Sea reveals the species <i>Lithophyllum pseudoracemosum</i> sp. nov. <i>Phycologia</i> , 2020, 59, 584-597.	0.6	14
9430	Complete mitochondrial genome of the Korean endemic firefly, <i>Luciola unmunsana</i> (Coleoptera: Lampyridae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 3165-3167.	0.2	4
9431	The complete mitochondrial genome of the yellowfin shiner, <i>Notropis lutipinnis</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 3185-3187.	0.2	0
9432	The complete chloroplast genome of <i>Eurya loquaiana</i> (Pentaphragmataceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 3293-3294.	0.2	0
9433	The complete chloroplast genome sequence of medicinal plant <i>Alpinia chinensis</i> (Retz.) Rosc. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 3328-3329.	0.2	2
9434	Global Epidemiology and Evolutionary History of <i>Staphylococcus aureus</i> ST45. <i>Journal of Clinical Microbiology</i> , 2020, 59, .	1.8	14
9435	Combined-evidence analyses of ultraconserved elements and morphological data: an empirical example in iguanian lizards. <i>Biology Letters</i> , 2020, 16, 20200356.	1.0	6
9436	Phylogenomics, biogeography, and evolution of the blue- or white-fruited dogwoods (<i>Cornus</i>)—insights into morphological and ecological niche divergence following intercontinental geographic isolation. <i>Journal of Systematics and Evolution</i> , 2020, 58, 604-645.	1.6	15
9437	Bradymonabacteria, a novel bacterial predator group with versatile survival strategies in saline environments. <i>Microbiome</i> , 2020, 8, 126.	4.9	37
9438	Subspecies Variation of <i>Daucus carota</i> Coastal (‘Gummifer’) Morphotypes (Apiaceae) Using Genotyping-by-Sequencing. <i>Systematic Botany</i> , 2020, 45, 688-702.	0.2	4
9439	Oral Infection by Mucosal and Cutaneous Human Papillomaviruses in the Men Who Have Sex with Men from the OHMAR Study. <i>Viruses</i> , 2020, 12, 899.	1.5	12
9440	Three Planctomycetes isolated from biotic surfaces in the Mediterranean Sea and the Pacific Ocean constitute the novel species <i>Symmachiella dynata</i> gen. nov., sp. nov. and <i>Symmachiella macrocystis</i> sp. nov.. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 1965-1977.	0.7	20
9441	The utility of DNA barcodes to confirm the identification of palm collections in botanical gardens. <i>PLoS ONE</i> , 2020, 15, e0235569.	1.1	7
9442	Comparative Genomics and Phylogenetic Analyses of <i>Christia vespertilionis</i> and <i>Urariopsis brevissima</i> in the Tribe Desmodieae (Fabaceae: Papilionoideae) Based on Complete Chloroplast Genomes. <i>Plants</i> , 2020, 9, 1116.	1.6	8
9443	Evolutionary analysis and protein family classification of chitin deacetylases in <i>Cryptococcus neoformans</i> . <i>Journal of Microbiology</i> , 2020, 58, 805-811.	1.3	3

#	ARTICLE	IF	CITATIONS
9444	The Phoebe genome sheds light on the evolution of magnoliids. Horticulture Research, 2020, 7, 146.	2.9	41
9445	Glacier retreat in the High Arctic: opportunity or threat for ectomycorrhizal diversity?. FEMS Microbiology Ecology, 2020, 96, .	1.3	5
9446	Genetic Adaptations of an Island Pit-Viper to a Unique Sedentary Life with Extreme Seasonal Food Availability. G3: Genes, Genomes, Genetics, 2020, 10, 1639-1646.	0.8	3
9447	Quinone perception in plants via leucine-rich-repeat receptor-like kinases. Nature, 2020, 587, 92-97.	13.7	77
9448	Genotypic and phylogenetic diversity of new isolates of terrestrial Xanthophyceae (Stramenopiles) from maritime sandy habitats. Phycologia, 2020, 59, 506-514.	0.6	5
9449	The Chloroplast Genome of <i>Salvia</i> : Genomic Characterization and Phylogenetic Analysis. International Journal of Plant Sciences, 2020, 181, 812-830.	0.6	15
9450	The Distribution and Spread of Susceptible and Resistant <i>Neisseria gonorrhoeae</i> Across Demographic Groups in a Major Metropolitan Center. Clinical Infectious Diseases, 2021, 73, e3146-e3155.	2.9	19
9451	Sympatric speciation in mountain roses (<i>Metrosideros</i>) on an oceanic island. Philosophical Transactions of the Royal Society B: Biological Sciences, 2020, 375, 20190542.	1.8	10
9452	Mapping genome variation of SARS-CoV-2 worldwide highlights the impact of COVID-19 super-spreaders. Genome Research, 2020, 30, 1434-1448.	2.4	91
9453	Introgression across evolutionary scales suggests reticulation contributes to Amazonian tree diversity. Molecular Ecology, 2020, 29, 4170-4185.	2.0	23
9454	Evolution of the African slippery frogs (<i>Anura</i> : <i>Conraua</i>), including the world's largest living frog. Zoologica Scripta, 2020, 49, 684-696.	0.7	5
9455	Curated multiple sequence alignment for the Adenomatous Polyposis Coli (APC) gene and accuracy of in silico pathogenicity predictions. PLoS ONE, 2020, 15, e0233673.	1.1	1
9456	Latitudinal Biogeographic Structuring in the Globally Distributed Moss <i>Ceratodon purpureus</i> . Frontiers in Plant Science, 2020, 11, 502359.	1.7	13
9457	Barthelonids represent a deep-branching metamonad clade with mitochondrion-related organelles predicted to generate no ATP. Proceedings of the Royal Society B: Biological Sciences, 2020, 287, 20201538.	1.2	13
9458	Endosymbionts of Metazoans Dwelling in the PACManus Hydrothermal Vent: Diversity and Potential Adaptive Features Revealed by Genome Analysis. Applied and Environmental Microbiology, 2020, 86, .	1.4	6
9459	Jennwenomyces, a new hyphomycete genus segregated from Belemnospora, producing versicolored phragmospores from percurrently extending conidiophores. Mycological Progress, 2020, 19, 869-883.	0.5	4
9460	Farysia magdalena sp. nov. and description of the anamorph of Anthracocystis heteropogonicola from the Americas. Mycological Progress, 2020, 19, 921-934.	0.5	1
9461	Hysterangium bonobo: A newly described truffle species that is eaten by bonobos in the Democratic Republic of Congo. Mycologia, 2020, 112, 1203-1211.	0.8	7

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9462	Microbiota in Dung and Milk Differ Between Organic and Conventional Dairy Farms. <i>Frontiers in Microbiology</i> , 2020, 11, 1746.	1.5	4
9463	Emergence of Resistance to Fluoroquinolones and Third-Generation Cephalosporins in <i>Salmonella</i> Typhi in Lahore, Pakistan. <i>Microorganisms</i> , 2020, 8, 1336.	1.6	35
9464	New Taxa of the Family Amniculicolaceae (Pleosporales, Dothideomycetes, Ascomycota) from Freshwater Habitats in Spain. <i>Microorganisms</i> , 2020, 8, 1355.	1.6	7
9465	Bacterial communities of the <i>Salvia lyrata</i> rhizosphere explained by spatial structure and sampling grain. <i>Microbial Ecology</i> , 2020, 80, 846-858.	1.4	8
9466	Molecular phylogeny and morphology reveal cryptic species in <i>Blackwellomyces</i> and <i>Cordyceps</i> (Cordycipitaceae) from Thailand. <i>Mycological Progress</i> , 2020, 19, 957-983.	0.5	21
9467	Sex-biased patterns shaped the genetic history of Roma. <i>Scientific Reports</i> , 2020, 10, 14464.	1.6	7
9468	Genome-wide patterns of divergence and introgression after secondary contact between <i>Pungitius</i> sticklebacks. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190548.	1.8	32
9469	A high-quality chromosome-level genome assembly reveals genetics for important traits in eggplant. <i>Horticulture Research</i> , 2020, 7, 153.	2.9	85
9470	The evolution of strong reproductive isolation between sympatric intertidal snails. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190545.	1.8	23
9471	Introduction of <i>Mycobacterium ulcerans</i> disease in the Bankim Health District of Cameroon follows damming of the Mapo River. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008501.	1.3	5
9472	Genomic Organization and Generation of Genetic Variability in the RHS (Retrotransposon Hot Spot) Protein Multigene Family in <i>Trypanosoma cruzi</i> . <i>Genes</i> , 2020, 11, 1085.	1.0	8
9473	Molecular Characterization of Hemorrhagic Enteritis Virus (HEV) Obtained from Clinical Samples in Western Canada 2017–2018. <i>Viruses</i> , 2020, 12, 941.	1.5	7
9474	Resurrecting the genus <i>Geomorium</i> : Systematic study of fungi in the genera <i>Underwoodia</i> and <i>Gymnohydnotrya</i> (<i>Pezizales</i>) with the description of three new South American species. <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2020, 44, 98-112.	1.6	6
9475	A first phylogenomic hypothesis for Eulophidae (Hymenoptera, Chalcidoidea). <i>Journal of Natural History</i> , 2020, 54, 597-609.	0.2	12
9476	Community composition of arctic root-associated fungi mirrors host plant phylogeny. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	16
9477	Skeletal muscle and cardiac transcriptomics of a regionally endothermic fish, the Pacific bluefin tuna, <i>Thunnus orientalis</i> . <i>BMC Genomics</i> , 2020, 21, 642.	1.2	2
9478	Annotated genome sequences of the carnivorous plant <i>Roridula gorgonias</i> and a non-carnivorous relative, <i>Clethra arborea</i> . <i>BMC Research Notes</i> , 2020, 13, 426.	0.6	5
9479	A Reference Genome Sequence for Giant Sequoia. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3907-3919.	0.8	67

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9480	Mcdadea: A New Genus of Acanthaceae Endemic to the Namib Desert of Southwestern Angola. Systematic Botany, 2020, 45, 200-211.	0.2	7
9481	The complete chloroplast genome of Sedum emarginatum (Crassulaceae). Mitochondrial DNA Part B: Resources, 2020, 5, 3082-3083.	0.2	5
9482	Main Routes of Entry and Genomic Diversity of SARS-CoV-2, Uganda. Emerging Infectious Diseases, 2020, 26, 2411-2415.	2.0	24
9484	Spidroin profiling of cribellate spiders provides insight into the evolution of spider prey capture strategies. Scientific Reports, 2020, 10, 15721.	1.6	23
9485	The Molecular Machinery of Gametogenesis in <i>Geodia</i> Demosponges (Porifera): Evolutionary Origins of a Conserved Toolkit across Animals. Molecular Biology and Evolution, 2020, 37, 3485-3506.	3.5	19
9486	Local acclimatisation-driven differential gene and protein expression patterns of Hsp70 in <i>Acropora muricata</i> : Implications for coral tolerance to bleaching. Molecular Ecology, 2020, 29, 4382-4394.	2.0	13
9487	Potential reverse spillover of infectious bursal disease virus at the interface of commercial poultry and wild birds. Virus Genes, 2020, 56, 705-711.	0.7	3
9488	How parasite exposure and time interact to determine <i>Australapatemon burti</i> (Trematoda: Digenea) infections in second intermediate hosts (<i>Erpobdella microstoma</i>) (Hirudinea: Erpobdellidae). Experimental Parasitology, 2020, 219, 108002.	0.5	2
9489	Phylogeny of Euclidieae (Brassicaceae) based on plastome and nuclear ribosomal DNA data. Molecular Phylogenetics and Evolution, 2020, 153, 106940.	1.2	7
9490	Molecular phylogeny and biogeography of the temperate Gondwanan family Triaenonychidae (Opiliones : Laniatores) reveals pre-Gondwanan regionalisation, common vicariance, and rare dispersal. Invertebrate Systematics, 2020, , .	0.5	12
9491	The origin and diversification of pteropods precede past perturbations in the Earth's carbon cycle. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 25609-25617.	3.3	25
9492	The complete chloroplast genome of <i>Phyllostachys glauca</i> (Bambusoideae), a dominant bamboo species in limestone mountains endemic to China. Mitochondrial DNA Part B: Resources, 2020, 5, 3193-3194.	0.2	3
9493	Long-read sequencing and de novo genome assembly of marine medaka (<i>Oryzias melastigma</i>). BMC Genomics, 2020, 21, 640.	1.2	7
9494	Leaf-footed bugs possess multiple hidden contrasting color signals, but only one is associated with increased body size. Ecology and Evolution, 2020, 10, 8571-8578.	0.8	7
9495	Linnaeus's folly – phylogeny, evolution and classification of <i>Sedum</i> (Crassulaceae) and Crassulaceae subfamily Sempervivoideae. Taxon, 2020, 69, 892-926.	0.4	26
9496	Rare Bolivian wild chile <i>Capsicum eshbaughii</i> (Solanaceae) located again: open ending on its identity and conservation. Plant Systematics and Evolution, 2020, 306, 1.	0.3	4
9497	The diversification and lineage-specific expansion of nitric oxide signaling in Placozoa: insights in the evolution of gaseous transmission. Scientific Reports, 2020, 10, 13020.	1.6	37
9498	The P-glycoprotein repertoire of the equine parasitic nematode <i>Parascaris univalens</i> . Scientific Reports, 2020, 10, 13586.	1.6	16

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9499	Diversity and pathogenicity of <i>Colletotrichum</i> species causing strawberry anthracnose in Taiwan and description of a new species, <i>Colletotrichum miaoliense</i> sp. nov.. <i>Scientific Reports</i> , 2020, 10, 14664.	1.6	49
9500	Early vertebrate origin of CTCFL, a CTCF paralog, revealed by proximity-guided shark genome scaffolding. <i>Scientific Reports</i> , 2020, 10, 14629.	1.6	5
9501	Silence as a way of niche adaptation: mecC-MRSA with variations in the accessory gene regulator (<i>agr</i>) functionality express kaleidoscopic phenotypes. <i>Scientific Reports</i> , 2020, 10, 14787.	1.6	11
9502	Three new species of <i>Gliocephalotrichum</i> causing fruit rot on different hosts from Brazil. <i>Mycologia</i> , 2020, 112, 1003-1016.	0.8	1
9503	Regional drivers of diversification in the late Quaternary in a widely distributed generalist species, the common pheasant <i>Phasianus colchicus</i> . <i>Journal of Biogeography</i> , 2020, 47, 2714-2727.	1.4	10
9504	A test of Generalized Bayesian dating: A new linguistic dating method. <i>PLoS ONE</i> , 2020, 15, e0236522.	1.1	5
9505	Genetic Diversity, Ochratoxin A and Fumonisin Profiles of Strains of <i>Aspergillus Section Nigri</i> Isolated from Dried Vine Fruits. <i>Toxins</i> , 2020, 12, 592.	1.5	8
9506	The complete mitochondrial genome of <i>Luffa acutangula</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 3208-3209.	0.2	2
9507	Mode and Tempo of Microsatellite Evolution across 300 Million Years of Insect Evolution. <i>Genes</i> , 2020, 11, 945.	1.0	5
9508	Rediscovery of <i>Lepisorus cespitosus</i> supported the floristic affinities between western Yunnan and southeast Tibet. <i>Plant Systematics and Evolution</i> , 2020, 306, 1.	0.3	3
9509	Novel species of <i>Pestalotiopsis</i> fungi on <i>Dracaena</i> from Thailand. <i>Mycology</i> , 2020, 11, 306-315.	2.0	7
9510	Characterization of the complete chloroplast genome of <i>Aconitum flavum</i> (Ranunculaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2982-2983.	0.2	7
9511	Complete chloroplast genome sequence of <i>Homalium hainanense</i> (Salicaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2819-2820.	0.2	0
9512	The complete chloroplast genome and phylogenetic analysis of <i>Pleurospermum amabile</i> Craib & W. W. Smith. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2966-2968.	0.2	1
9513	Comparative Genomics Underlines Multiple Roles of <i>Proffttella</i> , an Obligate Symbiont of Psyllids: Providing Toxins, Vitamins, and Carotenoids. <i>Genome Biology and Evolution</i> , 2020, 12, 1975-1987.	1.1	39
9514	Identification and Characterization of <i>Diaporthe</i> spp. Associated with Twig Cankers and Shoot Blight of Almonds in Spain. <i>Agronomy</i> , 2020, 10, 1062.	1.3	20
9515	Fatty Acid Biosynthesis in Chromerids. <i>Biomolecules</i> , 2020, 10, 1102.	1.8	1
9516	Phylogenetic and Chemotaxonomic Studies Confirm the Affinities of <i>Stromatoneurospora phoenix</i> to the Coprophilous Xylariaceae. <i>Journal of Fungi (Basel, Switzerland)</i> , 2020, 6, 144.	1.5	19

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9517	Chikungunya virus Detection in <i>Aedes aegypti</i> and <i>Culex quinquefasciatus</i> during an Outbreak in the Amazon Region. <i>Viruses</i> , 2020, 12, 853.	1.5	8
9518	Character evolution of modern flyspeck fungi and implications for interpreting thyrtothelial fossils. <i>American Journal of Botany</i> , 2020, 107, 1021-1040.	0.8	8
9519	The first report of two <i>Sphaeromyxa</i> species (Myxozoa: Bivalvulida) from the South China Sea: <i>Sphaeromyxa scorpaena</i> n. sp. from long-fingered scorpionfish (<i>Scorpaenodes albaiensis</i>) and <i>Sphaeromyxa theraponi</i> from tiger perch (<i>Terapon jarbua</i>). <i>Parasitology Research</i> , 2020, 119, 3617-3625.	0.6	2
9520	Nested whole-genome duplications coincide with diversification and high morphological disparity in Brassicaceae. <i>Nature Communications</i> , 2020, 11, 3795.	5.8	72
9521	A high-quality reference genome for cabbage obtained with SMRT reveals novel genomic features and evolutionary characteristics. <i>Scientific Reports</i> , 2020, 10, 12394.	1.6	29
9522	The complete chloroplast genome of <i>Tradescantia pallida</i> (Rose) D.R.Hunt. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2932-2933.	0.2	0
9523	Horizontal transmission and recombination maintain forever young bacterial symbiont genomes. <i>PLoS Genetics</i> , 2020, 16, e1008935.	1.5	87
9524	Phylogeny and multiple independent whole-genome duplication events in the Brassicales. <i>American Journal of Botany</i> , 2020, 107, 1148-1164.	0.8	32
9525	<i>Peronospora aquilegiicola</i> made its way to Germany: the start of a new pandemic?. <i>Mycological Progress</i> , 2020, 19, 791-798.	0.5	3
9526	<i>Euborlasia</i> Vaillant, 1890 (Nemertea: Piliidophora) from Bocas del Toro: description of a new species, with comments on the systematics of the genus. <i>Marine Biodiversity</i> , 2020, 50, 1.	0.3	4
9527	A genetic barcode of SARS-CoV-2 for monitoring global distribution of different clades during the COVID-19 pandemic. <i>International Journal of Infectious Diseases</i> , 2020, 100, 216-223.	1.5	43
9528	Species identification, phylogenetic analysis and detection of herbicide-resistant biotypes of <i>Amaranthus</i> based on ALS and ITS. <i>Scientific Reports</i> , 2020, 10, 11735.	1.6	3
9529	An ancient tropical origin, dispersals via land bridges and Miocene diversification explain the subcosmopolitan disjunctions of the liverwort genus <i>Lejeunea</i> . <i>Scientific Reports</i> , 2020, 10, 14123.	1.6	12
9530	A new gene order in the mitochondrial genome of the deep-sea diaphanous hatchet fish <i>Sternoptyx diaphana</i> Hermann, 1781 (Stomiiformes: Sternoptychidae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2850-2852.	0.2	2
9531	The complete chloroplast genome sequence of <i>Ulmus parvifolia</i> (Ulmaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2957-2958.	0.2	1
9532	The complete mitochondrial genome of <i>Polygonia c-aureum</i> (Lepidoptera: Nymphalidae) from Yizhou of China and its phylogeny. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2936-2937.	0.2	1
9533	Comparison of eight complete plastid genomes from three moss families Amblystegiaceae, Calliergonaceae and Pylaisiaceae. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 3091-3093.	0.2	2
9534	The complete mitochondrial genome of <i>Iphis elegans</i> (Reptilia: Squamata: Gymnophthalmidae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 3088-3090.	0.2	1

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9535	The mitochondrial genome of a horntail wasp, <i>Tremex fuscicornis</i> (Hymenoptera: Siricidae). Mitochondrial DNA Part B: Resources, 2020, 5, 3007-3008.	0.2	0
9536	The complete plastome and phylogenetic analysis of <i>Rhoiptelea chiliantha</i> (Juglandaceae). Mitochondrial DNA Part B: Resources, 2020, 5, 3091-3092.	0.2	1
9537	The climatic association of population divergence and future extinction risk of <i>Solanum pimpinellifolium</i> . AoB PLANTS, 2020, 12, plaa012.	1.2	9
9538	Chromosome-Level Assembly of the Common Lizard (<i>Zootoca vivipara</i>) Genome. Genome Biology and Evolution, 2020, 12, 1953-1960.	1.1	13
9539	Characterization of sponge-associated <i>Verrucomicrobia</i> : microcompartment-based sugar utilization and enhanced toxin-antitoxin modules as features of host-associated <i>Opiritales</i> . Environmental Microbiology, 2020, 22, 4669-4688.	1.8	26
9540	Phylogenetic relationships within the Mexican genus <i>Bakerantha</i> (Hechtioideae, Bromeliaceae) based on plastid and nuclear DNA: Implications for taxonomy. Journal of Systematics and Evolution, 2020, , .	1.6	6
9541	Strain Structure and Dynamics Revealed by Targeted Deep Sequencing of the Honey Bee Gut Microbiome. MSphere, 2020, 5, .	1.3	19
9542	Global transcriptomic responses orchestrate difenoconazole resistance in <i>Penicillium</i> spp. causing blue mold of stored apple fruit. BMC Genomics, 2020, 21, 574.	1.2	8
9543	Ophiostomatoid fungi associated with mites phoretic on bark beetles in Qinghai, China. IMA Fungus, 2020, 11, 15.	1.7	6
9544	First Report of a Neotropical Agaric (<i>Lepiota spiculata</i> , Agaricales, Basidiomycota) Containing Lethal \pm -Amanitin at Toxicologically Relevant Levels. Frontiers in Microbiology, 2020, 11, 1833.	1.5	6
9545	Baculovirus Expression and Functional Analysis of Vpa2 Proteins from <i>Bacillus thuringiensis</i> . Toxins, 2020, 12, 543.	1.5	1
9546	Plastome phylogenomics and phylogenetic diversity of endangered and threatened grassland species (Poaceae) in a North American tallgrass prairie. Ecology and Evolution, 2020, 10, 7602-7615.	0.8	3
9547	The complete chloroplast genome sequence of <i>Swertia diluta</i> (Gentianaceae). Mitochondrial DNA Part B: Resources, 2020, 5, 2763-2764.	0.2	1
9548	Characterization of the complete chloroplast genome of <i>styrax macrocarpus</i> (Styracaceae), an endemic species from China. Mitochondrial DNA Part B: Resources, 2020, 5, 2811-2812.	0.2	0
9549	The complete chloroplast genome sequence of medicinal plant: <i>Lepidium apetalum</i> (Brassicaceae). Mitochondrial DNA Part B: Resources, 2020, 5, 2842-2843.	0.2	0
9550	Complete mitochondrial genomes provide current refined phylogenomic hypotheses for relationships among ten <i>Hirundo</i> species. Mitochondrial DNA Part B: Resources, 2020, 5, 2881-2885.	0.2	1
9551	The mitochondrial genome sequence of a satyrid butterfly, <i>Lethe confuse</i> (Lepidoptera:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 100	0.2	0
9552	The complete chloroplast genome of <i>Verbascum chinense</i> (L.) Santapau. Mitochondrial DNA Part B: Resources, 2020, 5, 3021-3022.	0.2	2

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9553	Six additional mitochondrial genomes for North American nightsnakes (Dipsadidae: <i>Hypsiglena</i>) and a novel gene feature for advanced snakes. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 3056-3058.	0.2	2
9554	The complete mitochondrial genome of <i>Pedetontus zhejiangensis</i> (Microcoryphia: Machilidae) and its phylogeny. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 3143-3145.	0.2	0
9555	Analytical Performance Validation of Next-Generation Sequencing Based Clinical Microbiology Assays Using a K-mer Analysis Workflow. <i>Frontiers in Microbiology</i> , 2020, 11, 1883.	1.5	12
9556	The chloroplast genome of the moss <i>Haplocladium microphyllum</i> , first in family Thuidiaceae. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2813-2814.	0.2	0
9557	Characterization of the first chloroplast genome of <i>Tabebuia</i> (Bignoniaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2954-2956.	0.2	1
9558	The complete chloroplast genomes of <i>Heterotis rotundifolia</i> and <i>Heterocentron elegans</i> (Melastomataceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 3094-3095.	0.2	0
9559	The complete mitochondrial genome sequence of <i>Cletus rubidiventris</i> (Heteroptera: Coreidae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 3075-3076.	0.2	1
9560	The complete genome sequence of <i>Sorbus insignis</i> (Rosaceae: Amygdaloideae), an epiphytic shrub in this genus. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 3239-3240.	0.2	1
9561	Circumscription and phylogenetic position of <i>Ligularia</i> sect. <i>Stenostegia</i> (Asteraceae: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 69, 739-755.	0.4	5
9562	A revised subtribal classification of Gnaphalieae (Asteraceae). <i>Taxon</i> , 2020, 69, 778-806.	0.4	10
9563	Characterization of black spot resistance in diploid roses with QTL detection, meta-analysis and candidate-gene identification. <i>Theoretical and Applied Genetics</i> , 2020, 133, 3299-3321.	1.8	11
9564	The mitochondrial genome of an ectoparasitoid wasp, <i>Habrobracon hebetor</i> (Hymenoptera: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 5 69, 739-755.	0.2	5
9565	Chromosome-level genome assembly of the female western mosquitofish (<i>Gambusia affinis</i>). <i>GigaScience</i> , 2020, 9, .	3.3	5
9566	What is truth: Consensus and discordance in next-generation phylogenetic analyses of <i>Daucus</i> . <i>Journal of Systematics and Evolution</i> , 2020, 58, 1059-1070.	1.6	11
9567	Chlamydial contribution to anaerobic metabolism during eukaryotic evolution. <i>Science Advances</i> , 2020, 6, eabb7258.	4.7	18
9568	Microbial mats in the Turks and Caicos Islands reveal diversity and evolution of phototrophy in the Chloroflexota order Aggregatilineales. <i>Environmental Microbiomes</i> , 2020, 15, 9.	2.2	15
9569	Brassicaceous roots as an unexpected diversity hot-spot of helotialean endophytes. <i>IMA Fungus</i> , 2020, 11, 16.	1.7	15
9570	Natural variation in a glucuronosyltransferase modulates propionate sensitivity in a <i>C. elegans</i> propionic acidemia model. <i>PLoS Genetics</i> , 2020, 16, e1008984.	1.5	18

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9571	Genetic evolution of <i>in situ</i> follicular neoplasia to aggressive B-cell lymphoma of germinal center subtype. <i>Haematologica</i> , 2021, 106, 2673-2681.	1.7	21
9572	Evolutionary and Molecular Analysis of Complete Genome Sequences of Norovirus From Brazil: Emerging Recombinant Strain GII.P16/GII.4. <i>Frontiers in Microbiology</i> , 2020, 11, 1870.	1.5	10
9573	The Phylogeny of Class B Flavoprotein Monooxygenases and the Origin of the YUCCA Protein Family. <i>Plants</i> , 2020, 9, 1092.	1.6	5
9574	Origin of the critically endangered endemic species <i>Scrophularia takesimensis</i> (Scrophulariaceae) on Ulleung Island, Korea: implications for conservation. <i>Journal of Plant Research</i> , 2020, 133, 765-782.	1.2	5
9575	Palaeoclimate ocean conditions shaped the evolution of corals and their skeletons through deep time. <i>Nature Ecology and Evolution</i> , 2020, 4, 1531-1538.	3.4	90
9576	Supergene evolution via stepwise duplications and neofunctionalization of a floral-organ identity gene. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 23148-23157.	3.3	42
9577	Comprehensive Analysis of Codon Usage on Porcine Astrovirus. <i>Viruses</i> , 2020, 12, 991.	1.5	15
9578	<i>Lactifluus</i> (<i>Russulaceae</i>) diversity in Central America and the Caribbean: melting pot between realms. <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2020, 44, 278-300.	1.6	6
9579	Wireworm (Coleoptera: Elateridae) genomic analysis reveals putative cryptic species, population structure, and adaptation to pest control. <i>Communications Biology</i> , 2020, 3, 489.	2.0	21
9580	A new pinnotherid crab of the genus <i>Pinnixulala</i> Palacios Theil, Cuesta & Felder, 2016 from uncertain infaunal hosts in the northern Gulf of Mexico, with a rediagnosis and updated synonymy for the polychaete symbiont <i>Pinnixulala retinens</i> (Rathbun, 1918) (Decapoda: Brachyura: Tj ETQq1 1 0.784314 rrgBT / Overlock 10	0.3	3
9581	Mission impossible completed: unlocking the nomenclature of the largest and most complicated subgenus of <i>Cortinarius</i> , <i>Telamonia</i> . <i>Fungal Diversity</i> , 2020, 104, 291-331.	4.7	20
9582	Echolocation call frequency variation in horseshoe bats: molecular basis revealed by comparative transcriptomics. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20200875.	1.2	6
9583	Taxonomy and phylogeny of cercosporoid ascomycetes on <i>Diospyros</i> spp. with special emphasis on <i>Pseudocercospora</i> spp.. <i>Fungal Systematics and Evolution</i> , 2020, 6, 95-127.	0.9	9
9584	Phylogeny and species reassessment of <i>Hyalopterus</i> (Aphididae, Aphidinae). <i>Zoologica Scripta</i> , 2020, 49, 755-767.	0.7	3
9585	Ancient DNA shows domestic horses were introduced in the southern Caucasus and Anatolia during the Bronze Age. <i>Science Advances</i> , 2020, 6, .	4.7	27
9586	Distinct evolutionary trajectories of V1R clades across mouse species. <i>BMC Evolutionary Biology</i> , 2020, 20, 99.	3.2	8
9587	Phylogenetic structure in the <i>Sphagnum recurvum</i> complex (Bryophyta) in relation to taxonomy and geography. <i>American Journal of Botany</i> , 2020, 107, 1283-1295.	0.8	12
9588	Elucidating species richness in lichen fungi: The genus <i>Stictia</i> (Ascomycota: Peltigeraceae) in Puerto Rico. <i>Taxon</i> , 2020, 69, 851-891.	0.4	11

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9589	Resolving the Mortierellaceae phylogeny through synthesis of multi-gene phylogenetics and phylogenomics. <i>Fungal Diversity</i> , 2020, 104, 267-289.	4.7	57
9590	Tek/Tie2 is not required for cardiovascular development in zebrafish. <i>Development (Cambridge)</i> , 2020, 147, .	1.2	14
9591	A New Method for Next-Generation Sequencing of the Full Hepatitis B Virus Genome from A Clinical Specimen: Impact for Virus Genotyping. <i>Microorganisms</i> , 2020, 8, 1391.	1.6	7
9592	Early origin and global colonisation of foot-and-mouth disease virus. <i>Scientific Reports</i> , 2020, 10, 15268.	1.6	7
9593	Introgression Among Three Western North American Bilberries (<i>Vaccinium</i> section) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 582 Td	0.2	8
9594	Choricystis and Lewinosphaera gen. nov. (Trebouxiophyceae Chlorophyta), two different green algal endosymbionts in freshwater sponges. <i>Symbiosis</i> , 2020, 82, 175-188.	1.2	12
9595	The complete mitochondrial genome of <i>Xyrias revulsus</i> Jordan & Snyder, 1901. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 3154-3156.	0.2	0
9596	The unknown diversity of the genus <i>Characidium</i> (Characiformes: Crenuchidae) in the Chocó biogeographic region, Colombian Andes: Two new species supported by morphological and molecular data. <i>Journal of Fish Biology</i> , 2020, 97, 1662-1675.	0.7	6
9597	Occurrence of Chlamydiaceae in Raptors and Crows in Switzerland. <i>Pathogens</i> , 2020, 9, 724.	1.2	10
9598	<i>Yersinia pestis</i> strains from Latvia show depletion of the <i>pla</i> virulence gene at the end of the second plague pandemic. <i>Scientific Reports</i> , 2020, 10, 14628.	1.6	25
9599	Analysis of muntjac deer genome and chromatin architecture reveals rapid karyotype evolution. <i>Communications Biology</i> , 2020, 3, 480.	2.0	31
9600	Phylogenetic Characterization Reveals Prevalent <i>Shigella flexneri</i> ST100 Clone in Beijing, China, 2005 to 2018. <i>MSphere</i> , 2020, 5, .	1.3	1
9601	Swimming and Sinking Behavior of Warm Water Pelagic Snails. <i>Frontiers in Marine Science</i> , 2020, 7, .	1.2	5
9602	Sequencing the Genome of Indian Flying Fox, Natural Reservoir of Nipah Virus, Using Hybrid Assembly and Conservative Secondary Scaffolding. <i>Frontiers in Microbiology</i> , 2020, 11, 1807.	1.5	3
9603	Phylogenetic Analyses of Glycosyl Hydrolase Family 6 Genes in Tunicates: Possible Horizontal Transfer. <i>Genes</i> , 2020, 11, 937.	1.0	4
9604	Biogeography, phylogenetic relationships and morphological analyses of the South American genus <i>Mutisia</i> L.f. (Asteraceae) shows early connections of two disjunct biodiversity hotspots. <i>Organisms Diversity and Evolution</i> , 2020, 20, 639-656.	0.7	7
9605	Two New Species of <i>Laccaria</i> (Agaricales, Basidiomycota) from Korea. <i>Mycobiology</i> , 2020, 48, 288-295.	0.6	7
9606	The complete chloroplast genome sequence of <i>Monotropa uniflora</i> (Ericaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 3168-3169.	0.2	2

#	ARTICLE	IF	CITATIONS
9607	A review of the damselfly genus <i>Megalestes</i> Selys, 1862 (Insecta: Odonata: Zygoptera: Synlestidae) using integrative taxonomic methods. <i>Zootaxa</i> , 2020, 4851, zootaxa.4851.2.2.	0.2	2
9608	Integrin-alpha-6+ Candidate stem cells are responsible for whole body regeneration in the invertebrate chordate <i>Botrylloides diegensis</i> . <i>Nature Communications</i> , 2020, 11, 4435.	5.8	29
9609	Integrative taxonomy of the new millipede genus <i>Coxobolellus</i> , gen. nov. (Diplopoda : Spirobolida :). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5</i>	0.5	10
9610	Marasmioid rhizomorphs in bird nests: Species diversity, functional specificity, and new species from the tropics. <i>Mycologia</i> , 2020, 112, 1086-1103.	0.8	9
9611	Geographic distributions of <i>Pseudopaludicola boliviana</i> and congeneric long-legged species (Anura: Leiuperinae). <i>Studies on Neotropical Fauna and Environment</i> , 2022, 57, 66-82.	0.5	1
9612	The complete chloroplast genome sequence of <i>Taxillus yadoriki</i> (Loranthaceae): a hemi-parasitic evergreen shrub in East Asia. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 3172-3173.	0.2	3
9613	Intraspecific variations among the chloroplast genomes of <i>Artemisia scoparia</i> (asteraceae) from Pakistan and China. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 3182-3184.	0.2	3
9614	Induction of sexual reproduction reveals the presence of heterothallic <i>Spirogyra</i> strains (Zygnematophyceae, Streptophyta). <i>Phycological Research</i> , 2020, 68, 263-268.	0.8	1
9615	Molecular phylogeny of <i>Diphtherophora</i> de Man, 1880 (Nematoda:). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 422</i>	0.2	0
9616	Molecular phylogeny of Asian pipesnakes, genus <i>Cylindrophis</i> Wagler, 1828 (Squamata:). <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50</i> zootaxa.4851.3.5.	0.2	4
9617	Biphasic Outbreak of Invasive Group A <i>Streptococcus</i> Disease in Eldercare Facility, New Zealand. <i>Emerging Infectious Diseases</i> , 2020, 26, 841-848.	2.0	7
9618	Diversity and ochratoxin A-fumonisin profile of black <i>Aspergilli</i> isolated from grapes in China. <i>World Mycotoxin Journal</i> , 2020, 13, 225-234.	0.8	3
9619	Ultraconserved yet informative for species delimitation: Ultraconserved elements resolve long-standing systematic enigma in Central European bees. <i>Molecular Ecology</i> , 2020, 29, 4203-4220.	2.0	27
9620	Status, morphology, and phylogenetic relationships of <i>lyengaria</i> (Scytosiphonaceae). <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 5</i> <i>Research</i> , 2020, 68, 323-331.	0.8	5
9621	SARS-CoV-2 Polymorphisms and Multisystem Inflammatory Syndrome in Children. <i>Pediatrics</i> , 2020, 146, .	1.0	17
9622	A test of island biogeographic theory applied to estimates of gene flow in a Fijian bird is largely consistent with neutral expectations. <i>Molecular Ecology</i> , 2020, 29, 4059-4073.	2.0	7
9623	Survey of Early-Diverging Lineages of Fungi Reveals Abundant and Diverse Mycoviruses. <i>MBio</i> , 2020, 11, .	1.8	32
9624	The First Mitochondrial Genome for Geastrales (<i>Sphaerobolus stellatus</i>) Reveals Intron Dynamics and Large-Scale Gene Rearrangements of Basidiomycota. <i>Frontiers in Microbiology</i> , 2020, 11, 1970.	1.5	20

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9625	Molecular detection of pathogens in ticks associated with domestic animals from the Colombian Caribbean region. <i>Experimental and Applied Acarology</i> , 2020, 82, 137-150.	0.7	8
9626	The binding mechanism of the virulence factor <i>Streptococcus suis</i> adhesin P subtype to globotetraosylceramide is associated with systemic disease. <i>Journal of Biological Chemistry</i> , 2020, 295, 14305-14324.	1.6	10
9627	Another building block in the plant cell wall: Barley xyloglucan xyloglucosyl transferases link covalently xyloglucan and anionic oligosaccharides derived from pectin. <i>Plant Journal</i> , 2020, 104, 752-767.	2.8	17
9628	Adaptation to the cervical environment is associated with increased antibiotic susceptibility in <i>Neisseria gonorrhoeae</i> . <i>Nature Communications</i> , 2020, 11, 4126.	5.8	51
9629	Cryptic speciation of a pelagic <i>Roseobacter</i> population varying at a few thousand nucleotide sites. <i>ISME Journal</i> , 2020, 14, 3106-3119.	4.4	11
9630	From mainland to islands: colonization history in the tree frog <i>Kurixalus</i> (Anura: Rhacophoridae). <i>Environmental Epigenetics</i> , 2020, 66, 667-675.	0.9	8
9631	The chromosome-level draft genome of <i>Dalbergia odorifera</i> . <i>GigaScience</i> , 2020, 9, .	3.3	21
9632	Fine capsule variation affects bacteriophage susceptibility in <i>Klebsiella pneumoniae</i> ST258. <i>FASEB Journal</i> , 2020, 34, 10801-10817.	0.2	17
9633	Fungicide resistance in <i>Cercospora</i> species causing cercospora leaf blight and purple seed stain of soybean in Argentina. <i>Plant Pathology</i> , 2020, 69, 1678-1694.	1.2	17
9634	Taxonomic evaluation of two similar bent-toed geckos <i>Squamata</i> : 2020, 4830, 186-196.	0.2	4
9635	<i>Canthigaster aziz</i> , a new deep-dwelling toby fish (Tetraodontiformes: Tetraodontidae) from the Red Sea. <i>Zootaxa</i> , 2020, 4834, zootaxa.4834.1.5.	0.2	1
9636	Spider phyllosymbiosis: divergence of widow spider species and their tissues' microbiomes. <i>BMC Evolutionary Biology</i> , 2020, 20, 104.	3.2	14
9637	Rapid size change associated with intra-island evolutionary radiation in extinct Caribbean island-shrews. <i>BMC Evolutionary Biology</i> , 2020, 20, 106.	3.2	8
9638	Population structure and geographical segregation of <i>Cryptosporidium parvum</i> IId subtypes in cattle in China. <i>Parasites and Vectors</i> , 2020, 13, 425.	1.0	15
9639	The Genera of Fungi " G6: <i>Arthrographis</i> , <i>Kramasamuha</i> , <i>Melnikomyces</i> , <i>Thysanoreia</i> , and <i>Verruconis</i> . <i>Fungal Systematics and Evolution</i> , 2020, 6, 1-24.	0.9	13
9641	A haplotype-resolved, <i>de novo</i> genome assembly for the wood tiger moth (<i>Arctia</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	3.3	20
9642	Molecular Characterization of Newcastle Disease Viruses Isolated from Chickens in Tanzania and Ghana. <i>Viruses</i> , 2020, 12, 916.	1.5	17
9643	Phylogenetic reconstruction of <i>Ficus</i> subg. <i>Synoecia</i> and its allies (Moraceae), with implications on the origin of the climbing habit. <i>Taxon</i> , 2020, 69, 927-945.	0.4	7

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9644	Increased resolution of African swine fever virus genome patterns based on profile HMMs of protein domains. <i>Virus Evolution</i> , 2020, 6, veaa044.	2.2	7
9645	Use of Newly Designed Primers for Quantification of Complete Ammonia-Oxidizing (Comammox) Bacterial Clades and Strict Nitrite Oxidizers in the Genus <i>Nitrospira</i> . <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	38
9646	A Revised Sectional Classification of <i>Plukenetia</i> L. (Euphorbiaceae, Acalyphoideae) with Four New Species from South America. <i>Systematic Botany</i> , 2020, 45, 507-536.	0.2	2
9647	<i>Phytophthora acaciivora</i> sp. nov. associated with dying <i>Acacia mangium</i> in Vietnam. <i>Fungal Systematics and Evolution</i> , 2020, 6, 243-252.	0.9	10
9648	Molecular Epidemiology Analysis of SARS-CoV-2 Strains Circulating in Romania during the First Months of the Pandemic. <i>Life</i> , 2020, 10, 152.	1.1	9
9649	A Comparison of Whole Genome Sequencing of SARS-CoV-2 Using Amplicon-Based Sequencing, Random Hexamers, and Bait Capture. <i>Viruses</i> , 2020, 12, 895.	1.5	86
9650	The complete chloroplast genome of <i>Cymbidium longibracteatum</i> (Orchidaceae) and phylogenetic analysis. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2930-2931.	0.2	0
9651	Conserved Genomic Terminals of SARS-CoV-2 as Coevolving Functional Elements and Potential Therapeutic Targets. <i>MSphere</i> , 2020, 5, .	1.3	41
9652	Three redescrptions in <i>Tintinnopsis</i> (Protista: Ciliophora: Tintinnina) from coastal waters of China, with cytology and phylogenetic analyses based on ribosomal RNA genes. <i>BMC Microbiology</i> , 2020, 20, 374.	1.3	6
9653	Characterization and Diversity of 243 Complete Human Papillomavirus Genomes in Cervical Swabs Using Next Generation Sequencing. <i>Viruses</i> , 2020, 12, 1437.	1.5	11
9654	Do mangrove habitats serve as a reservoir for <i>Medicopsis romeroi</i> , a clinically important fungus. <i>Mycological Progress</i> , 2020, 19, 1267-1280.	0.5	2
9655	Horizontally acquired papGII-containing pathogenicity islands underlie the emergence of invasive uropathogenic <i>Escherichia coli</i> lineages. <i>Nature Communications</i> , 2020, 11, 5968.	5.8	42
9656	Resolving the systematics of Richtersiidae by multilocus phylogeny and an integrative redescription of the nominal species for the genus <i>Crenubiotus</i> (Tardigrada). <i>Scientific Reports</i> , 2020, 10, 19418.	1.6	13
9657	The importance of using whole genome sequencing and extended spectrum beta-lactamase selective media when monitoring antimicrobial resistance. <i>Scientific Reports</i> , 2020, 10, 19880.	1.6	27
9658	Physiological and molecular correlates of the screwworm fly attraction to wound and animal odors. <i>Scientific Reports</i> , 2020, 10, 20771.	1.6	3
9659	Phylogenetic comparison of egg transparency in ascidians by hyperspectral imaging. <i>Scientific Reports</i> , 2020, 10, 20829.	1.6	3
9660	Mutation of <i>hilD</i> in a <i>Salmonella</i> Derby lineage linked to swine adaptation and reduced risk to human health. <i>Scientific Reports</i> , 2020, 10, 21539.	1.6	7
9661	Deep Neighbor Information Learning From Evolution Trees for Phylogenetic Likelihood Estimates. <i>IEEE Access</i> , 2020, 8, 220692-220702.	2.6	4

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9662	Complete Genome Sequences of Four Natural <i>Pseudomonas</i> Isolates That Catabolize a Wide Range of Aromatic Compounds Relevant to Lignin Valorization. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	1
9663	The Neuromodulator-Encoding <i>sadA</i> Gene Is Widely Distributed in the Human Skin Microbiome. <i>Frontiers in Microbiology</i> , 2020, 11, 573679.	1.5	9
9664	RNAi-Mediated Suppression of <i>Laccase2</i> Impairs Cuticle Tanning and Molting in the Cotton Boll Weevil (<i>Anthonomus grandis</i>). <i>Frontiers in Physiology</i> , 2020, 11, 591569.	1.3	8
9665	Reassessment of molecular and morphological variation within the <i>Anagrus atomus</i> species complex (Hymenoptera: Mymaridae): egg parasitoids of leafhoppers (Hemiptera: Cicadellidae) in Europe and North America. <i>Journal of Natural History</i> , 2020, 54, 1735-1758.	0.2	6
9666	Phylogenetic relationships within <i>Pyrenodesmia</i> sensu lato and the role of pigments in its taxonomic interpretation. <i>Journal of Systematics and Evolution</i> , 2020, 59, 454.	1.6	6
9667	The 287,403 bp Mitochondrial Genome of Ectomycorrhizal Fungus <i>Tuber calosporum</i> Reveals Intron Expansion, tRNA Loss, and Gene Rearrangement. <i>Frontiers in Microbiology</i> , 2020, 11, 591453.	1.5	11
9668	Dissection for Floral Micromorphology and Plastid Genome of Valuable Medicinal Borages <i>Arnebia</i> and <i>Lithospermum</i> (Boraginaceae). <i>Frontiers in Plant Science</i> , 2020, 11, 606463.	1.7	16
9669	Survey and Sequence Characterization of Bovine Mastitis-Associated <i>Escherichia coli</i> in Dairy Herds. <i>Frontiers in Veterinary Science</i> , 2020, 7, 582297.	0.9	7
9670	Diversity within <i>Aspergillus niger</i> Clade and Description of a New Species: <i>Aspergillus vinaceus</i> sp. nov.. <i>Journal of Fungi</i> (Basel, Switzerland), 2020, 6, 371.	1.5	17
9671	Size Matters: An Evaluation of the Molecular Basis of Ontogenetic Modifications in the Composition of <i>Bothrops jararacussu</i> Snake Venom. <i>Toxins</i> , 2020, 12, 791.	1.5	18
9672	First identification of dopamine receptors in pikeperch, <i>Sander lucioperca</i> , during the pre-ovulatory period. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2020, 36, 100747.	0.4	0
9673	Under fire-simultaneous volatilome and transcriptome analysis unravels fine-scale responses of tansy chemotypes to dual herbivore attack. <i>BMC Plant Biology</i> , 2020, 20, 551.	1.6	12
9674	Species Delimitation of the <i>Eisenia nordenskioldi</i> Complex (Oligochaeta, Lumbricidae) Using Transcriptomic Data. <i>Frontiers in Genetics</i> , 2020, 11, 598196.	1.1	14
9675	Systematics and Multi-Gene Phylogeny of the Subfamily Nothoholostichinae (Ciliophora, Hypotrichia), With Integrative Description of a New Marine Species <i>Nothoholosticha luporinii</i> n. sp.. <i>Frontiers in Marine Science</i> , 2020, 7, .	1.2	6
9676	Novel Contributions to the Taxonomy of the Ciliates Genus <i>Euplotes</i> (Ciliophora, Euplotida): Redescription of Two Poorly Known Species, With a Brief Note on the Distributions of This Genus in Coastal Waters of Southern China. <i>Frontiers in Marine Science</i> , 2020, 7, .	1.2	4
9677	Comparative Genomic Analysis of Ochratoxin A Biosynthetic Cluster in Producing Fungi: New Evidence of a Cyclase Gene Involvement. <i>Frontiers in Microbiology</i> , 2020, 11, 581309.	1.5	19
9678	Dinoflagellate Host Chloroplasts and Mitochondria Remain Functional During Amoebophrya Infection. <i>Frontiers in Microbiology</i> , 2020, 11, 600823.	1.5	6
9679	Cultivation-Independent Analysis of the Bacterial Community Associated With the Calcareous Sponge <i>Clathrina clathrus</i> and Isolation of <i>Poriferisphaera corsica</i> Gen. Nov., Sp. Nov., Belonging to the Barely Studied Class Phycisphaerae in the Phylum Planctomycetes. <i>Frontiers in Microbiology</i> , 2020, 11, 602250.	1.5	23

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9680	Morphological and Molecular Characterization of <i>Kochinema farodai</i> Baqri and Bohra, 2001 (<i>Dorylaimida</i> : <i>Nordiidae</i>) from California, with the First Molecular Study and an Updated Taxonomy of the Genus. <i>Animals</i> , 2020, 10, 2300.	1.0	1
9681	Distribution of Important Probiotic Genes and Identification of the Biogenic Amines Produced by <i>Lactobacillus acidophilus</i> PNW3. <i>Foods</i> , 2020, 9, 1840.	1.9	5
9682	An Overview of Genomics, Phylogenomics and Proteomics Approaches in Ascomycota. <i>Life</i> , 2020, 10, 356.	1.1	12
9683	Establishment of a Challenge Model for Sheeppox Virus Infection. <i>Microorganisms</i> , 2020, 8, 2001.	1.6	6
9684	Identification and Characterization of 33 <i>Bacillus cereus</i> sensu lato Isolates from Agricultural Fields from Eleven Widely Distributed Countries by Whole Genome Sequencing. <i>Microorganisms</i> , 2020, 8, 2028.	1.6	11
9685	Molecular Phylogeny and Phylogeography of <i>Potentilla multifida</i> L. agg. (<i>Rosaceae</i>) in Northern Eurasia with Special Focus on Two Rare and Critically Endangered Endemic Species, <i>P. vulgarica</i> and <i>P. eversmanniana</i> . <i>Plants</i> , 2020, 9, 1798.	1.6	2
9686	Metagenomic insights into the metabolism and evolution of a new Thermoplasmata order (<i>Candidatus</i> Gimiplasmatales). <i>Environmental Microbiology</i> , 2021, 23, 3695-3709.	1.8	21
9687	Dissecting protein domain variability in the core RNA interference machinery of five insect orders. <i>RNA Biology</i> , 2021, 18, 1653-1681.	1.5	16
9688	The complete chloroplast genome of <i>Coelogyne barbata</i> (<i>Orchidaceae</i>), a rare and ornamental orchid. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 3728-3729.	0.2	0
9689	Benchmarking Orthogroup Inference Accuracy: Revisiting Orthobench. <i>Genome Biology and Evolution</i> , 2020, 12, 2258-2266.	1.1	23
9690	<i>Roussoella guttulata</i> (<i>Roussoellaceae</i> , <i>Pleosporales</i>), a novel bambusicolous ascomycete from Thailand. <i>Phytotaxa</i> , 2020, 471, 221-233.	0.1	6
9691	Metapangenomics of the oral microbiome provides insights into habitat adaptation and cultivar diversity. <i>Genome Biology</i> , 2020, 21, 293.	3.8	46
9692	Using target enrichment sequencing to study the higher-level phylogeny of the largest lichen-forming fungi family: <i>Parmeliaceae</i> (<i>Ascomycota</i>). <i>IMA Fungus</i> , 2020, 11, 27.	1.7	7
9693	Surface Microornamentation of Demosponge <i>Sterreraster</i> Spicules, Phylogenetic and Paleontological Implications. <i>Frontiers in Marine Science</i> , 2020, 7, .	1.2	5
9694	Simultaneous Genome Sequencing of <i>Prosthecochloris ethylica</i> and <i>Desulfuromonas acetoxidans</i> within a Syntrophic Mixture Reveals Unique Pili and Protein Interactions. <i>Microorganisms</i> , 2020, 8, 1939.	1.6	7
9695	Whole Genome Characterization and Evolutionary Analysis of G1P[8] Rotavirus A Strains during the Pre- and Post-Vaccine Periods in Mozambique (2012–2017). <i>Pathogens</i> , 2020, 9, 1026.	1.2	4
9696	Fasciclin-Like Arabinogalactan-Protein 16 (FLA16) Is Required for Stem Development in <i>Arabidopsis</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 615392.	1.7	28
9697	Simultaneous Quantification of <i>Vibrio metoecus</i> and <i>Vibrio cholerae</i> with Its O1 Serogroup and Toxigenic Subpopulations in Environmental Reservoirs. <i>Pathogens</i> , 2020, 9, 1053.	1.2	8

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9698	FireProtASR: A Web Server for Fully Automated Ancestral Sequence Reconstruction. Briefings in Bioinformatics, 2021, 22, .	3.2	37
9699	Taxonomy and Molecular Phylogeny of Three Species of Scuticociliates From China: <i>Citrithrix smalli</i> gen. nov., sp. nov., <i>Homalogastra binucleata</i> sp. nov. and <i>Uronema orientalis</i> Pan et al., 2015 (Protozoa), Tj ETQq1 1.0.784314 rgBT /Overlock	1.2	3
9700	Discovery of Novel Biosynthetic Gene Cluster Diversity From a Soil Metagenomic Library. Frontiers in Microbiology, 2020, 11, 585398.	1.5	16
9701	Phylogenetics and taxonomy of Telimenaceae (Phyllachorales) from Central America. Mycological Progress, 2020, 19, 1587-1599.	0.5	3
9702	Nonadaptive host-use specificity in tropical armored scale insects. Ecology and Evolution, 2020, 10, 12910-12919.	0.8	9
9703	Foliar fungal endophyte community structure is independent of phylogenetic relatedness in an Asteraceae common garden. Ecology and Evolution, 2020, 10, 13895-13912.	0.8	10
9704	Towards a complete phylogeny of African Melastomateae: Systematics of <i>Dissotis</i> and allies (Melastomataceae). Taxon, 2020, 69, 946-991.	0.4	14
9705	Phylogenomics supported by geometric morphometrics reveals delimitation of sexual species within the polyploid apomictic <i>Ranunculus auricomus</i> complex (Ranunculaceae). Taxon, 2020, 69, 1191-1220.	0.4	22
9706	Downy mildew of lavender caused by <i>Peronospora belbahrii</i> in Israel. Mycological Progress, 2020, 19, 1537-1543.	0.5	4
9707	The complete chloroplast genome of <i>Polygonatum odoratum</i> (Liliaceae), an endemic medicinal herb. Mitochondrial DNA Part B: Resources, 2020, 5, 3723-3724.	0.2	0
9708	The complete chloroplast genome of a medicinal plant, <i>Abutilon theophrasti</i> Medik. (Malvaceae). Mitochondrial DNA Part B: Resources, 2020, 5, 3759-3760.	0.2	1
9709	The complete mitochondrial genome of <i>Pseudoxenodon stejnegeri</i> (Squamata: Colubridae:) Tj ETQq1 1.0.784314 rgBT /Overlock	0.2	0
9710	The relationship between molar morphology and ecology within <i>Neotoma</i> . Journal of Mammalogy, 2020, 101, 1711-1726.	0.6	2
9711	Evolutionary fine-tuning of background-matching camouflage among geographical populations in the sandy beach tiger beetle. Proceedings of the Royal Society B: Biological Sciences, 2020, 287, 20202315.	1.2	12
9712	Using in silico predicted ancestral genomes to improve the efficiency of paleogenome reconstruction. Ecology and Evolution, 2020, 10, 12700-12709.	0.8	4
9713	Additions to the genus <i>Gimesia</i> : description of <i>Gimesia alba</i> sp. nov., <i>Gimesia algae</i> sp. nov., <i>Gimesia aquarii</i> sp. nov., <i>Gimesia aquatilis</i> sp. nov., <i>Gimesia fumaroli</i> sp. nov. and <i>Gimesia panarensis</i> sp. nov., isolated from aquatic habitats of the Northern Hemisphere. Antonie Van Leeuwenhoek, 2020, 113, 1999-2018.	0.7	41
9714	Description of a new marine predatory nematode <i>Latronema dyngi</i> sp. nov. (Nematoda, Chromadorida), Tj ETQq0 0.0 rgBT /Overlock	0.3	5
9715	The santalene synthase from <i>Cinnamomum camphora</i> : Reconstruction of a sesquiterpene synthase from a monoterpene synthase. Archives of Biochemistry and Biophysics, 2020, 695, 108647.	1.4	10

#	ARTICLE	IF	CITATIONS
9716	Genomic RNA Elements Drive Phase Separation of the SARS-CoV-2 Nucleocapsid. <i>Molecular Cell</i> , 2020, 80, 1078-1091.e6.	4.5	255
9717	A chromosome-scale genome assembly of a diploid alfalfa, the progenitor of autotetraploid alfalfa. <i>Horticulture Research</i> , 2020, 7, 194.	2.9	25
9718	A chromosome-scale reference genome of <i>Lobularia maritima</i> , an ornamental plant with high stress tolerance. <i>Horticulture Research</i> , 2020, 7, 197.	2.9	6
9719	Global emergence and evolutionary dynamics of bluetongue virus. <i>Scientific Reports</i> , 2020, 10, 21677.	1.6	26
9720	Complete mitochondrial genome of <i>Pterodecta felderi</i> (Lepidoptera: Callidulidae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 3730-3732.	0.2	1
9721	<i>PhyloWGA</i> : chromosome-aware phylogenetic interrogation of whole genome alignments. <i>Bioinformatics</i> , 2021, 37, 1923-1925.	1.8	1
9722	Phylogenomic Analysis of <i>Wolbachia</i> Strains Reveals Patterns of Genome Evolution and Recombination. <i>Genome Biology and Evolution</i> , 2020, 12, 2508-2520.	1.1	19
9723	Topology-dependent asymmetry in systematic errors affects phylogenetic placement of Ctenophora and Xenacoelomorpha. <i>Science Advances</i> , 2020, 6, .	4.7	102
9724	The evolution of a tropical biodiversity hotspot. <i>Science</i> , 2020, 370, 1343-1348.	6.0	179
9725	Genome Sequences of <i>Allochromatium palmeri</i> and <i>Allochromatium humboldtianum</i> Expand the <i>Allochromatium</i> Family Tree of Purple Sulfur Photosynthetic Bacteria within the Gammaproteobacteria and Further Refine the Genus. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	1
9726	Bioluminescence in an Undescribed Species of Carnivorous Sponge (Cladorhizidae) From the Deep Sea. <i>Frontiers in Marine Science</i> , 2020, 7, .	1.2	10
9727	Purification and Characterization of Two Novel Laccases from <i>Peniophora lycii</i> . <i>Journal of Fungi</i> (Basel, Switzerland), 2020, 6, 340.	1.5	12
9728	Current Status and Future Strategies to Increase Secondary Metabolite Production from Cyanobacteria. <i>Microorganisms</i> , 2020, 8, 1849.	1.6	21
9729	Genotyping of <i>Francisella tularensis</i> subsp. <i>holarctica</i> from Hares in Germany. <i>Microorganisms</i> , 2020, 8, 1932.	1.6	7
9730	Highly Pathogenic Avian Influenza Clade 2.3.4.4b Subtype H5N8 Virus Isolated from Mandarin Duck in South Korea, 2020. <i>Viruses</i> , 2020, 12, 1389.	1.5	30
9731	Increased HIV Subtype Diversity Reflecting Demographic Changes in the HIV Epidemic in New South Wales, Australia. <i>Viruses</i> , 2020, 12, 1402.	1.5	4
9732	Genome-wide identification of Argonautes in Solanaceae with emphasis on potato. <i>Scientific Reports</i> , 2020, 10, 20577.	1.6	10
9733	The complete chloroplast genome of <i>Mitreola yangchunensis</i> (Loganiaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 3794-3795.	0.2	0

#	ARTICLE	IF	CITATIONS
9734	Prokaryotic Community Compositions of the Hypersaline Sediments of Tuz Lake Demonstrated by Cloning and High-Throughput Sequencing. <i>Microbiology</i> , 2020, 89, 756-768.	0.5	10
9735	Organic Matter Composition at Ocean Station Papa Affects Its Bioavailability, Bacterioplankton Growth Efficiency and the Responding Taxa. <i>Frontiers in Marine Science</i> , 2021, 7, .	1.2	17
9736	<i>Peronosclerospora australiensis</i> is a synonym of <i>P. maydis</i> , which is widespread on Sumatra, and distinct from the most prevalent Java maize downy mildew pathogen. <i>Mycological Progress</i> , 2020, 19, 1309-1315.	0.5	8
9737	Parallel evolution in the emergence of highly pathogenic avian influenza A viruses. <i>Nature Communications</i> , 2020, 11, 5511.	5.8	23
9738	Distribution, autecology, genetic characterization, and conservation of the Western Mediterranean endemic dragonfly <i>Orthetrum nitidinerve</i> (Selys, 1841): insights from Italy. <i>International Journal of Odonatology</i> , 2020, 23, 405-422.	0.5	1
9739	A new species of <i>Clavariadelphus</i> (<i>Basidiomycota</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T <i>Phytotaxa</i> , 2020, 447, 61-67.	0.1	1
9740	<i>Sinosenecio ovatifolius</i> (Asteraceae), a new species from Guangxi, China. <i>Phytotaxa</i> , 2020, 460, 149-159.	0.1	6
9741	Genomic differences between the new <i>Fusarium oxysporum</i> f. sp. <i>apii</i> (Foa) race 4 on celery, the less virulent Foa races 2 and 3, and the avirulent on celery f. sp. <i>coriandrii</i> . <i>BMC Genomics</i> , 2020, 21, 730.	1.2	12
9742	Towards unravelling <i>Wolbachia</i> global exchange: a contribution from the <i>Bicyclus</i> and <i>Mylothris</i> butterflies in the Afrotropics. <i>BMC Microbiology</i> , 2020, 20, 319.	1.3	9
9743	Integrated omics unveil the secondary metabolic landscape of a basal dinoflagellate. <i>BMC Biology</i> , 2020, 18, 139.	1.7	17
9744	Dieback of <i>Euonymus alatus</i> (Celastraceae) Caused by <i>Cytospora haidianensis</i> sp. nov. in China. <i>Forests</i> , 2020, 11, 524.	0.9	9
9745	Molecular Phylogeny and Morphology of <i>Amphisphaeria</i> (= <i>Lepteutypa</i>) (<i>Amphisphaeriaceae</i>). <i>Journal of Fungi</i> (Basel, Switzerland), 2020, 6, 174.	1.5	13
9746	The Draft Genome of Red Lechwe, <i>Kobus lechwe lechwe</i> . <i>Frontiers in Genetics</i> , 2020, 11, 582638.	1.1	0
9747	Integrative taxonomy confirms two new West-Palaeartic species allied with <i>Chrysotoxum vernale</i> Loew, 1841 (Diptera: Syrphidae). <i>Organisms Diversity and Evolution</i> , 2020, 20, 821-833.	0.7	7
9748	The secrets of Sobek – A crocodile mummy mitogenome from ancient Egypt. <i>Journal of Archaeological Science: Reports</i> , 2020, 33, 102483.	0.2	4
9749	Portlandia-dominated Communities in the Arctic: Taxonomic Composition and Structure along the Geographical Gradient. <i>Doklady Earth Sciences</i> , 2020, 493, 645-648.	0.2	1
9750	Four myriapod relatives – but who are sisters? No end to debates on relationships among the four major myriapod subgroups. <i>BMC Evolutionary Biology</i> , 2020, 20, 144.	3.2	13
9751	The Transcriptome of <i>Cunninghamia lanceolata</i> male/female cone reveal the association between MIKC MADS-box genes and reproductive organs development. <i>BMC Plant Biology</i> , 2020, 20, 508.	1.6	15

#	ARTICLE	IF	CITATIONS
9752	Naming the untouchable “ environmental sequences and niche partitioning as taxonomical evidence in fungi. IMA Fungus, 2020, 11, 23.	1.7	15
9753	Genotypic and Phenotypic Characterization of Incompatibility Group FIB Positive Salmonella enterica Serovar Typhimurium Isolates from Food Animal Sources. Genes, 2020, 11, 1307.	1.0	8
9754	Yeast communities associated with cacti in Brazil and the description of <i>Kluyveromyces starmeri</i> sp. nov. based on phylogenomic analyses. Yeast, 2020, 37, 625-637.	0.8	6
9755	Predicted AS3MT Proteins Methylate Arsenic and Support Two Major Phylogenetic AS3MT Groups. Chemical Research in Toxicology, 2020, 33, 3041-3047.	1.7	13
9756	Resource conservation manifests in the genetic code. Science, 2020, 370, 683-687.	6.0	44
9757	Red Imported Fire Ant (<i>Solenopsis invicta</i>) Chemosensory Proteins Are Expressed in Tissue, Developmental, and Caste-Specific Patterns. Frontiers in Physiology, 2020, 11, 585883.	1.3	8
9758	Paratuberculosis in Captive Scimitar-Horned Oryxes (<i>Oryx dammah</i>). Animals, 2020, 10, 1949.	1.0	3
9759	Transcriptome Sequencing of the Striped Cucumber Beetle, <i>Acalymma vittatum</i> (F.), Reveals Numerous Sex-Specific Transcripts and Xenobiotic Detoxification Genes. BioTech, 2020, 9, 21.	1.3	7
9760	Molecular Epidemiology of Multi-Drug Resistant <i>Pseudomonas aeruginosa</i> Isolates from Hospitalized Patients in Greece. Microorganisms, 2020, 8, 1652.	1.6	3
9761	Comparative Analyses of the Chloroplast Genomes of Patchouli Plants and Their Relatives in <i>Pogostemon</i> (Lamiaceae). Plants, 2020, 9, 1497.	1.6	6
9762	The draft genome of the blood pheasant (<i>Thaginis cruentus</i>): Phylogeny and high-altitude adaptation. Ecology and Evolution, 2020, 10, 11440-11452.	0.8	1
9763	Morphometric and genetic evidence for four species of gentoo penguin. Ecology and Evolution, 2020, 10, 13836-13846.	0.8	12
9764	Gene Loss and Acquisition in Lineages of <i>Pseudomonas aeruginosa</i> Evolving in Cystic Fibrosis Patient Airways. MBio, 2020, 11, .	1.8	31
9765	Phylogenomics of the Andean Tetraploid Clade of the American Amaryllidaceae (Subfamily) <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 T</i> Frontiers in Plant Science, 2020, 11, 582422.	1.7	9
9766	Coupling Transcriptomics and Behaviour to Unveil the Olfactory System of <i>Spodoptera exigua</i> Larvae. Journal of Chemical Ecology, 2020, 46, 1017-1031.	0.9	13
9767	Rapid colour shift by reproductive character displacement in <i>Cupido</i> butterflies. Molecular Ecology, 2020, 29, 4942-4955.	2.0	10
9768	Taxonomic assessment and distribution of common toads (<i>Bufo</i> and <i>B. verrucosissimus</i>) in Turkey based on morphological and molecular data. Amphibia - Reptilia, 2020, 41, 399-411.	0.1	7
9769	Integrative systematics reveals the new land-snail genus <i>Taphrenalla</i> (Eupulmonata: Ariophantidae) with a description of nine new species from Thailand. Contributions To Zoology, 2020, 90, 21-69.	0.2	13

#	ARTICLE	IF	CITATIONS
9770	Reassessment of the moth genus <i>Bacotoma</i> , with a new species from Hainan Island (Lepidoptera: Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	0.2	4
9771	Molecular phylogeny and classification of <i>Chelidurella</i> Verhoeff, stat. restit. (Dermaptera: Tj ETQq1 1 0.784314 rgBT/Overlock 10 Tf 50	0.2	4
9772	Indo-European phylogenetics with R. Indo-European Linguistics, 2020, 8, 110-180.	0.3	4
9773	Comparative mitochondrial phylogeography of two legless lizards (Pygopodidae) from Queensland's fragmented woodlands. Israel Journal of Ecology and Evolution, 2020, 66, 142-150.	0.2	2
9774	Comparative Genome Analysis Reveals the Molecular Basis of Niche Adaptation of <i>Staphylococcus epidermidis</i> Strains. Frontiers in Genetics, 2020, 11, 566080.	1.1	5
9775	Phylogeny, Diversification Rate, and Divergence Time of <i>Agave sensu lato</i> (Asparagaceae), a Group of Recent Origin in the Process of Diversification. Frontiers in Plant Science, 2020, 11, 536135.	1.7	22
9776	Complete Plastid Genome Sequencing of Eight Species from <i>Hansenia</i> , <i>Haplosphaera</i> and <i>Sinodielsia</i> (Apiaceae): Comparative Analyses and Phylogenetic Implications. Plants, 2020, 9, 1523.	1.6	18
9777	Phylogeny, Taxonomy, and Biogeography of <i>Pterocarya</i> (Juglandaceae). Plants, 2020, 9, 1524.	1.6	15
9778	Proposal for a subdivision of the family Psathyrellaceae based on a taxon-rich phylogenetic analysis with iterative multigene guide tree. Mycological Progress, 2020, 19, 1151-1265.	0.5	24
9779	Comparative Genome Analysis of 33 <i>Chlamydia</i> Strains Reveals Characteristic Features of <i>Chlamydia Psittaci</i> and Closely Related Species. Pathogens, 2020, 9, 899.	1.2	24
9780	A Nationwide Study about the Dispersal Patterns of the Predominant HIV-1 Subtypes A1 and B in Greece: Inference of the Molecular Transmission Clusters. Viruses, 2020, 12, 1183.	1.5	8
9781	Heritability of the HIV-1 reservoir size and decay under long-term suppressive ART. Nature Communications, 2020, 11, 5542.	5.8	5
9782	Carbapenemase-Producing Gram-Negative Bacteria from American Crows in the United States. Antimicrobial Agents and Chemotherapy, 2020, 65, .	1.4	7
9783	Genome Sequences of Four <i>Shigella boydii</i> Strains Representative of the Major <i>S. boydii</i> Clades. Microbiology Resource Announcements, 2020, 9, .	0.3	1
9784	Evolution of Transmissible Gastroenteritis Virus (TGEV): A Codon Usage Perspective. International Journal of Molecular Sciences, 2020, 21, 7898.	1.8	14
9785	Population Genomic Analysis of <i>Mycoplasma bovis</i> Elucidates Geographical Variations and Genes associated with Host-Types. Microorganisms, 2020, 8, 1561.	1.6	13
9786	<i>Gambierdiscus</i> and <i>Fukuyoa</i> as potential indicators of ciguatera risk in the Balearic Islands. Harmful Algae, 2020, 99, 101913.	2.2	27
9787	Mitochondrial genome of <i>Cipangopaludina japonica</i> (Gastropoda: Viviparidae) with a tRNA gene rearrangement. Mitochondrial DNA Part B: Resources, 2020, 5, 1340-1341.	0.2	1

#	ARTICLE	IF	CITATIONS
9788	The complete chloroplast genome sequence of <i>Sauropus spatulifolius</i> Beille. Mitochondrial DNA Part B: Resources, 2020, 5, 1703-1704.	0.2	2
9789	Complete chloroplast genome of the endangered <i>Corybas taliensis</i> (Orchidaceae), a plant species with extremely small populations endemic to China. Mitochondrial DNA Part B: Resources, 2020, 5, 1884-1885.	0.2	3
9790	Understanding the Early Evolutionary Stages of a Tandem <i>Drosophilamelanogaster</i> -Specific Gene Family: A Structural and Functional Population Study. Molecular Biology and Evolution, 2020, 37, 2584-2600.	3.5	12
9791	No evidence for distinct types in the evolution of SARS-CoV-2. Virus Evolution, 2020, 6, veaa034.	2.2	85
9792	To bee or not to bee: The <i>raison d'être</i> ™ of toxic secondary compounds in the pollen of Boraginaceae. Functional Ecology, 2020, 34, 1345-1357.	1.7	12
9793	Genetic Diversity, Compartmentalization, and Age of HIV Proviruses Persisting in CD4 ⁺ T Cell Subsets during Long-Term Combination Antiretroviral Therapy. Journal of Virology, 2020, 94, .	1.5	21
9794	Genome Sequence of the Acidophilic Nonsulfur Purple Photosynthetic Alphaproteobacterium <i>Rhodovastum atsumiense</i> , a Divergent Member of the Acetobacteraceae Family. Microbiology Resource Announcements, 2020, 9, .	0.3	3
9795	Plasmids Shaped the Recent Emergence of the Major Nosocomial Pathogen <i>Enterococcus faecium</i> . MBio, 2020, 11, .	1.8	91
9796	Two new species of <i>Termitomyces</i> (Agaricales, Lyophyllaceae) from China and Thailand. Phytotaxa, 2020, 439, .	0.1	4
9797	Diversity trapped in cages: Revision of <i>Blumenavia</i> MÅ¶ller (Clathraceae, Basidiomycota) reveals three hidden species. PLoS ONE, 2020, 15, e0232467.	1.1	8
9798	Comparative Genomic Analysis Provides Insights into the Phylogeny, Resistome, Virulome, and Host Adaptation in the Genus <i>Ewingella</i> . Pathogens, 2020, 9, 330.	1.2	7
9799	Shedding light: a phylotranscriptomic perspective illuminates the origin of photosymbiosis in marine bivalves. BMC Evolutionary Biology, 2020, 20, 50.	3.2	11
9800	Comparative genomics in infectious disease. Current Opinion in Microbiology, 2020, 53, 61-70.	2.3	11
9801	High-throughput sequencing of litter and moss eDNA reveals a positive correlation between the diversity of Apicomplexa and their invertebrate hosts across alpine habitats. Soil Biology and Biochemistry, 2020, 147, 107837.	4.2	15
9802	Genomic analysis of fluoroquinolone-susceptible phylogenetic group B2 extraintestinal pathogenic <i>Escherichia coli</i> causing infections in cats. Veterinary Microbiology, 2020, 245, 108685.	0.8	12
9803	The first case of microsporidiosis in <i>Paramecium</i> . Parasitology, 2020, 147, 957-971.	0.7	12
9804	Genetic diversity, population structure, and relationships of apricot (<i>Prunus</i>) based on restriction site-associated DNA sequencing. Horticulture Research, 2020, 7, 69.	2.9	26
9805	Evolution of Sequence-Diverse Disordered Regions in a Protein Family: Order within the Chaos. Molecular Biology and Evolution, 2020, 37, 2155-2172.	3.5	20

#	ARTICLE	IF	CITATIONS
9806	Hemiptera phylogenomic resources: Tree-based orthology prediction and conserved exon identification. <i>Molecular Ecology Resources</i> , 2020, 20, 1346-1360.	2.2	5
9807	Metagenome Mining Reveals Hidden Genomic Diversity of Pelagimyophages in Aquatic Environments. <i>MSystems</i> , 2020, 5, .	1.7	23
9808	Epidemiological and Genomic Characterization of <i>Campylobacter jejuni</i> Isolates from a Foodborne Outbreak at Hangzhou, China. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3001.	1.8	33
9809	Feasibility of Known RNA Polymerase Inhibitors as Anti-SARS-CoV-2 Drugs. <i>Pathogens</i> , 2020, 9, 320.	1.2	26
9810	Repurposing a chemosensory macromolecular machine. <i>Nature Communications</i> , 2020, 11, 2041.	5.8	38
9811	The evolution of <i>Synchaetidae</i> (Rotifera: Monogononta) with a focus on <i>Synchaeta</i> : An integrative approach combining molecular and morphological data. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2020, 58, 823-857.	0.6	7
9812	A Fog-Irrigated Soil Substrate System Unifies and Optimizes Cyanobacterial Biocrust Inoculum Production. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	10
9813	The <i>Helvella corium</i> species aggregate in Nordic countries – phylogeny and species delimitation. <i>Fungal Systematics and Evolution</i> , 2020, 5, 169-186.	0.9	6
9814	Genomics of New Ciliate Lineages Provides Insight into the Evolution of Obligate Anaerobiosis. <i>Current Biology</i> , 2020, 30, 2037-2050.e6.	1.8	48
9815	Comparative analysis of phenolic compound metabolism among tea plants in the section <i>Thea</i> of the genus <i>Camellia</i> . <i>Food Research International</i> , 2020, 135, 109276.	2.9	24
9816	A protracted iGAS outbreak in a long-term care facility 2014–2015: control measures and the use of whole-genome sequencing. <i>Journal of Hospital Infection</i> , 2020, 105, 70-77.	1.4	1
9817	Resolving complicated relationships of the <i>Panax bipinnatifidus</i> complex in southwestern China by RAD-seq data. <i>Molecular Phylogenetics and Evolution</i> , 2020, 149, 106851.	1.2	12
9818	Barcoding helps threatened species: the case of <i>Iris marsica</i> (Iridaceae) from the protected areas of the Abruzzo (Central Italy). <i>Plant Biosystems</i> , 2020, 154, 961-972.	0.8	8
9819	The complete chloroplast genome of <i>Epimedium rhizomatosum</i> (Berberidaceae), an endemic plant species to China. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1886-1887.	0.2	1
9820	Tetracycline-inactivating enzymes from environmental, human commensal, and pathogenic bacteria cause broad-spectrum tetracycline resistance. <i>Communications Biology</i> , 2020, 3, 241.	2.0	97
9821	Bambusicolous <i>Fomitiporia</i> revisited: multilocus phylogeny reveals a clade of host-exclusive species. <i>Mycologia</i> , 2020, 112, 633-648.	0.8	8
9822	Closely related dinoflagellate species in vastly different habitats – an example of a marine–freshwater transition. <i>European Journal of Phycology</i> , 2020, 55, 478-489.	0.9	10
9823	Complete mitochondrial genome of <i>Gymnocypris waddellii</i> (Cypriniformes: Cyprinidae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1874-1875.	0.2	1

#	ARTICLE	IF	CITATIONS
9824	Chromosome-level genome assembly of a cyprinid fish <i>Onychostoma macrolepis</i> by integration of nanopore sequencing, Bionano and Hi-C technology. <i>Molecular Ecology Resources</i> , 2020, 20, 1361-1371.	2.2	27
9825	Large-scale DNA-based survey of frogs in Amazonia suggests a vast underestimation of species richness and endemism. <i>Journal of Biogeography</i> , 2020, 47, 1781-1791.	1.4	60
9826	Extended-Spectrum-β-Lactamase- and Plasmid AmpC-Producing <i>Escherichia coli</i> Causing Community-Onset Bloodstream Infection: Association of Bacterial Clones and Virulence Genes with Septic Shock, Source of Infection, and Recurrence. <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	1.4	17
9827	Two new foliicolous species of <i>Strigula</i> (Strigulaceae, Strigulales) in Korea offer insight in phorophyte-dependent variation of thallus morphology. <i>Phytotaxa</i> , 2020, 443, 1-12.	0.1	7
9828	Plant terpenoid metabolism co-opts a component of the cell wall biosynthesis machinery. <i>Nature Chemical Biology</i> , 2020, 16, 740-748.	3.9	67
9829	Agricultural intensification and the evolution of host specialism in the enteric pathogen <i>Campylobacter jejuni</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 11018-11028.	3.3	50
9830	The phylogenetic placement of a new species of <i>Belemia</i> in Nyctaginaceae, and the first plastome description for the genus. <i>Systematics and Biodiversity</i> , 2020, 18, 328-337.	0.5	0
9831	Prevalence of <i>Phytophthora</i> species in macadamia orchards in Australia and their ability to cause stem canker. <i>Plant Pathology</i> , 2020, 69, 1270-1280.	1.2	16
9832	Commensal Bacteria Impact a Protozoan's Integration into the Murine Gut Microbiota in a Dietary Nutrient-Dependent Manner. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	15
9833	Spiralian Genomes Reveal Gene Family Expansions Associated with Adaptation to Freshwater. <i>Journal of Molecular Evolution</i> , 2020, 88, 463-472.	0.8	4
9834	Investigating the genomic landscape of novel coronavirus (2019-nCoV) to identify non-synonymous mutations for use in diagnosis and drug design. <i>Journal of Clinical Virology</i> , 2020, 128, 104441.	1.6	27
9835	Tools for successful proliferation: diverse strategies of nutrient acquisition by a benthic cyanobacterium. <i>ISME Journal</i> , 2020, 14, 2164-2178.	4.4	33
9836	Allele-aware chromosome-level genome assembly and efficient transgene-free genome editing for the autotetraploid cultivated alfalfa. <i>Nature Communications</i> , 2020, 11, 2494.	5.8	224
9837	Precise phylogenetic analysis of microbial isolates and genomes from metagenomes using PhyloPhlAn 3.0. <i>Nature Communications</i> , 2020, 11, 2500.	5.8	368
9838	The genome of Mekong tiger perch (<i>Datnioides undecimradiatus</i>) provides insights into the phylogenetic position of Lobotiformes and biological conservation. <i>Scientific Reports</i> , 2020, 10, 8164.	1.6	3
9839	Positive epistasis between viral polymerase and the 3' untranslated region of its genome reveals the epidemiologic fitness of dengue virus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 11038-11047.	3.3	22
9840	Guppy Y Chromosome Integrity Maintained by Incomplete Recombination Suppression. <i>Genome Biology and Evolution</i> , 2020, 12, 965-977.	1.1	34
9841	Diversity and evolution of bacterial bioluminescence genes in the global ocean. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa018.	1.5	14

#	ARTICLE	IF	CITATIONS
9842	Emergence of Enteroaggregative <i>Escherichia coli</i> within the ST131 Lineage as a Cause of Extraintestinal Infections. <i>MBio</i> , 2020, 11, .	1.8	22
9843	<i>Akanthomyces neocoleopterorum</i> , a new verticillium-like species. <i>Phytotaxa</i> , 2020, 432, 119-124.	0.1	8
9844	A new velvet gecko (<i>Oedura</i> : <i>Diplodactylidae</i>) from Groote Eylandt, Northern Territory. <i>Zootaxa</i> , 2020, 4779, 438-450.	0.2	2
9845	Microbial Ecology of Methanotrophy in Streams Along a Gradient of CH ₄ Availability. <i>Frontiers in Microbiology</i> , 2020, 11, 771.	1.5	4
9846	Complete Mitochondrial Genome of the Fungal Biocontrol Agent <i>Trichoderma atroviride</i> : Genomic Features, Comparative Analysis and Insight Into the Mitochondrial Evolution in <i>Trichoderma</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 785.	1.5	11
9847	Linking Comparative Genomics of Nine Potato-Associated <i>Pseudomonas</i> Isolates With Their Differing Biocontrol Potential Against Late Blight. <i>Frontiers in Microbiology</i> , 2020, 11, 857.	1.5	32
9848	The Phylogeography of MERS-CoV in Hospital Outbreak-Associated Cases Compared to Sporadic Cases in Saudi Arabia. <i>Viruses</i> , 2020, 12, 540.	1.5	2
9849	<i>Peronospora monardae</i> , <i>Hyaloperonospora daughtreyae</i> and <i>H. iberidis</i> : new species associated with downy mildew diseases affecting ornamental plants in the United States. <i>European Journal of Plant Pathology</i> , 2020, 157, 311-326.	0.8	7
9850	Arabinogalactan-proteins of <i>Zostera marina</i> L. contain unique glycan structures and provide insight into adaption processes to saline environments. <i>Scientific Reports</i> , 2020, 10, 8232.	1.6	37
9851	Phylogenetic origin of <i>Magnolia pseudokobus</i> (Magnoliaceae), a rare <i>Magnolia</i> extinct in the wild, revealed by chloroplast genome sequencing, genome-wide SNP genotyping and microsatellite analysis. <i>Journal of Forest Research</i> , 2020, 25, 322-328.	0.7	2
9852	Complete plastid genome of two <i>Dalbergia</i> species (Fabaceae), and their significance in conservation and phylogeny. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1967-1969.	0.2	3
9853	Additional taxonomic coverage of the doubly uniparental inheritance in bivalves: Evidence of sex-linked heteroplasmy in the razor clam <i>Solen marginatus</i> Pulteney, 1799, but not in the lagoon cockle <i>Cerastoderma glaucum</i> (Bruguière, 1789). <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2020, 58, 561-570.	0.6	6
9854	Genetic and Virulence Profiles of Enteroaggregative <i>Escherichia coli</i> (EAEC) Isolated From Deployed Military Personnel (DMP) With Travelers' Diarrhea. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 200.	1.8	15
9855	Drug Resistance Prediction Using Deep Learning Techniques on HIV-1 Sequence Data. <i>Viruses</i> , 2020, 12, 560.	1.5	32
9856	Imaginal Disc Growth Factor 6 (<i>Idgf6</i>) Is Involved in Larval and Adult Wing Development in <i>Bactrocera correcta</i> (Bezzi) (Diptera: Tephritidae). <i>Frontiers in Genetics</i> , 2020, 11, 451.	1.1	10
9857	A mesopelagic ctenophore representing a new family, with notes on family-level taxonomy in Ctenophora: <i>Vampyroctena delmarvensis</i> gen. nov. sp. nov. (Vampyroctenidae, fam. nov.). <i>Marine Biodiversity</i> , 2020, 50, 1.	0.3	3
9858	Metabolic strategies of marine seafloor Chloroflexi inferred from genome reconstructions. <i>Environmental Microbiology</i> , 2020, 22, 3188-3204.	1.8	49
9859	Chloroplast genomes of Rubiaceae: Comparative genomics and molecular phylogeny in subfamily Ixoroideae. <i>PLoS ONE</i> , 2020, 15, e0232295.	1.1	18

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9860	Phylogenomics unravels Quaternary vicariance and allopatric speciation patterns in temperate–montane plant species: A case study on the <i>Ranunculus auricomus</i> species complex. <i>Molecular Ecology</i> , 2020, 29, 2031-2049.	2.0	41
9861	Densely sampled phylogenetic analyses of the Lesser Short-toed Lark (<i>Alaudala rufescens</i>) “Sand Lark (<i>A. Araytal</i>)” species complex (Aves, Passeriformes) reveal cryptic diversity. <i>Zoologica Scripta</i> , 2020, 49, 427-439.	0.7	14
9862	Phylogenomics, biogeography, and evolution of morphology and ecological niche of the eastern Asian–eastern North American <i>Nyssa</i> (Nyssaceae). <i>Journal of Systematics and Evolution</i> , 2020, 58, 571-603.	1.6	24
9863	Species IUCN threat status level increases with elevation: a phylogenetic approach for Neotropical tree frog conservation. <i>Biodiversity and Conservation</i> , 2020, 29, 2515-2537.	1.2	3
9864	Chromosome-level assembly of the horseshoe crab genome provides insights into its genome evolution. <i>Nature Communications</i> , 2020, 11, 2322.	5.8	57
9865	Molecular phylogeny of <i>Cremolobus</i> (Brassicaceae) supports the recognition of the new genus <i>Yunkia</i> and demonstrates the high habitat diversity of tribe Cremolobeae. <i>Systematics and Biodiversity</i> , 2020, 18, 295-314.	0.5	4
9866	<i>Tazarcus</i> , a new phylogenetically unplaced genus of two flightless weevils with metapleural ridge from the Eastern Arc Mountains, Tanzania (Coleoptera: Curculionidae: Molytinae). <i>Zootaxa</i> , 2020, 4766, 421-434.	0.2	1
9867	Distribution of <i>Macrobiotus shonaicus</i> Stec, Arakawa & Michalczyk, 2018 (Tardigrada: Tj ETQq1 1 0.784314 rgBT / Overlock 0,2	0.2	1
9868	<i>Sarcocheilichthys vittatus</i> , a new species of gudgeon (Teleostei: Tj ETQq0 0 0 rgBT / Overlock 10 Tf 50 201-220.	0.2	1
9869	Carnivorous sponges from the Australian Bathyal and Abyssal zones collected during the RV Investigator 2017 Expedition. <i>Zootaxa</i> , 2020, 4774, zootaxa.4774.1.1.	0.2	8
9870	The loss of photosynthesis pathway and genomic locations of the lost plastid genes in a holoparasitic plant <i>Aeginetia indica</i> . <i>BMC Plant Biology</i> , 2020, 20, 199.	1.6	16
9871	The trinity of ecological contrasts: a case study on rich insect assemblages by means of species, functional and phylogenetic diversity measures. <i>BMC Ecology</i> , 2020, 20, 29.	3.0	7
9872	Past and ongoing adaptation of human cytomegalovirus to its host. <i>PLoS Pathogens</i> , 2020, 16, e1008476.	2.1	19
9873	Correlations Between Prokaryotic Microbes and Stress-Resistant Algae in Different Corals Subjected to Environmental Stress in Hong Kong. <i>Frontiers in Microbiology</i> , 2020, 11, 686.	1.5	12
9874	The Genetic Basis of Morphological Diversity in Domesticated Goldfish. <i>Current Biology</i> , 2020, 30, 2260-2274.e6.	1.8	52
9875	A Novel Bat Coronavirus Closely Related to SARS-CoV-2 Contains Natural Insertions at the S1/S2 Cleavage Site of the Spike Protein. <i>Current Biology</i> , 2020, 30, 2196-2203.e3.	1.8	480
9876	The complete chloroplast genome of <i>Dendrobium pseudotenellum</i> (Orchidaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1880-1881.	0.2	0
9877	Chromosome-level reference genome of the jellyfish <i>Rhopilema esculentum</i> . <i>GigaScience</i> , 2020, 9, .	3.3	20

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9878	Chromosome-level reference genome assembly and gene editing of the dead-leaf butterfly <i>Kallima inachus</i> . <i>Molecular Ecology Resources</i> , 2020, 20, 1080-1092.	2.2	22
9879	A new cryptic species of fringe-toed lizards from southwestern Arizona with revised taxonomy of the <i>Uma notata</i> species complex (Squamata: Phrynosomatidae). <i>Zootaxa</i> , 2020, 4778, 67-100.	0.2	2
9880	Nosocomial outbreak of COVID-19 pneumonia in Wuhan, China. <i>European Respiratory Journal</i> , 2020, 55, 2000544.	3.1	150
9881	Multi-task learning sparse group lasso: a method for quantifying antigenicity of influenza A(H1N1) virus using mutations and variations in glycosylation of Hemagglutinin. <i>BMC Bioinformatics</i> , 2020, 21, 182.	1.2	10
9882	Polyploidy breaks speciation barriers in Australian burrowing frogs <i>Neobatrachus</i> . <i>PLoS Genetics</i> , 2020, 16, e1008769.	1.5	40
9883	De novo Assembly and Genome-Wide SNP Discovery in Rohu Carp, <i>Labeo rohita</i> . <i>Frontiers in Genetics</i> , 2020, 11, 386.	1.1	17
9884	Autographivirinae Bacteriophage Arno 160 Infects <i>Pectobacterium carotovorum</i> via Depolymerization of the Bacterial O-Polysaccharide. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3170.	1.8	12
9885	Genetic variants and source of introduction of SARS-CoV-2 in South America. <i>Journal of Medical Virology</i> , 2020, 92, 2139-2145.	2.5	33
9886	Fungal pathogens associated with branch and trunk cankers of nut crops in Iran. <i>European Journal of Plant Pathology</i> , 2020, 157, 327-351.	0.8	38
9887	Whole genome sequence analysis of <i>Cupriavidus campinensis</i> S14E4C, a heavy metal resistant bacterium. <i>Molecular Biology Reports</i> , 2020, 47, 3973-3985.	1.0	16
9888	Lichens and associated fungi from Glacier Bay National Park, Alaska. <i>Lichenologist</i> , 2020, 52, 61-181.	0.5	49
9889	Phylogeography of the iconic Australian red-tailed black-cockatoo (<i>Calyptorhynchus banksii</i>) and implications for its conservation. <i>Heredity</i> , 2020, 125, 85-100.	1.2	8
9890	High functionality of DNA barcodes and revealed cases of cryptic diversity in Korean curved-horn moths (Lepidoptera: Gelechioidea). <i>Scientific Reports</i> , 2020, 10, 6208.	1.6	10
9891	Evolution of vancomycin-resistant <i>Enterococcus faecium</i> during colonization and infection in immunocompromised pediatric patients. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 11703-11714.	3.3	36
9892	Identifying Invaders: The Case of <i>Ceratium furcoides</i> (Gonyaulacales, Dinophyceae) in South America. <i>Journal of Phycology</i> , 2020, 56, 1362-1366.	1.0	11
9893	The evolutionary origins of the cat attractant nepetalactone in catnip. <i>Science Advances</i> , 2020, 6, eaba0721.	4.7	70
9894	Description of Three New Genera of Metopidae (Metopida, Ciliophora): <i>Pileometopus</i> gen. nov., <i>Castula</i> gen. nov., and <i>Longitaenia</i> gen. nov., with Notes on the Phylogeny and Cryptic Diversity of Metopid Ciliates. <i>Protist</i> , 2020, 171, 125740.	0.6	14
9895	Molecular markers obtained from draft genomic sequence data characterise an isolate of <i>Oedogonium</i> (Chlorophyceae) used for biomass applications. <i>Phycologia</i> , 2020, 59, 340-345.	0.6	1

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9896	The complete chloroplast genome of an invasive herb <i>Bidens frondosa</i> L. (Asteraceae). Mitochondrial DNA Part B: Resources, 2020, 5, 1769-1770.	0.2	1
9897	De Novo Genome Assembly of Limpet <i>Bathycyba lactea</i> (Gastropoda: Pectinodontidae): The First Reference Genome of a Deep-Sea Gastropod Endemic to Cold Seeps. <i>Genome Biology and Evolution</i> , 2020, 12, 905-910.	1.1	15
9898	Uneven Missing Data Skew Phylogenomic Relationships within the Lories and Lorikeets. <i>Genome Biology and Evolution</i> , 2020, 12, 1131-1147.	1.1	28
9899	Molecular phylogeny and diversity of penaeid shrimps (Crustacea: Decapoda) from South-East Asian waters. <i>Zoologica Scripta</i> , 2020, 49, 596-613.	0.7	14
9900	Similar yet different: phylogenomic analysis to delineate <i>Salmonella</i> and <i>Citrobacter</i> species boundaries. <i>BMC Genomics</i> , 2020, 21, 377.	1.2	15
9901	Phylogenetic placement of <i>Paratrachaptum</i> and reconsideration of <i>Gloeophyllales</i> . <i>Fungal Systematics and Evolution</i> , 2020, 5, 119-130.	0.9	3
9902	Transcriptome Analysis of Zebrafish Olfactory Epithelium Reveal Sexual Differences in Odorant Detection. <i>Genes</i> , 2020, 11, 592.	1.0	8
9903	Tempo and Pattern of Avian Brain Size Evolution. <i>Current Biology</i> , 2020, 30, 2026-2036.e3.	1.8	72
9904	The genome sequence of star fruit (<i>Averrhoa carambola</i>). <i>Horticulture Research</i> , 2020, 7, 95.	2.9	18
9905	Characterization of the complete chloroplast genome and phylogenetic analysis of <i>Pittosporum tobira</i> (Pittosporaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1397-1398.	0.2	1
9906	Lineage-specific evolution and gene flow in <i>Listeria monocytogenes</i> are independent of bacteriophages. <i>Environmental Microbiology</i> , 2020, 22, 5058-5072.	1.8	16
9907	Tectonic evolution of the Tethyan region created the Eurasian extratropical biodiversity hotspots: tracing <i>Pireneitega</i> spiders' diversification history. <i>Ecography</i> , 2020, 43, 1400-1411.	2.1	8
9908	Interventions designed to control postpasteurization contamination in high-temperature, short-time-pasteurized fluid milk processing facilities: A case study on the effect of employee training, clean-in-place chemical modification, and preventive maintenance programs. <i>Journal of Dairy Science</i> , 2020, 103, 7569-7584.	1.4	11
9909	Hydrogen and Carbon Monoxide-Utilizing <i>Kyrpidia spormannii</i> Species From Pantelleria Island, Italy. <i>Frontiers in Microbiology</i> , 2020, 11, 951.	1.5	18
9910	Detection of Low Pathogenic Avian Influenza Virus Subtype H10N7 in Poultry and Environmental Water Samples During a Clinical Outbreak in Commercial Free-Range Layers, Netherlands 2017. <i>Frontiers in Veterinary Science</i> , 2020, 7, 237.	0.9	11
9911	The puzzling taxonomic rank of <i>Pijnackeria hispanica</i> , a chimerical hybrid androgen (Insecta.) Tj ETQq1 1 0.784314 rgBT / Overlock 10	0.9	2
9912	Illuminating Genetic Mysteries of the Dead Sea Scrolls. <i>Cell</i> , 2020, 181, 1218-1231.e27.	13.5	10
9913	Mitogenomic characterization and systematic placement of the Congo blind barb <i>Caecobarbus geertsii</i> (Cypriniformes: Cyprinidae). <i>International Journal of Biological Macromolecules</i> , 2020, 161, 292-298.	3.6	8

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9914	Two new bacilladnaviruses associated with the diatom <i>Haslea ostrearia</i> . <i>European Journal of Phycology</i> , 2020, 55, 444-453.	0.9	1
9915	The complete chloroplast genome of native <i>Prunus campanulata</i> in Taiwan. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1301-1302.	0.2	0
9916	The complete mitochondrial genome of a yellow passion fruit (<i>Passiflora edulis</i> Sims. f. <i>flavicarpa</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf . 1598-1600.	0.2	4
9917	The complete mitochondrial genome of the deep-water cartilaginous fish <i>Hydrolagus affinis</i> (de Brito Capello, 1868) (Holocephali: Chimaeridae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1810-1812.	0.2	5
9918	Correlation between Organelle Genetic Variation and RNA Editing in Dinoflagellates Associated with the Coral <i>Acropora digitifera</i> . <i>Genome Biology and Evolution</i> , 2020, 12, 203-209.	1.1	3
9919	An updated Chinese vascular plant tree of life: Phylogenetic diversity hotspots revisited. <i>Journal of Systematics and Evolution</i> , 2020, 58, 663-672.	1.6	31
9920	Unravelling evolutionary relationships between epifoliar Meliolaceae and angiosperms. <i>Journal of Systematics and Evolution</i> , 2022, 60, 23-42.	1.6	10
9921	Two-step mechanism of J-domain action in driving Hsp70 function. <i>PLoS Computational Biology</i> , 2020, 16, e1007913.	1.5	18
9922	Crystal structure of β -L-arabinobiosidase belonging to glycoside hydrolase family 121. <i>PLoS ONE</i> , 2020, 15, e0231513.	1.1	8
9923	<i>Dinastridium verrucosum</i> Baumeister from Bavaria (Germany) is a Borghiellacean Dinophyte (â€Šuessiales). <i>Protist</i> , 2020, 171, 125741.	0.6	3
9924	Integrating whole-genome sequencing within the National Antimicrobial Resistance Surveillance Program in the Philippines. <i>Nature Communications</i> , 2020, 11, 2719.	5.8	62
9925	An evolutionary path to altered cofactor specificity in a metalloenzyme. <i>Nature Communications</i> , 2020, 11, 2738.	5.8	22
9926	Complete mitogenome of the invasive land flatworm <i>Platydemus manokwari</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1689-1690.	0.2	8
9927	Characteristics of the mitochondrial genome of Qinling zokor (<i>Eospalax rufescens</i>). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2161-2162.	0.2	0
9928	High Levels of Acquired HIV Drug Resistance Following Virological Nonsuppression in HIV-Infected Women from a High-Risk Cohort in Uganda. <i>AIDS Research and Human Retroviruses</i> , 2020, 36, 782-791.	0.5	1
9929	Mapping of HIV-1C Transmission Networks Reveals Extensive Spread of Viral Lineages Across Villages in Botswana Treatment-as-Prevention Trial. <i>Journal of Infectious Diseases</i> , 2020, 222, 1670-1680.	1.9	12
9930	Mitogenomes Reveal Multiple Colonization of Mountains by <i>Rattus</i> in Sundaland. <i>Journal of Heredity</i> , 2020, 111, 392-404.	1.0	9
9931	A mitochondrial genetic divergence proxy predicts the reproductive compatibility of mammalian hybrids. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20200690.	1.2	14

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9932	Biochemical Convergence of Mitochondrial Hsp70 System Specialized in Iron-Sulfur Cluster Biogenesis. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3326.	1.8	13
9933	Nuclear phylogenomic analyses of asterids conflict with plastome trees and support novel relationships among major lineages. <i>American Journal of Botany</i> , 2020, 107, 790-805.	0.8	75
9934	Draft genome of the famous ornamental plant <i>Paeonia suffruticosa</i> . <i>Ecology and Evolution</i> , 2020, 10, 4518-4530.	0.8	34
9935	<i>Calycomorphotria hydatis</i> gen. nov., sp. nov., a novel species in the family Planctomycetaceae with conspicuous subcellular structures. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 1877-1887.	0.7	17
9936	A DNA Repair Inhibitor Isolated from an Ecuadorian Fungal Endophyte Exhibits Synthetic Lethality in PTEN-Deficient Glioblastoma. <i>Journal of Natural Products</i> , 2020, 83, 1899-1908.	1.5	2
9937	Genome-wide Identification and Characterization of Heat Shock Protein Family Reveals Role in Development and Stress Conditions in <i>Triticum aestivum</i> L.. <i>Scientific Reports</i> , 2020, 10, 7858.	1.6	44
9938	Taxonomy of Micronesian monitors (Reptilia: Squamata: <i>Varanus</i>): endemic status of new species argues for caution in pursuing eradication plans. <i>Royal Society Open Science</i> , 2020, 7, 200092.	1.1	7
9939	Extreme genomic volatility characterizes the evolution of the immunoglobulin heavy chain locus in cyprinodontiform fishes. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20200489.	1.2	11
9940	<i>Lindavia intermedia</i> (Bacillariophyceae) and Nuisance lake Snow in New Zealand: Chitin Content and Quantitative PCR Methods to Estimate Cell Concentrations and Expression of Chitin Synthase. <i>Journal of Phycology</i> , 2020, 56, 1232-1244.	1.0	6
9941	Genome Dynamics of <i>Vibrio cholerae</i> Isolates Linked to Seasonal Outbreaks of Cholera in Dhaka, Bangladesh. <i>MBio</i> , 2020, 11, .	1.8	39
9942	Optimizing taxon addition order and branch lengths in the construction of phylogenetic trees using maximum likelihood. <i>Journal of Bioinformatics and Computational Biology</i> , 2020, 18, 2050003.	0.3	4
9943	The green puzzle <i>Stichococcus</i> (Trebouxiophyceae, Tj ETQq1 1 0.784314 rgBT /Overlooked genus. <i>Phytotaxa</i> , 2020, 441, 113-142.	0.1	38
9944	A coarse-graining, ultrametric approach to resolve the phylogeny of prokaryotic strains with frequent homologous recombination. <i>BMC Evolutionary Biology</i> , 2020, 20, 52.	3.2	1
9945	Genomic evidence for a hybrid origin of the yeast opportunistic pathogen <i>Candida albicans</i> . <i>BMC Biology</i> , 2020, 18, 48.	1.7	46
9946	Leveraging plastomes for comparative analysis and phylogenomic inference within Scutellarioideae (Lamiaceae). <i>PLoS ONE</i> , 2020, 15, e0232602.	1.1	21
9947	First Report of Endolithic Members of <i>Rhodorus marinus</i> (Stylonematales, Rhodophyta) Growing Inside Rhodoliths Offshore Louisiana, Northwestern Gulf of Mexico. <i>Frontiers in Marine Science</i> , 2020, 7, .	1.2	5
9948	Does Molecular and Structural Evolution Shape the Speedy Grass Stomata?. <i>Frontiers in Plant Science</i> , 2020, 11, 333.	1.7	11
9949	News from the Sea: A New Genus and Seven New Species in the Pleosporalean Families Roussoellaceae and Thyridariaceae. <i>Diversity</i> , 2020, 12, 144.	0.7	20

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9950	Genomic Diversity, Population Structure, and Signature of Selection in Five Chinese Native Sheep Breeds Adapted to Extreme Environments. <i>Genes</i> , 2020, 11, 494.	1.0	20
9951	Pan-Genome Analyses of <i>Geobacillus</i> spp. Reveal Genetic Characteristics and Composting Potential. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3393.	1.8	7
9952	Reallocation of foliicolous species of the genus <i>Strigula</i> into six genera (lichenized Ascomycota). <i>Trends in Microbiology</i> , 2020, 28, 1015-1022.	4.7	9
9953	Global radiation in a rare biosphere soil diatom. <i>Nature Communications</i> , 2020, 11, 2382.	5.8	43
9954	Shale gas development has limited effects on stream biology and geochemistry in a gradient-based, multiparameter study in Pennsylvania. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 3670-3677.	3.3	22
9955	Genomic Epidemiology, Evolution, and Transmission Dynamics of Porcine Deltacoronavirus. <i>Molecular Biology and Evolution</i> , 2020, 37, 2641-2654.	3.5	76
9956	An integrative approach to the systematics of the <i>Berthella californica</i> species complex (Heterobranchia: Pleurobranchidae). <i>Journal of Molluscan Studies</i> , 2020, 86, 186-200.	0.4	2
9957	Tracking echovirus eleven outbreaks in Guangdong, China: a metatranscriptomic, phylogenetic, and epidemiological study. <i>Virus Evolution</i> , 2020, 6, veaa029.	2.2	14
9958	Genome Sequencing and Analysis of the Fungal Symbiont of <i>Sirex noctilio</i> , <i>Amylostereum areolatum</i> : Revealing the Biology of Fungus-Insect Mutualism. <i>MSphere</i> , 2020, 5, .	1.3	11
9959	Phylogenomic incongruence in <i>Ceratocystis</i> : a clue to speciation?. <i>BMC Genomics</i> , 2020, 21, 362.	1.2	11
9960	Population Biology and Epidemiological Studies of <i>Acinetobacter baumannii</i> in the Era of Whole Genome Sequencing: Is the Oxford Scheme Still Appropriate?. <i>Frontiers in Microbiology</i> , 2020, 11, 775.	1.5	10
9961	Chromosome-Level Reference Genome and Population Genomic Analysis Provide Insights into the Evolution and Improvement of Domesticated Mulberry (<i>Morus alba</i>). <i>Molecular Plant</i> , 2020, 13, 1001-1012.	3.9	59
9962	A widespread toxin-antitoxin system exploiting growth control via alarmone signaling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 10500-10510.	3.3	81
9963	Evolutionary relationships among <i>Massospora</i> spp. (Entomophthorales), obligate pathogens of cicadas. <i>Mycologia</i> , 2020, 112, 1060-1074.	0.8	15
9964	Characterization of the complete plastid genome of <i>Camellia amplexicaulis</i> (Theaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2091-2092.	0.2	0
9965	Integrating DNA Sequences with Morphological Analysis Clarifies Phylogenetic Position of <i>Salvia grandifolia</i> (Lamiaceae): An Enigmatic Species Endemic to Southwestern China. <i>International Journal of Plant Sciences</i> , 2020, 181, 787-799.	0.6	11
9966	Whole genome sequencing and antibiotic diffusion assays, provide new insight on drug resistance in the genus <i>Pedobacter</i> . <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	5
9967	Convergent Loss of an EDS1/PAD4 Signaling Pathway in Several Plant Lineages Reveals Coevolved Components of Plant Immunity and Drought Response. <i>Plant Cell</i> , 2020, 32, 2158-2177.	3.1	66

#	ARTICLE	IF	CITATIONS
9968	Genomic data reveal two distinct species from the widespread alpine ginger <i>Roscoea tibetica</i> Batalin (Zingiberaceae). <i>Journal of Systematics and Evolution</i> , 2021, 59, 1232-1243.	1.6	13
9969	Complete plastomes of 17 species of maples (Sapindaceae: Acer): comparative analyses and phylogenomic implications. <i>Plant Systematics and Evolution</i> , 2020, 306, 1.	0.3	4
9970	Treatment of Coronavirus Disease 2019 (COVID-19) Patients with Convalescent Plasma. <i>American Journal of Pathology</i> , 2020, 190, 1680-1690.	1.9	239
9971	<i>Grosmania tibetensis</i> , a new ophiostomatoid fungus associated with <i>Orthotomicus</i> sp. (Coleoptera) in Tibetan subalpine forests. <i>Mycoscience</i> , 2020, 61, 282-292.	0.3	2
9972	Identification of clonemates and genetic lineages using next-generation sequencing (ddRADseq) guides conservation of a rare species, <i>Bossiaea vombata</i> (Fabaceae). <i>Perspectives in Plant Ecology, Evolution and Systematics</i> , 2020, 45, 125544.	1.1	7
9973	Large-scale genome-wide analysis links lactic acid bacteria from food with the gut microbiome. <i>Nature Communications</i> , 2020, 11, 2610.	5.8	190
9974	Morphological, genotypic and metabolomic signatures confirm interfamilial hybridization between the ubiquitous kelps <i>Macrocystis</i> (Arthrothamnaceae) and <i>Lessonia</i> (Lessoniaceae). <i>Scientific Reports</i> , 2020, 10, 8279.	1.6	9
9975	The complete chloroplast genome of <i>Silvianthus bracteatus</i> (Carlemanniaceae) and phylogenetic analysis of Lamiales. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1132-1133.	0.2	2
9976	Complete chloroplast genome of <i>Pistacia chinensis</i> Bunge (Anacardiaceae: Rhoideae), an important economical and ornamental plant. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1931-1932.	0.2	4
9977	Exploring the phylogeny of the marattialean ferns. <i>Cladistics</i> , 2020, 36, 569-593.	1.5	20
9978	Evolution of feeding habits of sap beetles (Coleoptera: Nitidulidae) and placement of Calonecrinae. <i>Systematic Entomology</i> , 2020, 45, 911-923.	1.7	14
9979	Complete Chloroplast Genomes of 14 Mangroves: Phylogenetic and Comparative Genomic Analyses. <i>BioMed Research International</i> , 2020, 2020, 1-13.	0.9	14
9980	Phylogenomic synteny network analyses reveal ancestral transpositions of auxin response factor genes in plants. <i>Plant Methods</i> , 2020, 16, 70.	1.9	8
9981	Revalidation of the Argentinian pouched lamprey <i>Geotria macrostoma</i> (Burmeister, 1868) with molecular and morphological evidence. <i>PLoS ONE</i> , 2020, 15, e0233792.	1.1	30
9982	<i>Diatomophthoraceae</i> – a new family of olpidiopsis-like diatom parasitoids largely unrelated to <i>Ectrogella</i> . <i>Fungal Systematics and Evolution</i> , 2020, 5, 113-118.	0.9	13
9983	Phylogenetic position of <i>Diplostomum</i> spp. from New World herons based on complete mitogenomes, rDNA operons, and DNA barcodes, including a new species with partially elucidated life cycle. <i>Parasitology Research</i> , 2020, 119, 2129-2137.	0.6	15
9984	Chromosome-Level Genome Reveals the Origin of Neo-Y Chromosome in the Male Barred Knifejaw <i>Oplegnathus fasciatus</i> . <i>IScience</i> , 2020, 23, 101039.	1.9	14
9985	Epidemic of venereal treponematosi in wild monkeys: a paradigm for syphilis origin. <i>New Microbes and New Infections</i> , 2020, 35, 100670.	0.8	5

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9986	The phoma-like dilemma. <i>Studies in Mycology</i> , 2020, 96, 309-396.	4.5	87
9987	Plastome structure and phylogenetic position of <i>Rhus typhina</i> (Anacardiaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1794-1795.	0.2	0
9988	Tracking diversity and evolutionary pathways of Lebanese oak taxa through plastome analyses. <i>Botany Letters</i> , 2020, 167, 315-330.	0.7	5
9989	The origin of domestication genes in goats. <i>Science Advances</i> , 2020, 6, eaaz5216.	4.7	86
9990	Draft Genome Assembly of <i>Floccularia luteovirens</i> , an Edible and Symbiotic Mushroom on Qinghai-Tibet Plateau. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1167-1173.	0.8	5
9991	The reference genome of the selfing fish <i>Kryptolebias hermaphroditus</i> : Identification of phases I and II detoxification genes. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2020, 35, 100684.	0.4	2
9992	Lactobacilli Have a Niche in the Human Nose. <i>Cell Reports</i> , 2020, 31, 107674.	2.9	75
9993	Origin and Health Status of First-Generation Africans from Early Colonial Mexico. <i>Current Biology</i> , 2020, 30, 2078-2091.e11.	1.8	34
9994	Molecular characterization of <i>Brucella ovis</i> in Argentina. <i>Veterinary Microbiology</i> , 2020, 245, 108703.	0.8	2
9995	Cophylogenetic patterns in algal symbionts correlate with repeated symbiont switches during diversification and geographic expansion of lichen-forming fungi in the genus <i>Stictia</i> (Ascomycota). <i>Tj ETQq1 1 0.7843 14 rgBT /Overlock</i>		
9996	Supermatrix phylogeny resolves goby lineages and reveals unstable root of Gobiaria. <i>Molecular Phylogenetics and Evolution</i> , 2020, 151, 106862.	1.2	33
9997	The complete chloroplast genome of medicine and horticultural plant <i>Chloranthus spicatus</i> (Chloranthaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1293-1294.	0.2	2
9998	Integrative systematics untangles the evolutionary history of <i>Stenochrus</i> (Schizomida): <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 267</i> <i>Journal of the Linnean Society</i> , 2020, 130, 458-479.	0.7	8
9999	Phylogenetic signal in the topographic niche of trees: Current and historical significance of habitat structure on the species arrangement pattern within East Asian rugged forests. <i>Ecological Research</i> , 2020, 35, 613-624.	0.7	1
10000	<i>Macronychia</i> (Diptera: Sarcophagidae) goes cosmopolitan: description and molecular delineation of the first Australasian species. <i>Austral Entomology</i> , 2020, 59, 292-301.	0.8	4
10001	Genetic analysis of porcine circovirus type 2 (PCV2) in Queensland, Australia. <i>Australian Veterinary Journal</i> , 2020, 98, 388-395.	0.5	7
10002	Cryptic Haploid Stages in the Life Cycle of <i>Leathesia marina</i> (Chordariaceae, Phaeophyceae) Under In Vitro Culture. <i>Journal of Phycology</i> , 2020, 56, 1349-1361.	1.0	1
10003	Tax4Fun2: prediction of habitat-specific functional profiles and functional redundancy based on 16S rRNA gene sequences. <i>Environmental Microbiomes</i> , 2020, 15, 11.	2.2	323

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10004	Genome skimming and microsatellite analysis reveal contrasting patterns of genetic diversity in a rare sandhill endemic (<i>Erysimum teretifolium</i> , Brassicaceae). <i>PLoS ONE</i> , 2020, 15, e0227523.	1.1	2
10005	Co-Occurrence of the bla _{KPC-2} and Mcr-3 Gene in <i>Aeromonas caviae</i> SCAC2001 Isolated from Patients with Diarrheal Disease. <i>Infection and Drug Resistance</i> , 2020, Volume 13, 1527-1536.	1.1	10
10006	Large-Scale Hybridisation as an Extinction Threat to the Suweon Treefrog (Hylidae: Dryophytes) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 66</i>	1.0	8
10007	<i>Sporolithon franciscanum</i> sp. nov. (Sporolithales, Rhodophyta), a New Rhodolith-Forming Species from Northeast Brazil. <i>Diversity</i> , 2020, 12, 199.	0.7	5
10008	Comparison of Antimicrobial Resistance and Pan-Genome of Clinical and Non-Clinical <i>Enterococcus cecorum</i> from Poultry Using Whole-Genome Sequencing. <i>Foods</i> , 2020, 9, 686.	1.9	13
10009	Comparative Analyses of Five Complete Chloroplast Genomes from the Genus <i>Pterocarpus</i> (Fabaceae). <i>International Journal of Molecular Sciences</i> , 2020, 21, 3758.	1.8	52
10010	Actinomycetes from the Red Sea Sponge <i>Coscinoderma mathewsi</i> : Isolation, Diversity, and Potential for Bioactive Compounds Discovery. <i>Microorganisms</i> , 2020, 8, 783.	1.6	22
10011	Cryptic diversity and species boundaries within the <i>Paragalago zanzibaricus</i> species complex. <i>Molecular Phylogenetics and Evolution</i> , 2020, 150, 106887.	1.2	7
10012	Identifying SARS-CoV-2-related coronaviruses in Malayan pangolins. <i>Nature</i> , 2020, 583, 282-285.	13.7	1,453
10013	Genome-enabled phylogenetic and functional reconstruction of an araphid pennate diatom <i>Plagiostrata</i> sp. CCMP470, previously assigned as a radial centric diatom, and its bacterial commensal. <i>Scientific Reports</i> , 2020, 10, 9449.	1.6	25
10014	Faecal DNA to the rescue: Shotgun sequencing of non-invasive samples reveals two subspecies of Southeast Asian primates to be Critically Endangered species. <i>Scientific Reports</i> , 2020, 10, 9396.	1.6	9
10015	A treponemal genome from an historic plague victim supports a recent emergence of yaws and its presence in 15th century Europe. <i>Scientific Reports</i> , 2020, 10, 9499.	1.6	35
10016	Genetic cluster analysis of SARS-CoV-2 and the identification of those responsible for the major outbreaks in various countries. <i>Emerging Microbes and Infections</i> , 2020, 9, 1287-1299.	3.0	51
10017	Climate-driven vicariance and long-distance dispersal explain the Rand Flora pattern in the liverwort <i>Exormotheca pustulosa</i> (Marchantiophyta). <i>Biological Journal of the Linnean Society</i> , 2020, 130, 480-496.	0.7	2
10018	Phylogenomics indicates Amazonia as the major source of Neotropical swarm-founding social wasp diversity. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20200480.	1.2	28
10019	The <i>Chimonanthus salicifolius</i> genome provides insight into magnoliid evolution and flavonoid biosynthesis. <i>Plant Journal</i> , 2020, 103, 1910-1923.	2.8	41
10020	Determining the Genetic Characteristics of Resistance and Virulence of the <i>Epidermidis</i> Cluster Group Through Pan-Genome Analysis. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 274.	1.8	16
10021	Meta-Analysis and Evaluation by Insect-Mediated Baiting Reveal Different Patterns of Hypocrealean Entomopathogenic Fungi in the Soils From Two Regions of China. <i>Frontiers in Microbiology</i> , 2020, 11, 1133.	1.5	7

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10022	Estimating rates and patterns of diversification with incomplete sampling: a case study in the rosids. <i>American Journal of Botany</i> , 2020, 107, 895-909.	0.8	17
10023	Interfamilial relationships in order Fabales: new insights from the nuclear regions <i>sqd1</i> and 26S rDNA. <i>Plant Systematics and Evolution</i> , 2020, 306, 1.	0.3	2
10024	Bacterial symbionts support larval sap feeding and adult folivory in (semi-)aquatic reed beetles. <i>Nature Communications</i> , 2020, 11, 2964.	5.8	42
10025	Molecular phylogeny and biogeography of <i>Triplophysa</i> stone loaches in the Central Chinese Mountains. <i>Biological Journal of the Linnean Society</i> , 2020, 130, 563-577.	0.7	11
10026	Conserved white-rot enzymatic mechanism for wood decay in the Basidiomycota genus <i>Pycnoporus</i> . <i>DNA Research</i> , 2020, 27, .	1.5	32
10027	Recurrent Loss of <i>abaA</i> , a Master Regulator of Asexual Development in Filamentous Fungi, Correlates with Changes in Genomic and Morphological Traits. <i>Genome Biology and Evolution</i> , 2020, 12, 1119-1130.	1.1	16
10028	Production and evolution pattern of "fruity smell" aggregation pheromones in genus <i>Drosophila</i> . <i>Journal of Systematics and Evolution</i> , 2020, , .	1.6	2
10029	The fungal endophyte <i>Epichloa festucae</i> var. <i>lolii</i> plays a limited role in mediating crown rust severity in perennial ryegrass. <i>Crop Science</i> , 2020, 60, 1090-1104.	0.8	6
10030	Revisiting <i>Metarhizium</i> and the description of new species from Thailand. <i>Studies in Mycology</i> , 2020, 95, 171-251.	4.5	73
10031	Phylogenetic origins and family classification of typhuloid fungi, with emphasis on <i>Ceratellopsis</i> , <i>Macrotyphula</i> and <i>Typhula</i> (Basidiomycota). <i>Studies in Mycology</i> , 2020, 96, 155-184.	4.5	17
10032	Gene flow and rapid differentiation characterize a rapid insular radiation in the southwest Pacific (Aves: <i>Zosterops</i>). <i>Evolution; International Journal of Organic Evolution</i> , 2020, 74, 1788-1803.	1.1	23
10033	Historical assembly of Zygothrypetidae in the Atacama Desert. <i>Frontiers of Biogeography</i> , 2020, 12, .	0.8	11
10034	Understanding the Composition, Biosynthesis, Accumulation and Transport of Flavonoids in Crops for the Promotion of Crops as Healthy Sources of Flavonoids for Human Consumption. <i>Nutrients</i> , 2020, 12, 1717.	1.7	74
10035	A multilocus analysis of <i>Epicopeiidae</i> (Lepidoptera, Geometroidea) provides new insights into their relationships and the evolutionary history of mimicry. <i>Molecular Phylogenetics and Evolution</i> , 2020, 149, 106847.	1.2	9
10036	A new species of <i>Creptotrematina</i> (Trematoda: Allocreadiidae) from characid fishes of Brazil: morphological and molecular data. <i>Journal of Helminthology</i> , 2020, 94, e163.	0.4	4
10037	Global distribution of a chlorophyll <i>f</i> cyanobacterial marker. <i>ISME Journal</i> , 2020, 14, 2275-2287.	4.4	41
10038	Dissecting the genome of star fruit (<i>Averrhoa carambola</i> L.). <i>Horticulture Research</i> , 2020, 7, 94.	2.9	16
10039	The planctomycete <i>Stieleria maiorica</i> Mal15T employs stieleriocins to alter the species composition in marine biofilms. <i>Communications Biology</i> , 2020, 3, 303.	2.0	33

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10040	New species of aquatic chytrids from Oman. <i>Mycologia</i> , 2020, 112, 781-791.	0.8	3
10041	Genome-wide adaptive evolution to underground stresses in subterranean mammals: Hypoxia adaption, immunity promotion, and sensory specialization. <i>Ecology and Evolution</i> , 2020, 10, 7377-7388.	0.8	9
10042	Vibrios from the Norwegian marine environment: Characterization of associated antibiotic resistance and virulence genes. <i>MicrobiologyOpen</i> , 2020, 9, e1093.	1.2	28
10043	Characterization of the complete mitochondrial genome of <i>Amblyomma ovale</i> , comparative analyses and phylogenetic considerations. <i>Experimental and Applied Acarology</i> , 2020, 81, 421-439.	0.7	18
10044	Integrative taxonomy of <i>Pseudolepeophtheirus longicauda</i> (Crustacea: Copepoda: Caligidae) parasitic on <i>Platichthys stellatus</i> (Actinopterygii: Pleuronectidae). <i>Parasitology International</i> , 2020, 78, 102135.	0.6	4
10045	Cryptic species and host specificity in the bryozoan-associated hydrozoan <i>Zanclaea divergens</i> (Hydrozoa, Zanclidae). <i>Molecular Phylogenetics and Evolution</i> , 2020, 151, 106893.	1.2	15
10046	A REVISION OF GAGNEPAINIA AND HEMIORCHIS (GLOBBEAE: ZINGIBERACEAE). <i>Edinburgh Journal of Botany</i> , 2020, 77, 455-490.	0.4	1
10047	Culture-Independent Analysis of Linuron-Mineralizing Microbiota and Functions in on-Farm Biopurification Systems via DNA-Stable Isotope Probing: Comparison with Enrichment Culture. <i>Environmental Science & Technology</i> , 2020, 54, 9387-9397.	4.6	19
10048	The complete chloroplast genome of <i>Polygonatum ordoratum</i> (Mill.) Druce and its phylogenetic analysis. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1601-1602.	0.2	2
10049	Synteny-Guided Resolution of Gene Trees Clarifies the Functional Impact of Whole-Genome Duplications. <i>Molecular Biology and Evolution</i> , 2020, 37, 3324-3337.	3.5	28
10050	Revision of the pale-bellied <i>Micronycteris</i> Gray, 1866 (Chiroptera, Phyllostomidae) with descriptions of two new species. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2020, 58, 1411-1431.	0.6	6
10051	Lateral Gene Transfer Shapes Diversity of <i>Gardnerella</i> spp.. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 293.	1.8	18
10052	Importance of <i>Defluviitalea raffinosedens</i> for Hydrolytic Biomass Degradation in Co-Culture with <i>Hungateiclostridium thermocellum</i> . <i>Microorganisms</i> , 2020, 8, 915.	1.6	13
10053	Inducible aging in <i>Hydra oligactis</i> implicates sexual reproduction, loss of stem cells, and genome maintenance as major pathways. <i>GeroScience</i> , 2020, 42, 1119-1132.	2.1	13
10054	Evolutionary history of the Eurasian steppe plant <i>Schivereckia podolica</i> (Brassicaceae) and its close relatives. <i>Flora: Morphology, Distribution, Functional Ecology of Plants</i> , 2020, 268, 151602.	0.6	5
10055	<i>Desulfolutivibrio sulfoxidireducens</i> gen. nov., sp. nov., isolated from a pyrite-forming enrichment culture and reclassification of <i>Desulfovibrio sulfodismutans</i> as <i>Desulfolutivibrio sulfodismutans</i> comb. nov. <i>Systematic and Applied Microbiology</i> , 2020, 43, 126105.	1.2	26
10056	A multilocus phylogeny of the non-photosynthetic parasitic plant <i>Cistanche</i> (Orobanchaceae) refutes current taxonomy and identifies four major morphologically distinct clades. <i>Molecular Phylogenetics and Evolution</i> , 2020, 151, 106898.	1.2	11
10057	An integrative DNA barcoding framework of ladybird beetles (Coleoptera: Coccinellidae). <i>Scientific Reports</i> , 2020, 10, 10063.	1.6	19

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10058	Tropical plants evolve faster than their temperate relatives: a case from the bamboos (Poaceae: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 7 2020, 34, 482-493.	0.5	6
10059	The complete chloroplast genome sequence of <i>Pimpinella smithii</i> (Apiaceae). Mitochondrial DNA Part B: Resources, 2020, 5, 1155-1156.	0.2	2
10060	The complete chloroplast genome of <i>Styrax japonicus</i> (Styracaceae), a deciduous tree distributed in East Asia. Mitochondrial DNA Part B: Resources, 2020, 5, 1863-1864.	0.2	0
10061	Constructing the mitochondrial genome of the Peruvian grunt <i>Anisotremus scapularis</i> (Tschudi, 1846 (Lutjaniformes: Haemulidae) using RNA-seq data. Mitochondrial DNA Part B: Resources, 2020, 5, 1921-1923.	0.2	1
10062	Secondary contact zones of closely related <i>Erebia</i> butterflies overlap with narrow phenotypic and parasitic clines. Journal of Evolutionary Biology, 2020, 33, 1152-1163.	0.8	17
10063	The role of introgression and ecotypic parallelism in delineating intraspecific conservation units. Molecular Ecology, 2020, 29, 2793-2809.	2.0	31
10064	Whole genome characterization of autochthonous <i>Bos taurus brachyceros</i> and introduced <i>Bos indicus indicus</i> cattle breeds in Cameroon regarding their adaptive phenotypic traits and pathogen resistance. BMC Genetics, 2020, 21, 64.	2.7	7
10065	Native Arbuscular Mycorrhizal Fungi Characterization from Saline Lands in Arid Oases, Northwest China. Journal of Fungi (Basel, Switzerland), 2020, 6, 80.	1.5	8
10066	Genome-wide systematic characterization and expression analysis of the phosphatidylinositol 4-phosphate 5-kinases in plants. Gene, 2020, 756, 144915.	1.0	10
10067	Multivariate ratio analysis and DNA markers reveal a new Australian species and three synonymies in eucalypt-gall-associated <i>Megastigmus</i> (Hymenoptera: Megastigmidae). Bulletin of Entomological Research, 2020, 110, 709-724.	0.5	6
10068	Spatial genetic structure in the rock hyrax (<i>Procavia capensis</i>) across the Namaqualand and western Fynbos areas of South Africa: a mitochondrial and microsatellite perspective. Canadian Journal of Zoology, 2020, 98, 557-571.	0.4	4
10069	HIV-1 variants are archived throughout infection and persist in the reservoir. PLoS Pathogens, 2020, 16, e1008378.	2.1	37
10070	Genome-Wide Characterization and Comparative Analysis of MYB Transcription Factors in <i>Ganoderma</i> Species. G3: Genes, Genomes, Genetics, 2020, 10, 2653-2660.	0.8	12
10071	Protein signatures to identify the different genera within the Xanthomonadaceae family. Brazilian Journal of Microbiology, 2020, 51, 1515-1526.	0.8	6
10072	A new species of <i>Phrynobatrachus</i> (Amphibia: Anura: Phrynobatrachidae) from the Northern Mountains of Tanzania. Journal of Natural History, 2020, 54, 63-85.	0.2	3
10073	<i>Reticulocystis yunnanense</i> gen. et sp. nov., a new member of freshwater Oocystaceae algae (Trebouxiophyceae, Chlorophyta). European Journal of Phycology, 2020, 55, 507-516.	0.9	3
10074	The complete chloroplast genome of <i>Sibbaldia aphanopetala</i> (Rosaceae: Potentilleae). Mitochondrial DNA Part B: Resources, 2020, 5, 2026-2027.	0.2	3
10075	PIQMEE: Bayesian Phylodynamic Method for Analysis of Large Data Sets with Duplicate Sequences. Molecular Biology and Evolution, 2020, 37, 3061-3075.	3.5	12

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10076	Iterative subtractive binning of freshwater chronoserries metagenomes identifies over 400 novel species and their ecologic preferences. <i>Environmental Microbiology</i> , 2020, 22, 3394-3412.	1.8	69
10077	Unexpected conservation and global transmission of agrobacterial virulence plasmids. <i>Science</i> , 2020, 368, .	6.0	56
10078	An integrative phylogenomic approach to elucidate the evolutionary history and divergence times of Neuropterida (Insecta: Holometabola). <i>BMC Evolutionary Biology</i> , 2020, 20, 64.	3.2	48
10079	Ceratocystis wilt on <i>Eucalyptus</i> : first record from South Africa. <i>Southern Forests</i> , 2020, 82, 24-31.	0.2	9
10080	Contrasting bacteriome of the hornwort <i>Leiosporoceros dussii</i> in two nearby sites with emphasis on the hornwort-cyanobacterial symbiosis. <i>Symbiosis</i> , 2020, 81, 39-52.	1.2	24
10081	Phylogenomic insights into the temporal-spatial divergence history, evolution of leaf habit and hybridization in <i>Stachyurus</i> (Stachyuraceae). <i>Molecular Phylogenetics and Evolution</i> , 2020, 150, 106878.	1.2	12
10082	A molecular phylogenetic evaluation of the <i>Ramalina siliquosa</i> complex, with notes on species circumscription and relationships within <i>Ramalina</i> . <i>Lichenologist</i> , 2020, 52, 197-211.	0.5	7
10083	<i>Rhodachlya westii</i> sp. nov. (Rhodachlyales, Rhodophyta), a new species from Brazil, revealed by an integrative taxonomic approach. <i>Phycologia</i> , 2020, 59, 346-354.	0.6	7
10084	Molecular delimitation and taxonomic revision of the wimple piranha <i>Catoprion</i> (Characiformes: Serrasalminidae) with the description of a new species. <i>Journal of Fish Biology</i> , 2020, 97, 668-685.	0.7	9
10085	Finding complexity in complexes: Assessing the causes of mitonuclear discordance in a problematic species complex of Mesoamerican toads. <i>Molecular Ecology</i> , 2020, 29, 3543-3559.	2.0	29
10086	The nuclear and mitochondrial genomes of <i>Frieseomelitta varia</i> – a highly eusocial stingless bee (Meliponini) with a permanently sterile worker caste. <i>BMC Genomics</i> , 2020, 21, 386.	1.2	15
10087	A five-gene molecular phylogeny reveals <i>Parapanteles Ashmead</i> (Hymenoptera: Braconidae) to be polyphyletic as currently composed. <i>Molecular Phylogenetics and Evolution</i> , 2020, 150, 106859.	1.2	4
10088	Comparative Transcriptomics across Nematode Life Cycles Reveal Gene Expression Conservation and Correlated Evolution in Adjacent Developmental Stages. <i>Genome Biology and Evolution</i> , 2020, 12, 1019-1030.	1.1	15
10089	Whole-Genome Sequences of <i>Salmonella</i> Isolates from an Ecological Wastewater Treatment System. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	1
10090	Transcriptomes reveal expression of hemoglobins throughout insects and other Hexapoda. <i>PLoS ONE</i> , 2020, 15, e0234272.	1.1	6
10091	High-Quality Genome Assembly of <i>Chrysaora quinquecirrha</i> Provides Insights Into the Adaptive Evolution of Jellyfish. <i>Frontiers in Genetics</i> , 2020, 11, 535.	1.1	6
10092	Comparative Gene Analysis Focused on Silica Cell Wall Formation: Identification of Diatom-Specific SET Domain Protein Methyltransferases. <i>Marine Biotechnology</i> , 2020, 22, 551-563.	1.1	7
10093	Phylogenomics and molecular species delimitation reveals great cryptic diversity of leaf-toed geckos (Phyllodactylidae: <i>Phyllodactylus</i>), ancient origins, and diversification in Mexico. <i>Molecular Phylogenetics and Evolution</i> , 2020, 150, 106880.	1.2	11

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10094	Recent hybrids recapitulate ancient hybrid outcomes. <i>Nature Communications</i> , 2020, 11, 2179.	5.8	29
10095	Spitzenk�rper assembly mechanisms reveal conserved features of fungal and metazoan polarity scaffolds. <i>Nature Communications</i> , 2020, 11, 2830.	5.8	18
10096	Allelic sequence variation in the Sub1A, Sub1B and Sub1C genes among diverse rice cultivars and its association with submergence tolerance. <i>Scientific Reports</i> , 2020, 10, 8621.	1.6	14
10097	Characterization of the complete mitochondrial genome of <i>Ergatettix serrifemora</i> (Orthoptera: Tetrigidae) from China and its phylogenetic analysis. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2335-2336.	0.2	0
10098	A mitogenomic phylogeny of satyrid butterflies and complete mitochondrial genome of <i>Oeneis urda</i> (Lepidoptera: Nymphalidae: Satyrinae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1344-1345.	0.2	4
10099	The Ambrosia Beetle <i>Sueus niisimai</i> (Scolytinae: Hyorrhynchini) is Associated with the Canker Disease Fungus <i>Diatrypella japonica</i> (Xylariales). <i>Plant Disease</i> , 2020, 104, 3143-3150.	0.7	5
10100	Genome-Scale Phylogeny and Evolutionary Analysis of Ross River Virus Reveals Periodic Sweeps of Lineage Dominance in Western Australia, 1977–2014. <i>Journal of Virology</i> , 2020, 94, .	1.5	14
10101	Origin of OXA-23 Variant OXA-239 from a Recently Emerged Lineage of <i>Acinetobacter baumannii</i> International Clone V. <i>MSphere</i> , 2020, 5, .	1.3	50
10102	Diagnosis and prevalence of two new species of haplosporidians infecting shore crabs <i>Carcinus maenas</i> : <i>Haplosporidium carcini</i> n. sp., and <i>H. cranc</i> n. sp.. <i>Parasitology</i> , 2020, 147, 1229-1237.	0.7	12
10103	CobT and BzaC catalyze the regiospecific activation and methylation of the 5-hydroxybenzimidazole lower ligand in anaerobic cobamide biosynthesis. <i>Journal of Biological Chemistry</i> , 2020, 295, 10522-10534.	1.6	6
10104	Non-blue <i>Haslea</i> species (Bacillariophyceae: Naviculaceae) in the benthic marine flora of Guam (Mariana Islands, Western Pacific Ocean).. <i>Diatom Research</i> , 2020, 35, 163-183.	0.5	4
10105	A new section, <i>Lactifluus</i> section <i>Neotropicus</i> (Russulaceae), and two new <i>Lactifluus</i> species from the Atlantic Forest, Brazil. <i>Systematics and Biodiversity</i> , 2020, 18, 347-361.	0.5	6
10106	Phylogenetic relationships within <i>Pseudamnicola</i> Paulucci, 1878 (Caenogastropoda: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 267 T Islands. <i>Systematics and Biodiversity</i> , 2020, 18, 396-416.	0.5	7
10107	SARS-CoV-2 genomic surveillance in Taiwan revealed novel ORF8-deletion mutant and clade possibly associated with infections in Middle East. <i>Emerging Microbes and Infections</i> , 2020, 9, 1457-1466.	3.0	118
10108	Assembly and phylogenetic analysis of the complete chloroplast genome sequence of <i>Epimedium simplicifolium</i> (Berberidaceae), an endangered species endemic to China. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1865-1867.	0.2	1
10109	Comparative Analysis of Genomic Repeat Content in Gomphocerine Grasshoppers Reveals Expansion of Satellite DNA and Helitrons in Species with Unusually Large Genomes. <i>Genome Biology and Evolution</i> , 2020, 12, 1180-1193.	1.1	22
10110	High-throughput DNA sequencing of museum specimens sheds light on the long-missing species of the <i>Bokermannohyla claresignata</i> group (Anura: Hylidae: Cophomantini). <i>Zoological Journal of the Linnean Society</i> , 2020, 190, 1235-1255.	1.0	20
10111	Quaternary land bridges have not been universal conduits of gene flow. <i>Molecular Ecology</i> , 2020, 29, 2692-2706.	2.0	15

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10112	Ecological divergence in sympatry causes gene misexpression in hybrids. <i>Molecular Ecology</i> , 2020, 29, 2707-2721.	2.0	19
10113	On the origin of giant seeds: the macroevolution of the double coconut (<i>Lodoicea maldivica</i>) and its relatives (Borasseae, Arecaceae). <i>New Phytologist</i> , 2020, 228, 1134-1148.	3.5	15
10114	Hybrid Gene Origination Creates Human-Virus Chimeric Proteins during Infection. <i>Cell</i> , 2020, 181, 1502-1517.e23.	13.5	33
10115	The systematic position of the enigmatic rare South African endemic <i>Carex acocksii</i> : Its relevance on the biogeography and evolution of <i>Carex</i> sect. <i>Schoenoxiphium</i> (Cyperaceae). <i>South African Journal of Botany</i> , 2020, 131, 475-483.	1.2	6
10116	More is needed—Thousands of loci are required to elucidate the relationships of the “flowers of the sea” (Sabellida, Annelida). <i>Molecular Phylogenetics and Evolution</i> , 2020, 151, 106892.	1.2	24
10117	Disentangling the evolutionary history and biogeography of hill partridges (Phasianidae, Arborophila) from low coverage shotgun sequences. <i>Molecular Phylogenetics and Evolution</i> , 2020, 151, 106895.	1.2	2
10118	The potential of genome-wide RAD sequences for resolving rapid radiations: a case study in Cactaceae. <i>Molecular Phylogenetics and Evolution</i> , 2020, 151, 106896.	1.2	16
10119	First discovery of the sessile barnacle <i>Eochionelasmus</i> (Cirripedia: Balanomorpha) from a hydrothermal vent field in the Indian Ocean. <i>Journal of the Marine Biological Association of the United Kingdom</i> , 2020, 100, 585-593.	0.4	6
10120	Full-length transcript sequencing accelerates the transcriptome research of <i>Gymnocypris namensis</i> , an iconic fish of the Tibetan Plateau. <i>Scientific Reports</i> , 2020, 10, 9668.	1.6	12
10121	Draft genome of the European medicinal leech <i>Hirudo medicinalis</i> (Annelida, Clitellata.) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 38 1.6 27	1.6	27
10122	Systematics of <i>Hyperolius mitchelli</i> Loveridge, 1953 and <i>Hyperolius rubrovermiculatus</i> Schiitz, 1975 (Anura: Hyperoliidae) and assignment of populations from northern Tanzania. <i>African Journal of Herpetology</i> , 2020, 69, 165-181.	0.3	2
10123	Total-evidence analysis of an undescribed fauna: resolving the evolution and classification of Australia’s golden trapdoor spiders (Idiopidae: Arbanitinae: Euopliini). <i>Cladistics</i> , 2020, 36, 543-568.	1.5	8
10124	Identification of putative lignin biosynthesis genes in <i>Betula pendula</i> . <i>Trees - Structure and Function</i> , 2020, 34, 1255-1265.	0.9	5
10125	Recurrent horizontal transfer identifies mitochondrial positive selection in a transmissible cancer. <i>Nature Communications</i> , 2020, 11, 3059.	5.8	18
10126	Phylogenetic diversity in <i>fim</i> and <i>mfa</i> gene clusters between <i>Porphyromonas gingivalis</i> and <i>Porphyromonas gulae</i> , as a potential cause of host specificity. <i>Journal of Oral Microbiology</i> , 2020, 12, 1775333.	1.2	9
10127	The complete chloroplast genome of an endangered and endemic species, <i>Acer yangbiense</i> (Aceraceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 224-225.	0.2	3
10128	Episodic and guanine-cytosine-biased bursts of intragenomic and interspecific synonymous divergence in Ajugoideae (Lamiaceae) mitogenomes. <i>New Phytologist</i> , 2020, 228, 1107-1114.	3.5	13
10129	Epidemiology, genetic diversity and evolution of canine astrovirus. <i>Transboundary and Emerging Diseases</i> , 2020, 67, 2901-2910.	1.3	6

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10130	Involvement of Chromosomally Encoded Homologs of the RRNPP Protein Family in <i>Enterococcus faecalis</i> Biofilm Formation and Urinary Tract Infection Pathogenesis. <i>Journal of Bacteriology</i> , 2020, 202, .	1.0	6
10131	Tandem gene duplications drive divergent evolution of caffeine and crocin biosynthetic pathways in plants. <i>BMC Biology</i> , 2020, 18, 63.	1.7	94
10132	Spontaneous Tumor Regression in Tasmanian Devils Associated with <i>RASL11A</i> Activation. <i>Genetics</i> , 2020, 215, 1143-1152.	1.2	22
10133	Cross-Species Annotation of Expressed Genes and Detection of Different Functional Gene Modules Between 10 Cold- and 10 Hot-Propertied Chinese Herbal Medicines. <i>Frontiers in Genetics</i> , 2020, 11, 532.	1.1	2
10134	Insights Into Chloroplast Genome Evolution Across Opuntioideae (Cactaceae) Reveals Robust Yet Sometimes Conflicting Phylogenetic Topologies. <i>Frontiers in Plant Science</i> , 2020, 11, 729.	1.7	38
10135	Molecular Characterization and Antimicrobial Susceptibilities of <i>Nocardia</i> Species Isolated from the Soil; A Comparison with Species Isolated from Humans. <i>Microorganisms</i> , 2020, 8, 900.	1.6	4
10136	Diketopiperazines from <i>Batnamyces globulariicola</i> , gen. & sp. nov. (Chaetomiaceae), a fungus associated with roots of the medicinal plant <i>Globularia alypum</i> in Algeria. <i>Mycological Progress</i> , 2020, 19, 589-603.	0.5	17
10137	Cascading effects in freshwater microbial food webs by predatory Cercozoa, Katablepharidacea and ciliates feeding on aplastidic bacterivorous cryptophytes. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	14
10138	Detection of heterogeneous vancomycin intermediate resistance in MRSA isolates from Latin America. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 2424-2431.	1.3	8
10139	Evidence of repeated horizontal transfer of sterol C-5 desaturase encoding genes among dikarya fungi. <i>Molecular Phylogenetics and Evolution</i> , 2020, 150, 106850.	1.2	7
10140	Diversification history of clown tree frogs in Neotropical rainforests (Anura, Hylidae). <i>Trends in Ecology and Evolution</i> , 2020, 35, 1011-1021.	1.2	21
10141	Phylogenetic position of <i>Aculamprotula polysticta</i> , comb. res. (Bivalvia : Unionidae) inferred from phylogenetic relationships in Unionida. <i>Invertebrate Systematics</i> , 2020, 34, 192.	0.5	3
10142	Molecular phylogeny and ultrastructure of two novel parasitic dinoflagellates, <i>Haplozoon gracile</i> sp. nov. and <i>H. pugnus</i> sp. nov. <i>Phycologia</i> , 2020, 59, 305-319.	0.6	3
10143	The complete chloroplast genome of <i>Caryopteris incana</i> (Lamiaceae) and phylogenetic analysis. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1399-1400.	0.2	3
10144	First sexual morph record of <i>Sarcopodium vanillae</i> . <i>Mycotaxon</i> , 2020, 134, 707-717.	0.1	2
10145	Comparative Genomics Suggests Mechanisms of Genetic Adaptation toward the Catabolism of the Phenylurea Herbicide Linuron in <i>Variovorax</i> . <i>Genome Biology and Evolution</i> , 2020, 12, 827-841.	1.1	21
10146	Origin and evolution of dengue virus type 2 causing outbreaks in Kenya: Evidence of circulation of two cosmopolitan genotype lineages. <i>Virus Evolution</i> , 2020, 6, veaa026.	2.2	9
10147	Complete plastome sequencing resolves taxonomic relationships among species of <i>Calligonum</i> L. (Polygonaceae) in China. <i>BMC Plant Biology</i> , 2020, 20, 261.	1.6	30

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10148	Analysis of 1321 <i>Eubacterium rectale</i> genomes from metagenomes uncovers complex phylogeographic population structure and subspecies functional adaptations. <i>Genome Biology</i> , 2020, 21, 138.	3.8	72
10149	Comparative Genomics of the <i>Rhodococcus</i> Genus Shows Wide Distribution of Biodegradation Traits. <i>Microorganisms</i> , 2020, 8, 774.	1.6	25
10150	A Novel Retrovirus (Gunnison's Prairie Dog Retrovirus) Associated With Thymic Lymphoma in Gunnison's Prairie Dogs in Colorado, USA. <i>Viruses</i> , 2020, 12, 606.	1.5	6
10151	A sister lineage of the <i>Mycobacterium tuberculosis</i> complex discovered in the African Great Lakes region. <i>Nature Communications</i> , 2020, 11, 2917.	5.8	136
10152	Genomic consequences of dietary diversification and parallel evolution due to nectarivory in leaf-nosed bats. <i>GigaScience</i> , 2020, 9, .	3.3	18
10153	Inherent colistin resistance in genogroups of the <i>Enterobacter cloacae</i> complex: epidemiological, genetic and biochemical analysis from the BSAC Resistance Surveillance Programme. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 2452-2461.	1.3	20
10154	Model-Based Inference of Punctuated Molecular Evolution. <i>Molecular Biology and Evolution</i> , 2020, 37, 3308-3323.	3.5	13
10155	Phylogenetic reassessment of gorals with new evidence from northern Myanmar reveals five distinct species. <i>Mammal Review</i> , 2020, 50, 325-330.	2.2	7
10156	Depth-related variability in viral communities in highly stratified sulfidic mine tailings. <i>Microbiome</i> , 2020, 8, 89.	4.9	41
10157	Analysis of Pigment-Dispersing Factor Neuropeptides and Their Receptor in a Velvet Worm. <i>Frontiers in Endocrinology</i> , 2020, 11, 273.	1.5	4
10158	Whole Genome Sequencing and Spatial Analysis Identifies Recent Tuberculosis Transmission Hotspots in Ghana. <i>Frontiers in Medicine</i> , 2020, 7, 161.	1.2	15
10159	Patellariopsidaceae Fam. Nov. With Sexual-Asexual Connection and a New Host Record for <i>Cheirospora botryospora</i> (<i>Vibrissaceae</i> , <i>Ascomycota</i>). <i>Frontiers in Microbiology</i> , 2020, 11, 906.	1.5	2
10160	Chromosome Architecture and Gene Content of the Emergent Pathogen <i>Acinetobacter haemolyticus</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 926.	1.5	4
10161	Fungal Diversity in the Neptune Forest: Comparison of the Mycobiota of <i>Posidonia oceanica</i> , <i>Flabellia petiolata</i> , and <i>Padina pavonica</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 933.	1.5	13
10162	Single-Cell Genomics of Novel Actinobacteria With the Wood's Ljungdahl Pathway Discovered in a Serpentinizing System. <i>Frontiers in Microbiology</i> , 2020, 11, 1031.	1.5	41
10163	A Large-Scale Outbreak of Echovirus 30 in Gansu Province of China in 2015 and Its Phylodynamic Characterization. <i>Frontiers in Microbiology</i> , 2020, 11, 1137.	1.5	13
10164	Population Genomics and Phylogeography of a Clonal Bryophyte With Spatially Separated Sexes and Extreme Sex Ratios. <i>Frontiers in Plant Science</i> , 2020, 11, 495.	1.7	7
10165	Genomic Origin and Diversification of the Glucosinolate MAM Locus. <i>Frontiers in Plant Science</i> , 2020, 11, 711.	1.7	10

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10166	New Intranuclear Symbiotic Bacteria from Macronucleus of <i>Paramecium putrinum</i> "Candidatus Gortzia Yakutica". <i>Diversity</i> , 2020, 12, 198.	0.7	19
10167	Intestinal Microbiota Analyses of <i>Litopenaeus vannamei</i> During a Case of Atypical Massive Mortality in Northwestern Mexico. <i>Current Microbiology</i> , 2020, 77, 2312-2321.	1.0	3
10168	Phylogenomics indicates the "living fossil" Isoetes diversified in the Cenozoic. <i>PLoS ONE</i> , 2020, 15, e0227525.	1.1	20
10169	The 206 kbp mitochondrial genome of <i>Phanerochaete carnosae</i> reveals dynamics of introns, accumulation of repeat sequences and plasmid-derived genes. <i>International Journal of Biological Macromolecules</i> , 2020, 162, 209-219.	3.6	33
10170	Corrigendum to: Phylogeny, evolution and systematic revision of the mite harvestman family Neogoveidae (Opiliones Cyphophthalmi). <i>Invertebrate Systematics</i> , 2020, , .	0.5	0
10171	Phylogeny and historical biogeography of Hydrophyllaceae and Namaceae, with a special reference to <i>Phacelia</i> and <i>Wigandia</i> . <i>Systematics and Biodiversity</i> , 2020, 18, 757-770.	0.5	5
10172	Maximum Likelihood Estimation of Species Trees from Gene Trees in the Presence of Ancestral Population Structure. <i>Genome Biology and Evolution</i> , 2020, 12, 3977-3995.	1.1	5
10173	Host functional and phylogenetic composition rather than host diversity structure plant "herbivore networks. <i>Molecular Ecology</i> , 2020, 29, 2747-2762.	2.0	24
10174	Adaptation Evolution and Phylogenetic Analyses of Species in Chinese <i>Allium</i> Section <i>Pallasia</i> and Related Species Based on Complete Chloroplast Genome Sequences. <i>BioMed Research International</i> , 2020, 2020, 1-13.	0.9	9
10175	A chromosome-level assembly of the cat flea genome uncovers rampant gene duplication and genome size plasticity. <i>BMC Biology</i> , 2020, 18, 70.	1.7	29
10176	Comparative Mitogenome Analysis Reveals Mitochondrial Genome Differentiation in Ectomycorrhizal and Asymbiotic <i>Amanita</i> Species. <i>Frontiers in Microbiology</i> , 2020, 11, 1382.	1.5	42
10177	Comparison of Chloroplast Genomes among Species of Unisexual and Bisexual Clades of the Monocot Family Araceae. <i>Plants</i> , 2020, 9, 737.	1.6	23
10178	Signatures of TRI5, TRI8 and TRI11 Protein Sequences of <i>Fusarium incarnatum-equiseti</i> Species Complex (FIESC) Indicate Differential Trichothecene Analogue Production. <i>Toxins</i> , 2020, 12, 386.	1.5	1
10179	A high-quality genome sequence of alkaligrass provides insights into halophyte stress tolerance. <i>Science China Life Sciences</i> , 2020, 63, 1269-1282.	2.3	19
10180	Metabolomic-guided discovery of cyclic nonribosomal peptides from <i>Xylaria ellisii</i> sp. nov., a leaf and stem endophyte of <i>Vaccinium angustifolium</i> . <i>Scientific Reports</i> , 2020, 10, 4599.	1.6	22
10181	Metallomics reveals a persisting impact of cadmium on the evolution of metal-selective snail metallothioneins. <i>Metallomics</i> , 2020, 12, 702-720.	1.0	15
10182	Honey bees harbor a diverse gut virome engaging in nested strain-level interactions with the microbiota. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 7355-7362.	3.3	37
10183	Carbon Use Efficiency and Its Temperature Sensitivity Covary in Soil Bacteria. <i>MBio</i> , 2020, 11, .	1.8	52

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10184	Plastome Evolution in Dolomiaea (Asteraceae, Cardueae) Using Phylogenomic and Comparative Analyses. <i>Frontiers in Plant Science</i> , 2020, 11, 376.	1.7	18
10185	Taxonomic assignment of arbuscular mycorrhizal fungi in an 18S metagenomic dataset: a case study with saltcedar (<i>Tamarix aphylla</i>). <i>Mycorrhiza</i> , 2020, 30, 243-255.	1.3	26
10186	Fungal diversity notes 1151–1276: taxonomic and phylogenetic contributions on genera and species of fungal taxa. <i>Fungal Diversity</i> , 2020, 100, 5-277.	4.7	156
10187	The evolution of metabolism: How to test evolutionary hypotheses at the genomic level. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 482-500.	1.9	36
10188	Whole-Genome Analysis of Livestock-Associated Methicillin-Resistant <i>Staphylococcus aureus</i> Sequence Type 398 Strains Isolated From Patients With Bacteremia in China. <i>Journal of Infectious Diseases</i> , 2020, 221, S220-S228.	1.9	13
10189	The Tobacco Plant Genome. <i>Compendium of Plant Genomes</i> , 2020, , .	0.3	5
10190	Taxonomy on three novel species of <i>Sphaeromyxa</i> ThÃ©lohan 1892 (Myxozoa, Bivalvulida.) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 507 T</i> 1493-1503.	0.6	4
10191	Positive Selection of a Serine Residue in Bat IRF3 Confers Enhanced Antiviral Protection. <i>iScience</i> , 2020, 23, 100958.	1.9	34
10192	Pliocene–Early Pleistocene Geological Events Structure Pacific Martens (<i>Martes caurina</i>). <i>Journal of Heredity</i> , 2020, 111, 169-181.	1.0	5
10193	Out of Tibet: Genomic Perspectives on the Evolutionary History of Extant Pikas. <i>Molecular Biology and Evolution</i> , 2020, 37, 1577-1592.	3.5	39
10194	The invertebrate host of salmonid fish parasites <i>Ceratonova shasta</i> and <i>Parvicapsula minibicornis</i> (Cnidaria: Myxozoa), is a novel fabriciid annelid, <i>Manayunkia occidentalis</i> sp. nov. (Sabellida.) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 337</i>	1.0	5
10195	Delimitation of five astome ciliate species isolated from the digestive tube of three ecologically different groups of lumbricid earthworms, using the internal transcribed spacer region and the hypervariable D1/D2 region of the 28S rRNA gene. <i>BMC Evolutionary Biology</i> , 2020, 20, 37.	3.2	16
10196	Brown marmorated stink bug, <i>Halyomorpha halys</i> (Stål), genome: putative underpinnings of polyphagy, insecticide resistance potential and biology of a top worldwide pest. <i>BMC Genomics</i> , 2020, 21, 227.	1.2	60
10197	Genome of the webworm <i>Hyphantria cunea</i> unveils genetic adaptations supporting its rapid invasion and spread. <i>BMC Genomics</i> , 2020, 21, 242.	1.2	12
10198	Whole genome phylogeny of <i>Gallus</i> : introgression and data-type effects. <i>Avian Research</i> , 2020, 11, .	0.5	17
10199	Whole-Genome Analysis of <i>Salmonella enterica</i> Serovar Enteritidis Isolates in Outbreak Linked to Online Food Delivery, Shenzhen, China, 2018. <i>Emerging Infectious Diseases</i> , 2020, 26, 789-792.	2.0	26
10200	Comparative Mitogenome Analysis of the Genus <i>Trifolium</i> Reveals Independent Gene Fission of <i>ccmFn</i> and Intracellular Gene Transfers in Fabaceae. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1959.	1.8	17
10201	Evolution and Pathogenicity of the H1 and H3 Subtypes of Swine Influenza Virus in Mice between 2016 and 2019 in China. <i>Viruses</i> , 2020, 12, 298.	1.5	7

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10202	Reconstructing the Phylogeny of Corynebacteriales while Accounting for Horizontal Gene Transfer. <i>Genome Biology and Evolution</i> , 2020, 12, 381-395.	1.1	2
10203	Cave-adapted evolution in the North American amblyopsid fishes inferred using phylogenomics and geometric morphometrics. <i>Evolution; International Journal of Organic Evolution</i> , 2020, 74, 936-949.	1.1	13
10204	Draft Genome Analysis of <i>Christensenella minuta</i> DSM 22607, exhibiting an unusual expansion of transporter homologs of unknown function. <i>Journal of Genomics</i> , 2020, 8, 25-29.	0.6	5
10205	High Diversity of Testate Amoebae (Amoebozoa, Arcellinida) Detected by HTS Analyses in a New England Fen using Newly Designed Taxon-specific Primers. <i>Journal of Eukaryotic Microbiology</i> , 2020, 67, 450-462.	0.8	9
10206	Feeling sluggish: The extreme semislugs of Australia (Stylommatophora, Helicarionidae). <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2020, 58, 1021-1057.	0.6	3
10207	Phylogenetic Relationship Among Brackishwater <i>Vibrio</i> Species. <i>Evolutionary Bioinformatics</i> , 2020, 16, 117693432090328.	0.6	9
10208	Novel HPAIV H5N8 Reassortant (Clade 2.3.4.4b) Detected in Germany. <i>Viruses</i> , 2020, 12, 281.	1.5	41
10209	The transcription factor MML4_D12 regulates fiber development through interplay with the WD40-repeat protein WDR in cotton. <i>Journal of Experimental Botany</i> , 2020, 71, 3499-3511.	2.4	24
10210	Beyond Wallace: a new lineage of Chrysorthenches (Lepidoptera: Yponomeutoidea: Glyphipterigidae) reveals a journey tracking its host-plants, Podocarpus (Pinopsida: Podocarpaceae). <i>Zoological Journal of the Linnean Society</i> , 2020, 190, 709-736.	1.0	0
10211	Allopatric divergence and hybridization within <i>Cupressus chengiana</i> (Cupressaceae), a threatened conifer in the northern Hengduan Mountains of western China. <i>Molecular Ecology</i> , 2020, 29, 1250-1266.	2.0	46
10212	Assessing cryptic diversity in Neotropical rattlesnakes (Serpentes: Viperidae: Crotalus) with the description of two new species. <i>Zootaxa</i> , 2020, 4729, zootaxa.4729.4.1.	0.2	20
10213	Morphological Redescriptions and Molecular Phylogeny of Three Stentor Species (Ciliophora: Heterotrichea: Stentoridae) from Korea . <i>Zootaxa</i> , 2020, 4732, 435-452.	0.2	2
10214	A new species of the genus <i>Dendrelaphis</i> (Squamata: Colubridae) from Yunnan Province, China, with discussion of the occurrence of <i>D. cyanochloris</i> (Wall, 1921) in China. <i>Zootaxa</i> , 2020, 4743, 1-20.	0.2	3
10215	Using ggtree to Visualize Data on Tree-Like Structures. <i>Current Protocols in Bioinformatics</i> , 2020, 69, e96.	25.8	810
10216	Systematics and taxonomy of <i>Platyrrhinus chocoensis</i> (Chiroptera: Phyllostomidae) based on morphometric and genetic analyses: implications for biogeography and conservation. <i>Mammalian Biology</i> , 2020, 100, 113-124.	0.8	4
10217	Evolution of lifestyles in Capnodiales. <i>Studies in Mycology</i> , 2020, 95, 381-414.	4.5	76
10218	<i>Weda</i> , a new genus with two new species of Euphorbiaceae-Crotonoideae from Halmahera (North Maluku, Indonesia) and phylogenetic relationships of the Australasian tribe Ricinocarpeae. <i>Journal of Systematics and Evolution</i> , 2021, 59, 1000-1017.	1.6	5
10219	Revision of the <i>Psilota</i> Meigen, 1822 flower flies (Diptera: Syrphidae) of Australia. <i>Zootaxa</i> , 2020, 4737, zootaxa.4737.1.1.	0.2	3

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10220	Resolving the taxonomic puzzle of <i>Boana cinerascens</i> (Spix, 1824), with resurrection of <i>Hyla granosa gracilis</i> Melin, 1941 (Anura: Hylidae). <i>Zootaxa</i> , 2020, 4750, zootaxa.4750.1.1.	0.2	3
10221	<p>Description of a new snake eel Ophichthus olivaceus (Teleostei: Tj ETQq1 1 0,784314 rgBT /Overl	0.2	1
10222	Tunicate bulb size variation in monocots explained by temperature and phenology. <i>Ecology and Evolution</i> , 2020, 10, 2299-2309.	0.8	10
10223	Mitochondrial, metagenomic, and phylogenetic analysis of the ground beetle <i>Harpalus pensylvanicus</i> (Coleoptera: Carabidae). <i>Gene</i> , 2020, 740, 144540.	1.0	4
10224	Integrative taxonomic consideration of the Holarctic <i>Euconulus fulvus</i> group of land snails (Gastropoda, Stylommatophora). <i>Systematics and Biodiversity</i> , 2020, 18, 142-160.	0.5	10
10225	Regulators of an ancient polyphenism evolved through episodic protein divergence and parallel gene radiations. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20192595.	1.2	7
10226	A new species of the genus Pseudocrangonyx (Crustacea: Amphipoda:) Tj ETQq0 0 0 rgBT /Overl	0.2	10
10227	Exploring Micro-Eukaryotic Diversity in the Gut: Co-occurrence of Blastocystis Subtypes and Other Protists in Zoo Animals. <i>Frontiers in Microbiology</i> , 2020, 11, 288.	1.5	28
10228	Photosynthetic Picoeukaryotes Diversity in the Underlying Ice Waters of the White Sea, Russia. <i>Diversity</i> , 2020, 12, 93.	0.7	5
10229	Diverse patterns of constitutive and inducible overexpression of detoxifying enzyme genes among resistant <i>Aphis glycines</i> populations. <i>Pesticide Biochemistry and Physiology</i> , 2020, 164, 100-114.	1.6	13
10230	Vulnerability to Fishing and Life History Traits Correlate with the Load of Deleterious Mutations in Teleosts. <i>Molecular Biology and Evolution</i> , 2020, 37, 2192-2196.	3.5	12
10231	Discovery of a New TLR Gene and Gene Expansion Event through Improved Desert Tortoise Genome Assembly with Chromosome-Scale Scaffolds. <i>Genome Biology and Evolution</i> , 2020, 12, 3917-3925.	1.1	8
10232	Novel Insights into the Classification of Staphylococcal β -Lactamases in Relation to the Cefazolin Inoculum Effect. <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	1.4	13
10233	Genomic epidemiological characteristics of dengue fever in Guangdong province, China from 2013 to 2017. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008049.	1.3	9
10234	Green Fluorescence Patterns in Closely Related Symbiotic Species of <i>Zanclaea</i> (Hydrozoa, Capitata). <i>Diversity</i> , 2020, 12, 78.	0.7	8
10235	dsRNA-seq Reveals Novel RNA Virus and Virus-Like Putative Complete Genome Sequences from <i>Hymeniacidon</i> sp.<i>Sponge</i>. <i>Microbes and Environments</i> , 2020, 35, n/a.	0.7	21
10236	IsoSeq transcriptome assembly of <i>C₃</i> panicoid grasses provides tools to study evolutionary change in the Panicoideae. <i>Plant Direct</i> , 2020, 4, e00203.	0.8	2
10237	Characterization of <i>Myxidium spinibarba</i> sp. nov. (Cnidaria, Myxosporea, Myxidiidae) from <i>Spinibarbus sinensis</i> (Bleeker, 1871) in Chongqing China. <i>Parasitology Research</i> , 2020, 119, 1485-1491.	0.6	5

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10238	Global phylogenetic and morphological reassessment of <i>Fomitiporella</i> s.l. (Hymenochaetales,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 747 nov.. <i>Plant Systematics and Evolution</i> , 2020, 306, 1.	0.3	9
10239	Genetic diversification, population structure, and geophylogeny of the Scarface rockskipper <i>Istiblennius pox</i> (Teleostei: Blenniidae) in the Persian Gulf and Oman Sea. <i>Marine Biodiversity</i> , 2020, 50, 1.	0.3	9
10240	The large single-copy (LSC) region functions as a highly effective and efficient molecular marker for accurate authentication of medicinal <i>Dendrobium</i> species. <i>Acta Pharmaceutica Sinica B</i> , 2020, 10, 1989-2001.	5.7	23
10241	Morphology, morphogenesis, and molecular phylogeny of a novel saline soil ciliate, <i>Heterourosomoida sinica</i> n. sp. (Ciliophora, Hypotrichia). <i>European Journal of Protistology</i> , 2020, 73, 125666.	0.5	17
10242	Multiple evolutionary origins of sequestrate species in the agaricoid genus <i>Chlorophyllum</i> . <i>Mycologia</i> , 2020, 112, 400-422.	0.8	13
10243	Practical Speedup of Bayesian Inference of Species Phylogenies by Restricting the Space of Gene Trees. <i>Molecular Biology and Evolution</i> , 2020, 37, 1809-1818.	3.5	4
10244	Melanopsidae (Caenogastropoda: Cerithioidea) from the eastern Mediterranean: another case of morphostatic speciation. <i>Zoological Journal of the Linnean Society</i> , 2020, 190, 483-507.	1.0	7
10245	Stable species boundaries despite ten million years of hybridization in tropical eels. <i>Nature Communications</i> , 2020, 11, 1433.	5.8	53
10246	Live bird markets as evolutionary epicentres of H9N2 low pathogenicity avian influenza viruses in Korea. <i>Emerging Microbes and Infections</i> , 2020, 9, 616-627.	3.0	20
10247	Unmatched Level of Molecular Convergence among Deeply Divergent Complex Multicellular Fungi. <i>Molecular Biology and Evolution</i> , 2020, 37, 2228-2240.	3.5	23
10248	Evaluating the Performance of Probabilistic Algorithms for Phylogenetic Analysis of Big Morphological Datasets: A Simulation Study. <i>Systematic Biology</i> , 2020, 69, 1088-1105.	2.7	20
10249	A well-resolved transcriptomic phylogeny of the mite harvestman family Pettalidae (Arachnida,) Tj ETQq1 1 0.784314 rgBT /Overlock 1 2020, 47, 1345-1361.	1.4	20
10250	Genome Sequence Analysis of <i>Auricularia heimuer</i> Combined with Genetic Linkage Map. <i>Journal of Fungi (Basel, Switzerland)</i> , 2020, 6, 37.	1.5	14
10251	A Novel Hepe-Like Virus from Farmed Giant Freshwater Prawn <i>Macrobrachium rosenbergii</i> . <i>Viruses</i> , 2020, 12, 323.	1.5	13
10252	The genus <i>Ravenelia</i> (Pucciniales) in South Africa. <i>Mycological Progress</i> , 2020, 19, 259-290.	0.5	4
10253	A species complex within the red-reticulate <i>Goniobranchus</i> Pease, 1866 (Nudibranchia: Doridina:) Tj ETQq1 1 0.784314 rgBT /Overlock 1 0,3	0,3	5
10254	First draft genome for the sand-hopper <i>Trinorchestia longiramus</i> . <i>Scientific Data</i> , 2020, 7, 85.	2.4	8
10255	Systematics, biogeography, and diversification of <i>Scytalopus tapaculos</i> (Rhinocryptidae), an enigmatic radiation of Neotropical montane birds. <i>Auk</i> , 2020, 137, .	0.7	26

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10256	Functional Characterization of Sex Pheromone Receptors in the Fall Armyworm (Spodoptera) Tj ETQq0 0 0 rgBT /Oerlock 10 Tf 50 742	1.0	24
10257	Complete plastid genome of <i>Dendrocalamus brandisii</i> (Poaceae, Bambusoideae). Mitochondrial DNA Part B: Resources, 2020, 5, 1286-1287.	0.2	2
10258	Upgrading of Three Subspecies of <i>Eudigraphis takakuwai</i> to the Species Rank (Diplopoda: Penicillata: Polyxenida: Polyxenidae). Species Diversity, 2020, 25, 89-102.	0.1	0
10259	Animal Disease Surveillance in the 21st Century: Applications and Robustness of Phylodynamic Methods in Recent U.S. Human-Like H3 Swine Influenza Outbreaks. Frontiers in Veterinary Science, 2020, 7, 176.	0.9	1
10260	COVID-19: Epidemiology, Evolution, and Cross-Disciplinary Perspectives. Trends in Molecular Medicine, 2020, 26, 483-495.	3.5	470
10261	Novel phosphate-solubilizing bacteria enhance soil phosphorus cycling following ecological restoration of land degraded by mining. ISME Journal, 2020, 14, 1600-1613.	4.4	194
10262	Complete mitochondrial genome of the witch-hazel leaf gall aphid <i>Hamamelistes spinosus</i> (Hemiptera: Tj ETQq0 0 0 rgBT /Oerlock 10	0.2	3
10263	Hyena paleogenomes reveal a complex evolutionary history of cross-continental gene flow between spotted and cave hyena. Science Advances, 2020, 6, eaay0456.	4.7	38
10264	Insights into human genetic variation and population history from 929 diverse genomes. Science, 2020, 367, .	6.0	534
10265	Phylogeography of <i>Acartia tonsa</i> Dana, 1849 (Calanoida: Copepoda) and phylogenetic reconstruction of the genus <i>Acartia</i> Dana, 1846. Marine Biodiversity, 2020, 50, 1.	0.3	12
10266	The complete chloroplast genome sequence of <i>Oroxylum indicum</i> (L.) Kurz (Bignoniaceae) and its phylogenetic analysis. Mitochondrial DNA Part B: Resources, 2020, 5, 1429-1430.	0.2	5
10267	Recent mitochondrial lineage extinction in the critically endangered Javan rhinoceros. Zoological Journal of the Linnean Society, 2020, 190, 372-383.	1.0	13
10268	Observations on the relationships of some Sundaic passerine taxa (Aves: Passeriformes) previously unavailable for molecular phylogenetic study. Journal of Ornithology, 2020, 161, 651-664.	0.5	6
10269	Phylogenomics, Biogeography, and Morphometrics Reveal Rapid Phenotypic Evolution in Pythons After Crossing Wallace's Line. Systematic Biology, 2020, 69, 1039-1051.	2.7	24
10270	Dimorphic Leaf Development of the Aquatic Plant <i>Callitriche palustris</i> L. Through Differential Cell Division and Expansion. Frontiers in Plant Science, 2020, 11, 269.	1.7	19
10271	The complete chloroplast genome of <i>Malva verticillata</i> (Malvaceae). Mitochondrial DNA Part B: Resources, 2020, 5, 1609-1610.	0.2	1
10272	High-quality genome assembly and transcriptome of <i>Ancherythroculter nigrocauda</i> , an endemic Chinese cyprinid species. Molecular Ecology Resources, 2020, 20, 882-891.	2.2	11
10273	New Findings of the Rare Species <i>Rondeletia bicolor</i> (Stephanoberycoidei) Over the Mid-Atlantic Ridge and Some Peculiarities of the Rondeletiidae Family's Phylogeny. Journal of Ichthyology, 2020, 60, 13-21.	0.2	2

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10274	Taxonomy and phylogeny of hyaline-spored coelomycetes. <i>Fungal Diversity</i> , 2020, 100, 279-801.	4.7	58
10275	The grass squid <i>Pickfordiateuthis pulchella</i> is a paedomorphic loliginid. <i>Molecular Phylogenetics and Evolution</i> , 2020, 147, 106801.	1.2	8
10276	Phylogeny and divergence time estimation of the walnut family (Juglandaceae) based on nuclear RAD-Seq and chloroplast genome data. <i>Molecular Phylogenetics and Evolution</i> , 2020, 147, 106802.	1.2	45
10277	<i>Zygnema circumcarinatum</i> UTEX 1559 chloroplast and mitochondrial genomes provide insight into land plant evolution. <i>Journal of Experimental Botany</i> , 2020, 71, 3361-3373.	2.4	9
10278	Two Cobalt Chelatase Subunits Can Be Generated from a Single chlD Gene via Programed Frameshifting. <i>Molecular Biology and Evolution</i> , 2020, 37, 2268-2278.	3.5	9
10279	Combinatorial Evolution of a Terpene Synthase Gene Cluster Explains Terpene Variations in <i>Oryza</i> . <i>Plant Physiology</i> , 2020, 182, 480-492.	2.3	33
10280	A comparison of latitudinal species diversity patterns between riverine and terrestrial earthworms from the North American temperate zone. <i>Journal of Biogeography</i> , 2020, 47, 1373-1382.	1.4	4
10281	High diversity and pan-oceanic distribution of deep-sea polychaetes: <i>Prionospio</i> and <i>Aurospio</i> (Annelida: Spionidae) in the Atlantic and Pacific Ocean. <i>Organisms Diversity and Evolution</i> , 2020, 20, 171-187.	0.7	16
10282	Gut microbiota in neonates with congenital gastrointestinal surgical conditions: a prospective study. <i>Pediatric Research</i> , 2020, 88, 878-886.	1.1	11
10283	Characterization of the complete chloroplast genome of <i>Caesalpinia sappan</i> L. (Leguminosae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1642-1643.	0.2	1
10284	Expanding the mutualistic niche: parallel symbiont turnover along climatic gradients. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20192311.	1.2	31
10285	Genomic and transcriptomic evidence of light-sensing, porphyrin biosynthesis, Calvin-Benson-Bassham cycle, and urea production in Bathyarchaeota. <i>Microbiome</i> , 2020, 8, 43.	4.9	31
10286	A high-quality genome provides insights into the new taxonomic status and genomic characteristics of <i>Cladopus chinensis</i> (Podostemaceae). <i>Horticulture Research</i> , 2020, 7, 46.	2.9	11
10287	The <i>Litsea</i> genome and the evolution of the laurel family. <i>Nature Communications</i> , 2020, 11, 1675.	5.8	80
10288	Water lily (<i>Nymphaea thermarum</i>) genome reveals variable genomic signatures of ancient vascular cambium losses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 8649-8656.	3.3	33
10289	Deep genetic divergence and paraphyly in cryptic species of <i>Mugil</i> fishes (Actinopterygii): Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf	0.5	20
10290	Description of a new species of <i>Xylophis</i> Beddome, 1878 (Serpentes: Pareidae): Tj ETQq0 0 0 rgBT /Overlock 10 Tf	0.2	11
10291	Testing generic limits in Cercidoideae (Leguminosae): Insights from plastid and duplicated nuclear gene sequences. <i>Taxon</i> , 2020, 69, 67-86.	0.4	15

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10292	Exceptional diversity of opsin expression patterns in <i>Neogonodactylus oerstedii</i> (Stomatopoda) retinas. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 8948-8957.	3.3	22
10293	Species detection and delineation in the marine planktonic diatoms <i>Chaetoceros</i> and <i>Bacteriastrium</i> through metabarcoding: making biological sense of haplotype diversity. <i>Environmental Microbiology</i> , 2020, 22, 1917-1929.	1.8	15
10294	Functional colour genes and signals of selection in colour polymorphic salamanders. <i>Molecular Ecology</i> , 2020, 29, 1284-1299.	2.0	15
10295	Characterization of the Whole Mitogenome of Largehead Hairtail <i>Trichiurus lepturus</i> (Trichiuridae): Insights into Special Characteristics. <i>Biochemical Genetics</i> , 2020, 58, 430-451.	0.8	6
10296	Cryptic diversity of the genus <i>Beauveria</i> with a new species from Thailand. <i>Mycological Progress</i> , 2020, 19, 291-315.	0.5	18
10297	Multi-locus phylogeny and pathogenicity of <i>Stemphylium</i> species associated with legumes in Australia. <i>Mycological Progress</i> , 2020, 19, 381-396.	0.5	14
10298	A combined approach of mitochondrial DNA and anchored nuclear phylogenomics sheds light on unrecognized diversity, phylogeny, and historical biogeography of the torrent frogs, genus <i>Amolops</i> (Anura: Ranidae). <i>Molecular Phylogenetics and Evolution</i> , 2020, 148, 106789.	1.2	23
10299	<i>Anthoceros</i> genomes illuminate the origin of land plants and the unique biology of hornworts. <i>Nature Plants</i> , 2020, 6, 259-272.	4.7	225
10300	Antigenic characterization of novel H1 influenza A viruses in swine. <i>Scientific Reports</i> , 2020, 10, 4510.	1.6	19
10301	A new epiphyllous fly-speck fungus from the Early Cretaceous Potomac Group of Virginia (125–112 Ma): <i>Protographum luttrellii</i> , gen. et sp. nov.. <i>Mycologia</i> , 2020, 112, 504-518.	0.8	9
10302	<i>Commanderella</i> gen. nov. and new insights into foliose Kallymeniaceae (Rhodophyta) from the Russian Pacific coast based on molecular studies. <i>Phycologia</i> , 2020, 59, 200-207.	0.6	6
10303	What Is in <i>Umbilicaria pustulata</i> ? A Metagenomic Approach to Reconstruct the Holo-Genome of a Lichen. <i>Genome Biology and Evolution</i> , 2020, 12, 309-324.	1.1	37
10304	Multiple Genetic Trajectories to Extreme Abiotic Stress Adaptation in Arctic Brassicaceae. <i>Molecular Biology and Evolution</i> , 2020, 37, 2052-2068.	3.5	28
10305	Survival in the Tropics despite isolation, inbreeding and asexual reproduction: insights from the genome of the world's southernmost poplar (<i>Populus ilicifolia</i>). <i>Plant Journal</i> , 2020, 103, 430-442.	2.8	23
10306	Two new species of <i>Pristimantis</i> (Anura: Craugastoridae) with notes on the distribution of the genus in northeastern Colombia. <i>Zootaxa</i> , 2020, 4750, zootaxa.4750.4.3.	0.2	10
10307	Identification of a General Odorant Receptor for Repellents in the Asian Corn Borer <i>Ostrinia furnacalis</i> . <i>Frontiers in Physiology</i> , 2020, 11, 176.	1.3	13
10308	The Increase of Simple Sequence Repeats during Diversification of Marchantiidae, An Early Land Plant Lineage, Leads to the First Known Expansion of Inverted Repeats in the Evolutionarily-Stable Structure of Liverwort Plastomes. <i>Genes</i> , 2020, 11, 299.	1.0	11
10309	Phytoplankton thermal responses adapt in the absence of hard thermodynamic constraints. <i>Evolution; International Journal of Organic Evolution</i> , 2020, 74, 775-790.	1.1	32

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10310	Transmission of hepatitis C virus in HIV-1 positive and PrEP-using MSM in England. <i>Journal of Viral Hepatitis</i> , 2020, 27, 721-730.	1.0	16
10311	Diversification and cryptic diversity of <i>Ophisops elegans</i> (Sauria, Lacertidae). <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2020, 58, 1276-1289.	0.6	4
10312	Phylogeny and classification of Leptophlebiidae (Ephemeroptera) with an emphasis on Neotropical fauna. <i>Systematic Entomology</i> , 2020, 45, 415-429.	1.7	15
10313	Major Revisions in Arthropod Phylogeny Through Improved Supermatrix, With Support for Two Possible Waves of Land Invasion by Chelicerates. <i>Evolutionary Bioinformatics</i> , 2020, 16, 117693432090373.	0.6	19
10314	The draft nuclear genome sequence and predicted mitochondrial proteome of <i>Andalucia godoyi</i> , a protist with the most gene-rich and bacteria-like mitochondrial genome. <i>BMC Biology</i> , 2020, 18, 22.	1.7	43
10315	Identification of two novel adenoviruses in smooth-billed ani and tropical screech owl. <i>PLoS ONE</i> , 2020, 15, e0229415.	1.1	10
10316	Japanese species of <i>Alternaria</i> and their species boundaries based on host range. <i>Fungal Systematics and Evolution</i> , 2020, 5, 197-282.	0.9	39
10317	Genomic Stability of Composite SCCmec ACME and COMER-Like Genetic Elements in <i>Staphylococcus epidermidis</i> Correlates With Rate of Excision. <i>Frontiers in Microbiology</i> , 2020, 11, 166.	1.5	12
10318	Coexistence of Two bla _{NDM-5} Genes Carried on IncX3 and IncFII Plasmids in an <i>Escherichia coli</i> Isolate Revealed by Illumina and Nanopore Sequencing. <i>Frontiers in Microbiology</i> , 2020, 11, 195.	1.5	10
10319	A Phylogenomic Perspective on Evolution and Discordance in the Alpine-Arctic Plant Clade <i>Micranthes</i> (Saxifragaceae). <i>Frontiers in Plant Science</i> , 2019, 10, 1773.	1.7	28
10320	Aldoxime Metabolism Is Linked to Phenylpropanoid Production in <i>Camelina sativa</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 17.	1.7	16
10321	Complete Chloroplast Genome of <i>Michelia shiluensis</i> and a Comparative Analysis with Four Magnoliaceae Species. <i>Forests</i> , 2020, 11, 267.	0.9	21
10322	Geographic Life History Differences Predict Genomic Divergence Better than Mitochondrial Barcodes or Phenotype. <i>Genes</i> , 2020, 11, 265.	1.0	16
10323	Phylogeography and the Evolutionary History of Sunflower (<i>Helianthus annuus</i> L.): Wild Diversity and the Dynamics of Domestication. <i>Genes</i> , 2020, 11, 266.	1.0	10
10324	Comparative Studies on the Polymorphism and Copy Number Variation of mtSSU rDNA in Ciliates (Protista, Ciliophora): Implications for Phylogenetic, Environmental, and Ecological Research. <i>Microorganisms</i> , 2020, 8, 316.	1.6	28
10325	The First Plastid Genome of the Holoparasitic Genus <i>Prosopanche</i> (Hydnoraceae). <i>Plants</i> , 2020, 9, 306.	1.6	16
10326	Genotyping Porcine Circovirus 3 (PCV-3) Nowadays: Does It Make Sense?. <i>Viruses</i> , 2020, 12, 265.	1.5	47
10327	Longitudinal survey of microbiome associated with particulate matter in a megacity. <i>Genome Biology</i> , 2020, 21, 55.	3.8	59

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10328	VRC34-Antibody Lineage Development Reveals How a Required Rare Mutation Shapes the Maturation of a Broad HIV-Neutralizing Lineage. <i>Cell Host and Microbe</i> , 2020, 27, 531-543.e6.	5.1	23
10329	Asymmetron lucayanum: How many species are valid?. <i>PLoS ONE</i> , 2020, 15, e0229119.	1.1	7
10330	PromA Plasmids Are Instrumental in the Dissemination of Linuron Catabolic Genes Between Different Genera. <i>Frontiers in Microbiology</i> , 2020, 11, 149.	1.5	8
10331	Phylogenetic placement of Ivodea and biogeographic affinities of Malagasy Rutaceae. <i>Plant Systematics and Evolution</i> , 2020, 306, 1.	0.3	9
10332	Two small, cysteine-rich and cationic antifungal proteins from <i>Penicillium chrysogenum</i> : A comparative study of PAF and PAFB. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2020, 1862, 183246.	1.4	20
10333	Marine Sediments Illuminate Chlamydiae Diversity and Evolution. <i>Current Biology</i> , 2020, 30, 1032-1048.e7.	1.8	52
10334	Phylogenomic data resolve higher-level relationships within South American Liolaemus lizards. <i>Molecular Phylogenetics and Evolution</i> , 2020, 147, 106781.	1.2	15
10335	An alpine grasshopper radiation older than the mountains, on Kā-Tiritiri o te Moana (Southern Alps) of Aotearoa (New Zealand). <i>Molecular Phylogenetics and Evolution</i> , 2020, 147, 106783.	1.2	20
10336	The identity, ecology and distribution of <i>Polypyrrenula</i> (Ascomycota: Dothideomycetes): a new member of Trypetheliaceae revealed by molecular and anatomical data. <i>Lichenologist</i> , 2020, 52, 27-35.	0.5	3
10337	<i>Huriella flakusii</i> (Teloschistaceae, lichenized Ascomycota), a new species from the Colca Canyon region in Peru. <i>Lichenologist</i> , 2020, 52, 37-47.	0.5	3
10338	Genome-wide analysis of the HSP101/CLPB gene family for heat tolerance in hexaploid wheat. <i>Scientific Reports</i> , 2020, 10, 3948.	1.6	22
10339	An enigma no more: an integrated taxonomic revision of <i>Aenigmatopia Malloch</i> reveals novel phylogenetic placement and four new species (Diptera : Sarcophagidae : Miltogramminae). <i>Invertebrate Systematics</i> , 2020, , .	0.5	2
10340	Comparative Genomics and Antimicrobial Resistance Profiling of <i>Elizabethkingia</i> Isolates Reveal Nosocomial Transmission and <i>In Vitro</i> Susceptibility to Fluoroquinolones, Tetracyclines, and Trimethoprim-Sulfamethoxazole. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	1.8	27
10341	Clinical and Genomic Epidemiology of Carbapenem-Nonsusceptible <i>Citrobacter</i> spp. at a Tertiary Health Care Center over 2 Decades. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	1.8	21
10342	Museomics of tree squirrels: a dense taxon sampling of mitogenomes reveals hidden diversity, phenotypic convergence, and the need of a taxonomic overhaul. <i>BMC Evolutionary Biology</i> , 2020, 20, 77.	3.2	34
10343	Rationale and design of 'Hearts & Parks' study protocol for a pragmatic randomized clinical trial of an integrated clinic-community intervention to treat pediatric obesity. <i>BMC Pediatrics</i> , 2020, 20, 308.	0.7	6
10344	Ecological, morphological and molecular characterization of <i>Kryptoperidinium</i> sp. (Dinophyceae) from two Mediterranean coastal shallow lagoons. <i>Harmful Algae</i> , 2020, 97, 101855.	2.2	5
10345	First steps to restructuring the problematic genus <i>Lasiotocus</i> Looss, 1907 (Digenea: Monorchidae) with the proposal of four new genera. <i>Parasitology International</i> , 2020, 79, 102164.	0.6	11

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10346	Conflict and congruence between morphological and molecular data: revision of the <i>Merodon constans</i> group (Diptera : Syrphidae). <i>Invertebrate Systematics</i> , 2020, .	0.5	8
10347	Characterization of the chloroplast genome of <i>Calanthe henryi</i> (Epidendroideae; Orchidaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2273-2275.	0.2	2
10348	A Comprehensive Multi-Omic Approach Reveals a Relatively Simple Venom in a Diet Generalist, the Northern Short-Tailed Shrew, <i>Blarina brevicauda</i> . <i>Genome Biology and Evolution</i> , 2020, 12, 1148-1166.	1.1	12
10349	Single-locus DNA barcoding and species delimitation of the sandfly subgenus <i>Evandromyia</i> (<i>Aldamyia</i>). <i>Medical and Veterinary Entomology</i> , 2020, 34, 420-431.	0.7	10
10350	Municipal Wastewater Surveillance Revealed a High Community Disease Burden of a Rarely Reported and Possibly Subclinical <i>Salmonella enterica</i> Serovar Derby Strain. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	19
10351	<i>Bimuria omanensis</i> , sp. nov. (Didymosphaeriaceae.) <i>Trends in Microbiology</i> , 2020, 28, 101-103.	0.1	3
10352	A new species of succulent plants from the Mukojima group of the Bonin Islands, Japan: <i>Sedum mukojimense</i> (Crassulaceae). <i>Phytotaxa</i> , 2020, 450, 188-198.	0.1	1
10353	Taxonomic scheme of the order Chaetophorales (Chlorophyceae, Chlorophyta) based on chloroplast genomes. <i>BMC Genomics</i> , 2020, 21, 442.	1.2	13
10354	Distribution of alfalfa weevil (Coleoptera: Curculionidae) and its parasitoids on the Canadian Prairies, with a key to described species of Nearctic <i>Bathyplectes</i> (Hymenoptera: Ichneumonidae). <i>Canadian Entomologist</i> , 2020, 152, 663-701.	0.4	8
10355	Ultrastructural, Cytochemical, and Comparative Genomic Evidence of Peroxisomes in Three Genera of Pathogenic Free-Living Amoebae, Including the First Morphological Data for the Presence of This Organelle in Heteroloboseans. <i>Genome Biology and Evolution</i> , 2020, 12, 1734-1750.	1.1	4
10356	The Complete Protist Symbiont Communities of <i>Coptotermes formosanus</i> and <i>Coptotermes gestroi</i> : Morphological and Molecular Characterization of Five New Species. <i>Journal of Eukaryotic Microbiology</i> , 2020, 67, 626-641.	0.8	19
10357	The Large pBS32/pLS32 Plasmid of Ancestral <i>Bacillus subtilis</i> . <i>Journal of Bacteriology</i> , 2020, 202, .	1.0	6
10358	A New Species of <i>Osedax</i> (Siboglinidae: Annelida) From Colonization Experiments in the Arctic Deep Sea. <i>Frontiers in Marine Science</i> , 2020, 7, .	1.2	5
10359	Investigation of a Salmonellosis Outbreak Caused by Multidrug Resistant <i>Salmonella</i> Typhimurium in China. <i>Frontiers in Microbiology</i> , 2020, 11, 801.	1.5	39
10360	Zoantharia (Cnidaria: Hexacorallia) of the Dutch Caribbean and One New Species of Parazoanthus. <i>Diversity</i> , 2020, 12, 190.	0.7	11
10362	Morphology, molecular phylogeny, and taxonomy of trichodinids (Ciliophora, Mobilida) from Calanoid copepods. <i>Parasitology Research</i> , 2020, 119, 2597-2608.	0.6	2
10363	Characteristic and phylogenetic analyses of chloroplast genome for <i>Mentha haplocalyx</i> (Lamiaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2099-2100.	0.2	3
10364	Complete mitochondrial genome of <i>Hestina assimilis</i> (Lepidoptera: Nymphalidae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1269-1271.	0.2	1

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10365	Characterization of the complete chloroplast genome of an important medicinal plant, <i>Sinomenium acutum</i> (Menispermaceae, Ranunculales). Mitochondrial DNA Part B: Resources, 2020, 5, 1305-1306.	0.2	1
10366	The complete mitochondrial genome of <i>Athetis pallidipennis</i> (Lepidoptera: Noctuidae). Mitochondrial DNA Part B: Resources, 2020, 5, 1346-1348.	0.2	1
10367	The first complete chloroplast genome of a mangrove fern, <i>Acrostichum speciosum</i> . Mitochondrial DNA Part B: Resources, 2020, 5, 1413-1414.	0.2	2
10368	Complete mitochondrial genome of the imperiled Trispot Darter (<i>Etheostoma trisella</i>). Mitochondrial DNA Part B: Resources, 2020, 5, 1523-1524.	0.2	0
10369	Complete plastome sequence of <i>Tetrataenium yunnanense</i> (tribe Tordylieae, Apiaceae) with anti-tumor activity. Mitochondrial DNA Part B: Resources, 2020, 5, 1525-1527.	0.2	0
10370	The complete chloroplast genome of <i>Chromolaena odorata</i> (Compositae), a noxious invasive weed to South China. Mitochondrial DNA Part B: Resources, 2020, 5, 1510-1511.	0.2	1
10371	The complete chloroplast genome of <i>Catalpa ovata</i> (Bignoniaceae): an important ornamental and medicinal plant. Mitochondrial DNA Part B: Resources, 2020, 5, 1675-1676.	0.2	3
10372	Complete mitochondrial genome of <i>Henricia pachyderma</i> (Asteroidea, Spinulosida, Echinasteridae) and phylogenetic analysis. Mitochondrial DNA Part B: Resources, 2020, 5, 1483-1484.	0.2	1
10373	The complete chloroplast genome sequence of <i>Malva verticillata</i> . Mitochondrial DNA Part B: Resources, 2020, 5, 1669-1670.	0.2	1
10374	The complete chloroplast genome of a well-known medicinal herb, <i>Senna tora</i> . Mitochondrial DNA Part B: Resources, 2020, 5, 1659-1660.	0.2	1
10375	The complete chloroplast genome sequence of <i>Heracleum yungningense</i> . Mitochondrial DNA Part B: Resources, 2020, 5, 1783-1784.	0.2	2
10376	Complete mitochondrial genome of <i>Eudarcia gwangneungensis</i> (Lepidoptera: Meessiidae). Mitochondrial DNA Part B: Resources, 2020, 5, 1746-1747.	0.2	3
10377	The complete plastid genome of <i>Vanda subconcolor</i> (Orchidaceae, Aeridinae). Mitochondrial DNA Part B: Resources, 2020, 5, 1712-1713.	0.2	2
10378	The complete chloroplast genome sequence of <i>Thymus quinquecostatus</i> var. <i>japonicus</i> (Lamiaceae), an endemic to Ullenung Island of Korea. Mitochondrial DNA Part B: Resources, 2020, 5, 2401-2402.	0.2	2
10379	The Complete chloroplast genome of <i>Geodorum densiflorum</i> (Orchidaceae). Mitochondrial DNA Part B: Resources, 2020, 5, 2056-2057.	0.2	1
10380	The complete chloroplast genome of <i>Catalpa speciosa</i> (Warder) Engelman (Bignoniaceae). Mitochondrial DNA Part B: Resources, 2020, 5, 2089-2090.	0.2	1
10381	Complete chloroplast genome sequence of an endangered <i>Ottelia cordata</i> and its phylogenetic analysis. Mitochondrial DNA Part B: Resources, 2020, 5, 2209-2210.	0.2	1
10382	The complete chloroplast genome of <i>Toxicodendron griffithii</i> . Mitochondrial DNA Part B: Resources, 2020, 5, 2211-2212.	0.2	4

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10383	Complete chloroplast genome sequence of <i>Ampelocalamus scandens</i> (Arundinaceae). Mitochondrial DNA Part B: Resources, 2020, 5, 2237-2238.	0.2	0
10384	The complete chloroplast genomes of the mangrove fern <i>Acrostichum aureum</i> . Mitochondrial DNA Part B: Resources, 2020, 5, 2258-2259.	0.2	2
10385	The complete chloroplast genome of <i>Akebia trifoliata</i> (Lardizabalaceae), a traditional herb in China. Mitochondrial DNA Part B: Resources, 2020, 5, 2330-2331.	0.2	2
10386	The complete chloroplast genome of <i>Melanosciadium pimpinelloideum</i> (Apiaceae), an endemic species of China. Mitochondrial DNA Part B: Resources, 2020, 5, 2371-2372.	0.2	3
10387	The complete chloroplast genome of <i>Aesculus chinensis</i> var. <i>wilsonii</i> . Mitochondrial DNA Part B: Resources, 2020, 5, 2547-2549.	0.2	2
10388	Prospects for the accelerated improvement of the resilient crop quinoa. <i>Journal of Experimental Botany</i> , 2020, 71, 5333-5347.	2.4	49
10389	Ancestral mitogenome capture of the Southeast Asian banded linsang. <i>PLoS ONE</i> , 2020, 15, e0234385.	1.1	9
10390	Continent-Scale Sampling Reveals Fine-Scale Turnover in a Beneficial Bug Symbiont. <i>Frontiers in Microbiology</i> , 2020, 11, 1276.	1.5	7
10391	Ribosomal and Protein Gene Phylogeny Reveals Novel Saprobic Fungal Species From <i>Juglans regia</i> and <i>Urtica dioica</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 1303.	1.5	8
10392	Degradative Capacity of Two Strains of <i>Rhodonia placenta</i> : From Phenotype to Genotype. <i>Frontiers in Microbiology</i> , 2020, 11, 1338.	1.5	9
10393	Miocene Diversification in the Savannas Precedes Tetraploid Rainforest Radiation in the African Tree Genus <i>Azobium</i> (Detarioideae, Fabaceae). <i>Frontiers in Plant Science</i> , 2020, 11, 798.	1.7	5
10394	The Loss of the Inverted Repeat in the Putranjivoid Clade of Malpighiales. <i>Frontiers in Plant Science</i> , 2020, 11, 942.	1.7	22
10395	Diversification of African Rainforest Restricted Clades: Piptostigmatidae and Annonaceae. <i>Diversity</i> , 2020, 12, 227.	0.7	11
10396	Class I KNOX Is Related to Determinacy during the Leaf Development of the Fern <i>Mickelia scandens</i> (Dryopteridaceae). <i>International Journal of Molecular Sciences</i> , 2020, 21, 4295.	1.8	16
10397	Gene Expression and Functional Analyses of Odorant Receptors in Small Hive Beetles (<i>Aethina tumida</i>). <i>International Journal of Molecular Sciences</i> , 2020, 21, 4582.	1.8	4
10398	Recombination Analysis of Non-Poliovirus Members of the Enterovirus C Species: Restriction of Recombination Events to Members of the Same 3DPol Cluster. <i>Viruses</i> , 2020, 12, 706.	1.5	7
10399	Optimizing the widely used nuclear protein-coding gene primers in beetle phylogenies and their application in the genus <i>Sasajiscymnus</i> Vandenberg (Coleoptera: Coccinellidae). <i>Ecology and Evolution</i> , 2020, 10, 7731-7738.	0.8	5
10400	Variation in the bank of microscopic forms in urchin barren coast: detection using DNA metabarcoding based on high-throughput sequencing. <i>Journal of Applied Phycology</i> , 2020, 32, 2115-2124.	1.5	4

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10401	Metagenomics: Applications of functional and structural approaches and meta-omics. , 2020, , 471-505.		4
10402	The Genomes of the Allohexaploid <i>Echinochloa crus-galli</i> and Its Progenitors Provide Insights into Polyploidization-Driven Adaptation. <i>Molecular Plant</i> , 2020, 13, 1298-1310.	3.9	47
10403	A novel <i>Borrelia</i> species, intermediate between Lyme disease and relapsing fever groups, in neotropical passerine-associated ticks. <i>Scientific Reports</i> , 2020, 10, 10596.	1.6	32
10404	Complete mitochondrial genome of <i>Anarta trifolii</i> (Lepidoptera: Noctuidae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1290-1292.	0.2	1
10405	The complete chloroplast genome of <i>Chrysopogon aciculatus</i> (Retz.) Trin. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1272-1274.	0.2	0
10406	Complete chloroplast genome sequence of <i>Epimedium dewuense</i> (Berberidaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1361-1362.	0.2	0
10407	The complete chloroplast genome of <i>Axonopus compressus</i> (Sw.) Beauv. and its phylogenetic position. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1441-1442.	0.2	0
10408	The complete chloroplast genome sequences of <i>Anoectochilus nandanensis</i> and <i>A. calcareus</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1381-1382.	0.2	0
10409	The complete chloroplast genome and phylogenetic analysis of <i>Gentiana manshurica</i> Kitag from China. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1625-1626.	0.2	2
10410	The complete chloroplast genome of <i>Elsholtzia densa</i> var. <i>ianthina</i> (Lamiaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1671-1672.	0.2	2
10411	The complete plastome of the coccoid green alga <i>Jenufa minuta</i> (Chlorophyceae, incertae sedis) unveils a noncanonical genetic code and a previously unrecognized trans-spliced group II intron in the <i>rpl32</i> gene. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1728-1730.	0.2	0
10412	Characterization of the complete chloroplast genome of two <i>Hovenia</i> species (Rhamnaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1731-1732.	0.2	3
10413	The complete chloroplast genome sequence of <i>Anogeissus acuminata</i> (combretaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2032-2033.	0.2	1
10414	Characterization of the complete plastid genome of Chinese medicinal plant <i>Isodon serra</i> (Lamiaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2111-2112.	0.2	4
10415	Characterization of the complete chloroplast genome sequence of <i>Pistia stratiotes</i> (Araceae) and its phylogenetic implications. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2168-2169.	0.2	2
10416	The complete plastome of a folk medicinal herb <i>Isodon lophanthoides</i> var. <i>graciliflorus</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2219-2221.	0.2	3
10417	The complete mitochondrial genomes of two Japanese endemic Satyrinae butterflies, <i>Neope goshkevitschii</i> and <i>Lethe sicelis</i> (Lepidoptera, Nymphalidae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2243-2245.	0.2	1
10418	The complete chloroplast genome of <i>Semiaquilegia guangxiensis</i> , a rare and endemic herb in Guangxi, China. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2324-2325.	0.2	0

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10419	The complete chloroplast genome of <i>Cymbidium serratum</i> (Orchidaceae): a rare and Endangered species endemic to Southwest China. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2429-2431.	0.2	1
10420	Architecture and Self-Assembly of <i>Clostridium sporogenes</i> and <i>Clostridium botulinum</i> Spore Surfaces Illustrate a General Protective Strategy across Spore Formers. <i>MSphere</i> , 2020, 5, .	1.3	12
10421	Genome assembly of the basket willow, <i>Salix viminalis</i> , reveals earliest stages of sex chromosome expansion. <i>BMC Biology</i> , 2020, 18, 78.	1.7	39
10422	Microbial succession during the transition from active to inactive stages of deep-sea hydrothermal vent sulfide chimneys. <i>Microbiome</i> , 2020, 8, 102.	4.9	62
10423	The Importance of Genomics for Deciphering the Invasion Success of the Seagrass <i>Halophila stipulacea</i> in the Changing Mediterranean Sea. <i>Diversity</i> , 2020, 12, 263.	0.7	6
10424	Comparative mitochondrial genome analysis of <i>Neodontobutis hainanensis</i> and <i>Perccottus glenii</i> reveals conserved genome organization and phylogeny. <i>Genomics</i> , 2020, 112, 3862-3870.	1.3	10
10425	Characterization of the complete chloroplast genome of <i>Sclerolaena napiformis</i> Wilson, an endangered Australian chenopod. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1332-1333.	0.2	1
10426	The complete chloroplast genome of a hemiparasitic plant <i>Santalum boninense</i> (Santalaceae), endemic to the Bonin (Ogasawara) Islands. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1386-1387.	0.2	0
10427	The complete plastid genome of a drought-tolerant moss, <i>Anomodon attenuatus</i> (Hedw.) h ¹ / ₄ b. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1554-1555.	0.2	0
10428	The complete mitogenomes of the green algae <i>Jenufa minuta</i> and <i>Jenufa perforata</i> (Chlorophyceae,) Tj ETQq1 1 0.784314 rgBT /Overbo. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1516-1518.	0.2	4
10429	The complete chloroplast genome of <i>Rheum nobile</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1519-1520.	0.2	2
10430	The complete chloroplast genome of <i>Neolamarckia macrophylla</i> (Rubiaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1611-1612.	0.2	5
10431	Complete mitogenome of the noble volute <i>Cymbiola nobilis</i> from the Vietnamese Island of Ph ^o Qu ^a c. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1661-1662.	0.2	0
10432	Complete chloroplast genome of <i>Morinda parvifolia</i> (Rubiaceae), a traditional medicinal plant in China. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1845-1847.	0.2	2
10433	Phylogenetic analysis of the complete chloroplast genome of <i>Prunus persica</i> seed as the Chinese herbal medicine to China. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1892-1893.	0.2	0
10434	The complete chloroplast genome of <i>Roscoea tibetica</i> , an alpine ginger species. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1878-1879.	0.2	0
10435	The complete chloroplast genome of <i>Clematis fruticosa</i> Turcz. (Ranunculaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1908-1909.	0.2	2
10436	The complete mitochondrial genome of <i>Haliotis ovina</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2312-2313.	0.2	2

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10437	The complete chloroplast genome sequence of <i>Begonia versicolor</i> Irmsch. (Begoniaceae). Mitochondrial DNA Part B: Resources, 2020, 5, 2113-2114.	0.2	1
10438	Complete mitogenome of the invasive land flatworm <i>Parakontikia ventrolineata</i> , the second Geoplanidae (Platyhelminthes) to display an unusually long <i>cox2</i> gene. Mitochondrial DNA Part B: Resources, 2020, 5, 2115-2116.	0.2	5
10439	The complete chloroplast genome of <i>Prunus conradinae</i> (Rosaceae), a wild flowering cherry from China. Mitochondrial DNA Part B: Resources, 2020, 5, 2153-2154.	0.2	2
10440	The complete mitochondrial genome of <i>Schoutedenia ralumensis</i> RÅ¼bsaamen, 1905 (Hemiptera: Tj ETQq1 1 0.784314 rgBT	0.2	5
10441	The complete chloroplast genome of <i>Zelkova serrata</i> and its phylogenetic position within Ulmaceae. Mitochondrial DNA Part B: Resources, 2020, 5, 2182-2183.	0.2	1
10442	High genetic similarity between non-typhoidal <i>Salmonella</i> isolated from paired blood and stool samples of children in the Democratic Republic of the Congo. PLoS Neglected Tropical Diseases, 2020, 14, e0008377.	1.3	11
10443	Analysis and characterization of the Aldehyde dehydrogenase (ALDH) gene superfamily in the desert moss <i>Syntrichia caninervis</i> in response to abiotic stress. Environmental and Experimental Botany, 2020, 178, 104176.	2.0	8
10444	Distribution and characteristics of Beilong virus among wild rodents and shrews in China. Infection, Genetics and Evolution, 2020, 85, 104454.	1.0	8
10445	Recent accelerated diversification in rosids occurred outside the tropics. Nature Communications, 2020, 11, 3333.	5.8	43
10446	The new truffle genus <i>Babosia</i> and a new species of <i>Stouffera</i> from semiarid grasslands of Hungary. Mycologia, 2020, 112, 808-818.	0.8	1
10447	Complete mitogenome of the shortfin spiny eel, <i>Notacanthus bonaparte</i> (Elopomorpha; Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 342 Td (0.2	1
10448	Characterization and phylogenetic analysis of the complete mitogenome of the Arctic skate <i>Amblyraja hyperborea</i> (Rajiformes; Rajidae). Mitochondrial DNA Part B: Resources, 2020, 5, 1588-1589.	0.2	2
10449	Phylogenetic inference of <i>Plebejus argus</i> (Lepidoptera: Lycaenidae) using its complete mitochondrial genome with an extra copy of tRNASer. Mitochondrial DNA Part B: Resources, 2020, 5, 1584-1585.	0.2	4
10450	The complete chloroplast genome sequence of <i>Clematis Montana</i> Buch.-Ham. (Ranunculaceae) and its phylogenetic analysis. Mitochondrial DNA Part B: Resources, 2020, 5, 2246-2247.	0.2	1
10451	The Chromosome-Level Genome Assembly and Comprehensive Transcriptomes of the Razor Clam (<i>Sinonovacula constricta</i>). Frontiers in Genetics, 2020, 11, 664.	1.1	18
10452	Adaptive evolution of low-salinity tolerance and hypoosmotic regulation in a euryhaline teleost, <i>Takifugu obscurus</i> . Marine Biology, 2020, 167, 1.	0.7	16
10453	Microfungi associated with <i>Clematis</i> (Ranunculaceae) with an integrated approach to delimiting species boundaries. Fungal Diversity, 2020, 102, 1-203.	4.7	93
10454	Description of <i>Massilia rubra</i> sp. nov., <i>Massilia aquatica</i> sp. nov., <i>Massilia mucilaginoso</i> sp. nov., <i>Massilia frigida</i> sp. nov., and one <i>Massilia</i> genomospecies isolated from Antarctic streams, lakes and regoliths. Systematic and Applied Microbiology, 2020, 43, 126112.	1.2	60

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10455	Predominance of influenza virus A(H3N2) 3C.2a1b and A(H1N1)pdm09 6B.1A5A genetic subclades in the WHO European Region, 2018–2019. <i>Vaccine</i> , 2020, 38, 5707-5717.	1.7	5
10456	Comparison of the transcriptomes of different life history stages of the freshwater Rhodophyte <i>Thorea hispida</i> . <i>Genomics</i> , 2020, 112, 3978-3990.	1.3	3
10457	Whole-genome, transcriptome, and methylome analyses provide insights into the evolution of platycoside biosynthesis in <i>Platycodon grandiflorus</i> , a medicinal plant. <i>Horticulture Research</i> , 2020, 7, 112.	2.9	38
10458	Plastome Structural Conservation and Evolution in the Clusioid Clade of Malpighiales. <i>Scientific Reports</i> , 2020, 10, 9091.	1.6	22
10459	Identification and characterization of <i>Colletotrichum</i> species causing apple bitter rot in New York and description of <i>C. noveboracense</i> sp. nov.. <i>Scientific Reports</i> , 2020, 10, 11043.	1.6	55
10460	The complete chloroplast genome of <i>Epimedium pudingense</i> (Berberidaceae), a narrowly distributed plant species in China. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2631-2633.	0.2	1
10461	Predicting regional hotspots of phylogenetic diversity across multiple species groups. <i>Diversity and Distributions</i> , 2020, 26, 1305-1314.	1.9	7
10462	How being synanthropic affects the gut bacteriome and mycobiome: comparison of two mouse species with contrasting ecologies. <i>BMC Microbiology</i> , 2020, 20, 194.	1.3	14
10463	Taxonomic determination of the cryptogenic red alga, <i>Chondria tumulosa</i> sp. nov., (Rhodomelaceae), and its invasive characteristics. <i>PLoS ONE</i> , 2020, 15, e0234358.	1.1	15
10464	The Origin and Evolution of Plastid Genome Downsizing in Southern Hemispheric Cupresses (Cupressaceae). <i>Frontiers in Plant Science</i> , 2020, 11, 901.	1.7	6
10465	Population genetics of wild <i>Macaca fascicularis</i> with low-coverage shotgun sequencing of museum specimens. <i>American Journal of Physical Anthropology</i> , 2020, 173, 21-33.	2.1	11
10466	Molecular characterization of <i>Acomys louisiae</i> from Somaliland: a deep divergence and contrasting genetic patterns in a rift zone. <i>Mammalian Biology</i> , 2020, 100, 385-398.	0.8	4
10467	Mandarin fish (Sinipercaidae) genomes provide insights into innate predatory feeding. <i>Communications Biology</i> , 2020, 3, 361.	2.0	33
10468	Adaptation of plasticity to projected maximum temperatures and across climatically defined bioregions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 17112-17121.	3.3	44
10469	Kpi, a chaperone-usher pili system associated with the worldwide-disseminated high-risk clone <i>Klebsiella pneumoniae</i> ST-15. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 17249-17259.	3.3	23
10470	Kissing cousins: a review of the African genus <i>Limnophis</i> Günther, 1865 (Colubridae: Natricinae), with the description of a new species from north-eastern Angola. <i>African Journal of Herpetology</i> , 2020, 69, 79-107.	0.3	9
10471	A dwarf among giants: phylogenetic position of the elusive Angolan Adder (<i>Bitis heraldica</i>) and biogeographic affinities of Angolan Afrotropical regions. <i>African Journal of Herpetology</i> , 2020, 69, 108-118.	0.3	4
10472	Characterization of the complete chloroplast genome of <i>Xanthium sibiricum</i> , one of the traditional Chinese medicines in China. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1202-1203.	0.2	0

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10473	Complete genome and phylogenetic analysis of <i>Agrimonia pilosa</i> Idb. Mitochondrial DNA Part B: Resources, 2020, 5, 1435-1436.	0.2	4
10474	The complete chloroplast genome of <i>Youngia gracilipes</i> (Asteraceae). Mitochondrial DNA Part B: Resources, 2020, 5, 2004-2005.	0.2	0
10475	The complete chloroplast genome of <i>Myxopyrum hainanense</i> and phylogenic analysis of Oleaceae. Mitochondrial DNA Part B: Resources, 2020, 5, 2103-2104.	0.2	0
10476	Genetic recombination in fast-spreading coxsackievirus A6 variants: a potential role in evolution and pathogenicity. <i>Virus Evolution</i> , 2020, 6, veaa048.	2.2	13
10477	Chytrid rhizoid morphogenesis resembles hyphal development in multicellular fungi and is adaptive to resource availability. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20200433.	1.2	18
10478	East Asian origin of the widespread alpine snowbed herb, <i>Primula cuneifolia</i> (Primulaceae), in the northern Pacific region. <i>Journal of Biogeography</i> , 2020, 47, 2181-2193.	1.4	16
10479	Molecular adaptation and convergent evolution of frugivory in Old World and neotropical fruit bats. <i>Molecular Ecology</i> , 2020, 29, 4366-4381.	2.0	32
10480	An outbreak of Shiga toxin-producing <i>Escherichia coli</i> O157:H7 linked to a mud-based obstacle course, England, August 2018. <i>Zoonoses and Public Health</i> , 2020, 67, 467-473.	0.9	6
10481	Genomic Analysis of Early SARS-CoV-2 Variants Introduced in Mexico. <i>Journal of Virology</i> , 2020, 94, .	1.5	32
10482	Lateral Gene Transfer Drives Metabolic Flexibility in the Anaerobic Methane-Oxidizing Archaeal Family <i>Methanoperedenaceae</i> . <i>MBio</i> , 2020, 11, .	1.8	51
10483	Impact of insertion sequences on convergent evolution of <i>Shigella</i> species. <i>PLoS Genetics</i> , 2020, 16, e1008931.	1.5	43
10484	Influence of hydrostatic pressure on the behaviour of three ciliate species isolated from the deep-sea floor. <i>Marine Biology</i> , 2020, 167, 1.	0.7	6
10485	Next generation sequencing reveals past and current widespread occurrence of maize yellow mosaic virus in South Africa. <i>European Journal of Plant Pathology</i> , 2020, 158, 237-249.	0.8	4
10486	Morphology, taxonomy and molecular phylogeny of three marine peritrich ciliates, including two new species: <i>Zoothamnium apoarbuscula</i> n. sp. and <i>Z. apohentscheli</i> n. sp. (Protozoa, Ciliophora,) <i>Tj ETQq1 1 0.784314 egBT /Overl</i>	1.2	6
10487	New insights into the systematics of <i>Bactrodesmium</i> and its allies and introducing new genera, species and morphological patterns in the Pleurotheciales and Savoryellales (Sordariomycetes). <i>Studies in Mycology</i> , 2020, 95, 415-466.	4.5	25
10488	Phylogenetic characterization of two novel species of the genus <i>Bifidobacterium</i> : <i>Bifidobacterium saimiriisciurei</i> sp. nov. and <i>Bifidobacterium platyrrhinorum</i> sp. nov.. <i>Systematic and Applied Microbiology</i> , 2020, 43, 126111.	1.2	6
10489	Molecular evolutionary and 3D protein structural analyses of <i>Lactobacillus fermentum</i> elongation factor Tu, a novel brain health promoting factor. <i>Genomics</i> , 2020, 112, 3915-3924.	1.3	1
10490	The evolutionary history of the cellophane bee genus <i>Colletes</i> Latreille (Hymenoptera: Colletidae): Molecular phylogeny, biogeography and implications for a global infrageneric classification. <i>Molecular Phylogenetics and Evolution</i> , 2020, 146, 106750.	1.2	8

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10491	Phylogenomics of the genus <i>Tursiops</i> and closely related Delphininae reveals extensive reticulation among lineages and provides inference about eco-evolutionary drivers. <i>Molecular Phylogenetics and Evolution</i> , 2020, 146, 106756.	1.2	40
10492	Complex evolutionary history of coffees revealed by full plastid genomes and 28,800 nuclear SNP analyses, with particular emphasis on <i>Coffea canephora</i> (Robusta coffee). <i>Molecular Phylogenetics and Evolution</i> , 2020, 151, 106906.	1.2	13
10493	Extinction rates of non-avian dinosaur species are uncorrelated with the rate of evolution of phylogenetically informative characters. <i>Biology Letters</i> , 2020, 16, 20200231.	1.0	3
10494	Stool Samples of Acute Diarrhea Inpatients as a Reservoir of ST11 Hypervirulent KPC-2-Producing <i>Klebsiella pneumoniae</i> . <i>MSystems</i> , 2020, 5, .	1.7	42
10495	Ecological Assembly Processes Are Coordinated between Bacterial and Viral Communities in Fractured Shale Ecosystems. <i>MSystems</i> , 2020, 5, .	1.7	15
10496	Comparative chloroplast genome analysis of <i>Artemisia</i> (Asteraceae) in East Asia: insights into evolutionary divergence and phylogenomic implications. <i>BMC Genomics</i> , 2020, 21, 415.	1.2	45
10497	Population genomics of <i>Vibrionaceae</i> isolated from an endangered oasis reveals local adaptation after an environmental perturbation. <i>BMC Genomics</i> , 2020, 21, 418.	1.2	6
10498	Viral RNA Genomes Identified from Marine Macroalgae and a Diatom. <i>Microbes and Environments</i> , 2020, 35, n/a.	0.7	17
10499	Comprehensive integrated NGS-based surveillance and contact-network modeling unravels transmission dynamics of vancomycin-resistant enterococci in a high-risk population within a tertiary care hospital. <i>PLoS ONE</i> , 2020, 15, e0235160.	1.1	21
10500	Metabolism of Soy Isoflavones by Intestinal Bacteria: Genome Analysis of an <i>Adlercreutzia equolifaciens</i> Strain That Does Not Produce Equol. <i>Biomolecules</i> , 2020, 10, 950.	1.8	11
10501	Patterns of host-parasite associations in tropical lice and their passerine hosts in Cameroon. <i>Ecology and Evolution</i> , 2020, 10, 6512-6524.	0.8	2
10502	Target protection as a key antibiotic resistance mechanism. <i>Nature Reviews Microbiology</i> , 2020, 18, 637-648.	13.6	100
10503	Comparative and Phylogenetic Analyses of the Complete Chloroplast Genomes of Six Almond Species (<i>Prunus</i> spp. L.). <i>Scientific Reports</i> , 2020, 10, 10137.	1.6	18
10504	Characterization of the complete chloroplast genome of <i>Rumex nepalensis</i> (Polygonaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2458-2459.	0.2	2
10505	Characterization of the complete mitogenomes of the Asian Paradise Flycatcher <i>Terpsiphone paradisi</i> (Monarchidae) and phylogenetic analysis. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2542-2543.	0.2	0
10506	Leaf reflectance spectra capture the evolutionary history of seed plants. <i>New Phytologist</i> , 2020, 228, 485-493.	3.5	72
10507	Molecular characterization of foot-and-mouth disease viruses circulating in Ethiopia between 2008 and 2019. <i>Transboundary and Emerging Diseases</i> , 2020, 67, 2983-2992.	1.3	13
10508	ZapE/Afg1 interacts with Oxa1 and its depletion causes a multifaceted phenotype. <i>PLoS ONE</i> , 2020, 15, e0234918.	1.1	7

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10509	Genome Report: Whole Genome Sequence and Annotation of the Parasitoid Jewel Wasp <i>Nasonia giraulti</i> Laboratory Strain RV2X[u]. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2565-2572.	0.8	12
10510	A Genomic and Transcriptomic Overview of MATE, ABC, and MFS Transporters in <i>Citrus sinensis</i> Interaction with <i>Xanthomonas citri</i> subsp. <i>citri</i> . <i>Plants</i> , 2020, 9, 794.	1.6	9
10511	<i>Thalassoglobus polymorphus</i> sp. nov., a novel Planctomycete isolated close to a public beach of Mallorca Island. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 1915-1926.	0.7	15
10512	Increasing incidence of group B streptococcus neonatal infections in the Netherlands is associated with clonal expansion of CC17 and CC23. <i>Scientific Reports</i> , 2020, 10, 9539.	1.6	25
10513	A new phylogenetic protocol: dealing with model misspecification and confirmation bias in molecular phylogenetics. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa041.	1.5	15
10514	CoreSimul: a forward-in-time simulator of genome evolution for prokaryotes modeling homologous recombination. <i>BMC Bioinformatics</i> , 2020, 21, 264.	1.2	10
10515	Comparative genomics of four strains of the edible brown alga, <i>Cladosiphon okamuranus</i> . <i>BMC Genomics</i> , 2020, 21, 422.	1.2	9
10516	Can the anatomy of abnormal flowers elucidate relationships of the androecial members in the ginger (<i>Zingiberaceae</i>)?. <i>EvoDevo</i> , 2020, 11, 12.	1.3	4
10517	Evolutionary History of the <i>Marchantia polymorpha</i> Complex. <i>Frontiers in Plant Science</i> , 2020, 11, 829.	1.7	15
10518	<i>Maioricimonas rarisocia</i> gen. nov., sp. nov., a novel planctomycete isolated from marine sediments close to Mallorca Island. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 1901-1913.	0.7	17
10519	Effects of irradiance, temperature, nutrients, and pCO ₂ on the growth and biochemical composition of cultivated <i>Ulva fenestrata</i> . <i>Journal of Applied Phycology</i> , 2020, 32, 3243-3254.	1.5	39
10520	DNA barcoding of a stowaway reef coral in the international aquarium trade results in a new distribution record. <i>Marine Biodiversity</i> , 2020, 50, 1.	0.3	4
10521	A mitogenomic phylogeny of pierid butterflies and complete mitochondrial genome of the yellow tip <i>Anthocharis scolymus</i> (Lepidoptera: Pieridae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2587-2589.	0.2	4
10522	Molecular phylogeny and species delimitation of Stachyuraceae: Advocating a herbarium specimen-based phylogenomic approach in resolving species boundaries. <i>Journal of Systematics and Evolution</i> , 2020, 58, 710-724.	1.6	6
10523	Genomic analysis of <i>Escherichia coli</i> strains isolated from diseased chicken in the Czech Republic. <i>BMC Veterinary Research</i> , 2020, 16, 189.	0.7	30
10524	Transposable element abundance correlates with mode of transmission in microsporidian parasites. <i>Mobile DNA</i> , 2020, 11, 19.	1.3	21
10525	The complete chloroplast genome sequence of the medicinal plant <i>Mesona chinensis</i> (Labiatae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2721-2722.	0.2	0
10526	The evolution of flowering phenology: an example from the wind-pollinated African Restionaceae. <i>Annals of Botany</i> , 2020, 126, 1141-1153.	1.4	2

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10527	Impacts of the Toba eruption and montane forest expansion on diversification in Sumatran parachuting frogs (<i>Rhacophorus</i>). <i>Molecular Ecology</i> , 2020, 29, 2994-3009.	2.0	4
10528	Cooperation between passive and active silicon transporters clarifies the ecophysiology and evolution of biosilicification in sponges. <i>Science Advances</i> , 2020, 6, eaba9322.	4.7	22
10529	Ancient Divergence Driven by Geographic Isolation and Ecological Adaptation in Forest Dependent Sundaland Tree Squirrels. <i>Frontiers in Ecology and Evolution</i> , 2020, 8, .	1.1	9
10530	The Microbiome of <i>Posidonia oceanica</i> Seagrass Leaves Can Be Dominated by Planctomycetes. <i>Frontiers in Microbiology</i> , 2020, 11, 1458.	1.5	40
10531	Complete Genome Sequencing and Transcriptome Analysis of Nitrogen Metabolism of <i>Succinivibrio dextrinosolvens</i> Strain Z6 Isolated From Dairy Cow Rumen. <i>Frontiers in Microbiology</i> , 2020, 11, 1826.	1.5	22
10532	<i>Pseudomonas</i> Phage PaBCA Jumbo Member of an Old Parasite Family. <i>Viruses</i> , 2020, 12, 721.	1.5	9
10533	Phylogeny and biogeography of <i>Astraea</i> with new insights into the evolutionary history of Crotonaceae (Euphorbiaceae). <i>Molecular Phylogenetics and Evolution</i> , 2020, 145, 106738.	1.2	9
10534	Evolution of non-lichenized, saprotrophic species of <i>Arthonia</i> (Ascomycota, Arthoniales) and resurrection of <i>Naevia</i> , with notes on <i>Mycoporium</i> . <i>Fungal Diversity</i> , 2020, 102, 205-224.	4.7	12
10535	Molecular and morphological phylogeny of thistle fruit flies <i>Acanthiophilus</i> Becker 1908 and <i>Tephritomyia</i> Hendel 1927 (Diptera: Tephritidae). <i>Zoologischer Anzeiger</i> , 2020, 287, 67-76.	0.4	0
10536	Evolutionary epidemiology of <i>Streptococcus iniae</i> : Linking mutation rate dynamics with adaptation to novel immunological landscapes. <i>Infection, Genetics and Evolution</i> , 2020, 85, 104435.	1.0	11
10537	Diversity, phylogeny, and historical biogeography of large-eye seabreams (Teleostei: Lethrinidae). <i>Molecular Phylogenetics and Evolution</i> , 2020, 151, 106902.	1.2	9
10538	A novel cyanobacterial geosmin producer, revising GeoA distribution and dispersion patterns in Bacteria. <i>Scientific Reports</i> , 2020, 10, 8679.	1.6	17
10539	The complete chloroplast genome sequence of <i>Acorus calamus</i> (Acoraceae) from Fujian, China. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1334-1335.	0.2	1
10540	The complete chloroplast genome of <i>Uraria lagopodioides</i> (Fabaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1365-1366.	0.2	1
10541	The complete chloroplast genome sequence of <i>Rosa filipes</i> (Rosaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1376-1377.	0.2	6
10542	The complete chloroplast genome sequence of <i>Rubus cochinchinensis</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1636-1637.	0.2	2
10543	Complete mitochondrial genome of <i>Gymnodiptychus pachycheilus weiheensis</i> (Teleostei: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 102 Td	0.2	0
10544	Complete chloroplast genome sequence of <i>Epimedium shuichengense</i> S. Z. He (Berberidaceae), an endangered species endemic to China. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1804-1805.	0.2	0

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10545	The complete chloroplast genome of <i>Altingia chinensis</i> (Hamamelidaceae). Mitochondrial DNA Part B: Resources, 2020, 5, 1808-1809.	0.2	2
10546	Chloroplast genome features and phylogenomic placement of <i>Lespedeza bicolor</i> (Fabaceae). Mitochondrial DNA Part B: Resources, 2020, 5, 1870-1871.	0.2	0
10547	Characterization of the complete chloroplast genome of <i>Swertia souliei</i> (Gentianaceae). Mitochondrial DNA Part B: Resources, 2020, 5, 1901-1902.	0.2	3
10548	The complete chloroplast genome of <i>Polygala tenuifolia</i> , a critically endangered species in Korea. Mitochondrial DNA Part B: Resources, 2020, 5, 1919-1920.	0.2	3
10549	Complete chloroplast genomes of <i>Camellia perpetua</i> and <i>Camellia indochinensis</i> . Mitochondrial DNA Part B: Resources, 2020, 5, 1979-1980.	0.2	0
10550	The complete chloroplast genome sequence of <i>Brainea insignis</i> (Blechnaceae). Mitochondrial DNA Part B: Resources, 2020, 5, 2034-2035.	0.2	0
10551	The complete chloroplast genome sequence of <i>Liparis bootanensis</i> (Orchidaceae). Mitochondrial DNA Part B: Resources, 2020, 5, 2058-2059.	0.2	1
10552	The complete chloroplast genome of paradox (<i>Juglans major</i> × <i>J. regia</i>), an interspecific hybrid in China. Mitochondrial DNA Part B: Resources, 2020, 5, 2087-2088.	0.2	0
10553	The complete chloroplast genome and phylogenetic analysis of <i>Paris delavayi</i> (Melanthiaceae). Mitochondrial DNA Part B: Resources, 2020, 5, 2126-2128.	0.2	0
10554	Characterization of the complete chloroplast genome of <i>Eleutherococcus senticosus</i> (Araliaceae) as an herb in China. Mitochondrial DNA Part B: Resources, 2020, 5, 2133-2134.	0.2	2
10555	The first complete chloroplast genome sequence of <i>Paris polyphylla</i> var. <i>emeiensis</i> , a rare and endangered species. Mitochondrial DNA Part B: Resources, 2020, 5, 2172-2173.	0.2	3
10556	The complete chloroplast genome of <i>Mitrasacme pygmaea</i> (Loganiaceae). Mitochondrial DNA Part B: Resources, 2020, 5, 2406-2407.	0.2	0
10557	The complete chloroplast genome of <i>Ampelopsis grossedentata</i> (Hand.-Mazz.) W. T. Wang (Family: Vitaceae) and its phylogenetic analysis. Mitochondrial DNA Part B: Resources, 2020, 5, 2423-2424.	0.2	6
10558	Macroevolutionary Patterns of Sexual Size Dimorphism Among African Tree Frogs (Family: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	1.0	8
10559	Ciliate diversity and distribution across horizontal and vertical scales in the open ocean. Molecular Ecology, 2020, 29, 2824-2839.	2.0	18
10560	<i>Burrowsia</i> , a new genus of lichenized fungi (Caliciaceae), plus the new species <i>B. cataractae</i> and <i>Scoliosporum fabisporum</i> , from Mpumalanga, South Africa. South African Journal of Botany, 2020, 132, 471-481.	1.2	3
10561	Methane, arsenic, selenium and the origins of the DMSO reductase family. Scientific Reports, 2020, 10, 10946.	1.6	20
10562	The complete chloroplast genome of <i>Myricaria laxiflora</i> (Tamaricaceae): an endemic and endangered species from China. Mitochondrial DNA Part B: Resources, 2020, 5, 1153-1154.	0.2	4

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10563	The complete chloroplast genome of <i>Philadelphus pekinensis</i> Rupr. (Hydrangeaceae). Mitochondrial DNA Part B: Resources, 2020, 5, 1178-1179.	0.2	0
10564	The complete plastid genome of <i>Stenotaphrum subulatum</i> Trin. (Panicoidae) and phylogenetic analysis. Mitochondrial DNA Part B: Resources, 2020, 5, 1378-1380.	0.2	0
10565	Complete mitogenome of the entomopathogenic fungus <i>Metarhizium rileyi</i> . Mitochondrial DNA Part B: Resources, 2020, 5, 1494-1495.	0.2	3
10566	The complete mitochondrial genome of <i>Teratoscincus roborowskii</i> (Squamata: Gekkonidae) and its phylogeny. Mitochondrial DNA Part B: Resources, 2020, 5, 1575-1577.	0.2	2
10567	Complete chloroplast genome sequence of <i>Pedicularis verticillata</i> and chloroplast genome reconstruction of <i>P.</i> <i>cheilanthifolia</i> (Orobanchaceae). Mitochondrial DNA Part B: Resources, 2020, 5, 1578-1579.	0.2	2
10568	The first complete chloroplast genome of <i>Gentiana rigescens</i> and its phylogenetic position in Gentianaceae. Mitochondrial DNA Part B: Resources, 2020, 5, 1603-1604.	0.2	1
10569	The complete chloroplast genome of <i>Catalpa ovata</i> G. Don. (Bignoniaceae). Mitochondrial DNA Part B: Resources, 2020, 5, 1800-1801.	0.2	5
10570	Complete chloroplast genome sequence of <i>Betula microphylla</i> (Betulaceae). Mitochondrial DNA Part B: Resources, 2020, 5, 2151-2152.	0.2	0
10571	The complete chloroplast genome of <i>Camellia nitidissima</i> (Theaceae). Mitochondrial DNA Part B: Resources, 2020, 5, 2228-2230.	0.2	1
10572	Spatial predictors of genomic and phenotypic variation differ in a lowland Middle American bird (<i>Tij ETQq1 1 0.784314 rgBT /Overloc</i>)	2.0	8
10573	Population genetic structure of <i>Anoplophora glabripennis</i> in South Korea: Invasive populations in the native range?. <i>Journal of Pest Science</i> , 2020, 93, 1181-1196.	1.9	12
10574	Pathogenic Allodiploid Hybrids of <i>Aspergillus Fungi</i> . <i>Current Biology</i> , 2020, 30, 2495-2507.e7.	1.8	39
10575	Integrative taxonomy and species delimitation of <i>Rhipicephalus turanicus</i> (Acari: Ixodida: Ixodidae). <i>International Journal for Parasitology</i> , 2020, 50, 577-594.	1.3	34
10576	Disentangling the evolutionary history of peri-Mediterranean cyprinids using host-specific gill monogeneans. <i>International Journal for Parasitology</i> , 2020, 50, 969-984.	1.3	14
10577	Infection of hard ticks in the Caspian Sea littoral of Iran with Lyme borreliosis and relapsing fever borreliae. <i>Ticks and Tick-borne Diseases</i> , 2020, 11, 101500.	1.1	8
10578	The delayed and geographically heterogeneous diversification of flowering plant families. <i>Nature Ecology and Evolution</i> , 2020, 4, 1232-1238.	3.4	131
10579	Chloroplast DNA analysis of the invasive weed, Himalayan balsam (<i>Impatiens glandulifera</i>), in the British Isles. <i>Scientific Reports</i> , 2020, 10, 10966.	1.6	7
10580	<i>Nigrospora</i> Species Associated with Various Hosts from Shandong Peninsula, China. <i>Mycobiology</i> , 2020, 48, 169-183.	0.6	31

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10581	Phylogenetic and codon usage analysis of atypical porcine pestivirus (APPV). <i>Virulence</i> , 2020, 11, 916-926.	1.8	10
10582	The complete chloroplast genome of <i>Juglans cathayensis</i> var. <i>formosana</i> (Hayata), an endemic in China. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1802-1803.	0.2	0
10583	Sequence and phylogenetic analysis of the mitochondrial genome for the groundhopper <i>Mazarredia convexa</i> (Orthoptera: Tetrigidae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2276-2277.	0.2	1
10584	Comparative mitogenome analysis of two ectomycorrhizal fungi (<i>Paxillus</i>) reveals gene rearrangement, intron dynamics, and phylogeny of basidiomycetes. <i>IMA Fungus</i> , 2020, 11, 12.	1.7	36
10585	Convergent morphological responses to loss of flight in rails (Aves: Rallidae). <i>Ecology and Evolution</i> , 2020, 10, 6186-6207.	0.8	9
10586	Genetic factors for short life span associated with evolution of the loss of flight ability. <i>Ecology and Evolution</i> , 2020, 10, 6020-6029.	0.8	1
10587	Phylogenomic Insights into Deep Phylogeny of Angiosperms Based on Broad Nuclear Gene Sampling. <i>Plant Communications</i> , 2020, 1, 100027.	3.6	61
10588	Genome-scale data reveal the role of hybridization in lichen-forming fungi. <i>Scientific Reports</i> , 2020, 10, 1497.	1.6	26
10589	Complete mitochondrial genome of <i>Mustela sibirica</i> (Carnivora: Mustelidae), a protected and endangered species in China. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1081-1083.	0.2	2
10590	Integration of culture-dependent and independent methods provides a more coherent picture of the pig gut microbiome. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	28
10591	Into the wild: new yeast genomes from natural environments and new tools for their analysis. <i>FEMS Yeast Research</i> , 2020, 20, .	1.1	29
10592	CRK2 and C-terminal Phosphorylation of NADPH Oxidase RBOHD Regulate Reactive Oxygen Species Production in Arabidopsis. <i>Plant Cell</i> , 2020, 32, 1063-1080.	3.1	115
10593	Phosphatidic acid produced by phospholipase D is required for hyphal cell-cell fusion and fungal-plant symbiosis. <i>Molecular Microbiology</i> , 2020, 113, 1101-1121.	1.2	16
10594	Nanopore sequencing-based genome assembly and evolutionary genomics of circum-basmati rice. <i>Genome Biology</i> , 2020, 21, 21.	3.8	73
10595	Selective sweeps on novel and introgressed variation shape mimicry loci in a butterfly adaptive radiation. <i>PLoS Biology</i> , 2020, 18, e3000597.	2.6	60
10596	High-Quality Genome Assembly of <i>Eriocheir japonica sinensis</i> Reveals Its Unique Genome Evolution. <i>Frontiers in Genetics</i> , 2019, 10, 1340.	1.1	32
10597	Distribution of Bacterial β -1,3-Galactosyltransferase Genes in the Human Gut Microbiome. <i>Frontiers in Immunology</i> , 2019, 10, 3000.	2.2	39
10598	Genome-Based Metabolic Reconstruction Unravels the Key Role of B12 in Methionine Auxotrophy of an Ortho-Phenylphenol-Degrading <i>Sphingomonas haloaromaticamans</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 3009.	1.5	8

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10599	Untangling the Evolution of American Wild Grapes: Admixed Species and How to Find Them. <i>Frontiers in Plant Science</i> , 2019, 10, 1814.	1.7	16
10600	A transcriptome-based study on the phylogeny and evolution of the taxonomically controversial subfamily Apiioideae (Apiaceae). <i>Annals of Botany</i> , 2020, 125, 937-953.	1.4	35
10601	Phenotypic Convergence Is Not Mirrored at the Protein Level in a Lizard Adaptive Radiation. <i>Molecular Biology and Evolution</i> , 2020, 37, 1604-1614.	3.5	19
10602	Molecular and biological analysis revealed genetic diversity and high virulence strain of <i>Toxoplasma gondii</i> in Japan. <i>PLoS ONE</i> , 2020, 15, e0227749.	1.1	8
10603	Deep-sea amphipods around cobalt-rich ferromanganese crusts: Taxonomic diversity and selection of candidate species for connectivity analysis. <i>PLoS ONE</i> , 2020, 15, e0228483.	1.1	8
10604	Two-way evolution of root form in the riverweed family Podostemaceae, with implications for phenotypic evolution. <i>Plant Systematics and Evolution</i> , 2020, 306, 1.	0.3	3
10605	Identification and sex-biased profiles of candidate olfactory genes in the antennal transcriptome of the parasitoid wasp <i>Cotesia vestalis</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2020, 34, 100657.	0.4	18
10606	<i>Cunea russae</i> n. sp. (Amoebozoa, Dactylopodida), another cryptic species of <i>Cunea</i> Kudryavtsev and Pawlowski, 2015, inhabits a continental brackish-water biotope. <i>European Journal of Protistology</i> , 2020, 73, 125685.	0.5	4
10607	Complete genome sequence and genome-scale metabolic modelling of <i>Acinetobacter baumannii</i> type strain ATCC 19606. <i>International Journal of Medical Microbiology</i> , 2020, 310, 151412.	1.5	11
10608	A cross-sectional study to characterize local HIV-1 dynamics in Washington, DC using next-generation sequencing. <i>Scientific Reports</i> , 2020, 10, 1989.	1.6	9
10609	Cryptic and extensive hybridization between ancient lineages of American crows. <i>Molecular Ecology</i> , 2020, 29, 956-969.	2.0	24
10610	Whole-Genome Sequencing of <i>Corynebacterium diphtheriae</i> Isolates Recovered from an Inner-City Population Demonstrates the Predominance of a Single Molecular Strain. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	1.8	13
10611	Predicting nitroimidazole antibiotic resistance mutations in <i>Mycobacterium tuberculosis</i> with protein engineering. <i>PLoS Pathogens</i> , 2020, 16, e1008287.	2.1	51
10612	Phylogenetic Systematics of the Water Toad (<i>Bufo stejnegeri</i>) Elucidates the Evolution of Semi-aquatic Toad Ecology and Pleistocene Glacial Refugia. <i>Frontiers in Ecology and Evolution</i> , 2020, 7, .	1.1	13
10613	Succession and Colonization Dynamics of Endolithic Phototrophs within Intertidal Carbonates. <i>Microorganisms</i> , 2020, 8, 214.	1.6	12
10614	Key Transitions in the Evolution of Rapid and Slow Growing <i>Mycobacteria</i> Identified by Comparative Genomics. <i>Frontiers in Microbiology</i> , 2019, 10, 3019.	1.5	37
10615	Identification and Comparative Analysis of Venom Proteins in a Pupal Ectoparasitoid, <i>Pachycrepoideus vindemmiae</i> . <i>Frontiers in Physiology</i> , 2020, 11, 9.	1.3	21
10616	Rodents as intermediate hosts of cestode parasites of mammalian carnivores and birds of prey in Poland, with the first data on the life-cycle of <i>Mesocestoides melesi</i> . <i>Parasites and Vectors</i> , 2020, 13, 95.	1.0	14

#	ARTICLE	IF	CITATIONS
10617	A Beetle in a Haystack: Are There Alternate Hosts of the Coffee Berry Borer (<i>Hypothenemus hampei</i>) in Puerto Rico?. <i>Agronomy</i> , 2020, 10, 228.	1.3	5
10618	Characterization of novel Î±-galactosidase in glycohydrolase family 97 from <i>Bacteroides thetaiotaomicron</i> and its immobilization for industrial application. <i>International Journal of Biological Macromolecules</i> , 2020, 152, 727-734.	3.6	12
10619	Prickly waterlily and rigid hornwort genomes shed light on early angiosperm evolution. <i>Nature Plants</i> , 2020, 6, 215-222.	4.7	88
10620	Reevaluating Cryphonectriaceae and allied families in Diaporthales. <i>Mycologia</i> , 2020, 112, 267-292.	0.8	25
10621	Phenotypic divergence of thermotolerance: Molecular basis and cold adaptive evolution related to intrinsic DNA flexibility of glacier-inhabiting <i>Cryobacterium</i> strains. <i>Environmental Microbiology</i> , 2020, 22, 1409-1420.	1.8	7
10622	The complete chloroplast genome sequence of the Chinese endemic species <i>Sorbus setschwanensis</i> (Rosaceae) and its phylogenetic analysis. <i>Nordic Journal of Botany</i> , 2020, 38, .	0.2	7
10623	Southern Chinese populations harbour non-nucleatum <i>Fusobacteria</i> possessing homologues of the colorectal cancer-associated FadA virulence factor. <i>Gut</i> , 2020, 69, 1998-2007.	6.1	42
10624	Evolution of Ty1 copy number control in yeast by horizontal transfer and recombination. <i>PLoS Genetics</i> , 2020, 16, e1008632.	1.5	30
10625	One step beyond a broad molecular phylogenetic analysis: Species delimitation of <i>Adenomera marmorata</i> Steindachner, 1867 (Anura: Leptodactylidae). <i>PLoS ONE</i> , 2020, 15, e0229324.	1.1	9
10626	Dominance of Mating Type A1 and Indication of Epigenetic Effects During Early Stages of Mating in <i>Phytophthora infestans</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 252.	1.5	9
10627	Species delimitation of <i>Planosiphon gracilis</i> morphospecies (Scytosiphonaceae, Phaeophyceae) from Japan and the description of <i>Pl. nakamurae</i> sp. nov. <i>Phycologia</i> , 2020, 59, 116-126.	0.6	5
10628	Chromosomal-level assembly of <i>Juglans sigillata</i> genome using Nanopore, BioNano, and Hi-C analysis. <i>GigaScience</i> , 2020, 9, .	3.3	33
10629	Draft Genome Resource for <i>Macrophomina phaseolina</i> Associated With Charcoal Rot in Sorghum. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 724-726.	1.4	11
10630	Genomic evidence for two phylogenetic species and long-term population bottlenecks in red pandas. <i>Science Advances</i> , 2020, 6, eaax5751.	4.7	86
10631	Identification of a novel base J binding protein complex involved in RNA polymerase II transcription termination in trypanosomes. <i>PLoS Genetics</i> , 2020, 16, e1008390.	1.5	33
10632	Phase variation in <i>latB</i> associated with a fatal <i>Pasteurella multocida</i> outbreak in captive squirrel gliders. <i>Veterinary Microbiology</i> , 2020, 243, 108612.	0.8	6
10633	A comparative genomics study of 23 <i>Aspergillus</i> species from section Flavi. <i>Nature Communications</i> , 2020, 11, 1106.	5.8	125
10634	Standardized phylogenetic and molecular evolutionary analysis applied to species across the microbial tree of life. <i>Scientific Reports</i> , 2020, 10, 1723.	1.6	65

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10635	Complex Evolution of Insect Insulin Receptors and Homologous Decoy Receptors, and Functional Significance of Their Multiplicity. <i>Molecular Biology and Evolution</i> , 2020, 37, 1775-1789.	3.5	58
10636	Genomic consequences of population decline in critically endangered pangolins and their demographic histories. <i>National Science Review</i> , 2020, 7, 798-814.	4.6	45
10637	Evaluating character partitioning and molecular models in plastid phylogenomics at low taxonomic levels: A case study using <i>Amphilophium</i> (Bignoniaceae). <i>Journal of Systematics and Evolution</i> , 2020, 58, 1071-1089.	1.6	29
10638	Shared Mutations in a Novel Glutaredoxin Repressor of Multicellular Trichome Fate Underlie Parallel Evolution of <i>Antirrhinum</i> Species. <i>Current Biology</i> , 2020, 30, 1357-1366.e4.	1.8	10
10639	High rates of tenofovir failure in a CRF01_AE-predominant HIV epidemic in the Philippines. <i>International Journal of Infectious Diseases</i> , 2020, 95, 125-132.	1.5	10
10640	Developmental and molecular characterization of novel staminodes in <i>Aquilegia</i> . <i>Annals of Botany</i> , 2020, 126, 231-243.	1.4	9
10641	Using genomic information for management planning of an endangered perennial, <i>Viola uliginosa</i> . <i>Ecology and Evolution</i> , 2020, 10, 2638-2649.	0.8	11
10642	Specialized bacteriome uncovered in the coralloid roots of the epiphytic gymnosperm, <i>Zamia pseudoparasitica</i> . <i>Environmental DNA</i> , 2020, 2, 418-428.	3.1	22
10643	Morpho-molecular traits of Indo-Pacific and Caribbean Halofolliculina ciliate infections. <i>Coral Reefs</i> , 2020, 39, 375-386.	0.9	6
10644	Soybean aphid biotype 1 genome: Insights into the invasive biology and adaptive evolution of a major agricultural pest. <i>Insect Biochemistry and Molecular Biology</i> , 2020, 120, 103334.	1.2	15
10645	Major Changes in Plastid Protein Import and the Origin of the Chloroplastida. <i>IScience</i> , 2020, 23, 100896.	1.9	21
10646	Stem rust resistance in wheat is suppressed by a subunit of the mediator complex. <i>Nature Communications</i> , 2020, 11, 1123.	5.8	52
10647	Hybridization and introgression drive genome evolution of Dutch elm disease pathogens. <i>Nature Ecology and Evolution</i> , 2020, 4, 626-638.	3.4	44
10648	Whole genome sequencing reveals extended natural transformation in <i>Campylobacter</i> impacting diagnostics and the pathogens adaptive potential. <i>Scientific Reports</i> , 2020, 10, 3686.	1.6	24
10649	Toward an understanding of the systematics and evolution of the genus <i>Acrapex</i> Hampson, 1894 (Lepidoptera: Noctuidae: Apameini: Sesamiina): molecular phylogenetics of the genus and review of the species-rich <i>Acrapex</i> aenigma group. <i>Annales De La Societe Entomologique De France</i> , 2020, 56, 29-91.	0.4	4
10650	Characterization of <i>Martensia</i> (Delesseriaceae; Rhodophyta) from shallow and mesophotic habitats in the Hawaiian Islands: description of four new species. <i>European Journal of Phycology</i> , 2020, 55, 172-185.	0.9	12
10651	Tick-borne encephalitis foci in northeast Italy revealed by combined virus detection in ticks, serosurvey on goats and human cases. <i>Emerging Microbes and Infections</i> , 2020, 9, 474-484.	3.0	31
10652	Identification of novel mobile colistin resistance gene <i>mcr-10</i> . <i>Emerging Microbes and Infections</i> , 2020, 9, 508-516.	3.0	346

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10653	The complete chloroplast genome sequence of a traditional Chinese medicine plant <i>Bulbophyllum disciflorum</i> Rolfe (Orchidaceae). Mitochondrial DNA Part B: Resources, 2020, 5, 59-60.	0.2	3
10654	The complete chloroplast genome of <i>Reevesia thyrsoidea</i> (Malvaceae). Mitochondrial DNA Part B: Resources, 2020, 5, 292-293.	0.2	3
10655	The complete chloroplast genome sequence of <i>Acorus gramineus</i> (Acoraceae). Mitochondrial DNA Part B: Resources, 2020, 5, 488-489.	0.2	1
10656	Complete mitochondrial genome of coconut hispine beetle <i>Brontispa longissima</i> (Coleoptera: Tj ETQq1 1 0.784314 rgBT /Overlock 107	0.2	2
10657	Phylogenetic relationships and characterization of the complete mitochondrial genome of <i>Eriobotrya japonica</i> in southeast of China. Mitochondrial DNA Part B: Resources, 2020, 5, 269-270.	0.2	0
10658	The mitochondrial genome of <i>Apis mellifera simensis</i> (Hymenoptera: Apidae), an Ethiopian honey bee. Mitochondrial DNA Part B: Resources, 2020, 5, 9-10.	0.2	13
10659	The complete chloroplast genome sequence of <i>Hypolepis sparsisora</i> (Dennstaedtiaceae). Mitochondrial DNA Part B: Resources, 2020, 5, 298-299.	0.2	0
10660	The mitochondrial genome of the Spanish honey bee, <i>Apis mellifera iberiensis</i> (Insecta: Tj ETQq1 1 0.784314 rgBT /Overlock 107	0.2	7
10661	Complete chloroplast genome sequence of <i>Pueraria lobata</i> (Willd.) Ohwi (Fabaceae): a traditional Chinese medicinal herb. Mitochondrial DNA Part B: Resources, 2020, 5, 25-26.	0.2	2
10662	The complete chloroplast genome of <i>Plantago fengdouensis</i> (Plantaginaceae): an endemic and Endangered species from China. Mitochondrial DNA Part B: Resources, 2020, 5, 51-52.	0.2	3
10663	The complete chloroplast genome of <i>Phlomoides betonicoides</i> (Lamiaceae), a traditional Tibetan medicinal herb. Mitochondrial DNA Part B: Resources, 2020, 5, 75-76.	0.2	8
10664	The complete chloroplast genome of "black tiger 2" (<i>Kadsura coccinea</i> (lem.) A.C. Smith) in southeast of China and phylogenetic relationshipsAQ1. Mitochondrial DNA Part B: Resources, 2020, 5, 296-297.	0.2	3
10665	The complete chloroplast genome sequence of <i>Actinidia styracifolia</i> C. F. Liang. Mitochondrial DNA Part B: Resources, 2020, 5, 90-91.	0.2	2
10666	Complete plastid genome of <i>Cheirostylis chinensis</i> (Orchidaceae, Goodyerinae). Mitochondrial DNA Part B: Resources, 2020, 5, 127-128.	0.2	0
10667	Complete mitogenomes of the chlorophyte green algae <i>Scherffelia dubia</i> and <i>Tetraselmis</i> sp. CCMP 881 (Chlorodendrophyceae). Mitochondrial DNA Part B: Resources, 2020, 5, 138-139.	0.2	4
10668	The complete chloroplast genome sequence of a traditional Chinese medicine: <i>Achyranthes bidentata</i> (Amaranthaceae). Mitochondrial DNA Part B: Resources, 2020, 5, 158-159.	0.2	1
10669	Complete chloroplast genome of <i>Physalis chenopodifolia</i> Lam. (Solanaceae). Mitochondrial DNA Part B: Resources, 2020, 5, 162-163.	0.2	5
10670	Complete mitogenomes of the marine picoplanktonic green algae <i>Prasinoderma</i> sp. MBIC 10622 and <i>Prasinococcus capsulatus</i> CCMP 1194 (Palmophyllophyceae). Mitochondrial DNA Part B: Resources, 2020, 5, 166-168.	0.2	3

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10671	Characterization of the complete chloroplast genome of <i>Engelhardia roxburghiana</i> (Juglandaceae). Mitochondrial DNA Part B: Resources, 2020, 5, 250-251.	0.2	1
10672	Complete plastid genome of <i>Holcoglossum tsii</i> (Orchidaceae, Aeridinae) and phylogenetic analysis. Mitochondrial DNA Part B: Resources, 2020, 5, 281-282.	0.2	0
10673	Complete chloroplast genome sequence of <i>Gigantochloa verticillata</i> (Bambusodae). Mitochondrial DNA Part B: Resources, 2020, 5, 306-307.	0.2	0
10674	Complete mitochondrial genome of the spotted lanternfly, <i>Lycorma delicatula</i> White, 1845 (Hemiptera: Tj ETQq1 1 0,784314 2 rgBT /Ov	0.2	0
10675	The complete chloroplast genome of a species <i>Cansjera rheedei</i> (Opiliaceae). Mitochondrial DNA Part B: Resources, 2020, 5, 314-316.	0.2	1
10676	Characterization of the complete chloroplast genome of <i>Aquilaria sinensis</i> , an endangered agarwood-producing tree. Mitochondrial DNA Part B: Resources, 2020, 5, 422-423.	0.2	3
10677	The complete chloroplast genome of the traditional Chinese herb, <i>Uncaria rhynchophylla</i> (Rubiaceae). Mitochondrial DNA Part B: Resources, 2020, 5, 424-425.	0.2	5
10678	Characterization and phylogenetic analysis of the complete plastome of <i>Alopecurus japonicus</i> (Gramineae), an annual weed. Mitochondrial DNA Part B: Resources, 2020, 5, 396-397.	0.2	7
10679	Characterization of the complete chloroplast genome of <i>Ottelia alismoides</i> (Hydrocharitaceae), a vulnerable submerged macrophyte in China. Mitochondrial DNA Part B: Resources, 2020, 5, 404-405.	0.2	1
10680	Sequence and phylogeny of the complete mitochondrial genome of the Himalayan jungle crow (<i>Corvidae:Corvus macrorhynchos intermedius</i>) from Pakistan. Mitochondrial DNA Part B: Resources, 2020, 5, 348-350.	0.2	1
10681	The complete chloroplast genome of <i>Epimedium davidii</i> Franch. (Berberidaceae). Mitochondrial DNA Part B: Resources, 2020, 5, 445-446.	0.2	0
10682	The complete plastid genome of <i>Ruppia brevipedunculata</i> Shuo Yu & den Hartog. Mitochondrial DNA Part B: Resources, 2020, 5, 474-475.	0.2	2
10683	Characterization of the complete chloroplast genome and phylogenetic analysis of <i>Silene jennisseensis</i> (Caryophyllaceae). Mitochondrial DNA Part B: Resources, 2020, 5, 476-477.	0.2	1
10684	Characterization of the complete chloroplast genome of a well-known Chinese medicinal herb, <i>Scrophularia ningpoensis</i> . Mitochondrial DNA Part B: Resources, 2020, 5, 484-485.	0.2	3
10685	Complete mitogenome of the chlorophyte green alga <i>Marsupiomonas</i> sp. NIES 1824 (Pedinophyceae). Mitochondrial DNA Part B: Resources, 2020, 5, 548-550.	0.2	1
10686	The complete mitochondrial genome of <i>Annamanum lunulatum</i> (Coleoptera: Lamiinae) and its phylogeny. Mitochondrial DNA Part B: Resources, 2020, 5, 551-553.	0.2	6
10687	Characterization and phylogenetic relationships analysis of the complete chloroplast genome of <i>Capsicum annuum</i> (Solanaceae). Mitochondrial DNA Part B: Resources, 2020, 5, 570-571.	0.2	0
10688	Complete chloroplast genome sequence of <i>Bambusa pervariabilis</i> (Bambusodae). Mitochondrial DNA Part B: Resources, 2020, 5, 790-791.	0.2	0

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10689	Complete mitochondrial genome of <i>Plodia interpunctella</i> (Lepidoptera: Pyralidae). Mitochondrial DNA Part B: Resources, 2020, 5, 583-585.	0.2	4
10690	The re-sequencing of complete chloroplast genome of <i>Cinnamomum camphora</i> (Lauraceae) from Quanzhou, China. Mitochondrial DNA Part B: Resources, 2020, 5, 520-521.	0.2	2
10691	Complete plastome sequence of <i>Hoya carnosa</i> (L. f.) R. Br. (Apocynaceae). Mitochondrial DNA Part B: Resources, 2020, 5, 522-523.	0.2	3
10692	The complete chloroplast genome of <i>Protea kilimandscharica</i> Engl. (Proteaceae). Mitochondrial DNA Part B: Resources, 2020, 5, 603-604.	0.2	0
10693	Complete chloroplast genome sequence of <i>Acer ginnala</i> , an important ornamental tree. Mitochondrial DNA Part B: Resources, 2020, 5, 609-610.	0.2	3
10694	Characterization of the complete plastid genome of <i>Astelia australiana</i> (J. H. Willis) L. B. Moore (Asteliaceae, Asparagales). Mitochondrial DNA Part B: Resources, 2020, 5, 656-657.	0.2	0
10695	The complete chloroplast genome of <i>Hovenia dulcis</i> (Rhamnaceae). Mitochondrial DNA Part B: Resources, 2020, 5, 665-666.	0.2	0
10696	The complete chloroplast genome and phylogenetic analysis of <i>Indofevillea khasiana</i> (Cucurbitaceae). Mitochondrial DNA Part B: Resources, 2020, 5, 669-670.	0.2	0
10697	The complete mitochondrial genome of the green alga <i>Chloroidium</i> sp. UTEX 3077 (Watanabea clade), Tj ETQq0 0 0 1gBT /Overlock 10	0.2	0
10698	Complete mitochondrial genome of <i>Mycalesis intermedia</i> (Lepidoptera: Nymphalidae). Mitochondrial DNA Part B: Resources, 2020, 5, 703-704.	0.2	2
10699	Characterization of the complete chloroplast genome of <i>Hovenia acerba</i> (Rhamnaceae). Mitochondrial DNA Part B: Resources, 2020, 5, 934-935.	0.2	7
10700	Characterization of the complete chloroplast genome of <i>Angelica dahurica</i> (Apiaceae) as an herb in China. Mitochondrial DNA Part B: Resources, 2020, 5, 678-679.	0.2	2
10701	The complete chloroplast genome of <i>Mahonia oiwakensis</i> (Berberidaceae), a traditional Chinese medicinal plant. Mitochondrial DNA Part B: Resources, 2020, 5, 692-694.	0.2	2
10702	The complete chloroplast genome of <i>Semiliquidambar cathayensis</i> (Hamamelidaceae). Mitochondrial DNA Part B: Resources, 2020, 5, 695-696.	0.2	4
10703	The complete chloroplast genome sequence of <i>Sinojackia huangmeiensis</i> (Styracaceae). Mitochondrial DNA Part B: Resources, 2020, 5, 715-717.	0.2	0
10704	Complete chloroplast genome sequence and phylogenetic analysis of <i>Magnolia pilocarpa</i> , a highly ornamental species endemic in central China. Mitochondrial DNA Part B: Resources, 2020, 5, 720-722.	0.2	3
10705	The complete chloroplast genome of <i>Epimedium wushanense</i> T. S. Ying. (Berberidaceae), a traditional Chinese medicinal herb. Mitochondrial DNA Part B: Resources, 2020, 5, 817-818.	0.2	0
10706	A mitogenomic phylogeny of spiders and complete mitochondrial genome of <i>Cyriopagopus hainanus</i> (Araneae:Theraphosidae). Mitochondrial DNA Part B: Resources, 2020, 5, 782-783.	0.2	4

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10707	Characterization of the complete plastome of <i>Saposhnikovia divaricata</i> (Turcz.) Schischk. Mitochondrial DNA Part B: Resources, 2020, 5, 786-787.	0.2	2
10708	Complete mitochondrial genome of a parasitic wasp <i>Microplitis pallidipes</i> (Hymenoptera: Braconidae): Tj ETQq1 1 0,784314 rgBT /Over	0.2	1
10709	The complete chloroplast genome sequence of <i>Plagiogyria euphlebia</i> , a fascinating fern with important taxonomic significance. Mitochondrial DNA Part B: Resources, 2020, 5, 843-844.	0.2	1
10710	Complete plastid genome of the Chinese medicinal herb <i>Paeonia obovata</i> subsp. <i>Willmottiae</i> (Paeoniaceae): characterization and phylogeny. Mitochondrial DNA Part B: Resources, 2020, 5, 845-847.	0.2	1
10711	The mitochondrial genome of the Maltese honey bee, <i>Apis mellifera ruttneri</i> (Insecta): Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 582 T	0.2	4
10712	Characterization of the complete chloroplast genome sequence of <i>Anisodus acutangulus</i> (Solanaceae). Mitochondrial DNA Part B: Resources, 2020, 5, 893-894.	0.2	2
10713	The complete mitochondrial genome of the least horseshoe bat (<i>Rhinolophus pusillus</i>). Mitochondrial DNA Part B: Resources, 2020, 5, 881-882.	0.2	1
10714	Complete chloroplast genome sequences of <i>Lagotis yunnanensis</i> (Scrophulariaceae): an Endangered species endemic to the Hengduan Mountains region. Mitochondrial DNA Part B: Resources, 2020, 5, 897-898.	0.2	1
10715	Characterization of the complete chloroplast genome of <i>Gentiana rhodantha</i> (Gentianaceae). Mitochondrial DNA Part B: Resources, 2020, 5, 902-903.	0.2	3
10716	The complete chloroplast genome of <i>Epimedium brevicornu</i> (Berberidaceae), a traditional Chinese medicinal herb. Mitochondrial DNA Part B: Resources, 2020, 5, 887-888.	0.2	1
10717	The complete chloroplast genome of <i>Bougainvillea glabra</i> . Mitochondrial DNA Part B: Resources, 2020, 5, 889-890.	0.2	5
10718	The complete chloroplast genome of <i>Aquilegia barnebyi</i> , a basal eudicot species. Mitochondrial DNA Part B: Resources, 2020, 5, 1060-1061.	0.2	0
10719	Characterization of the complete mitochondrial genome of <i>Caryopemon giganteus</i> Pic (Coleoptera: Chrysomelidae: Bruchinae). Mitochondrial DNA Part B: Resources, 2020, 5, 929-931.	0.2	1
10720	Characterization of the complete chloroplast genome of <i>Prunus davidiana</i> , an excellent horticultural species. Mitochondrial DNA Part B: Resources, 2020, 5, 932-933.	0.2	1
10721	The complete plastid genome of <i>Rhamnus taquetii</i> , an endemic shrub on the Jeju Island of Korea. Mitochondrial DNA Part B: Resources, 2020, 5, 924-926.	0.2	2
10722	Mitochondrial genome of the <i>Harpiocephalus harpia</i> (Chiroptera: Vespertilionidae) from China. Mitochondrial DNA Part B: Resources, 2020, 5, 996-998.	0.2	1
10723	Sequencing and characterization of mitochondrial genome of <i>Idea effusaria</i> (Lepidoptera): Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 102 T	0.2	1
10724	The complete plastome of <i>Hyacinthoides non-scripta</i> (L.) Chouard ex Rothm. (Asparagaceae). Mitochondrial DNA Part B: Resources, 2020, 5, 1003-1004.	0.2	2

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10725	Complete mitochondrial genome of <i>Eilema ussircum</i> (Lepidoptera: Erebidae). Mitochondrial DNA Part B: Resources, 2020, 5, 1065-1066.	0.2	1
10726	Complete mitochondrial genome of <i>Dioryctria yiai</i> (Lepidoptera: Pyralidae). Mitochondrial DNA Part B: Resources, 2020, 5, 1062-1064.	0.2	3
10727	The complete chloroplast genome of <i>Epimedium elachyphyllum</i> Stearn (Berberidaceae), an endangered species endemic to China. Mitochondrial DNA Part B: Resources, 2020, 5, 1027-1028.	0.2	0
10728	Characterization of the complete chloroplast genome of <i>Chlorophytum comosum</i> (Liliaceae). Mitochondrial DNA Part B: Resources, 2020, 5, 1046-1047.	0.2	0
10729	Characterization of the complete chloroplast genome of <i>Salix maizhokunggarensis</i> (Salicaceae). Mitochondrial DNA Part B: Resources, 2020, 5, 1054-1055.	0.2	1
10730	Complete mitochondrial genome of <i>Chrysolophus pictus</i> (Galliformes: Phasianidae), a national protected wild pheasant in China. Mitochondrial DNA Part B: Resources, 2020, 5, 1031-1033.	0.2	1
10731	The complete mitochondrial genome of the meerkat (<i>Suricata suricatta</i>) and its phylogenetic relationship with other feliform species. Mitochondrial DNA Part B: Resources, 2020, 5, 1100-1101.	0.2	1
10732	The complete chloroplast genome sequence of <i>Acidosasa gigantea</i> (Bambusoideae: Tj ETQq1 1 0.784314 rgBT /Overlock 10 T 5 Resources, 2020, 5, 1119-1121.	0.2	6
10733	Origin and Evolution of Polycyclic Triterpene Synthesis. <i>Molecular Biology and Evolution</i> , 2020, 37, 1925-1941.	3.5	38
10734	On the origin and continuing evolution of SARS-CoV-2. <i>National Science Review</i> , 2020, 7, 1012-1023.	4.6	1,248
10735	Occurrence and High-Throughput Sequencing of Viruses in Ohio Wheat. <i>Plant Disease</i> , 2020, 104, 1789-1800.	0.7	13
10736	Parechovirus A prevalence in adults in The Netherlands. <i>Archives of Virology</i> , 2020, 165, 963-966.	0.9	6
10737	Genome-based classification of <i>Micromonospora craterilacus</i> sp. nov., a novel actinobacterium isolated from Nemrut Lake. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 791-801.	0.7	11
10738	Integrative taxonomy reveals new taxa of Trochidae (Gastropoda: Vetigastropoda) from seamounts in the tropical western Pacific. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2020, 159, 103234.	0.6	1
10739	Characterizing ciguatoxin (CTX)- and Non-CTX-producing strains of <i>Gambierdiscus balechii</i> using comparative transcriptomics. <i>Science of the Total Environment</i> , 2020, 717, 137184.	3.9	12
10740	Local adaptation fuels cryptic speciation in terrestrial annelids. <i>Molecular Phylogenetics and Evolution</i> , 2020, 146, 106767.	1.2	6
10741	Utility of targeted sequence capture for phylogenomics in rapid, recent angiosperm radiations: Neotropical <i>Burmeistera</i> bellflowers as a case study. <i>Molecular Phylogenetics and Evolution</i> , 2020, 152, 106769.	1.2	34
10742	First Report of <i>Kosakonia radincitans</i> Bacteraemia from Europe (Austria) - Identification and Whole-Genome Sequencing of Strain DSM 107547. <i>Scientific Reports</i> , 2020, 10, 1948.	1.6	10

#	ARTICLE	IF	CITATIONS
10743	Disentangling the taxonomy of the subfamily Rasborinae (Cypriniformes, Danionidae) in Sundaland using DNA barcodes. <i>Scientific Reports</i> , 2020, 10, 2818.	1.6	28
10744	Different from tracheophytes, liverworts commonly have mixed 35S and 5S arrays. <i>Annals of Botany</i> , 2020, 125, 1057-1064.	1.4	8
10745	Shedding of Yellow Fever Virus From an Imported Case in the Netherlands After Travel to Brazil. <i>Open Forum Infectious Diseases</i> , 2020, 7, ofaa020.	0.4	2
10746	Exploration of Plastid Phylogenomic Conflict Yields New Insights into the Deep Relationships of Leguminosae. <i>Systematic Biology</i> , 2020, 69, 613-622.	2.7	131
10747	Substantially adaptive potential in polyploid cyprinid fishes: evidence from biogeographic, phylogenetic and genomic studies. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20193008.	1.2	30
10748	A metagenomic assessment of microbial eukaryotic diversity in the global ocean. <i>Molecular Ecology Resources</i> , 2020, 20, 718-731.	2.2	70
10749	Reconstructing the evolutionary history of nitrogenases: Evidence for ancestral molybdenum cofactor utilization. <i>Geobiology</i> , 2020, 18, 394-411.	1.1	58
10750	Phylogenetics and seed morphology of African Nymphaeoides (Menyanthaceae). <i>Nordic Journal of Botany</i> , 2020, 38, .	0.2	1
10751	Exceptional Enlargement of the Mitochondrial Genome Results from Distinct Causes in Different Rain Frogs (Anura: Brevicipitidae: <i>Breviceps</i>). <i>International Journal of Genomics</i> , 2020, 2020, 1-12.	0.8	7
10752	A three-year whole genome sequencing perspective of <i>Enterococcus faecium</i> sepsis in Australia. <i>PLoS ONE</i> , 2020, 15, e0228781.	1.1	14
10753	Taxonomic revision of the genus <i>Zygorhizidium</i> : <i>Zygorhizidiales</i> and <i>Zygorhizidiales</i> ord. nov. (<i>Chytridiomycetes</i> , <i>Chytridiomycota</i>). <i>Fungal Systematics and Evolution</i> , 2020, 5, 17-38.	0.9	26
10754	Target Nuclear and Off-Target Plastid Hybrid Enrichment Data Inform a Range of Evolutionary Depths in the Orchid Genus <i>Epidendrum</i> . <i>Frontiers in Plant Science</i> , 2019, 10, 1761.	1.7	42
10755	Morphological and molecular investigation on freshwater choanoflagellates (<i>Craspedida</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 267 Td (73, 125687.	0.5	5
10756	Inferring putative ancient whole-genome duplications in the 1000 Plants (1KP) initiative: access to gene family phylogenies and age distributions. <i>GigaScience</i> , 2020, 9, .	3.3	49
10757	Genomic analysis and antimicrobial resistance of <i>Neisseria gonorrhoeae</i> isolates from Vietnam in 2011 and 2015–16. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 1432-1438.	1.3	28
10758	Global Diversification Dynamics Since the Jurassic: Low Dispersal and Habitat-Dependent Evolution Explain Hotspots of Diversity and Shell Disparity in River Snails (<i>Viviparidae</i>). <i>Systematic Biology</i> , 2020, 69, 944-961.	2.7	18
10759	Longer is Not Always Better: Optimizing Barcode Length for Large-Scale Species Discovery and Identification. <i>Systematic Biology</i> , 2020, 69, 999-1015.	2.7	45
10760	Evidence for widespread selection in shaping the genomic landscape during speciation of <i>Populus</i> . <i>Molecular Ecology</i> , 2020, 29, 1120-1136.	2.0	31

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10761	Genome-Wide Analysis of Cyclophilin Proteins in 21 Oomycetes. <i>Pathogens</i> , 2020, 9, 24.	1.2	3
10762	Reappraising plastid markers of the red algae for phylogenetic community ecology in the genomic era. <i>Ecology and Evolution</i> , 2020, 10, 1299-1310.	0.8	6
10763	<i>Lysobacter prati</i> sp. nov., isolated from a plateau meadow sample. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 763-772.	0.7	17
10764	Whole genomic sequencing and sex-dependent abundance estimation of <i>Cardinium</i> sp., a common and hyperabundant bacterial endosymbiont of the American house dust mite, <i>Dermatophagoides farinae</i> . <i>Experimental and Applied Acarology</i> , 2020, 80, 363-380.	0.7	24
10765	Genome of <i>Tripterygium wilfordii</i> and identification of cytochrome P450 involved in triptolide biosynthesis. <i>Nature Communications</i> , 2020, 11, 971.	5.8	103
10766	Response of the human gut and saliva microbiome to urbanization in Cameroon. <i>Scientific Reports</i> , 2020, 10, 2856.	1.6	27
10767	Expansion of the genus <i>Imleria</i> in North America to include <i>Imleria floridana</i> , sp. nov., and <i>Imleria pallida</i> , comb. nov.. <i>Mycologia</i> , 2020, 112, 423-437.	0.8	2
10768	Novel de Novo Genome of <i>Cynopterus brachyotis</i> Reveals Evolutionarily Abrupt Shifts in Gene Family Composition across Fruit Bats. <i>Genome Biology and Evolution</i> , 2020, 12, 259-272.	1.1	12
10769	Phylogeny of African fruit bats (Chiroptera, Pteropodidae) based on complete mitochondrial genomes. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2020, 58, 1395-1410.	0.6	17
10770	Genomic epidemiology of <i>Vibrio cholerae</i> reveals the regional and global spread of two epidemic non-toxigenic lineages. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008046.	1.3	16
10771	Increasing prevalence of a fluoroquinolone resistance mutation amongst <i>Campylobacter jejuni</i> isolates from four human infectious intestinal disease studies in the United Kingdom. <i>PLoS ONE</i> , 2020, 15, e0227535.	1.1	9
10772	<i>Geodina</i> (<i>Pezizomycetes</i> : <i>Wynneaceae</i>) has a single widespread species in tropical America. <i>Fungal Systematics and Evolution</i> , 2020, 5, 131-138.	0.9	6
10773	The Evolution, Gene Expression Profile, and Secretion of Digestive Peptidases in Lepidoptera Species. <i>Catalysts</i> , 2020, 10, 217.	1.6	6
10774	Inducing the attachment of cable bacteria on oxidizing electrodes. <i>Biogeosciences</i> , 2020, 17, 597-607.	1.3	10
10775	It is not a disaster: molecular and morphologically based phylogenetic analysis of <i>Rondeletieae</i> and the <i>Rondeletia</i> complex (Cinchonoideae, Rubiaceae). <i>Plant Systematics and Evolution</i> , 2020, 306, 1.	0.3	6
10776	<i>Euwallacea perbrevis</i> (Coleoptera: Curculionidae: Scolytinae), a confirmed pest on <i>Acacia crassicarpa</i> in Riau, Indonesia, and a new fungal symbiont; <i>Fusarium rekanum</i> sp. nov.. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 803-823.	0.7	21
10777	Molecular characterisation of acanthocephalans from Australian marine teleosts: proposal of a new family, synonymy of another and transfer of taxa between orders. <i>Systematic Parasitology</i> , 2020, 97, 1-23.	0.5	21
10778	Hidden diversity in two widespread snake species (Serpentes: Xenodontini: <i>Erythrolamprus</i>) from South America. <i>Molecular Phylogenetics and Evolution</i> , 2020, 146, 106772.	1.2	6

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10779	Symbiont replacements reset the co-evolutionary relationship between insects and their heritable bacteria. <i>ISME Journal</i> , 2020, 14, 1384-1395.	4.4	36
10780	The genome of Shaw's sea snake (<i>Hydrophis curtus</i>) reveals secondary adaptation to its marine environment. <i>Molecular Biology and Evolution</i> , 2020, 37, 1744-1760.	3.5	28
10781	The uncharacterized gene <i>EVE</i> contributes to vessel element dimensions in <i>Populus</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 5059-5066.	3.3	11
10782	Linking influenza virus evolution within and between human hosts. <i>Virus Evolution</i> , 2020, 6, veaa010.	2.2	47
10783	Transcriptome-based target enrichment baits for stony corals (Cnidaria: Anthozoa: Scleractinia). <i>Molecular Ecology Resources</i> , 2020, 20, 807-818.	2.2	26
10784	Evolution of the Small Family of Alternative Splicing Modulators Nuclear Speckle RNA-Binding Proteins in Plants. <i>Genes</i> , 2020, 11, 207.	1.0	10
10785	Genomic and Epidemiological Surveillance of Zika Virus in the Amazon Region. <i>Cell Reports</i> , 2020, 30, 2275-2283.e7.	2.9	37
10786	Emergence of human-adapted <i>Salmonella enterica</i> is linked to the Neolithization process. <i>Nature Ecology and Evolution</i> , 2020, 4, 324-333.	3.4	72
10787	EasyPrimer: user-friendly tool for pan-PCR/HRM primers design. Development of an HRM protocol on <i>wzi</i> gene for fast <i>Klebsiella pneumoniae</i> typing. <i>Scientific Reports</i> , 2020, 10, 1307.	1.6	12
10788	Two new species of Solieriaceae (Rhodophyta, Gigartinales) from the euphotic and mesophotic zones off Bermuda, <i>Meristotheca odontoloma</i> and <i>Tepoztequiella muriamans</i> . <i>Phycologia</i> , 2020, 59, 177-185.	0.6	4
10789	Loss of a conserved MAPK causes catastrophic failure in assembly of a specialized cilium-like structure in <i>Toxoplasma gondii</i> . <i>Molecular Biology of the Cell</i> , 2020, 31, 881-888.	0.9	35
10790	Untangling cryptic diversity in the High Andes: Revision of the <i>Scytalopus [magellanicus]</i> complex (Rhinocryptidae) in Peru reveals three new species. <i>Auk</i> , 2020, 137, .	0.7	20
10791	Larval development of the stygobitic shrimp <i>Creaseria morleyi</i> (Creaser, 1936) (Decapoda: Caridea). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5</i>	0.3	2
10792	Genetic diversity and novel lineages in the cosmopolitan copepod <i>Pleuromamma abdominalis</i> in the Southeast Pacific. <i>Scientific Reports</i> , 2020, 10, 1115.	1.6	7
10793	Ancient DNA and high-resolution chronometry reveal a long-term human role in the historical diversity and biogeography of the Bahamian hutia. <i>Scientific Reports</i> , 2020, 10, 1373.	1.6	20
10794	Analysis of <i>Plasmodium falciparum</i> Rh2b deletion polymorphism across different transmission areas. <i>Scientific Reports</i> , 2020, 10, 1498.	1.6	3
10795	Evaluation of the population structure and phylogeography of the Japanese Genji firefly, <i>Luciola cruciata</i> , at the nuclear DNA level using RAD-Seq analysis. <i>Scientific Reports</i> , 2020, 10, 1533.	1.6	16
10796	Phylogenomic analysis of trichomycterid catfishes (Teleostei: Siluriformes) inferred from ultraconserved elements. <i>Scientific Reports</i> , 2020, 10, 2697.	1.6	45

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10797	Complementary molecular methods reveal comprehensive phylogenetic diversity integrating inconspicuous lineages of early-diverged wood-decaying mushrooms. <i>Scientific Reports</i> , 2020, 10, 3057.	1.6	5
10798	A recently evolved diflavin-containing monomeric nitrate reductase is responsible for highly efficient bacterial nitrate assimilation. <i>Journal of Biological Chemistry</i> , 2020, 295, 5051-5066.	1.6	27
10799	Desiccation tolerance in streptophyte algae and the algae to land plant transition: evolution of LEA and MIP protein families within the Viridiplantae. <i>Journal of Experimental Botany</i> , 2020, 71, 3270-3278.	2.4	23
10800	Mycoheterotrophic plants living on arbuscular mycorrhizal fungi are generally enriched in ¹³ C, ¹⁵ N and ² H isotopes. <i>Journal of Ecology</i> , 2020, 108, 1250-1261.	1.9	15
10801	A method to generate multilocus barcodes of pinned insect specimens using MiSeq. <i>Molecular Ecology Resources</i> , 2020, 20, 692-705.	2.2	3
10802	A classification framework for <i>Bacillus anthracis</i> defined by global genomic structure. <i>Evolutionary Applications</i> , 2020, 13, 935-944.	1.5	13
10803	Population genetic structure and predominance of cyclical parthenogenesis in the bird cherry-aphid <i>Rhopalosiphum padi</i> in England. <i>Evolutionary Applications</i> , 2020, 13, 1009-1025.	1.5	16
10804	Genomic insight into the origins and evolution of symbiosis genes in <i>Phaseolus vulgaris</i> microsymbionts. <i>BMC Genomics</i> , 2020, 21, 186.	1.2	24
10805	Molecular evolution of GII.P17-GII.17 norovirus associated with sporadic acute gastroenteritis cases during 2013-2018 in Zhoushan Islands, China. <i>Virus Genes</i> , 2020, 56, 279-287.	0.7	8
10806	Three new species of <i>Allobacciger</i> Hafeezullah & Siddiqi, 1970 (Digenea: Monorchidae) from Australia and French Polynesia. <i>Marine Biodiversity</i> , 2020, 50, 1.	0.3	9
10807	Insights into the Tricholomatineae (Agaricales, Agaricomycetes): a new arrangement of Biannulariaceae and Callistosporium, Callistosporiaceae fam. nov., Xerophorus stat. nov., and Pleurocollybia incorporated into Callistosporium. <i>Fungal Diversity</i> , 2020, 101, 211-259.	4.7	15
10808	Growth, enzymatic production and morphology of the white-rot fungi <i>Lentinus crinitus</i> (L.) Fr. upon 2,4-D herbicide exposition. <i>International Journal of Environmental Science and Technology</i> , 2020, 17, 2995-3012.	1.8	19
10809	Deep mitochondrial DNA phylogeographic divergence in the threatened aoudad <i>Ammotragus lervia</i> (Bovidae, Caprini). <i>Gene</i> , 2020, 739, 144510.	1.0	5
10810	Phylogenetic analysis and transcriptional profiling of WRKY genes in sunflower (<i>Helianthus annuus</i>) Tj ETQq1 1 0.784314 rgBT /Overl... <i>Products</i> , 2020, 148, 112268.	2.5	27
10811	Morphological and molecular taxonomy of <i>Timea</i> (Porifera: Timeidae) from the Gulf of Mexico with the description of a new species and re-description of <i>T. hechteli</i> . <i>Journal of the Marine Biological Association of the United Kingdom</i> , 2020, 100, 375-387.	0.4	1
10812	Community-acquired in name only: A cluster of carbapenem-resistant <i>Acinetobacter baumannii</i> in a burn intensive care unit and beyond. <i>Infection Control and Hospital Epidemiology</i> , 2020, 41, 531-538.	1.0	10
10813	An exceptional case of mitochondrial tRNA duplication-deletion events in blood-feeding leeches. <i>Organisms Diversity and Evolution</i> , 2020, 20, 221-231.	0.7	2
10814	Genomic epizootiology of a <i>Brucella abortus</i> outbreak in Northern Ireland (1997-2012). <i>Infection, Genetics and Evolution</i> , 2020, 81, 104235.	1.0	10

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10815	ddRAD analyses reveal a credible phylogenetic relationship of the four main genera of Bambusa-Dendrocalamus-Gigantochloa complex (Poaceae: Bambusoideae). <i>Molecular Phylogenetics and Evolution</i> , 2020, 146, 106758.	1.2	19
10816	Phylogeny of Echiura updated, with a revised taxonomy to reflect their placement in Annelida as sister group to Capitellidae. <i>Invertebrate Systematics</i> , 2020, 34, 101.	0.5	17
10817	Genetic differentiation in mountain-dwelling clam shrimp, Paralimnadia (Crustacea : Branchiopoda : Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.5	4
10818	Plastid-encoded gene comparison reveals usefulness of <i>atpB</i> , <i>psaA</i> , and <i>rbcL</i> for identification and phylogeny of plastid-containing cryptophyte clades. <i>Phycologia</i> , 2020, 59, 154-164.	0.6	1
10819	The complete chloroplast genome and phylogenetic analysis of <i>Cuminum cyminum</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1079-1080.	0.2	1
10820	Molecular Evolution of the Glutathione S-Transferase Family in the <i>Bemisia tabaci</i> Species Complex. <i>Genome Biology and Evolution</i> , 2020, 12, 3857-3872.	1.1	17
10821	Conflicting signal in transcriptomic markers leads to a poorly resolved backbone phylogeny of chalcidoid wasps. <i>Systematic Entomology</i> , 2020, 45, 783-802.	1.7	23
10822	Phylogenomic Reconstruction Sheds Light on New Relationships and Timescale of Rails (Aves: Rallidae) Evolution. <i>Diversity</i> , 2020, 12, 70.	0.7	17
10823	Rapid inference of antibiotic resistance and susceptibility by genomic neighbour typing. <i>Nature Microbiology</i> , 2020, 5, 455-464.	5.9	74
10824	Clades of huge phages from across Earth's ecosystems. <i>Nature</i> , 2020, 578, 425-431.	13.7	331
10825	The complete mitochondrial genome of the West African honey bee <i>Apis mellifera adansonii</i> (Insecta: Hymenoptera: Apidae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 11-12.	0.2	6
10826	The complete mitochondrial genome of <i>Apis mellifera jemenitica</i> (Insecta: Hymenoptera: Apidae), the Arabian honey bee. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 875-876.	0.2	8
10827	Comparative genomics applied to <i>Mucor</i> species with different lifestyles. <i>BMC Genomics</i> , 2020, 21, 135.	1.2	23
10828	The draft genome of horseshoe crab <i>Tachypleus tridentatus</i> reveals its evolutionary scenario and well-developed innate immunity. <i>BMC Genomics</i> , 2020, 21, 137.	1.2	22
10829	A new redescription of <i>Richtersius coronifer</i> , supported by transcriptome, provides resources for describing concealed species diversity within the monotypic genus <i>Richtersius</i> (Eutardigrada). <i>Zoological Letters</i> , 2020, 6, 2.	0.7	25
10830	Whole Genome Sequencing Results Associated with Minimum Inhibitory Concentrations of 14 Anti-Tuberculosis Drugs among Rifampicin-Resistant Isolates of <i>Mycobacterium Tuberculosis</i> from Iran. <i>Journal of Clinical Medicine</i> , 2020, 9, 465.	1.0	20
10832	Prevalent pH Controls the Capacity of <i>Galdieria maxima</i> to Use Ammonia and Nitrate as a Nitrogen Source. <i>Plants</i> , 2020, 9, 232.	1.6	11
10833	Reconstruction and Characterization of Full-Length Begomovirus and Alphasatellite Genomes Infecting Pepper through Metagenomics. <i>Viruses</i> , 2020, 12, 202.	1.5	12

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10834	Detection of a novel <i>Chlamydia</i> species in captive spur-thighed tortoises (<i>Testudo graeca</i>) in southeastern Spain and proposal of <i>Candidatus Chlamydia testudinis</i> . <i>Systematic and Applied Microbiology</i> , 2020, 43, 126071.	1.2	30
10835	Evolution of self-compatibility by a mutant Sm-RNase in citrus. <i>Nature Plants</i> , 2020, 6, 131-142.	4.7	85
10836	The earliest farmers of northwest China exploited grain-fed pheasants not chickens. <i>Scientific Reports</i> , 2020, 10, 2556.	1.6	18
10837	Chloroplast characterization and phylogenetic relationship of <i>Cymbidium aloifolium</i> (Orchidaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 478-479.	0.2	2
10838	Novel Reassortant Avian Influenza A(H9N2) Virus Isolate in Migratory Waterfowl in Hubei Province, China. <i>Frontiers in Microbiology</i> , 2020, 11, 220.	1.5	16
10839	16S rRNA Sequencing Detected <i>Proffella</i> , <i>Liberibacter</i> , <i>Wolbachia</i> , and <i>Diplorickettsia</i> from Relatives of the Asian Citrus Psyllid. <i>Microbial Ecology</i> , 2020, 80, 410-422.	1.4	24
10840	Phylogenetic relationships between fungus-associated Neotropical species of the genera <i>Hirtodrosophila</i> , <i>Mycodrosophila</i> and <i>Zygothrica</i> (Diptera, Drosophilidae), with insights into the evolution of breeding sites usage. <i>Molecular Phylogenetics and Evolution</i> , 2020, 145, 106733.	1.2	8
10841	New data from Monoplacophora and a carefully-curated dataset resolve molluscan relationships. <i>Scientific Reports</i> , 2020, 10, 101.	1.6	56
10842	Multiple evolutionary lineages detected in giant reed (<i>Arundo donax</i> L.): Applied and evolutionary perspectives. <i>Annals of Applied Biology</i> , 2020, 176, 285-295.	1.3	3
10843	Molecular phylogenetics provides a novel hypothesis of chromosome evolution in Neotropical fishes of the genus <i>Potamorhina</i> (Teleostei, Curimatidae). <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2020, 58, 1067-1075.	0.6	4
10844	Phylogenomics changes our understanding about earwig evolution. <i>Systematic Entomology</i> , 2020, 45, 516-526.	1.7	15
10845	<i>Dentipellis fimbriata</i> sp. nov. (Russulales, Basidiomycota) from subtropical Taiwan. <i>Phytotaxa</i> , 2020, 428, 131-138.	0.1	3
10846	A competence-regulated toxin-antitoxin system in <i>Haemophilus influenzae</i> . <i>PLoS ONE</i> , 2020, 15, e0217255.	1.1	5
10847	Isolation of an archaeon at the prokaryote-eukaryote interface. <i>Nature</i> , 2020, 577, 519-525.	13.7	449
10848	Phosphatase POPX2 interferes with cell cycle by interacting with Chk1. <i>Cell Cycle</i> , 2020, 19, 405-418.	1.3	3
10849	Paralogization and New Protein Architectures in Planctomycetes Bacteria with Complex Cell Structures. <i>Molecular Biology and Evolution</i> , 2020, 37, 1020-1040.	3.5	6
10850	Untangling systematics of the <i>Paramacrobiotus areolatus</i> species complex by an integrative redescription of the nominal species for the group, with multilocus phylogeny and species delineation in the genus <i>Paramacrobiotus</i> . <i>Zoological Journal of the Linnean Society</i> , 2020, 188, 694-716.	1.0	43
10851	Conservation Genetics in Mammals. , 2020, , .		6

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10852	Candidatus Mcinerneyibacterium aminivorans gen. nov., sp. nov., the first representative of the candidate phylum Mcinerneyibacteriota phyl. nov. recovered from a high temperature, high salinity tertiary oil reservoir in north central Oklahoma, USA. Systematic and Applied Microbiology, 2020, 43, 126057.	1.2	23
10853	High diversity of fish ectoparasitic monogeneans (<i>Dactylogyrus</i>) in the Iberian Peninsula: a case of adaptive radiation?. Parasitology, 2020, 147, 418-430.	0.7	14
10854	Phylogenetic informativeness analyses to clarify past diversification processes in Cucurbitaceae. Scientific Reports, 2020, 10, 488.	1.6	17
10855	Culture-independent tracking of <i>Vibrio cholerae</i> lineages reveals complex spatiotemporal dynamics in a natural population. Environmental Microbiology, 2020, 22, 4244-4256.	1.8	15
10856	Multiple lineages of hyperdiverse Zopheridae beetles survived the New Zealand Oligocene Drowning. Journal of Biogeography, 2020, 47, 927-940.	1.4	17
10857	Phylogeographical patterns and a cryptic species provide new insights into Western Indian Ocean giant clams phylogenetic relationships and colonization history. Journal of Biogeography, 2020, 47, 1086-1105.	1.4	22
10858	Complex patterns of differentiation and gene flow underly the divergence of aposematic phenotypes in <i>Oophaga</i> poison frogs. Molecular Ecology, 2020, 29, 1944-1956.	2.0	17
10859	Evolutionary Dynamics of Oropouche Virus in South America. Journal of Virology, 2020, 94, .	1.5	17
10860	<i>Genlisea hawkingii</i> (Lentibulariaceae), a new species from Serra da Canastra, Minas Gerais, Brazil. PLoS ONE, 2020, 15, e0226337.	1.1	4
10861	Biogeographic study of human gut-associated crAssphage suggests impacts from industrialization and recent expansion. PLoS ONE, 2020, 15, e0226930.	1.1	38
10862	Phylogenetic Analysis and Substitution Rate Estimation of Colonial Volvocine Algae Based on Mitochondrial Genomes. Genes, 2020, 11, 115.	1.0	5
10863	Phylogeny and highland adaptation of Chinese species in <i>Allium</i> section <i>Daghestanica</i> (Amaryllidaceae) revealed by transcriptome sequencing. Molecular Phylogenetics and Evolution, 2020, 146, 106737.	1.2	10
10864	Environmental and genetic determinants of plasmid mobility in pathogenic <i>Escherichia coli</i> . Science Advances, 2020, 6, eaax3173.	4.7	45
10865	Reevaluation of the "well-known" <i>Paraurostyla weissei</i> complex, with notes on the ontogenesis of a new <i>Paraurostyla</i> species (Ciliophora, Hypotrichia). European Journal of Protistology, 2020, 73, 125672.	0.5	21
10866	Genetic structure and phylogeographic relationships of the <i>Bellamya</i> complex: A nascent aquacultural snail in the Pearl River basin, China. Aquaculture Research, 2020, 51, 1323-1335.	0.9	4
10867	"Little Red Jellies" in Monterey Bay, California (Cnidaria: Hydrozoa: Trachymedusae): Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	1.2	6
10868	<i>Crepis desertorum</i> (Asteraceae, Cichorieae), a new species from northern Xinjiang (China) based on morphological and molecular data. Plant Diversity, 2020, 42, 74-82.	1.8	1
10869	Turkey tick news: A molecular investigation into the presence of tick-borne pathogens in host-seeking ticks in Anatolia; Initial evidence of putative vectors and pathogens, and footsteps of a secretly rising vector tick, <i>Haemaphysalis parva</i> . Ticks and Tick-borne Diseases, 2020, 11, 101373.	1.1	14

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10870	Two plastomes of <i>Phyllostachys</i> and reconstruction of phylogenetic relationship amongst selected <i>Phyllostachys</i> species using genome skimming. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 69-70.	0.2	9
10871	Complete mitogenomes of the chlorophycean green algae <i>Bulbochaete rectangularis</i> var. <i>hiloensis</i> (Oedogoniales) and <i>Stigeoclonium helveticum</i> (Chaetophorales) provide insight into the sequence of events that led to the acquisition of a reduced-derived pattern of evolution in the Chlamydomonadales and Sphaeropleales. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 611-613.	0.2	6
10872	tRNA 2'-O-methylation by a duo of TRM7/FTSJ1 proteins modulates small RNA silencing in <i>Drosophila</i> . <i>Nucleic Acids Research</i> , 2020, 48, 2050-2072.	6.5	30
10873	Disentangling drivers of small mammal diversity in a highly fragmented forest system. <i>Biotropica</i> , 2020, 52, 182-195.	0.8	15
10874	Subchromosome-Scale Nuclear and Complete Mitochondrial Genome Characteristics of <i>Morchella crassipes</i> . <i>International Journal of Molecular Sciences</i> , 2020, 21, 483.	1.8	27
10875	Having the balls to colonize "The Ephydatia fluviatilis group and the origin of (ancient) lake "endemic" sponge lineages. <i>Journal of Great Lakes Research</i> , 2020, 46, 1140-1145.	0.8	9
10876	Into-India or out-of-India? Historical biogeography of the freshwater gastropod genus <i>Pila</i> (Caenogastropoda: Ampullariidae). <i>Biological Journal of the Linnean Society</i> , 2020, 129, 752-764.	0.7	13
10877	Detection of natural hybridization and delimitation of two closely related operational taxonomic units of the <i>Astyanax fasciatus</i> (Teleostei: Characidae) complex through integrative approaches. <i>Biological Journal of the Linnean Society</i> , 2020, 129, 687-700.	0.7	3
10878	Insights into the Evolutionary History of the Hawaiian <i>Bidens</i> (Asteraceae) Adaptive Radiation Revealed Through Phylogenomics. <i>Journal of Heredity</i> , 2020, 111, 119-137.	1.0	22
10879	<i>Synnematotriadelphia</i> gen. nov. (<i>S. stilboidea</i> comb. nov. and <i>S. synnematofera</i> comb. nov.) and <i>Triadelphia hexaformispora</i> sp. nov. in the family Triadelpiaceae. <i>Mycological Progress</i> , 2020, 19, 127-137.	0.5	5
10880	Quantitative immunology for physicists. <i>Physics Reports</i> , 2020, 849, 1-83.	10.3	39
10881	Identification and stable expression of vitellogenin receptor through vitellogenesis in the European eel. <i>Animal</i> , 2020, 14, 1213-1222.	1.3	12
10882	Integrating multiple genomic technologies to investigate an outbreak of carbapenemase-producing <i>Enterobacter hormaechei</i> . <i>Nature Communications</i> , 2020, 11, 466.	5.8	34
10883	Comparative Genomics Identifies Putative Signatures of Sociality in Spiders. <i>Genome Biology and Evolution</i> , 2020, 12, 122-133.	1.1	16
10884	Evaluation of reported sediment samples from 20 Ma using a molecular phylogenetic approach: comment on Liu et al. (2017). <i>Environmental Microbiology</i> , 2020, 22, 813-818.	1.8	0
10885	Intraclonal competitive fitness of longitudinal cystic fibrosis <i>Pseudomonas aeruginosa</i> airway isolates in liquid cultures. <i>Environmental Microbiology</i> , 2020, 22, 2536-2549.	1.8	7
10886	Genomic features of the fall armyworm (<i>Spodoptera frugiperda</i>) (J.E. Smith) yield insights into its defense system and flight capability. <i>Entomological Research</i> , 2020, 50, 100-112.	0.6	10
10887	Genomic analyses of a "living fossil" The endangered dove "tree. <i>Molecular Ecology Resources</i> , 2020, 20, 756-769.	2.2	26

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10888	Biodiversity inventory of the grey mullets (Actinopterygii: Mugilidae) of the Indo-Australian Archipelago through the iterative use of DNA-based species delimitation and specimen assignment methods. <i>Evolutionary Applications</i> , 2020, 13, 1451-1467.	1.5	23
10889	The <i>Pseudomphalina kalchbrenneri</i> complex in North America. <i>Botany</i> , 2020, 98, 91-101.	0.5	2
10890	Genome assembly and characterization of a complex zBED-NLR gene-containing disease resistance locus in Carolina Gold Select rice with Nanopore sequencing. <i>PLoS Genetics</i> , 2020, 16, e1008571.	1.5	112
10891	A molecular phylogeny of Southeast Asian <i>Cyrtandra</i> (Gesneriaceae) supports an emerging paradigm for Malesian plant biogeography. <i>Frontiers of Biogeography</i> , 2020, 12, .	0.8	16
10892	Unique Clindamycin-Resistant <i>Clostridioides difficile</i> Strain Related to Fluoroquinolone-Resistant Epidemic BI/RT027 Strain. <i>Emerging Infectious Diseases</i> , 2020, 26, 247-254.	2.0	4
10893	Mountains as Islands: Species Delimitation and Evolutionary History of the Ant-Loving Beetle Genus <i>Panabachia</i> (Coleoptera, Staphylinidae) from the Northern Andes. <i>Insects</i> , 2020, 11, 64.	1.0	5
10894	Conjugation in <i>Euplotes raikovi</i> (Protista, Ciliophora): New Insights into Nuclear Events and Macronuclear Development from Micronucleate and Amicronucleate Cells. <i>Microorganisms</i> , 2020, 8, 162.	1.6	26
10895	Genomic characterisation and epidemiology of 2019 novel coronavirus: implications for virus origins and receptor binding. <i>Lancet, The</i> , 2020, 395, 565-574.	6.3	9,430
10896	DIX Domain Polymerization Drives Assembly of Plant Cell Polarity Complexes. <i>Cell</i> , 2020, 180, 427-439.e12.	13.5	54
10897	Mechanisms of β -lactam resistance of <i>Streptococcus uberis</i> isolated from bovine mastitis cases. <i>Veterinary Microbiology</i> , 2020, 242, 108592.	0.8	18
10898	Soft sponges with tricky tree: On the phylogeny of dictyoceratid sponges. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2020, 58, 27-40.	0.6	14
10899	Structural evolution drives diversification of the large LRR-ERLK gene family. <i>New Phytologist</i> , 2020, 226, 1492-1505.	3.5	53
10900	The round goby genome provides insights into mechanisms that may facilitate biological invasions. <i>BMC Biology</i> , 2020, 18, 11.	1.7	32
10901	Host-Specific Evolutionary and Transmission Dynamics Shape the Functional Diversification of <i>Staphylococcus epidermidis</i> in Human Skin. <i>Cell</i> , 2020, 180, 454-470.e18.	13.5	102
10902	101 Dothideomycetes genomes: A test case for predicting lifestyles and emergence of pathogens. <i>Studies in Mycology</i> , 2020, 96, 141-153.	4.5	135
10903	Complete Chloroplast Genome Sequence of Chinese Lacquer Tree (<i>Toxicodendron vernicifluum</i>), Tj ETQq1 1,0784314 rgBT /Ove 0,9 15	0.9	15
10904	BioInfoPortal: A scientific gateway for integrating bioinformatics applications on the Brazilian national high-performance computing network. <i>Future Generation Computer Systems</i> , 2020, 107, 192-214.	4.9	7
10905	Comparative genomics shows differences in the electron transport and carbon metabolic pathways of <i>Mycobacterium africanum</i> relative to <i>Mycobacterium tuberculosis</i> and suggests an adaptation to low oxygen tension. <i>Tuberculosis</i> , 2020, 120, 101899.	0.8	15

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10906	Evolution of a supergene that regulates a trans-species social polymorphism. <i>Nature Ecology and Evolution</i> , 2020, 4, 240-249.	3.4	62
10907	Stepwise evolution and convergent recombination underlie the global dissemination of carbapenemase-producing <i>Escherichia coli</i> . <i>Genome Medicine</i> , 2020, 12, 10.	3.6	40
10908	Genome-Based Comparison of All Species of the Genus <i>Moorella</i> , and Status of the Species <i>Moorella thermoacetica</i> and <i>Moorella thermoautotrophica</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 3070.	1.5	12
10909	Evolutionary strategies drive a balance of the interacting gene products for the <i>CBL</i> and <i>CIPK</i> gene families. <i>New Phytologist</i> , 2020, 226, 1506-1516.	3.5	52
10910	Eocene–Oligocene sea-level fall drove amphipod habitat shift from marine to freshwater in the Far East. <i>Zoologica Scripta</i> , 2020, 49, 357-365.	0.7	3
10911	Plant Mitochondrial Carriers: Molecular Gatekeepers That Help to Regulate Plant Central Carbon Metabolism. <i>Plants</i> , 2020, 9, 117.	1.6	23
10912	Cross-species transmission of the newly identified coronavirus 2019-nCoV. <i>Journal of Medical Virology</i> , 2020, 92, 433-440.	2.5	688
10913	Phylogenomics and biogeography of the world's thrushes (<i>Aves</i> , <i>Turdus</i>): new evidence for a more parsimonious evolutionary history. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20192400.	1.2	16
10914	Complete mitochondrial genome of <i>Atractomorpha sagittaris</i> (Orthoptera: Pyrgomorphidae) and its phylogenetic analysis for Acrididea. <i>Biologia (Poland)</i> , 2020, 75, 1571-1583.	0.8	5
10915	Bacterial endosymbionts of <i>Placobdella</i> (Annelida: Hirudinea: Glossiphoniidae): phylogeny, genetic distance, and vertical transmission. <i>Hydrobiologia</i> , 2020, 847, 1177-1194.	1.0	2
10916	Morphology and molecular analyses of four epibiotic peritrichs on crustacean and polychaete hosts, including descriptions of two new species (<i>Ciliophora</i> , <i>Peritrichia</i>). <i>European Journal of Protistology</i> , 2020, 73, 125670.	0.5	27
10917	Adaption and parallel evolution of human-isolated H5 avian influenza viruses. <i>Journal of Infection</i> , 2020, 80, 630-638.	1.7	10
10918	Exploring Diversity, Taxonomy and Phylogeny of Diatoms (Bacillariophyta) from Marine Habitats. Novel Taxa with Internal Costae. <i>Protist</i> , 2020, 171, 125713.	0.6	11
10919	A taxonomic conundrum: Characterizing a cryptic radiation of Asian gracile skinks (<i>Squamata</i>): Tj ETQq1 1 0.784314,rgBT /Oyerlock 10	1.2	2
10920	Discovery of a Fungal Copper Radical Oxidase with High Catalytic Efficiency toward 5-Hydroxymethylfurfural and Benzyl Alcohols for Bioprocessing. <i>ACS Catalysis</i> , 2020, 10, 3042-3058.	5.5	46
10921	Diversity and metabolism of <i>Woeseiales</i> bacteria, global members of marine sediment communities. <i>ISME Journal</i> , 2020, 14, 1042-1056.	4.4	51
10922	Phylogenetic relationships of the Chinese torrent frogs (<i>Ranidae</i> : <i>Amolops</i>) revealed by phylogenomic analyses of AFLP-Capture data. <i>Molecular Phylogenetics and Evolution</i> , 2020, 146, 106753.	1.2	13
10923	Persistent Transmission of Shigellosis in England Is Associated with a Recently Emerged Multidrug-Resistant Strain of <i>Shigella sonnei</i> . <i>Journal of Clinical Microbiology</i> , 2020, 58, .	1.8	45

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10924	Phylogeographic analyses point to long-term survival on the spot in micro-endemic Lycian salamanders. <i>PLoS ONE</i> , 2020, 15, e0226326.	1.1	6
10925	New insights on evolutionary aspects of <i>Pythium insidiosum</i> and other peronosporaleans. <i>Mycoses</i> , 2020, 63, 395-406.	1.8	4
10926	Unusual genome expansion and transcription suppression in ectomycorrhizal <i>Tricholoma matsutake</i> by insertions of transposable elements. <i>PLoS ONE</i> , 2020, 15, e0227923.	1.1	15
10927	Evolution of Photorespiratory Glycolate Oxidase among Archaeplastida. <i>Plants</i> , 2020, 9, 106.	1.6	9
10928	Implementing Large Genomic Single Nucleotide Polymorphism Data Sets in Phylogenetic Network Reconstructions: A Case Study of Particularly Rapid Radiations of Cichlid Fish. <i>Systematic Biology</i> , 2020, 69, 848-862.	2.7	37
10929	Tropical Niche Conservatism Explains the Eocene Migration from India to Southeast Asia in Ochyroceratid Spiders. <i>Systematic Biology</i> , 2020, 69, 987-998.	2.7	12
10930	Phylogenetic relationships of <i>Atractylodes lancea</i> , <i>A. chinensis</i> and <i>A. macrocephala</i> , revealed by complete plastome and nuclear gene sequences. <i>PLoS ONE</i> , 2020, 15, e0227610.	1.1	10
10931	Multigene phylogeny and taxonomy of <i>Dendryphion hydei</i> and <i>Torula hydei</i> spp. nov. from herbaceous litter in northern Thailand. <i>PLoS ONE</i> , 2020, 15, e0228067.	1.1	7
10932	Hybrid Genome Assembly and Annotation of a Pandrug-Resistant <i>Klebsiella pneumoniae</i> Strain Using Nanopore and Illumina Sequencing. <i>Infection and Drug Resistance</i> , 2020, Volume 13, 199-206.	1.1	26
10933	Two Distinct Genotypes of <i>Spissistilus festinus</i> (Say, 1830) (Hemiptera, Membracidae) in the United States Revealed by Phylogenetic and Morphological Analyses. <i>Insects</i> , 2020, 11, 80.	1.0	4
10934	The first mitochondrial genome for Phaudidae (Lepidoptera) with phylogenetic analyses of Zygaenoidea. <i>International Journal of Biological Macromolecules</i> , 2020, 149, 951-961.	3.6	10
10935	The chloroplast genome sequence of the green macroalga <i>Caulerpa okamurae</i> (Ulvophyceae). <i>Trends in Plant Science</i> , 2020, 25, 100752.	0.4	3
10936	Honey-bee-associated prokaryotic viral communities reveal wide viral diversity and a profound metabolic coding potential. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 10511-10519.	3.3	36
10937	Taxonomic review of the Asian Horned Frogs (Amphibia: Megophrys Kuhl & Van Hasselt) of Northeast India and Bangladesh previously misidentified as <i>M. parva</i> (Boulenger), with descriptions of three new species. <i>Journal of Natural History</i> , 2020, 54, 119-194.	0.2	12
10938	Characterization of complete chloroplast genome of artificial hybrid passion fruit "Ziyan"™, <i>Passiflora edulis</i> Sims – <i>P. edulis</i> f. <i>edulis</i> Sims (Passifloraceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1720-1721.	0.2	1
10939	No Evidence for Single-Copy Immune-Genes Specific Signals of Selection in Termites. <i>Frontiers in Ecology and Evolution</i> , 2020, 8, .	1.1	5
10940	Patterns in Microbial Assemblages Exported From the Meltwater of Arctic and Sub-Arctic Glaciers. <i>Frontiers in Microbiology</i> , 2020, 11, 669.	1.5	24
10941	Evolutionary Changes in DnaA-Dependent Chromosomal Replication in Cyanobacteria. <i>Frontiers in Microbiology</i> , 2020, 11, 786.	1.5	12

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10942	A consensus phylogenomic approach highlights paleopolyploid and rapid radiation in the history of Ericales. <i>American Journal of Botany</i> , 2020, 107, 773-789.	0.8	38
10943	QIIME 2 Enables Comprehensive End-to-End Analysis of Diverse Microbiome Data and Comparative Studies with Publicly Available Data. <i>Current Protocols in Bioinformatics</i> , 2020, 70, e100.	25.8	212
10944	On the identity of <i>Goodyera rosulacea</i> (Orchidaceae: Orchidoideae: Cranichideae: Goodyerinae). <i>Kew Bulletin</i> , 2020, 75, 1.	0.4	1
10945	The Reference Genome of Tea Plant and Resequencing of 81 Diverse Accessions Provide Insights into Its Genome Evolution and Adaptation. <i>Molecular Plant</i> , 2020, 13, 1013-1026.	3.9	257
10946	Radiation of the coralline red algae (Corallinophycidae, Rhodophyta) crown group as inferred from a multilocus time-calibrated phylogeny. <i>Molecular Phylogenetics and Evolution</i> , 2020, 150, 106845.	1.2	33
10947	The Great Oxidation Event expanded the genetic repertoire of arsenic metabolism and cycling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 10414-10421.	3.3	96
10948	Colonize, radiate, decline: Unraveling the dynamics of island community assembly with Fijian trapjaw ants. <i>Evolution; International Journal of Organic Evolution</i> , 2020, 74, 1082-1097.	1.1	8
10949	Evolution of NLR resistance genes with noncanonical N-terminal domains in wild tomato species. <i>New Phytologist</i> , 2020, 227, 1530-1543.	3.5	60
10950	Tracing the Evolutionary History and Global Expansion of <i>Candida auris</i> Using Population Genomic Analyses. <i>MBio</i> , 2020, 11, .	1.8	224
10951	Marine tardigrades from Lützow-Holm Bay, East Antarctica with the description of a new species. <i>Polar Biology</i> , 2020, 43, 679-693.	0.5	6
10952	<i>Neodeightonia phoenicum</i> CMIB-151: Isolation, Molecular Identification, and Production and Characterization of an Exopolysaccharide. <i>Journal of Polymers and the Environment</i> , 2020, 28, 1954-1966.	2.4	3
10953	Characterization of a specific odorant receptor for linalool in the Chinese citrus fly <i>Bactrocera minax</i> (Diptera: Tephritidae). <i>Insect Biochemistry and Molecular Biology</i> , 2020, 122, 103389.	1.2	19
10954	The complete mitochondrial genome of <i>Choroterpides apiculata</i> (Ephemeroptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 267 Td (1159-1160.	0.2	8
10955	Mitochondrial genome of <i>Apis mellifera anatoliaca</i> (Hymenoptera: Apidae) – the Anatolian honey bee. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1876-1877.	0.2	2
10956	Medium-Chain Fatty Acid Synthesis by <i>Candidatus</i> <i>Weimeria bifida</i> gen. nov., sp. nov., and <i>Candidatus</i> <i>Pseudoramibacter fermentans</i> sp. nov. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	42
10957	Draft Genome Sequences of <i>Thiorhodococcus mannitoliphagus</i> and <i>Thiorhodococcus minor</i> , Purple Sulfur Photosynthetic Bacteria in the Gammaproteobacterial Family Chromatiaceae. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	1
10958	Comparison of the Bacterial Gut Microbiome of North American <i>Triatoma</i> spp. With and Without <i>Trypanosoma cruzi</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 364.	1.5	20
10959	Pathogenomes of Atypical Non-shigatoxigenic <i>Escherichia coli</i> NSF/SF O157:H7/NM: Comprehensive Phylogenomic Analysis Using Closed Genomes. <i>Frontiers in Microbiology</i> , 2020, 11, 619.	1.5	11

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10960	Abundance of Colistin-Resistant, OXA-23- and ArmA-Producing <i>Acinetobacter baumannii</i> Belonging to International Clone 2 in Greece. <i>Frontiers in Microbiology</i> , 2020, 11, 668.	1.5	29
10961	More Knot Worms: Four New <i>Polygordius</i> (Annelida) Species from the Pacific and Caribbean. <i>Diversity</i> , 2020, 12, 146.	0.7	2
10962	Unraveling the Phylogenomic Relationships of the Most Diverse African Palm Genus <i>Raphia</i> (Calamoideae, Arecaceae). <i>Plants</i> , 2020, 9, 549.	1.6	16
10963	Comparative genetic analysis of grayling (<i>Thymallus</i> spp. Salmonidae) across the paleohydrologically dynamic river drainages of the Altai-Sayan mountain region. <i>Hydrobiologia</i> , 2020, 847, 2823-2844.	1.0	6
10964	Transcriptome analysis and metabolic profiling reveal the key role of carotenoids in the petal coloration of <i>Liriodendron tulipifera</i> . <i>Horticulture Research</i> , 2020, 7, 70.	2.9	47
10965	Haplotype-resolved genomes provide insights into structural variation and gene content in Angus and Brahman cattle. <i>Nature Communications</i> , 2020, 11, 2071.	5.8	84
10966	Gene Function Rather than Reproductive Mode Drives the Evolution of RNA Helicases in Sexual and Apomictic <i>Boechera</i> . <i>Genome Biology and Evolution</i> , 2020, 12, 656-673.	1.1	7
10967	Revision of the Bark Beetle Genera Within the Former <i>Cryphalini</i> (Curculionidae: Scolytinae). <i>Insect Systematics and Diversity</i> , 2020, 4, .	0.7	22
10968	Emergence of Fluoroquinolone-Resistant <i>Campylobacter jejuni</i> and <i>Campylobacter coli</i> among Australian Chickens in the Absence of Fluoroquinolone Use. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	39
10969	Genomic characterization of <i>Lactobacillus fermentum</i> DSM 20052. <i>BMC Genomics</i> , 2020, 21, 328.	1.2	15
10970	Evaluation of the relative roles of the Tabanidae and Glossinidae in the transmission of trypanosomiasis in drug resistance hotspots in Mozambique. <i>Parasites and Vectors</i> , 2020, 13, 219.	1.0	20
10971	Phylogenomics reveals conservation challenges and opportunities for cryptic endangered species in a rapidly disappearing desert ecosystem. <i>Biodiversity and Conservation</i> , 2020, 29, 2185-2200.	1.2	3
10972	<i>Serratia marcescens</i> : a key pathogen caused ginger rhizomes soft rot disease. <i>Journal of Plant Diseases and Protection</i> , 2020, 127, 379-391.	1.6	2
10973	Netrin expressed by the ventral ectoderm lineage guides mesoderm migration in epibolic gastrulation of the leech. <i>Developmental Biology</i> , 2020, 463, 39-52.	0.9	4
10974	The negative regulator SMAX1 controls mycorrhizal symbiosis and strigolactone biosynthesis in rice. <i>Nature Communications</i> , 2020, 11, 2114.	5.8	101
10975	Bioinformatic prospecting and phylogenetic analysis reveals 94 undescribed circular bacteriocins and key motifs. <i>BMC Microbiology</i> , 2020, 20, 77.	1.3	20
10976	Comparative Genomic and Transcriptomic Analyses of <i>Mycobacterium kansasii</i> Subtypes Provide New Insights Into Their Pathogenicity and Taxonomy. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 122.	1.8	10
10977	Phylogenetic Analyses of Sites in Different Protein Structural Environments Result in Distinct Placements of the Metazoan Root. <i>Biology</i> , 2020, 9, 64.	1.3	20

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10978	Complete Chloroplast Genome Sequence and Phylogenetic Inference of the Canary Islands Dragon Tree (<i>Dracaena draco</i> L.). <i>Forests</i> , 2020, 11, 309.	0.9	14
10979	Genomic Features of <i>Cladobotryum dendroides</i> , Which Causes Cobweb Disease in Edible Mushrooms, and Identification of Genes Related to Pathogenicity and Mycoparasitism. <i>Pathogens</i> , 2020, 9, 232.	1.2	15
10980	Extremely low genetic diversity in the European clade of the model bryophyte <i>Anthoceros agrestis</i> . <i>Plant Systematics and Evolution</i> , 2020, 306, 1.	0.3	1
10981	Multilocus phylogeny of Paratelmatobiinae (Anura: Leptodactylidae) reveals strong spatial structure and previously unknown diversity in the Atlantic Forest hotspot. <i>Molecular Phylogenetics and Evolution</i> , 2020, 148, 106819.	1.2	22
10982	Compartmentalization and Clonal Amplification of HIV-1 in the Male Genital Tract Characterized Using Next-Generation Sequencing. <i>Journal of Virology</i> , 2020, 94, .	1.5	11
10983	Genome- and Community-Level Interaction Insights into Carbon Utilization and Element Cycling Functions of <i>Hydrothermarchaeota</i> in Hydrothermal Sediment. <i>MSystems</i> , 2020, 5, .	1.7	75
10984	Towards a rigorous species delimitation framework for scleractinian corals based on RAD sequencing: the case study of <i>Leptastrea</i> from the Indo-Pacific. <i>Coral Reefs</i> , 2020, 39, 1001-1025.	0.9	38
10985	Phylogenetic relationships within the subtribe Cynoglossinae (Cynoglossoideae: Boraginaceae): new insights from nuclear and plastid DNA sequence data. <i>Plant Systematics and Evolution</i> , 2020, 306, 1.	0.3	5
10986	<i>Aureliella helgolandensis</i> gen. nov., sp. nov., a novel Planctomycete isolated from a jellyfish at the shore of the island Helgoland. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 1839-1849.	0.7	19
10987	Description of <i>Polystyrenella longa</i> gen. nov., sp. nov., isolated from polystyrene particles incubated in the Baltic Sea. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 1851-1862.	0.7	14
10988	<i>Lignipirellula cremea</i> gen. nov., sp. nov., a planctomycete isolated from wood particles in a brackish river estuary. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 1863-1875.	0.7	15
10989	Two new species in a new genus and a critical revision of Brachybasidiaceae (Exobasidiales). <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 T5</i>	0.5	3
10990	Speciation Associated with Shifts in Migratory Behavior in an Avian Radiation. <i>Current Biology</i> , 2020, 30, 1312-1321.e6.	1.8	45
10991	Enriching indigenous microbial consortia as a promising strategy for xenobioticsâ€™ cleanup. <i>Journal of Cleaner Production</i> , 2020, 261, 121234.	4.6	24
10992	Frequency of mutations associated with resistance to first- and second-line drugs in multidrug-resistant <i>Mycobacterium tuberculosis</i> isolates. <i>Journal of Global Antimicrobial Resistance</i> , 2020, 22, 275-282.	0.9	4
10993	Genomic characteristics of clinically important ST11 <i>Klebsiella pneumoniae</i> strains worldwide. <i>Journal of Global Antimicrobial Resistance</i> , 2020, 22, 519-526.	0.9	36
10994	Evaluation of haplotype callers for next-generation sequencing of viruses. <i>Infection, Genetics and Evolution</i> , 2020, 82, 104277.	1.0	29
10995	Phylogenetic overview of Erysiphaceae based on nrDNA and MCM7 sequences. <i>Mycoscience</i> , 2020, 61, 249-258.	0.3	6

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10996	Diverse responses of common vole (<i>Microtus arvalis</i>) populations to Late Glacial and Early Holocene climate changes – Evidence from ancient DNA. <i>Quaternary Science Reviews</i> , 2020, 233, 106239.	1.4	23
10997	Epidemiology and evolutionary analysis of Torque teno sus virus. <i>Veterinary Microbiology</i> , 2020, 244, 108668.	0.8	3
10998	Comparative genomic analysis of <i>Erwinia amylovora</i> reveals novel insights in phylogenetic arrangement, plasmid diversity, and streptomycin resistance. <i>Genomics</i> , 2020, 112, 3762-3772.	1.3	31
10999	A large-scale systematic framework of Chinese snakes based on a unified multilocus marker system. <i>Molecular Phylogenetics and Evolution</i> , 2020, 148, 106807.	1.2	42
11000	Testing morphological trait evolution and assessing species delimitations in the grape genus using a phylogenomic framework. <i>Molecular Phylogenetics and Evolution</i> , 2020, 148, 106809.	1.2	10
11001	Outstanding diversity and microendemism in a clade of rare Atlantic Forest montane frogs. <i>Molecular Phylogenetics and Evolution</i> , 2020, 149, 106813.	1.2	8
11002	Is dispersal mode a driver of diversification and geographical distribution in the tropical plant family Melastomataceae?. <i>Molecular Phylogenetics and Evolution</i> , 2020, 148, 106815.	1.2	50
11003	Genomic analyses reveal two species of the matamata (<i>Testudines: Chelidae: Chelus</i> spp.) and clarify their phylogeography. <i>Molecular Phylogenetics and Evolution</i> , 2020, 148, 106823.	1.2	20
11004	A timetree for phytoplasmas (<i>Mollicutes</i>) with new insights on patterns of evolution and diversification. <i>Molecular Phylogenetics and Evolution</i> , 2020, 149, 106826.	1.2	14
11005	The sterlet sturgeon genome sequence and the mechanisms of segmental rediploidization. <i>Nature Ecology and Evolution</i> , 2020, 4, 841-852.	3.4	159
11006	Genome sequence of <i>Gossypium herbaceum</i> and genome updates of <i>Gossypium arboreum</i> and <i>Gossypium hirsutum</i> provide insights into cotton A-genome evolution. <i>Nature Genetics</i> , 2020, 52, 516-524.	9.4	240
11007	Draft genomes of two Atlantic bay scallop subspecies <i>Argopecten irradians irradians</i> and <i>A. i. concentricus</i> . <i>Scientific Data</i> , 2020, 7, 99.	2.4	37
11008	Phylogenomics of <i>Rhodocyclales</i> and its distribution in wastewater treatment systems. <i>Scientific Reports</i> , 2020, 10, 3883.	1.6	22
11009	Genomic Epidemiology of Vancomycin-Resistant <i>Enterococcus faecium</i> (VREfm) in Latin America: Revisiting The Global VRE Population Structure. <i>Scientific Reports</i> , 2020, 10, 5636.	1.6	39
11010	Metagenomic views of microbial dynamics influenced by hydrocarbon seepage in sediments of the Gulf of Mexico. <i>Scientific Reports</i> , 2020, 10, 5772.	1.6	21
11011	Phylogeny, biogeography and systematics of Pacific vent, methane seep, and whale-fall <i>Parougia</i> (<i>Dorvilleidae</i> : <i>Annelida</i>), with eight new species. <i>Invertebrate Systematics</i> , 2020, 34, 200.	0.5	7
11012	Phylogenetic relationships and taxonomic issues in <i>Gastridium</i> (<i>Poaceae</i>) inferred from plastid and nuclear DNA sequence analysis. <i>Plant Biosystems</i> , 2020, 154, 947-960.	0.8	1
11013	Molecular biodiversity of Iranian shallow water sponges. <i>Systematics and Biodiversity</i> , 2020, 18, 192-202.	0.5	11

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11014	The complete chloroplast genome sequence of <i>Althaea rosea</i> (L.) Cavan. (Malvaceae) and its phylogenetic analysis. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1433-1434.	0.2	4
11015	A revision of <i>Neusticomys peruviansis</i> (Rodentia: Cricetidae) with the description of a new subspecies. <i>Journal of Mammalogy</i> , 2020, 101, 858-871.	0.6	4
11016	Type II and type IV toxin-antitoxin systems show different evolutionary patterns in the global <i>Klebsiella pneumoniae</i> population. <i>Nucleic Acids Research</i> , 2020, 48, 4357-4370.	6.5	14
11017	Hide-and-seek with hoverflies: <i>Merodon aureus</i> – a species, a complex or a subgroup?. <i>Zoological Journal of the Linnean Society</i> , 2020, 190, 974-1001.	1.0	12
11018	Phylogenetic conservation of soil bacterial responses to simulated global changes. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190242.	1.8	46
11019	A dated phylogeny of Lardizabalaceae reveals an unusual long-distance dispersal across the Pacific Ocean and the rapid rise of East Asian subtropical evergreen broadleaved forests in the late Miocene. <i>Cladistics</i> , 2020, 36, 447-457.	1.5	20
11020	Trentepohlialean Algae (Trentepohliales, Ulvophyceae) Show Preference to Selected Mycobiont Lineages in Lichen Symbioses. <i>Journal of Phycology</i> , 2020, 56, 979-993.	1.0	16
11021	The Taxonomy and Diversity of <i>Proschkinia</i> (Bacillariophyta), A Common But Enigmatic Genus from Marine Coasts. <i>Journal of Phycology</i> , 2020, 56, 953-978.	1.0	5
11022	Description of <i>Freudenthalidium</i> gen. nov. and <i>Halluxium</i> gen. nov. to Formally Recognize Clades Fr3 and H as Genera in the Family Symbiodiniaceae (Dinophyceae). <i>Journal of Phycology</i> , 2020, 56, 923-940.	1.0	56
11023	High genomic diversity in the bank vole at the northern apex of a range expansion: The role of multiple colonizations and end-glacial refugia. <i>Molecular Ecology</i> , 2020, 29, 1730-1744.	2.0	27
11024	Speciation and gene flow in two sympatric small mammals from Madagascar, <i>Microgale fotsifotsy</i> and <i>M. Ásoricoides</i> (Mammalia: Tenrecidae). <i>Molecular Ecology</i> , 2020, 29, 1717-1729.	2.0	2
11025	The genome of a cave plant, <i>Primulina huaijiensis</i> , provides insights into adaptation to limestone karst habitats. <i>New Phytologist</i> , 2020, 227, 1249-1263.	3.5	32
11026	How well do multispecies coalescent methods perform with mitochondrial genomic data? A case study of butterflies and moths (Insecta: Lepidoptera). <i>Systematic Entomology</i> , 2020, 45, 857-873.	1.7	15
11027	MEKK2 inhibits activation of MAP kinases in <i>Arabidopsis</i> . <i>Plant Journal</i> , 2020, 103, 705-714.	2.8	16
11028	Polyploidization events shaped the transcription factor repertoires in legumes (Fabaceae). <i>Plant Journal</i> , 2020, 103, 726-741.	2.8	17
11029	From the Inside Out: an Epibiotic <i>Bdellovibrio</i> Predator with an Expanded Genomic Complement. <i>Journal of Bacteriology</i> , 2020, 202, .	1.0	14
11030	Flexible Cobamide Metabolism in <i>Clostridioides</i> (<i>Clostridium</i>) <i>difficile</i> 630 [†] <i>erm</i> . <i>Journal of Bacteriology</i> , 2020, 202, .	1.0	13
11031	– <i>Candidatus</i> <i>Desulfobulbus rimicarenis</i> , an Uncultivated Deltaproteobacterial Epibiont from the Deep-Sea Hydrothermal Vent Shrimp <i>Rimicaris exoculata</i> . <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	24

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11032	Outbreak Severity of Highly Pathogenic Avian Influenza A(H5N8) Viruses Is Inversely Correlated to Polymerase Complex Activity and Interferon Induction. <i>Journal of Virology</i> , 2020, 94, .	1.5	10
11033	A Novel <i>Legionella</i> Genomic Island Encodes a Copper-Responsive Regulatory System and a Single Icm/Dot Effector Protein Transcriptionally Activated by Copper. <i>MBio</i> , 2020, 11, .	1.8	7
11034	<i>Paenibacillus odorifer</i> , the Predominant <i>Paenibacillus</i> Species Isolated from Milk in the United States, Demonstrates Genetic and Phenotypic Conservation of Psychrotolerance but Clade-Associated Differences in Nitrogen Metabolic Pathways. <i>MSphere</i> , 2020, 5, .	1.3	9
11035	Toxin-Antitoxin Gene Pairs Found in Tn ₃ Family Transposons Appear To Be an Integral Part of the Transposition Module. <i>MBio</i> , 2020, 11, .	1.8	25
11036	Ancient DNA From Museum Specimens and Next Generation Sequencing Help Resolve the Controversial Evolutionary History of the Critically Endangered Puebla Deer Mouse. <i>Frontiers in Ecology and Evolution</i> , 2020, 8, .	1.1	18
11037	Genomic and Phenotypic Analyses of <i>Acinetobacter baumannii</i> Isolates From Three Tertiary Care Hospitals in Thailand. <i>Frontiers in Microbiology</i> , 2020, 11, 548.	1.5	26
11038	Tracing the Origin of Planktonic Protists in an Ancient Lake. <i>Microorganisms</i> , 2020, 8, 543.	1.6	28
11039	Pathological, Morphological, Cytogenomic, Biochemical and Molecular Data Support the Distinction between <i>Colletotrichum cigarro</i> comb. et stat. nov. and <i>Colletotrichum kahawae</i> . <i>Plants</i> , 2020, 9, 502.	1.6	21
11040	Severe Plastid Genome Size Reduction in a Mycoheterotrophic Orchid, <i>Danxiaorchis singchiana</i> , Reveals Heavy Gene Loss and Gene Relocations. <i>Plants</i> , 2020, 9, 521.	1.6	4
11041	Phylogenomic Analysis of Secondary Metabolism in the Toxic Cyanobacterial Genera <i>Anabaena</i> , <i>Dolichospermum</i> and <i>Aphanizomenon</i> . <i>Toxins</i> , 2020, 12, 248.	1.5	34
11042	A Complex of Badnavirus Species Infecting Cacao Reveals Mixed Infections, Extensive Genomic Variability, and Interspecific Recombination. <i>Viruses</i> , 2020, 12, 443.	1.5	19
11043	<i>Volvariella turcica</i> , a new species from Turkey, and a multigene phylogeny of <i>Volvariella</i> . <i>Mycologia</i> , 2020, 112, 577-587.	0.8	6
11044	The mitochondrial genome of <i>Caenis</i> sp. (Ephemeroptera: Caenidae) from Fujian and the phylogeny of Caenidae within Ephemeroptera. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 192-193.	0.2	8
11045	Characterization of the complete chloroplast genome of <i>Salix variegata</i> (Salicaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 196-197.	0.2	2
11046	The complete chloroplast genome sequence of a rambler rose, <i>Rosa wichuraiana</i> (Rosaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 252-253.	0.2	5
11047	Complete mitochondrial genome of <i>Carijoa riisei</i> (Duchassaing & Michelotti, 1860) (Octocorallia: Tj ETQq1 1 0.784314 rgBT ₃ /Overlook _{0,2}	0.2	0
11048	Genetic bases for variation in structure and biological activity of trichothecene toxins produced by diverse fungi. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 5185-5199.	1.7	21
11049	Characterization of the complete chloroplast genome of <i>Salvia hispanica</i> (Lamiaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1748-1750.	0.2	10

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11050	<i>Candidatus</i> <i>Ethanoperedens</i> , a Thermophilic Genus of Archaea Mediating the Anaerobic Oxidation of Ethane. <i>MBio</i> , 2020, 11, .	1.8	66
11051	Selection Is a Significant Driver of Gene Gain and Loss in the Pangenome of the Bacterial Genus <i>Sulfurovum</i> in Geographically Distinct Deep-Sea Hydrothermal Vents. <i>MSystems</i> , 2020, 5, .	1.7	35
11052	Invalidation of taxa within the silvery woolly monkey (<i>Lagothrix lagothricha poeppigii</i> , Atelidae). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 66</i>	0.7	1
11053	Mitochondrial sequences of <i>Rhipicephalus</i> and <i>Coxiella</i> endosymbiont reveal evidence of lineages co-cladogenesis. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	9
11054	Identification and Characterization of Fungi Causing Thread Blight Diseases on Cacao in Ghana. <i>Plant Disease</i> , 2020, 104, 3033-3042.	0.7	11
11055	Toward a preliminary assessment of the diversity and origin of Cyprinid fish genus <i>Carassius</i> in Iran. <i>Journal of Applied Ichthyology</i> , 2020, 36, 422-430.	0.3	6
11056	Shifting ecosystem connectivity during the Pleistocene drove diversification and gene flow in a species complex of Neotropical birds (Tityridae: <i>Pachyrhamphus</i>). <i>Journal of Biogeography</i> , 2020, 47, 1714-1726.	1.4	7
11057	Iconic, threatened, but largely unknown: Biogeography of the Macaronesian dragon trees (<i>Dracaena</i>). <i>Tj ETQq1 1 0,784314 rgBT /Overlock 14</i>	0.4	14
11058	Lineage-specific evolution of mangrove plastid genomes. <i>Plant Genome</i> , 2020, 13, e20019.	1.6	4
11059	A functionally informed evolutionary framework for the study of LRR-RLKs during stem cell maintenance. <i>Journal of Plant Research</i> , 2020, 133, 331-342.	1.2	10
11060	Phylogeny and cultivation of the holocarpic oomycete <i>Diatomophthora perforans</i> comb. nov., an endoparasitoid of marine diatoms. <i>Mycological Progress</i> , 2020, 19, 441-454.	0.5	10
11061	Host preference and sorus location correlate with parasite phylogeny in the smut fungal genus <i>Microbotryum</i> (Basidiomycota, Microbotryales). <i>Mycological Progress</i> , 2020, 19, 481-493.	0.5	16
11062	Morphology, Ultrastructure, and Phylogeny of Two Novel Species of <i>Ventrifissura</i> (<i>V. oblonga</i> n. sp.). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 66</i>	0.6	2
11063	The complete plastid genome of <i>Dendrocalamus yunnanicus</i> (Poaceae, Bambuseae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1521-1522.	0.2	0
11064	The Remarkable Dual-Level Diversity of Prokaryotic Flagellins. <i>MSystems</i> , 2020, 5, .	1.7	11
11065	Pattern and timing of diversification in the African freshwater fish genus <i>Distichodus</i> (Characiformes: Distichodontidae). <i>BMC Evolutionary Biology</i> , 2020, 20, 48.	3.2	6
11066	Analysis of 1,000+ Type-Strain Genomes Substantially Improves Taxonomic Classification of Alphaproteobacteria. <i>Frontiers in Microbiology</i> , 2020, 11, 468.	1.5	1,537
11067	Lysine Acetyltransferase p300/CBP Plays an Important Role in Reproduction, Embryogenesis and Longevity of the Pea Aphid <i>Acyrtosiphon pisum</i> . <i>Insects</i> , 2020, 11, 265.	1.0	13

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11068	Insights into the Diversification and Evolution of R2R3-MYB Transcription Factors in Plants. <i>Plant Physiology</i> , 2020, 183, 637-655.	2.3	102
11069	Physiological and genomic characterization of a new <i>Candidatus</i> Nitrotoga™ isolate. <i>Environmental Microbiology</i> , 2020, 22, 2365-2382.	1.8	26
11070	Whole-Genome-Sequence-Based Characterization of Extensively Drug-Resistant <i>Acinetobacter baumannii</i> Hospital Outbreak. <i>MSphere</i> , 2020, 5, .	1.3	36
11071	Genome-centric resolution of novel microbial lineages in an excavated Centrosaurus dinosaur fossil bone from the Late Cretaceous of North America. <i>Environmental Microbiomes</i> , 2020, 15, 8.	2.2	8
11072	Conserved nuclear hormone receptors controlling a novel plastic trait target fast-evolving genes expressed in a single cell. <i>PLoS Genetics</i> , 2020, 16, e1008687.	1.5	44
11073	Draft Genome Assembly for the Tibetan Black Bear (<i>Ursus thibetanus thibetanus</i>). <i>Frontiers in Genetics</i> , 2020, 11, 231.	1.1	8
11074	Decoding diversity in a coral reef fish species complex with restricted range using metagenomic sequencing of gut contents. <i>Ecology and Evolution</i> , 2020, 10, 3413-3423.	0.8	2
11075	High Prevalence of Sequences Included in Transmission Clusters Within Newly Diagnosed HIV-1 Patients in Southern Spain (2004-2015). <i>Microbial Drug Resistance</i> , 2020, 26, 1090-1097.	0.9	2
11076	Characterization of <i>Klebsiella pneumoniae</i> isolates from a mother-child cohort in Madagascar. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 1736-1746.	1.3	9
11077	Convergent evolution of seasonal camouflage in response to reduced snow cover across the snowshoe hare range*. <i>Evolution; International Journal of Organic Evolution</i> , 2020, 74, 2033-2045.	1.1	19
11078	A deeper meaning for shallow-level phylogenomic studies: nested anchored hybrid enrichment offers great promise for resolving the tiger moth tree of life (Lepidoptera: Erebidæ). <i>Tj ETQq0 0 0 rgBT 10 rlock 10 Tf 50 33</i>	1.0	10
11079	Using Colonization Assays and Comparative Genomics To Discover Symbiosis Behaviors and Factors in <i>Vibrio fischeri</i> . <i>MBio</i> , 2020, 11, .	1.8	17
11080	Evolutionary Dynamics of the SKN-1 MED END-1,3 Regulatory Gene Cascade in <i>Caenorhabditis</i> Endoderm Specification. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 333-356.	0.8	14
11081	Chromosome-level genome assembly of an important pine defoliator, <i>Dendrolimus punctatus</i> (Lepidoptera; Lasiocampidae). <i>Molecular Ecology Resources</i> , 2020, 20, 1023-1037.	2.2	34
11082	Inter-Lineage Variation of Lassa Virus Glycoprotein Epitopes: A Challenge to Lassa Virus Vaccine Development. <i>Viruses</i> , 2020, 12, 386.	1.5	27
11083	Contemporary integrative taxonomy for sexually deprived protists: A case study of <i>Trachelomonas</i> (Euglenaceae) from western Ukraine. <i>Taxon</i> , 2020, 69, 28-42.	0.4	4
11084	Morphogenesis and molecular phylogeny of two soil ciliates <i>Australocirrus australis</i> (Foissner, 1995) Kumar and Foissner, 2015 and <i>A. aspoECKi</i> (Foissner, 2004) Kumar and Foissner, 2015 (Ciliophora). <i>Tj ETQq0 0 0 rgBT 10 rlock 10 Tf 50 33</i>	0.5	10
11085	<i>Alienimonas chondri</i> sp. nov., a novel planctomycete isolated from the biofilm of the red alga <i>Chondrus crispus</i> . <i>Systematic and Applied Microbiology</i> , 2020, 43, 126083.	1.2	17

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11086	Apcdd1 is a dual BMP/Wnt inhibitor in the developing nervous system and skin. <i>Developmental Biology</i> , 2020, 464, 71-87.	0.9	11
11087	Red Coloration in an Anchialine Shrimp: Carotenoids, Genetic Variation, and Candidate Genes. <i>Biological Bulletin</i> , 2020, 238, 119-130.	0.7	14
11088	Insights into phylogeny, age and evolution of <i>Allium</i> (Amaryllidaceae) based on the whole plastome sequences. <i>Annals of Botany</i> , 2020, 125, 1039-1055.	1.4	49
11089	Transmission Potential of Asymptomatic and Paucisymptomatic Severe Acute Respiratory Syndrome Coronavirus 2 Infections: A 3-Family Cluster Study in China. <i>Journal of Infectious Diseases</i> , 2020, 221, 1948-1952.	1.9	80
11090	Diversity and Complexity of the Large Surface Protein Family in the Compacted Genomes of Multiple <i>Pneumocystis</i> Species. <i>MBio</i> , 2020, 11, .	1.8	11
11091	Chloroplast genomes of seven species of Coryloideae (Betulaceae): structures and comparative analysis. <i>Genome</i> , 2020, 63, 337-348.	0.9	11
11092	Phylogenomics Helps to Evaluate the Impact of an HIV Prevention Intervention. <i>Viruses</i> , 2020, 12, 469.	1.5	17
11093	The impact of intragenomic rRNA variation on metabarcoding-derived diversity estimates: A case study from marine nematodes. <i>Environmental DNA</i> , 2020, 2, 519-534.	3.1	8
11094	Research in Computational Molecular Biology. <i>Lecture Notes in Computer Science</i> , 2020, , .	1.0	0
11095	<i>Methylobacterium planium</i> sp. nov., isolated from a lichen sample. <i>Archives of Microbiology</i> , 2020, 202, 1709-1715.	1.0	12
11096	Symbiotic yeasts from the mycangium, larval gut and woody substrate of an African stag beetle <i>Xiphodontus antilope</i> (Coleoptera: Lucanidae). <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 1123-1134.	0.7	4
11097	A ddRAD-based population genetics and phylogenetics of an endangered freshwater fish from Japan. <i>Conservation Genetics</i> , 2020, 21, 641-652.	0.8	7
11098	Phylogenetic revision of <i>Petrakia</i> and <i>Seifertia</i> (Melanommataceae, Pleosporales): new and rediscovered species from Europe and North America. <i>Mycological Progress</i> , 2020, 19, 417-440.	0.5	6
11099	The genome of the Java medaka (<i>Oryzias javanicus</i>): Potential for its use in marine molecular ecotoxicology. <i>Marine Pollution Bulletin</i> , 2020, 154, 111118.	2.3	5
11100	Phylogeny and biogeography of Pachygoneae (Menispermaceae), with consideration of the boreotropical flora hypothesis and resurrection of the genera <i>Cebatha</i> and <i>Nephroia</i> . <i>Molecular Phylogenetics and Evolution</i> , 2020, 148, 106825.	1.2	13
11101	Current status of freshwater red algal diversity (Rhodophyta) of the African continent including description of new taxa (<i>Batrachospermales</i>). <i>Phycologia</i> , 2020, 59, 187-199.	0.6	10
11102	Genome-informed integrative taxonomic description of three cryptic species in the earthworm genus <i>Carpetania</i> (Oligochaeta, Hormogastridae). <i>Systematics and Biodiversity</i> , 2020, 18, 203-215.	0.5	16
11103	New insights into the phylogeny of the dark-spored Myxomycetes (Amoebozoa: Conosa: Myxogastria:) <i>Tj ETQq1 1 0.784314 rgBT /Over</i> 228-236.	0.5	7

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11104	Jamestown Canyon virus in Massachusetts: clinical case series and vector screening. <i>Emerging Microbes and Infections</i> , 2020, 9, 903-912.	3.0	20
11105	Radiation history of Asian <i>Asarum</i> (sect. <i>Heterotropa</i> , <i>Aristolochiaceae</i>) resolved using a phylogenomic approach based on double-digested RAD-seq data. <i>Annals of Botany</i> , 2020, 126, 245-260.	1.4	13
11106	Mitochondrial genomes and thousands of ultraconserved elements resolve the taxonomy and historical biogeography of the <i>Euphonia</i> and <i>Chlorophonia</i> finches (Passeriformes: <i>Fringillidae</i>). <i>Auk</i> , 2020, 137, .	0.7	14
11107	Phylogenetics of the mycoheterotrophic genus <i>Thismia</i> (<i>Thismiaceae</i> : <i>Dioscoreales</i>) with a focus on the Old World taxa: delineation of novel natural groups and insights into the evolution of morphological traits. <i>Botanical Journal of the Linnean Society</i> , 2020, 193, 287-315.	0.8	24
11108	A new mouse of the <i>Peromyscus maniculatus</i> species complex (<i>Cricetidae</i>) from the highlands of central Mexico. <i>Journal of Mammalogy</i> , 2020, 101, 1117-1132.	0.6	4
11109	Large X-Linked Palindromes Undergo Arm-to-Arm Gene Conversion across <i>Mus</i> Lineages. <i>Molecular Biology and Evolution</i> , 2020, 37, 1979-1985.	3.5	8
11110	A New Analysis of Archaea's Bacteria Domain Separation: Variable Phylogenetic Distance and the Tempo of Early Evolution. <i>Molecular Biology and Evolution</i> , 2020, 37, 2332-2340.	3.5	37
11111	Dispersal versus vicariance in the Aegean: combining molecular and morphological phylogenies of eastern Mediterranean <i>Dendarus</i> (<i>Coleoptera</i> : <i>Tenebrionidae</i>) sheds new light on the phylogeography of the Aegean area. <i>Zoological Journal of the Linnean Society</i> , 2020, 190, 824-843.	1.0	9
11112	Evolutionary dynamics in the dispersal of sign languages. <i>Royal Society Open Science</i> , 2020, 7, 191100.	1.1	11
11113	Pleistocene expansion and connectivity of mesic forests inside the South American Dry Diagonal supported by the phylogeography of a small lizard*. <i>Evolution; International Journal of Organic Evolution</i> , 2020, 74, 1988-2004.	1.1	7
11114	<i>Paludicola</i> gen. nov. and Revision of the Species Formerly in <i>Batrachospermum</i> Section <i>Turfosa</i> (<i>Batrachospermales</i> , <i>Rhodophyta</i>). <i>Journal of Phycology</i> , 2020, 56, 844-861.	1.0	14
11115	Spatial phylogenetics of the North American flora. <i>Journal of Systematics and Evolution</i> , 2020, 58, 393-405.	1.6	39
11116	Demography and adaptation promoting evolutionary transitions in a mammalian genus that diversified during the Pleistocene. <i>Molecular Ecology</i> , 2020, 29, 2777-2792.	2.0	13
11117	Transovarial Transmission of Bacteriome-Associated Symbionts in the Cicada <i>Pycna repanda</i> (<i>Hemiptera</i> : <i>Cicadidae</i>). <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	14
11118	Temperature and Nutrient Levels Correspond with Lineage-Specific Microdiversification in the Ubiquitous and Abundant Freshwater Genus <i>Limnohabitans</i> . <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	16
11119	Insights on Population Structure and Within-Host Genetic Changes among Meningococcal Carriage Isolates from U.S. Universities. <i>MSphere</i> , 2020, 5, .	1.3	3
11120	From the frying pan: an unusual dwarf shrub from Namibia turns out to be a new brassicacean family. <i>Phytotaxa</i> , 2020, 439, 171-185.	0.1	7
11121	A morphological and molecular revision of lizards of the genus <i>Marisora</i> (Hedges & Conn (Squamata: <i>Mabuyidae</i>) from Central America and Mexico, with descriptions of four new species. <i>Zootaxa</i> , 2020, 4763, zootaxa.4763.3.1.	0.2	6

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11122	<p><p>On systematic status of Spindasis syama Horsfield, [1829] in Taiwan and the Philippines (Lepidoptera: Lycaenidae: Aphnaeini)</p>. Zootaxa, 2020, 4763, 485-500.</p>	0.2	0
11123	Isolation and characterization of diverse microbial representatives from the human skin microbiome. Microbiome, 2020, 8, 58.	4.9	42
11124	Genomic analysis of natural intra-specific hybrids among Ethiopian isolates of Leishmania donovani. PLoS Neglected Tropical Diseases, 2020, 14, e0007143.	1.3	17
11125	Persistence of Brucella abortus lineages revealed by genomic characterization and phylogenetic analysis. PLoS Neglected Tropical Diseases, 2020, 14, e0008235.	1.3	13
11126	<i>De Novo</i> Genome Assembly of <i>Populus simonii</i> Further Supports That <i>Populus simonii</i> and <i>Populus trichocarpa</i> Belong to Different Sections. G3: Genes, Genomes, Genetics, 2020, 10, 455-466.	0.8	21
11127	MetaEukâ€”sensitive, high-throughput gene discovery, and annotation for large-scale eukaryotic metagenomics. Microbiome, 2020, 8, 48.	4.9	119
11128	Small and mighty: adaptation of superphylum Patescibacteria to groundwater environment drives their genome simplicity. Microbiome, 2020, 8, 51.	4.9	205
11129	Egyptian Roussette IFN-γ Subtypes Elicit Distinct Antiviral Effects and Transcriptional Responses in Conspicuous Cells. Frontiers in Immunology, 2020, 11, 435.	2.2	15
11130	The Genomic Context for the Evolution and Transmission of Community-Associated Staphylococcus aureus ST59 Through the Food Chain. Frontiers in Microbiology, 2020, 11, 422.	1.5	21
11131	Nuclear and Chloroplast Sequences Resolve the Enigmatic Origin of the Concord Grape. Frontiers in Plant Science, 2020, 11, 263.	1.7	17
11132	Deep Functional Profiling Facilitates the Evaluation of the Antibacterial Potential of the Antibiotic Amicoumacin. Antibiotics, 2020, 9, 157.	1.5	14
11133	Functional Divergence of Microtubule-Associated TPX2 Family Members in Arabidopsis thaliana. International Journal of Molecular Sciences, 2020, 21, 2183.	1.8	17
11134	Characterization of Nuclear and Mitochondrial Genomes of Two Tobacco Endophytic Fungi Leptosphaerulina chartarum and Curvularia trifolii and Their Contributions to Phylogenetic Implications in the Pleosporales. International Journal of Molecular Sciences, 2020, 21, 2461.	1.8	7
11135	Insight into the Functional Diversification of Lipases in the Endoparasitoid Pteromalus puparum (Hymenoptera: Pteromalidae) by Genome-scale Annotation and Expression Analysis. Insects, 2020, 11, 227.	1.0	7
11136	Whole-Genome Sequencing-Based Characteristics in Extended-Spectrum Beta-Lactamase-Producing Escherichia coli Isolated from Retail Meats in Korea. Microorganisms, 2020, 8, 508.	1.6	6
11137	Isolation of Anti-Inflammatory and Epithelium Reinforcing Bacteroides and Parabacteroides Spp. from A Healthy Fecal Donor. Nutrients, 2020, 12, 935.	1.7	97
11138	Complete Genome Sequencing, Molecular Epidemiological, and Pathogenicity Analysis of Pigeon Paramyxoviruses Type 1 Isolated in Guangxi, China during 2012â€”2018. Viruses, 2020, 12, 366.	1.5	13
11139	A Heterologous Viral Protein Scaffold for Chimeric Antigen Design: An Example PCV2 Virus Vaccine Candidate. Viruses, 2020, 12, 385.	1.5	1

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11140	Urocystis cumminsii sp. nov., a smut fungus on Themidaceae from Arizona. Mycotaxon, 2020, 134, 591-599.	0.1	2
11141	Detection of human papillomaviruses in paired healthy skin and actinic keratosis by next generation sequencing. Papillomavirus Research (Amsterdam, Netherlands), 2020, 9, 100196.	4.5	14
11142	Diversification dynamics of freshwater bivalves (Unionidae: Parreysiinae: Coelaturini) indicate historic hydrographic connections throughout the East African Rift System. Molecular Phylogenetics and Evolution, 2020, 148, 106816.	1.2	11
11143	Restriction site associated DNA sequencing data reveal a radiation of willow species (<i>Salix</i> L.), Tj ETQq1 1 0.784314 rgBT /Ov... 59, 44-57.	1.6	27
11144	Joint Phylogenetic Estimation of Geographic Movements and Biome Shifts during the Global Diversification of <i>Viburnum</i> . Systematic Biology, 2021, 70, 67-85.	2.7	33
11145	Genomic and morphological data help uncover extinction progress of an unsustainably traded hill myna radiation. Ibis, 2021, 163, 38-51.	1.0	2
11146	Ultra-conserved Elements and morphology reciprocally illuminate conflicting phylogenetic hypotheses in Chalcididae (Hymenoptera, Chalcidoidea). Cladistics, 2021, 37, 1-35.	1.5	20
11147	The phylogeny of the Casque-headed Treefrogs (Hylidae: Hylinae: Lophyohylini). Cladistics, 2021, 37, 36-72.	1.5	24
11148	Correlations among oligonucleotide repeats, nucleotide substitutions, and insertion-deletion mutations in chloroplast genomes of plant family Malvaceae. Journal of Systematics and Evolution, 2021, 59, 388-402.	1.6	43
11149	Phylogenetic relationships, biogeography and taxonomic delimitation of Astragalus sect. Acanthophaea (Fabaceae) using cpDNA and nrDNA ITS sequences analyses. Plant Biosystems, 2021, 155, 291-301.	0.8	6
11150	Morphological Characters Can Strongly Influence Early Animal Relationships Inferred from Phylogenomic Data Sets. Systematic Biology, 2021, 70, 360-375.	2.7	21
11151	Functional characterization of pheromone receptor candidates in codling moth <i>Cydia pomonella</i> (Lepidoptera: Tortricidae). Insect Science, 2021, 28, 445-456.	1.5	7
11152	Hidden diversity within the <i>Diopatra cuprea</i> complex (Annelida: Onuphidae): morphological and genetics analyses reveal four new species in the south-west Atlantic. Zoological Journal of the Linnean Society, 2021, 191, 637-671.	1.0	13
11153	Phylogenomics Reveals Ancient Gene Tree Discordance in the Amphibian Tree of Life. Systematic Biology, 2021, 70, 49-66.	2.7	124
11154	DNA Barcoding and Demographic History of <i>Peromyscus yucatanicus</i> (Rodentia: Cricetidae) Endemic to the Yucatan Peninsula, Mexico. Journal of Mammalian Evolution, 2021, 28, 481-495.	1.0	4
11155	The Origin of the Legumes is a Complex Paleopolyploid Phylogenomic Tangle Closely Associated with the Cretaceous-Paleogene (K-Pg) Mass Extinction Event. Systematic Biology, 2021, 70, 508-526.	2.7	83
11156	Earlier treatment initiation is associated with a decreased number of HIV-1 subtype A1 transmissions in Greece. Sexually Transmitted Infections, 2021, 97, 232-237.	0.8	2
11157	Molecular surveillance of methicillin-resistant <i>Staphylococcus aureus</i> genomes in hospital unexpectedly reveals discordance between temporal and genetic clustering. American Journal of Infection Control, 2021, 49, 59-64.	1.1	6

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11158	Phylogeny and classification of the Sematophyllaceae s.l. (Hypnales, Bryophyta). <i>Journal of Systematics and Evolution</i> , 2021, 59, 524-540.	1.6	2
11159	The origin and evolution of the diosgenin biosynthetic pathway in yam. <i>Plant Communications</i> , 2021, 2, 100079.	3.6	44
11160	Nonbifurcating Phylogenetic Tree Inference via the Adaptive LASSO. <i>Journal of the American Statistical Association</i> , 2021, 116, 858-873.	1.8	1
11161	Out of Sight, Out of Mind: Widespread Nuclear and Plastid-Nuclear Discordance in the Flowering Plant Genus <i>Polemonium</i> (Polemoniaceae) Suggests Widespread Historical Gene Flow Despite Limited Nuclear Signal. <i>Systematic Biology</i> , 2021, 70, 162-180.	2.7	64
11162	Evidence for re-infection and persistent carriage of <i>Shigella</i> species in adult males reporting domestically acquired infection in England. <i>Clinical Microbiology and Infection</i> , 2021, 27, 126.e7-126.e13.	2.8	18
11163	Genes with evidence of positive selection as potentially related to coloniality and the evolution of morphological features among the lophophorates and entoprocts. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2021, 336, 267-280.	0.6	7
11164	Near-complete phylogeny of extant Crocodylia (Reptilia) using mitogenome-based data. <i>Zoological Journal of the Linnean Society</i> , 2021, 191, 1075-1089.	1.0	20
11165	Protein-encoding ultraconserved elements provide a new phylogenomic perspective of Oestroidea flies (Diptera: Calypterae). <i>Systematic Entomology</i> , 2021, 46, 5-27.	1.7	32
11166	Does the Gonostomum-patterned oral apparatus in hypotrichia carry a phylogenetic signal? Evidence from morphological and molecular data based on extended taxon sampling using three nuclear genes (Ciliophora, Spirotrichea). <i>Science China Life Sciences</i> , 2021, 64, 311-322.	2.3	34
11167	Composition of the North American Wood Frog (<i>Rana sylvatica</i>) Bacterial Skin Microbiome and Seasonal Variation in Community Structure. <i>Microbial Ecology</i> , 2021, 81, 78-92.	1.4	25
11168	Cryptic Patterns of Speciation in Cryptic Primates: Microendemic Mouse Lemurs and the Multispecies Coalescent. <i>Systematic Biology</i> , 2021, 70, 203-218.	2.7	42
11169	Using RAD seq for reconstructing phylogenies of highly diverged taxa: A test using the tribe Scandiceae (Apiaceae). <i>Journal of Systematics and Evolution</i> , 2021, 59, 58-72.	1.6	8
11170	Geoclimatic factors influence the population genetic connectivity of <i>Incarvillea arguta</i> (Bignoniaceae) in the Himalaya-Hengduan Mountains biodiversity hotspot. <i>Journal of Systematics and Evolution</i> , 2021, 59, 151-168.	1.6	28
11171	Insect biomass is not a consistent proxy for biodiversity metrics in wild bees. <i>Ecological Indicators</i> , 2021, 121, 107132.	2.6	26
11172	Unraveling elephant-shrews: Phylogenetic relationships and unexpected introgression among giant sengis. <i>Molecular Phylogenetics and Evolution</i> , 2021, 154, 107001.	1.2	1
11173	A systematic study of North American <i>Angelica</i> species (Apiaceae) based on nrDNA ITS and cpDNA sequences and fruit morphology. <i>Journal of Systematics and Evolution</i> , 2022, 60, 789-808.	1.6	10
11174	The interplay of colour and bioacoustic traits in the differentiation of a Southeast Asian songbird complex. <i>Molecular Ecology</i> , 2021, 30, 297-309.	2.0	12
11175	A phantom on the trees: Integrative taxonomy supports a reappraisal of rear-fanged snakes classification (Dipsadidae: Philodryadini). <i>Zoologischer Anzeiger</i> , 2021, 290, 19-39.	0.4	7

#	ARTICLE	IF	CITATIONS
11176	Serendipita restingae sp. nov. (Sebacinales): an orchid mycorrhizal agaricomycete with wide host range. Mycorrhiza, 2021, 31, 1-15.	1.3	15
11177	Multilocus phylogeny of African striped grass mice (Lemniscomys): Stripe pattern only partly reflects evolutionary relationships. Molecular Phylogenetics and Evolution, 2021, 155, 107007.	1.2	11
11178	Habitat-scale heterogeneity maintains fungal endophyte diversity in two native prairie legumes. Mycologia, 2021, 113, 20-32.	0.8	8
11179	Computational strategies to combat COVID-19: useful tools to accelerate SARS-CoV-2 and coronavirus research. Briefings in Bioinformatics, 2021, 22, 642-663.	3.2	110
11180	Phylogeny of Lithobiidae Newport, 1844, with emphasis on the megadiverse genus Lithobius Leach, 1814 (Myriapoda, Chilopoda). Cladistics, 2021, 37, 162-184.	1.5	5
11181	Phylogenetic relationships and revised classification of the true bug infraorder Dipsocoromorpha (Insecta: Hemiptera: Heteroptera). Cladistics, 2021, 37, 248-275.	1.5	1
11182	Radiation of nitrogenâ€­metabolizing enzymes across the tree of life tracks environmental transitions in Earth history. Geobiology, 2021, 19, 18-34.	1.1	36
11183	Elevated rates of positive selection drive the evolution of pestiferousness in the Colorado potato beetle (<i>Leptinotarsa decemlineata</i> , Say). Molecular Ecology, 2021, 30, 237-254.	2.0	16
11184	RepeatFS: a file system providing reproducibility through provenance and automation. Bioinformatics, 2021, 37, 1292-1296.	1.8	0
11185	Paleotemperatures and recurrent habitat shifts drive diversification of treefrogs across distinct biodiversity hotspots in subâ€­Amazonian South America. Journal of Biogeography, 2021, 48, 305-320.	1.4	7
11186	Variability analyses of the maternal lineage of horses and donkeys. Gene, 2021, 769, 145231.	1.0	3
11187	Unity in diversity: phylogenetics and taxonomy of Rhabdoweisiaceae (Dicranales, Bryophyta). Botanical Journal of the Linnean Society, 2021, 195, 545-567.	0.8	14
11188	IS²⁶-mediated amplification of bla_{OXA-1} and bla_{CTX-M-15} with concurrent outer membrane porin disruption associated with de novo carbapenem resistance in a recurrent bacteraemia cohort. Journal of Antimicrobial Chemotherapy, 2021, 76, 385-395.	1.3	29
11189	Combination of Sanger and target-enrichment markers supports revised generic delimitation in the problematic "Ureia clade" of the nettle family (Urticaceae). Molecular Phylogenetics and Evolution, 2021, 158, 107008.	1.2	11
11190	Natural polymorphisms in a pair of NSP2 homoeologs can cause loss of nodulation in peanut. Journal of Experimental Botany, 2021, 72, 1104-1118.	2.4	15
11191	Morphological and molecular phylogeny of Epiperipatus (Onychophora: Peripatidae): a combined approach. Zoological Journal of the Linnean Society, 2021, 192, 763-793.	1.0	4
11192	Tracing the Origin and Evolutionary History of Pyricularia oryzae Infecting Maize and Barnyard Grass. Phytopathology, 2021, 111, 128-136.	1.1	14
11193	Going against the flow: Barriers to gene flow impact patterns of connectivity in cryptic coral reef gobies throughout the western Atlantic. Journal of Biogeography, 2021, 48, 427-439.	1.4	16

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11194	New approaches to species delimitation and population structure of anthozoans: Two case studies of octocorals using ultraconserved elements and exons. <i>Molecular Ecology Resources</i> , 2021, 21, 78-92.	2.2	34
11195	Do Alignment and Trimming Methods Matter for Phylogenomic (UCE) Analyses?. <i>Systematic Biology</i> , 2021, 70, 440-462.	2.7	30
11196	Metabarcoding unsorted kickâ€s samples facilitates macroinvertebrateâ€b based biomonitoring with increased taxonomic resolution, while outperforming environmental DNA. <i>Environmental DNA</i> , 2021, 3, 353-371.	3.1	16
11197	An integrative approach distinguishes three new species of Abyssochrysoidea (Mollusca: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 of the Linnean Society, 2021, 191, 748-771.	1.0	14
11198	Phylogenetic analysis and osteological comparison of the cave-dwelling spined loach, <i>Bibarba parvocolus</i> (Cypriniformes: Cobitidae), and its surface congener. <i>Zoological Journal of the Linnean Society</i> , 2021, 191, 1059-1074.	1.0	2
11199	Impacts of subchronic exposure to a commercial 2,4-D herbicide on developmental stages of multiple freshwater fish species. <i>Chemosphere</i> , 2021, 263, 127638.	4.2	14
11200	Phytophthora Species Associated with Roots of Native and Non-native Trees in Natural and Managed Forests. <i>Microbial Ecology</i> , 2021, 81, 122-133.	1.4	13
11201	Italian odonates in the Pandora's box: A comprehensive DNA barcoding inventory shows taxonomic warnings at the Holarctic scale. <i>Molecular Ecology Resources</i> , 2021, 21, 183-200.	2.2	37
11202	Recent hybrid speciation at the origin of the narrow endemic <i>Pulmonaria helvetica</i> . <i>Annals of Botany</i> , 2021, 127, 21-31.	1.4	12
11203	PoSeiDon: a Nextflow pipeline for the detection of evolutionary recombination events and positive selection. <i>Bioinformatics</i> , 2021, 37, 1018-1020.	1.8	8
11204	Resolving robust phylogenetic relationships of core Brassicaceae using genome skimming data. <i>Journal of Systematics and Evolution</i> , 2021, 59, 442-453.	1.6	16
11205	The genome sequence of the giant phototrophic gammaproteobacterium <i>Thiospirillum jenense</i> gives insight into its physiological properties and phylogenetic relationships. <i>Archives of Microbiology</i> , 2021, 203, 97-105.	1.0	5
11206	A new pleosporalean fungus isolated from superficial to deep human clinical specimens. <i>Medical Mycology</i> , 2021, 59, 278-288.	0.3	5
11207	<i>Esteya floridanum</i> sp. nov.: An Ophiostomatalean Nematophagous Fungus and Its Potential to Control the Pine Wood Nematode. <i>Phytopathology</i> , 2021, 111, 304-311.	1.1	8
11208	An Unbiased Molecular Approach Using 3â€²-UTRs Resolves the Avian Family-Level Tree of Life. <i>Molecular Biology and Evolution</i> , 2021, 38, 108-127.	3.5	99
11209	Dasycerine rove beetles: Cretaceous diversification, phylogeny and historical biogeography (Coleoptera: Staphylinidae: Dasycerinae). <i>Cladistics</i> , 2021, 37, 185-210.	1.5	11
11210	Cryptic lineage diversity within Forest Dormice (Mammalia: <i>Dryomys nitedula</i>) revealed by deep genetic divergence among different subspecies on the Iranian Plateau and in adjacent areas. <i>Mammalian Biology</i> , 2021, 101, 21-34.	0.8	2
11211	Culturable mycobiota from Karst caves in China II, with descriptions of 33 new species. <i>Fungal Diversity</i> , 2021, 106, 29-136.	4.7	53

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11212	Phylogeny Estimation Given Sequence Length Heterogeneity. <i>Systematic Biology</i> , 2021, 70, 268-282.	2.7	29
11213	What Could Explain $\delta^{13}\text{C}$ Signatures in Biocrust Cyanobacteria of Drylands?. <i>Microbial Ecology</i> , 2021, 81, 134-145.	1.4	1
11214	Multiple Merger Genealogies in Outbreaks of <i>Mycobacterium tuberculosis</i> . <i>Molecular Biology and Evolution</i> , 2021, 38, 290-306.	3.5	11
11215	Livestock-associated methicillin-resistant <i>Staphylococcus aureus</i> : Establishing links between animals and humans on livestock holdings. <i>Transboundary and Emerging Diseases</i> , 2021, 68, 789-801.	1.3	6
11216	A Southeast Asian origin for present-day non-African human Y chromosomes. <i>Human Genetics</i> , 2021, 140, 299-307.	1.8	14
11217	Spatiotemporal Genetic Diversity of Lions Reveals the Influence of Habitat Fragmentation across Africa. <i>Molecular Biology and Evolution</i> , 2021, 38, 48-57.	3.5	27
11218	Congruence and Conflict in the Higher-Level Phylogenetics of Squamate Reptiles: An Expanded Phylogenomic Perspective. <i>Systematic Biology</i> , 2021, 70, 542-557.	2.7	35
11219	Chloroplast Genome of Native <i>Silene latifolia</i> subsp. <i>alba</i> from Fennoscandia Shows High Level of Differences from Invasive White Campion. <i>Plant Molecular Biology Reporter</i> , 2021, 39, 226-239.	1.0	2
11220	A novel chorismate mutase from <i>Erysiphe quercicola</i> performs dual functions of synthesizing amino acids and inhibiting plant salicylic acid synthesis. <i>Microbiological Research</i> , 2021, 242, 126599.	2.5	8
11221	Phylotranscriptomic evidence for pervasive ancient hybridization among Old World salamanders. <i>Molecular Phylogenetics and Evolution</i> , 2021, 155, 106967.	1.2	22
11222	Systematics, biogeography and evolution of the Saharo-Arabian naked-toed geckos genus <i>Tropicolotes</i> . <i>Molecular Phylogenetics and Evolution</i> , 2021, 155, 106969.	1.2	8
11223	Phylogeny resolved, metabolism revealed: functional radiation within a widespread and divergent clade of sponge symbionts. <i>ISME Journal</i> , 2021, 15, 503-519.	4.4	24
11224	Concerted and birth-and-death evolution of 26S ribosomal DNA in <i>Camellia</i> L. <i>Annals of Botany</i> , 2021, 127, 63-73.	1.4	7
11225	An updated phylogeny of the metallo- β -lactamases. <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 76, 117-123.	1.3	14
11226	Genomic and phenotypic analysis of siderophore-producing <i>Rhodococcus qingshengii</i> strain S10 isolated from an arid weathered serpentine rock environment. <i>Archives of Microbiology</i> , 2021, 203, 855-860.	1.0	6
11227	Phylogenomic relationships and character evolution of the grape family (Vitaceae). <i>Molecular Phylogenetics and Evolution</i> , 2021, 154, 106948.	1.2	31
11228	Phylogeny and biogeography of South American marsh pitcher plant genus <i>Heliampora</i> (Sarraceniaceae) endemic to the Guiana Highlands. <i>Molecular Phylogenetics and Evolution</i> , 2021, 154, 106961.	1.2	3
11229	A multi-layered approach to the diversification of squirrels. <i>Mammal Review</i> , 2021, 51, 66-81.	2.2	22

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11230	Uncovering DNA-PKcs ancient phylogeny, unique sequence motifs and insights for human disease. <i>Progress in Biophysics and Molecular Biology</i> , 2021, 163, 87-108.	1.4	45
11231	Ancient DNA Suggests Single Colonization and Within-Archipelago Diversification of Caribbean Caviomorph Rodents. <i>Molecular Biology and Evolution</i> , 2021, 38, 84-95.	3.5	19
11232	Molecular and morphological evidence for a new species of <i>Isodon</i> (Lamiaceae) from southern China. <i>Plant Diversity</i> , 2021, 43, 54-62.	1.8	3
11233	Plastid phylogenomic insights into the evolution of subfamily Dialioideae (Leguminosae). <i>Plant Diversity</i> , 2021, 43, 27-34.	1.8	16
11234	Systematics of a Neotropical clade of dead-leaf-foraging antwrens (Aves: Thamnophilidae). <i>Trends in Ecology and Evolution</i> , 2021, 36, 582-592.	1.2	3
11235	Phylogenomics of the Mesoamerican alligator-lizard genera <i>Abronia</i> and <i>Mesaspis</i> (Anguillidae). <i>Trends in Ecology and Evolution</i> , 2021, 36, 1069-1073.	1.2	13
11236	A symbiotic nutrient exchange within the cyanosphere microbiome of the biocrust cyanobacterium, <i>Microcoleus vaginatus</i> . <i>ISME Journal</i> , 2021, 15, 282-292.	4.4	44
11237	A conserved α -helix plays a key role in thermoadaptation of catalysis in the glycoside hydrolase family 4. <i>Biochimica et Biophysica Acta - Proteins and Proteomics</i> , 2021, 1869, 140523.	1.1	3
11238	Identification of ancient viruses from metagenomic data of the Jomon people. <i>Journal of Human Genetics</i> , 2021, 66, 287-296.	1.1	5
11239	Complex Evolution of Light-Dependent Protochlorophyllide Oxidoreductases in Aerobic Anoxygenic Phototrophs: Origin, Phylogeny, and Function. <i>Molecular Biology and Evolution</i> , 2021, 38, 819-837.	3.5	6
11240	Molecular phylogeny, biogeography and character evolution of the montane genus <i>Incarvillea</i> Juss. (Bignoniaceae). <i>Plant Diversity</i> , 2021, 43, 1-14.	1.8	7
11241	Reduced Influenza A Virus Specific Postvaccination Antibody Cross-reactivity in the B/Victoria Lineage—Predominant 2019/20 Season. <i>Clinical Infectious Diseases</i> , 2021, 72, e776-e783.	2.9	4
11242	The Origins of Coca: Museum Genomics Reveals Multiple Independent Domestications from Progenitor <i>Erythroxylum gracilipes</i> . <i>Systematic Biology</i> , 2021, 70, 1-13.	2.7	10
11243	Foliose <i>Ulva</i> Species Show Considerable Inter-specific Genetic Diversity, Low Intra-specific Genetic Variation, and the Rare Occurrence of Inter-specific Hybrids in the Wild. <i>Journal of Phycology</i> , 2021, 57, 219-233.	1.0	24
11244	Additive Uncorrelated Relaxed Clock Models for the Dating of Genomic Epidemiology Phylogenies. <i>Molecular Biology and Evolution</i> , 2021, 38, 307-317.	3.5	28
11245	A Truncated Singleton NLR Causes Hybrid Necrosis in <i>Arabidopsis thaliana</i> . <i>Molecular Biology and Evolution</i> , 2021, 38, 557-574.	3.5	26
11246	Population Genomics Reveals Incipient Speciation, Introgression, and Adaptation in the African Mona Monkey (<i>Cercopithecus mona</i>). <i>Molecular Biology and Evolution</i> , 2021, 38, 876-890.	3.5	15
11247	Disentangling Sources of Gene Tree Discordance in Phylogenomic Data Sets: Testing Ancient Hybridizations in <i>Amaranthaceae</i> s.l. <i>Systematic Biology</i> , 2021, 70, 219-235.	2.7	112

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11248	Giant African snail genomes provide insights into molluscan whole-genome duplication and aquatic-terrestrial transition. <i>Molecular Ecology Resources</i> , 2021, 21, 478-494.	2.2	33
11249	Chromosome-level genome assembly of <i>Paralithodes platypus</i> provides insights into evolution and adaptation of king crabs. <i>Molecular Ecology Resources</i> , 2021, 21, 511-525.	2.2	14
11250	Elongation factor P is required for EII Glc translation in <i>Corynebacterium glutamicum</i> due to an essential polyproline motif. <i>Molecular Microbiology</i> , 2021, 115, 320-331.	1.2	4
11251	<i>Marinomyxa</i> Gen. Nov. Accommodates Gall-Forming Parasites of the Tropical to Subtropical Seagrass Genus <i>Halophila</i> and Constitutes a Novel Deep-Branching Lineage Within Phytomyxea (Rhizaria: Tj ETQq1 1 0.784314 rgBT / Overlock	1.4	1
11252	Acidobacteria are active and abundant members of diverse atmospheric H ₂ -oxidizing communities detected in temperate soils. <i>ISME Journal</i> , 2021, 15, 363-376.	4.4	23
11253	New species boundaries and the diversification history of marsh rat taxa clarify historical connections among ecologically and geographically distinct wetlands of South America. <i>Molecular Phylogenetics and Evolution</i> , 2021, 155, 106992.	1.2	12
11254	raxmlGUI 2.0: A graphical interface and toolkit for phylogenetic analyses using RAxML. <i>Methods in Ecology and Evolution</i> , 2021, 12, 373-377.	2.2	394
11255	Single dominant diatom can host diverse parasitic fungi with different degree of host specificity. <i>Limnology and Oceanography</i> , 2021, 66, 667-677.	1.6	16
11256	New contributions to the phylogeny of the ciliate class Heterotrichea (Protista, Ciliophora): analyses at family-genus level and new evolutionary hypotheses. <i>Science China Life Sciences</i> , 2021, 64, 606-620.	2.3	34
11257	Evolutionary history of histamine receptors: Early vertebrate origin and expansion of the H ₃ -H ₄ subtypes. <i>Molecular Phylogenetics and Evolution</i> , 2021, 154, 106989.	1.2	6
11258	Metabolic resistance to organophosphate insecticides in natural populations of the whitefly <i>Bemisia tabaci</i> (Hemiptera: Aleyrodidae) in Egypt and molecular identification of mitotypes. <i>Phytoparasitica</i> , 2021, 49, 443-457.	0.6	5
11259	Population Genomics Trace Clonal Diversification and Intercontinental Migration of an Emerging Fungal Pathogen of Boxwood. <i>Phytopathology</i> , 2021, 111, 184-193.	1.1	16
11260	Microeukaryotic Communities Associated With the Seagrass <i>Zostera marina</i> Are Spatially Structured. <i>Journal of Eukaryotic Microbiology</i> , 2021, 68, e12827.	0.8	12
11261	Shotgun metagenomics and microscopy indicate diverse cyanophytes, other bacteria, and microeukaryotes in the epimicrobiota of a northern Chilean wetland <i>Nostoc</i> (Cyanobacteria). <i>Journal of Phycology</i> , 2021, 57, 39-50.	1.0	3
11262	Multiple species delimitation approaches applied to the avian lark genus <i>Alaudala</i> . <i>Molecular Phylogenetics and Evolution</i> , 2021, 154, 106994.	1.2	14
11263	Plastome evolution and phylogenetic relationships among Malvaceae subfamilies. <i>Gene</i> , 2021, 765, 145103.	1.0	27
11264	Phylogenies from mitochondrial genomes of 120 species of ticks: Insights into the evolution of the families of ticks and of the genus <i>Amblyomma</i> . <i>Ticks and Tick-borne Diseases</i> , 2021, 12, 101577.	1.1	38
11265	Phylogenetic relationships of the <i>Boana pulchella</i> Group (Anura: Hylidae). <i>Molecular Phylogenetics and Evolution</i> , 2021, 155, 106981.	1.2	15

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11266	Experimentally-validated correlation analysis reveals new anaerobic methane oxidation partnerships with consortium-level heterogeneity in diazotrophy. <i>ISME Journal</i> , 2021, 15, 377-396.	4.4	31
11267	Genomic Adaptations to Salinity Resist Gene Flow in the Evolution of Floridian Watersnakes. <i>Molecular Biology and Evolution</i> , 2021, 38, 745-760.	3.5	11
11268	Asymmetric acoustic signal recognition led to asymmetric gene flow between two parapatric frogs. <i>Zoological Journal of the Linnean Society</i> , 2021, 192, 130-143.	1.0	3
11269	Culturing novel and abundant pelagiphages in the ocean. <i>Environmental Microbiology</i> , 2021, 23, 1145-1161.	1.8	27
11270	A chromosome-level genome assembly of rice leaffolder, <i>Cnaphalocrocis medinalis</i> . <i>Molecular Ecology Resources</i> , 2021, 21, 561-572.	2.2	15
11271	A high-quality <i>Brassica napus</i> genome reveals expansion of transposable elements, subgenome evolution and disease resistance. <i>Plant Biotechnology Journal</i> , 2021, 19, 615-630.	4.1	56
11272	Phylogeny and biogeography of <i>Fagus</i> (Fagaceae) based on 28 nuclear single-copy loci. <i>Journal of Systematics and Evolution</i> , 2022, 60, 759-772.	1.6	15
11273	Mitochondrial Genome Evolution of Placozoans: Gene Rearrangements and Repeat Expansions. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	13
11274	Repeated hybridization increased diversity in the door snail complex <i>Charpentieria itala</i> in the Southern Alps. <i>Molecular Phylogenetics and Evolution</i> , 2021, 155, 106982.	1.2	6
11275	Genomic fingerprints of palaeogeographic history: The tempo and mode of rift tectonics across tropical Africa has shaped the diversification of the killifish genus <i>Nothobranchius</i> (Teleostei). <i>Trends in Ecology & Evolution</i> , 2021, 36, 1073-1083.	1.0	8
11276	Another stripe on the tiger makes no difference? Unexpected diversity in the widespread tiger tarantula <i>Davus pentaloris</i> (Araneae: Theraphosidae: Theraphosinae). <i>Zoological Journal of the Linnean Society</i> , 2021, 192, 75-104.	1.0	8
11277	Etiology of Halo Blight in Michigan Hopyards. <i>Plant Disease</i> , 2021, 105, 859-872.	0.7	5
11278	Evolution and dissemination of L and M plasmid lineages carrying antibiotic resistance genes in diverse Gram-negative bacteria. <i>Plasmid</i> , 2021, 113, 102528.	0.4	10
11279	Relatedness and the composition of communities over time: Evaluating phylogenetic community structure in the late Cenozoic record of bivalves. <i>Paleobiology</i> , 2021, 47, 301-313.	1.3	4
11280	Idiosyncratic responses to drivers of genetic differentiation in the complex landscapes of Isthmian Central America. <i>Heredity</i> , 2021, 126, 251-265.	1.2	5
11281	Evidence of introgression in endemic frogs from the <i>campo rupestre</i> contradicts the reduced hybridization hypothesis. <i>Biological Journal of the Linnean Society</i> , 2021, 133, 561-576.	0.7	6
11282	Genomic Characterization and Curation of UCEs Improves Species Tree Reconstruction. <i>Systematic Biology</i> , 2021, 70, 307-321.	2.7	24
11283	Chromosome-level genome assembly of <i>Lethenteron reissneri</i> provides insights into lamprey evolution. <i>Molecular Ecology Resources</i> , 2021, 21, 448-463.	2.2	25

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11284	Comparative analysis reveals the expansion of mitochondrial DNA control region containing unusually high G-C tandem repeat arrays in <i>Nasonia vitripennis</i> . <i>International Journal of Biological Macromolecules</i> , 2021, 166, 1246-1257.	3.6	9
11285	Population Genomics of Bacterial Plant Pathogens. <i>Phytopathology</i> , 2021, 111, 23-31.	1.1	10
11286	Indo-Asian <i>Eriolaena</i> expanded to include two Malagasy genera, and other generic realignments based on molecular phylogenetics of <i>Dombeyoideae</i> (Malvaceae). <i>Taxon</i> , 2021, 70, 99-126.	0.4	4
11287	Highly divergent cuticular hydrocarbon profiles in the cleptobiotic ants of the <i>Ectatomma ruidum</i> species complex. <i>Chemoecology</i> , 2021, 31, 125-135.	0.6	8
11288	Heat resistance and genomics of spoilage <i>Alicyclobacillus</i> spp. Isolated from fruit juice and fruit-based beverages. <i>Food Microbiology</i> , 2021, 94, 103662.	2.1	6
11289	Evidence for non-methanogenic metabolisms in globally distributed archaeal clades basal to the <i>Methanomassiliicoccales</i> . <i>Environmental Microbiology</i> , 2021, 23, 340-357.	1.8	19
11290	The phylogenetic relationship within SARS-CoV-2s: An expanding basal clade. <i>Molecular Phylogenetics and Evolution</i> , 2021, 157, 107017.	1.2	15
11291	Karyotype evolution and preliminary molecular assessment of genera in the family <i>Scorpiopidae</i> (Arachnida: <i>Scorpiones</i>). <i>Zoology</i> , 2021, 144, 125882.	0.6	7
11292	Unique genomic traits for cold adaptation in <i>Naganishia vishniacii</i> , a polyextremophile yeast isolated from Antarctica. <i>FEMS Yeast Research</i> , 2021, 21, .	1.1	14
11293	A review of <i>Triops granarius</i> (Lucas, 1864) sensu lato (Notostraca: <i>Triopsidae</i>) of southern Africa and Madagascar, with comments on the group. <i>Journal of Crustacean Biology</i> , 2021, 41, .	0.3	7
11294	Structural Basis for Bacterial Ribosome-Associated Quality Control by RqcH and RqcP. <i>Molecular Cell</i> , 2021, 81, 115-126.e7.	4.5	41
11295	Comparative genomics of <i>Fusarium oxysporum</i> f. sp. <i>melonis</i> strains reveals nine lineages and a new sequence type of <i>AvrFom2</i> . <i>Environmental Microbiology</i> , 2021, 23, 2035-2053.	1.8	5
11296	Chromosome level assembly reveals a unique immune gene organization and signatures of evolution in the common pheasant. <i>Molecular Ecology Resources</i> , 2021, 21, 897-911.	2.2	10
11297	Method comparison of targeted influenza A virus typing and whole-genome sequencing from respiratory specimens of companion animals. <i>Journal of Veterinary Diagnostic Investigation</i> , 2021, 33, 191-201.	0.5	7
11298	Multigene phylogeny and taxonomic revision of <i>Atheliales</i> s.l.: Reinstatement of three families and one new family, <i>Lobuliciaceae</i> fam. nov.. <i>Fungal Biology</i> , 2021, 125, 239-255.	1.1	12
11299	Inter- and intra-archipelago dynamics of population structure and gene flow in a Polynesian bird. <i>Molecular Phylogenetics and Evolution</i> , 2021, 156, 107034.	1.2	4
11300	Sister species, different histories: comparative phylogeography of two bird species associated with Amazonian open vegetation. <i>Biological Journal of the Linnean Society</i> , 2021, 132, 161-173.	0.7	16
11301	Mitogenomes Reveal Alternative Initiation Codons and Lineage-Specific Gene Order Conservation in Echinoderms. <i>Molecular Biology and Evolution</i> , 2021, 38, 981-985.	3.5	13

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11302	The Legacy of Recurrent Introgression during the Radiation of Hares. <i>Systematic Biology</i> , 2021, 70, 593-607.	2.7	47
11303	Description of <i>Phaeobola aeris</i> gen. nov., sp. nov (Rhizaria, Cercozoa, Euglyphida) Sheds Light on Euglyphida's Dark Matter. <i>Journal of Eukaryotic Microbiology</i> , 2021, 68, e12835.	0.8	2
11304	A Needle in the Haystack – Mapping Sequences to Morphology Exemplified by the Loricata Choanoflagellate <i>Enibas thessalia</i> sp. nov. (Acanthoecida, Acanthoecidae). <i>Protist</i> , 2021, 172, 125782.	0.6	7
11305	Genome-wide RAD sequencing resolves the evolutionary history of serrate leaf <i>Juniperus</i> and reveals discordance with chloroplast phylogeny. <i>Molecular Phylogenetics and Evolution</i> , 2021, 156, 107022.	1.2	13
11306	Phylogenomic analyses recover a clade of large-bodied decapodiform cephalopods. <i>Molecular Phylogenetics and Evolution</i> , 2021, 156, 107038.	1.2	29
11307	Host shifting and host sharing in a genus of specialist flies diversifying alongside their sunflower hosts. <i>Journal of Evolutionary Biology</i> , 2021, 34, 364-379.	0.8	3
11308	Phylogeny of <i>Neobursaridium</i> reshapes the systematics of <i>Paramecium</i> (Oligohymenophorea, Ciliophora). <i>Zoologica Scripta</i> , 2021, 50, 241-268.	0.7	12
11309	Proteome size reduction in Apicomplexans is linked with loss of DNA repair and host redundant pathways. <i>Infection, Genetics and Evolution</i> , 2021, 87, 104642.	1.0	4
11310	Carbapenemase-producing Enterobacterales causing secondary infections during the COVID-19 crisis at a New York City hospital. <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 76, 380-384.	1.3	58
11311	Determination of Genomic Epidemiology of Historical <i>Clostridium perfringens</i> Outbreaks in New York State by Use of Two Web-Based Platforms: National Center for Biotechnology Information Pathogen Detection and FDA GalaxyTrakr. <i>Journal of Clinical Microbiology</i> , 2021, 59, .	1.8	7
11312	Morphology, morphogenesis and molecular phylogeny of a novel soil ciliate, <i>Afrokahliella paramacrostoma</i> n. sp. (Ciliophora, Hypotrichia). <i>European Journal of Protistology</i> , 2021, 77, 125748.	0.5	12
11313	Prevalence and antimicrobial susceptibility of <i>Campylobacter</i> isolated from retail chickens in Thailand. <i>International Journal of Food Microbiology</i> , 2021, 339, 109017.	2.1	13
11314	PCR identification of <i>Salmonella</i> serovars for the E serogroup based on novel specific targets obtained by pan-genome analysis. <i>LWT - Food Science and Technology</i> , 2021, 145, 110535.	2.5	7
11315	Phylogenomics resolves the invasion history of <i>Acacia auriculiformis</i> in Florida. <i>Journal of Biogeography</i> , 2021, 48, 453-464.	1.4	12
11316	Genome surveying reveals the complete chloroplast genome and nuclear genomic features of the crocin-producing plant <i>Gardenia jasminoides</i> Ellis. <i>Genetic Resources and Crop Evolution</i> , 2021, 68, 1165-1180.	0.8	5
11317	First Report of <i>Xanthomonas fragariae</i> Causing Angular Leaf Spot on Strawberry (<i>Fragaria</i> – <i>ananassa</i>) in Taiwan. <i>Plant Disease</i> , 2021, 105, 1187-1187.	0.7	10
11318	Phylogenetic diversity metrics from molecular phylogenies: modelling expected degree of error under realistic rate variation. <i>Diversity and Distributions</i> , 2021, 27, 164-178.	1.9	11
11319	<i>Dictyota cyanoloma</i> (Dictyotales, Phaeophyceae), a Newly Introduced Brown Algal Species in California. <i>Journal of Phycology</i> , 2021, 57, 370-378.	1.0	3

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11320	Unexpected Discovery and Expression of Amphibian Class II Endogenous Retroviruses. <i>Journal of Virology</i> , 2021, 95, .	1.5	5
11321	<i>Haemoproteus synnii</i> (Haemosporida: Haemoproteidae) in owls from Brazil: morphological and molecular characterization, potential cryptic species, and exo-erythrocytic stages. <i>Parasitology Research</i> , 2021, 120, 243-255.	0.6	6
11322	Conserved keratin gene clusters in ancient fish: An evolutionary seed for terrestrial adaptation. <i>Genomics</i> , 2021, 113, 1120-1128.	1.3	7
11323	Partitioned Gene-Tree Analyses and Gene-Based Topology Testing Help Resolve Incongruence in a Phylogenomic Study of Host-Specialist Bees (Apidae: Eucerinae). <i>Molecular Biology and Evolution</i> , 2021, 38, 1090-1100.	3.5	23
11324	Genomic signals reveal past evolutionary dynamics of <i>Quercus schottkyana</i> and its response to future climate change. <i>Journal of Systematics and Evolution</i> , 2021, 59, 985.	1.6	4
11325	Whole-Genome Transcriptome Analyses of Native Symbionts Reveal Host Coral Genomic Novelty for Establishing Coral-Algae Symbioses. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	23
11326	Early presence of <i>Batrachochytrium dendrobatidis</i> in Mexico with a contemporary dominance of the global panzootic lineage. <i>Molecular Ecology</i> , 2021, 30, 424-437.	2.0	21
11327	Phylogenomics of the North American Plecoptera. <i>Systematic Entomology</i> , 2021, 46, 287-305.	1.7	19
11328	Extended-spectrum beta-lactamase-producing <i>Escherichia coli</i> and antimicrobial resistance in municipal and hospital wastewaters in Czech Republic: Culture-based and metagenomic approaches. <i>Environmental Research</i> , 2021, 193, 110487.	3.7	24
11329	Enrichment and physiological characterization of a novel comammox <i>Nitrospira</i> indicates ammonium inhibition of complete nitrification. <i>ISME Journal</i> , 2021, 15, 1010-1024.	4.4	117
11330	Biallelic variants in HPDL, encoding 4-hydroxyphenylpyruvate dioxygenase-like protein, lead to an infantile neurodegenerative condition. <i>Genetics in Medicine</i> , 2021, 23, 524-533.	1.1	17
11331	A unique porin mediates iron-selective transport through cyanobacterial outer membranes. <i>Environmental Microbiology</i> , 2021, 23, 376-390.	1.8	31
11332	Genetic diversity and population structure of <i>Acanthopagrus schlegelii</i> inferred from mtDNA sequences. <i>Regional Studies in Marine Science</i> , 2021, 41, 101532.	0.4	4
11333	Subgroup level differences of physiological activities in marine Lokiarchaeota. <i>ISME Journal</i> , 2021, 15, 848-861.	4.4	23
11334	Evidence for speciation underground in diving beetles (Dytiscidae) from a subterranean archipelago. <i>Evolution; International Journal of Organic Evolution</i> , 2021, 75, 166-175.	1.1	26
11335	Genomic Analysis Enlightens Agaricales Lifestyle Evolution and Increasing Peroxidase Diversity. <i>Molecular Biology and Evolution</i> , 2021, 38, 1428-1446.	3.5	72
11336	Divergent Evolution of a Protein-Protein Interaction Revealed through Ancestral Sequence Reconstruction and Resurrection. <i>Molecular Biology and Evolution</i> , 2021, 38, 152-167.	3.5	8
11337	Comparative genomics reveals the <i>in planta</i> -secreted <i>Verticillium dahliae</i> Av2 effector protein recognized in tomato plants that carry the <i>scp-V2</i> resistance locus. <i>Environmental Microbiology</i> , 2021, 23, 1941-1958.	1.8	32

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11338	Exploring systematic biases, rooting methods and morphological evidence to unravel the evolutionary history of the genus <i>Ficus</i> (Moraceae). <i>Cladistics</i> , 2021, 37, 402-422.	1.5	11
11339	A new species of <i>Wallinia</i> Pearse, 1920 (Digenea: Allocreadiidae), in <i>Astyanax bimaculatus</i> (Linnaeus). <i>Tj ETQq1 1 0.784314 rgBT /Overle</i> Research, 2021, 120, 37-44.	0.6	5
11340	Phylogenomics of manakins (Aves: Pipridae) using alternative locus filtering strategies based on informativeness. <i>Molecular Phylogenetics and Evolution</i> , 2021, 155, 107013.	1.2	20
11341	The Windblown: Possible Explanations for Dinophyte DNA in Forest Soils. <i>Journal of Eukaryotic Microbiology</i> , 2021, 68, e12833.	0.8	9
11342	Description of <i>Flexiglena</i> gen. nov. and new members of <i>Discoplastis</i> and <i>Euglenaformis</i> (Euglenida). <i>Journal of Phycology</i> , 2021, 57, 766-779.	1.0	12
11343	Hybrid speciation via inheritance of alternate alleles of parental isolating genes. <i>Molecular Plant</i> , 2021, 14, 208-222.	3.9	68
11344	Hidden in plain sight: Morphological and phylogenetic evidence for <i>Bouteloua arizonica</i> , a species distinct from <i>Bouteloua aristoides</i> (Poaceae, Chloridoideae). <i>Plant Diversity</i> , 2021, 43, 125-133.	1.8	1
11345	Mitochondrial evolution in the Demospongiae (Porifera): Phylogeny, divergence time, and genome biology. <i>Molecular Phylogenetics and Evolution</i> , 2021, 155, 107011.	1.2	17
11346	Anaerobic bacterial degradation of protein and lipid macromolecules in subarctic marine sediment. <i>ISME Journal</i> , 2021, 15, 833-847.	4.4	38
11347	Drivers and dynamics of a massive adaptive radiation in cichlid fishes. <i>Nature</i> , 2021, 589, 76-81.	13.7	151
11348	Intra-specific genetic variability drives carbon metabolism and symbiotic host interactions in the ectomycorrhizal fungus <i>Pisolithus microcarpus</i> . <i>Environmental Microbiology</i> , 2021, 23, 2004-2020.	1.8	14
11349	Diversity and biomass dynamics of unicellular marine fungi during a spring phytoplankton bloom. <i>Environmental Microbiology</i> , 2021, 23, 448-463.	1.8	22
11350	Utility of large subunit for environmental sequencing of arbuscular mycorrhizal fungi: a new reference database and pipeline. <i>New Phytologist</i> , 2021, 229, 3048-3052.	3.5	20
11351	Concatenated data and dense taxon sampling clarify phylogeny and ecological transitions within <i>Hypotricha</i> . <i>Zoologica Scripta</i> , 2021, 50, 125-139.	0.7	4
11352	Phylogenetic and Biogeographic Patterns of <i>Vibrio parahaemolyticus</i> Strains from North America Inferred from Whole-Genome Sequence Data. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	6
11353	Diversification of Fungal Chitinases and Their Functional Differentiation in <i>Histoplasma capsulatum</i> . <i>Molecular Biology and Evolution</i> , 2021, 38, 1339-1355.	3.5	12
11354	F-box protein CFK1 interacts with and degrades <i>de novo</i> DNA methyltransferase in <i>Arabidopsis</i> . <i>New Phytologist</i> , 2021, 229, 3303-3317.	3.5	13
11355	Genetic admixture increases phenotypic diversity in the nectar yeast <i>Metschnikowia reukaufii</i> . <i>Fungal Ecology</i> , 2021, 49, 101016.	0.7	4

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11356	Morphological and molecular identification reveals that waters from an isolated oasis in Tamanrasset (extreme South of Algerian Sahara) are colonized by opportunistic and pollution-tolerant diatom species. <i>Ecological Indicators</i> , 2021, 121, 107104.	2.6	9
11357	The Perfect Storm: Gene Tree Estimation Error, Incomplete Lineage Sorting, and Ancient Gene Flow Explain the Most Recalcitrant Ancient Angiosperm Clade, Malpighiales. <i>Systematic Biology</i> , 2021, 70, 491-507.	2.7	61
11358	Expansion and expression diversity of FAR1/FRS-like genes provides insights into flowering time regulation in roses. <i>Plant Diversity</i> , 2021, 43, 173-179.	1.8	8
11359	A phylogenetic assessment of Pholiota and the new genus Pyrrhulomyces. <i>Mycologia</i> , 2021, 113, 146-167.	0.8	10
11360	<i>Amanita</i> in the Guineo-Congolian rainforest: Epitypes and new species from the Dja Biosphere Reserve, Cameroon. <i>Mycologia</i> , 2021, 113, 168-190.	0.8	6
11361	Spatial and temporal variations in <i>Synechococcus</i> microdiversity in the Southern California coastal ecosystem. <i>Environmental Microbiology</i> , 2021, 23, 252-266.	1.8	10
11362	SNP-based genotyping and whole-genome sequencing reveal previously unknown genetic diversity in <i>Xanthomonas vasicola</i> pv. <i>musacearum</i> , causal agent of banana xanthomonas wilt, in its presumed Ethiopian origin. <i>Plant Pathology</i> , 2021, 70, 534-543.	1.2	3
11363	Evidence for Two Main Domestication Trajectories in <i>Saccharomyces cerevisiae</i> Linked to Distinct Bread-Making Processes. <i>Current Biology</i> , 2021, 31, 722-732.e5.	1.8	43
11364	Genomic-based classification of <i>Catenulispora pinisilvae</i> sp. nov., novel actinobacteria isolated from a pine forest soil in Poland and emended description of <i>Catenulispora rubra</i> . <i>Systematic and Applied Microbiology</i> , 2021, 44, 126164.	1.2	14
11365	Integrating phylogenetics, morphology, and osteology to delimit a new species of endemic montane sheep frog (Microhylidae: <i>Hypopachus</i>) from the Lenca Highlands of Honduras. <i>Systematics and Biodiversity</i> , 2021, 19, 186-208.	0.5	0
11366	Reticulate Evolution, Ancient Chloroplast Haplotypes, and Rapid Radiation of the Australian Plant Genus <i>Adenanthos</i> (Proteaceae). <i>Frontiers in Ecology and Evolution</i> , 2021, 8, .	1.1	25
11367	Unraveling Reticulate Evolution in <i>Opuntia</i> (Cactaceae) From Southern Mexico. <i>Frontiers in Plant Science</i> , 2021, 11, 606809.	1.7	8
11368	Molecular and morphometric characterization of fruit bats of the genus <i>Rousettus</i> Gray, 1821 (Chiroptera: Pteropodidae) in Iran. <i>Zoology in the Middle East</i> , 2021, 67, 1-11.	0.2	2
11369	An emerging view of the diversity, ecology and function of Archaea in alkaline hydrothermal environments. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	6
11370	Chromosome-level genome assembly of the aphid parasitoid <i>Aphidius gifuensis</i> using Oxford Nanopore sequencing and Hi-C technology. <i>Molecular Ecology Resources</i> , 2021, 21, 941-954.	2.2	10
11371	A genome-wide investigation of adaptive signatures in protein-coding genes related to tool behaviour in New Caledonian and Hawaiian crows. <i>Molecular Ecology</i> , 2021, 30, 973-986.	2.0	2
11372	Cytosuclear discordance, reticulation and cryptic diversity in one of North America's most common frogs. <i>Molecular Phylogenetics and Evolution</i> , 2021, 156, 107042.	1.2	4
11373	The pico-sized Mamiellophyceae and a novel <i>Bathycoccus</i> clade from the summer plankton of Russian Arctic Seas and adjacent waters. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	10

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11374	Horizontal chromosome transfer and independent evolution drive diversification in <i>Fusarium oxysporum</i> f. sp. <i>fragariae</i> . <i>New Phytologist</i> , 2021, 230, 327-340.	3.5	26
11375	Integrative taxonomy recognized a new cryptic species within <i>Stipa grandis</i> from Loess Plateau of China. <i>Journal of Systematics and Evolution</i> , 2022, 60, 901-913.	1.6	5
11376	Molecular phylogeny of <i>Eremias</i> spp. from Pakistan contributes to a better understanding of the diversity of racerunners. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2021, 59, 466-483.	0.6	4
11377	Parasitic flatworms infecting thorny skate, <i>Amblyraja radiata</i> : Infection by the monogeneans <i>Acanthocotyle verrilli</i> and <i>Rajonchocotyle emarginata</i> in Svalbard. <i>Parasitology International</i> , 2021, 81, 102261.	0.6	1
11378	Unraveling the history of the genus <i>Gallus</i> through whole genome sequencing. <i>Molecular Phylogenetics and Evolution</i> , 2021, 158, 107044.	1.2	9
11379	Identification of Evolutionarily Conserved Nuclear Matrix Proteins and Their Prokaryotic Origins. <i>Journal of Proteome Research</i> , 2021, 20, 518-530.	1.8	9
11380	Chromosome-level reference genome assembly provides insights into aroma biosynthesis in passion fruit (<i>Passiflora edulis</i>). <i>Molecular Ecology Resources</i> , 2021, 21, 955-968.	2.2	31
11381	Comparative insight into the genomic landscape of SARS-CoV-2 and identification of mutations associated with the origin of infection and diversity. <i>Journal of Medical Virology</i> , 2021, 93, 2406-2419.	2.5	13
11382	Revisiting the systematics of the <i>Leptodactylus melanonotus</i> group (Anura: Leptodactylidae): Redescription of <i>L. Petersii</i> and revalidation of its junior synonyms. <i>Zoologischer Anzeiger</i> , 2021, 290, 117-134.	0.4	11
11383	Stepwise evolution of <i>Salmonella</i> Typhimurium ST313 causing bloodstream infection in Africa. <i>Nature Microbiology</i> , 2021, 6, 327-338.	5.9	68
11384	Evidence of cryptic speciation in South American lungfish. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2021, 59, 760-771.	0.6	3
11385	Overlooked biodiversity of mitochondrial lineages in <i>Hemiodus</i> (Ostariophysi, Characiformes). <i>Zoologica Scripta</i> , 2021, 50, 337-351.	0.7	5
11386	Genomic Insights Into the Lifestyles of Thaumarchaeota Inside Sponges. <i>Frontiers in Microbiology</i> , 2020, 11, 622824.	1.5	16
11387	Sourcing Elephant Ivory from a Sixteenth-Century Portuguese Shipwreck. <i>Current Biology</i> , 2021, 31, 621-628.e4.	1.8	7
11388	Phylogeny and biogeography of <i>Myrcia</i> sect. <i>Aguava</i> (Myrtaceae, Myrteae) based on phylogenomic and Sanger data provide evidence for a Cerrado origin and geographically structured clades. <i>Molecular Phylogenetics and Evolution</i> , 2021, 157, 107043.	1.2	13
11389	Discovery of divided RdRp sequences and a hitherto unknown genomic complexity in fungal viruses. <i>Virus Evolution</i> , 2021, 7, veaa101.	2.2	33
11390	Toxin- and species-dependent regulation of ATP-binding cassette (ABC) transporters in scallops after exposure to paralytic shellfish toxin-producing dinoflagellates. <i>Aquatic Toxicology</i> , 2021, 230, 105697.	1.9	13
11391	Illumination enhances the protein abundance of sarcoplasmic reticulum Ca ²⁺ -ATPases-like transporter in the ctenidium and whitish inner mantle of the giant clam, <i>Tridacna squamosa</i> , to augment exogenous Ca ²⁺ uptake and shell formation, respectively. <i>Comparative Biochemistry and Physiology Part A. Molecular & Integrative Physiology</i> , 2021, 251, 110811.	0.8	7

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11392	Colpodean ciliate phylogeny and reference alignments for phylogenetic placements. <i>European Journal of Protistology</i> , 2021, 77, 125747.	0.5	5
11393	New distributional records, taxonomy, morphology, and genetic variations of the endangered brackish-water species <i>Lamprothamnium succinctum</i> (Charales: Charophyceae) in Japan. <i>Journal of Asia-Pacific Biodiversity</i> , 2021, 14, 15-22.	0.2	4
11394	Diverse lineages of multidrug resistant clinical <i>Salmonella enterica</i> and a cryptic outbreak in New Hampshire, USA revealed from a year-long genomic surveillance. <i>Infection, Genetics and Evolution</i> , 2021, 87, 104645.	1.0	6
11395	Plastome and phylogenetic relationship of the woody buckwheat <i>Fagopyrum tibeticum</i> in the Qinghai-Tibet Plateau. <i>Plant Diversity</i> , 2021, 43, 198-205.	1.8	10
11396	<i>Thermogemmata fonticola</i> gen. nov., sp. nov., the first thermophilic planctomycete of the order Gemmatales from a Kamchatka hot spring. <i>Systematic and Applied Microbiology</i> , 2021, 44, 126157.	1.2	22
11397	Comparison of historical and contemporary isolates of <i>Senecavirus A</i> . <i>Veterinary Microbiology</i> , 2021, 253, 108946.	0.8	14
11398	<i>Salmonella enterica</i> serovar Typhi H58 clone has been endemic in Zimbabwe from 2012 to 2019. <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 76, 1160-1167.	1.3	13
11399	Phylogenomic species delimitation in the ants of the <i>Temnothorax salvini</i> group (Hymenoptera: Formicidae): an integrative approach. <i>Systematic Entomology</i> , 2021, 46, 307-326.	1.7	25
11400	<i>Phlebopus roseus</i> , a new edible bolete from China, is associated with insects and plants. <i>Mycologia</i> , 2021, 113, 33-42.	0.8	4
11401	Systematics, distribution, and sexual compatibility of six <i>Scytosiphon</i> species (Scytosiphonaceae, Phaeophyceae) from Japan and the description of four new species. <i>Journal of Phycology</i> , 2021, 57, 416-434.	1.0	7
11402	Precise Species Identification by Whole-Genome Sequencing of <i>Enterobacter</i> Bloodstream Infection, China. <i>Emerging Infectious Diseases</i> , 2021, 27, 161-169.	2.0	14
11403	Disruption of duplicated yellow genes in <i>Bactrocera tryoni</i> modifies pigmentation colouration and impacts behaviour. <i>Journal of Pest Science</i> , 2021, 94, 917-932.	1.9	5
11404	Phylogenetic reconstruction of early diverging tapeworms (Cestoda: Caryophyllidea) reveals ancient radiations in vertebrate hosts and biogeographic regions. <i>International Journal for Parasitology</i> , 2021, 51, 263-277.	1.3	13
11405	Genome-wide genetic variation coupled with demographic and ecological niche modeling of the dusky-footed woodrat (<i>Neotoma fuscipes</i>) reveal patterns of deep divergence and widespread Holocene expansion across northern California. <i>Heredity</i> , 2021, 126, 521-536.	1.2	3
11406	Phylogenetic and ecological correlates of pollen morphological diversity in a Neotropical rainforest. <i>Biotropica</i> , 2021, 53, 74-85.	0.8	7
11407	Mitochondrial genomes of the <i>Dorcus velutinus</i> complex (Coleoptera: Lucanidae) with the large intergenic spacer showing unique short sequence repeats and their implications for systematics. <i>Journal of Asia-Pacific Entomology</i> , 2021, 24, 493-501.	0.4	3
11408	Electrochemical and phylogenetic comparisons of oxygen-reducing electroautotrophic communities. <i>Biosensors and Bioelectronics</i> , 2021, 171, 112700.	5.3	2
11409	First detection of <i>Amblyomma variegatum</i> and molecular finding of <i>Rickettsia africae</i> in Sardinia, Italy. <i>Ticks and Tick-borne Diseases</i> , 2021, 12, 101561.	1.1	13

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11410	On Sea Turtle-associated <i>Craspedostauros</i> (Bacillariophyta), with Description of Three Novel Species. <i>Journal of Phycology</i> , 2021, 57, 199-218.	1.0	9
11411	Newly discovered cichlid fish biodiversity threatened by hybridization with non-native species. <i>Molecular Ecology</i> , 2021, 30, 895-911.	2.0	24
11412	The Function and Evolution of Motile DNA Replication Systems in Ciliates. <i>Current Biology</i> , 2021, 31, 66-76.e6.	1.8	76
11413	Ciliates as bioindicators of water quality: A case study in the neotropical region and evidence of phylogenetic signals (18S-rDNA). <i>Environmental Pollution</i> , 2021, 268, 115760.	3.7	10
11414	Biogeography of land snail genus <i>Acusta</i> (Gastropoda: Camaenidae): Diversification on East Asian islands. <i>Molecular Phylogenetics and Evolution</i> , 2021, 155, 106999.	1.2	4
11415	Molecular and morphological diversity in species of <i>Kronichthys</i> (Teleostei, Loricariidae) from Atlantic coastal rivers of Brazil. <i>Journal of Fish Biology</i> , 2021, 98, 668-679.	0.7	2
11416	Tiny treefrogs in the Pleistocene: Phylogeography of <i>Dendropsophus oliveirai</i> in the Atlantic Forest and associated enclaves in northeastern Brazil. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2021, 59, 179-194.	0.6	5
11417	Like myovirus community shaped by dispersal and deterministic processes in the South China Sea. <i>Environmental Microbiology</i> , 2021, 23, 1038-1052.	1.8	5
11418	High-throughput sequencing of 5S rDNA in oaks: Exploring intragenomic variation and algorithms to recognize target species in pure and mixed samples. <i>Molecular Ecology Resources</i> , 2021, 21, 495-510.	2.2	7
11419	Extensive photobiont sharing in a rapidly radiating cyanolichen clade. <i>Molecular Ecology</i> , 2021, 30, 1755-1776.	2.0	19
11420	Mitochondrial genomes of Danish vertebrate species generated for the national DNA reference database, DNAMark. <i>Environmental DNA</i> , 2021, 3, 472-480.	3.1	24
11421	DNA-barcoding identification of <i>Dothistroma septosporum</i> on <i>Pinus contorta</i> var. <i>latifolia</i> , <i>P. banksiana</i> and their hybrid in northern Alberta, Canada. <i>Canadian Journal of Plant Pathology</i> , 2021, 43, 472-479.	0.8	6
11422	Systematics, distribution, and conservation status of Dice's cottontail, <i>Sylvilagus dicei</i> Harris, 1932 (Mammalia, Lagomorpha, Leporidae), in Central America. <i>Systematics and Biodiversity</i> , 2021, 19, 74-88.	0.5	1
11423	Chasing Waterborne Pathogens in Antarctic Human-Made and Natural Environments, with Special Reference to <i>Legionella</i> spp. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	13
11424	Molecular phylogeny and trait evolution in an ancient terrestrial arthropod lineage: Systematic revision and implications for ecological divergence (Collembola, Tomocerinae). <i>Molecular Phylogenetics and Evolution</i> , 2021, 154, 106995.	1.2	9
11425	Quantifying acquisition and transmission of <i>Enterococcus faecium</i> using genomic surveillance. <i>Nature Microbiology</i> , 2021, 6, 103-111.	5.9	53
11426	Global Diversity and Geographic Distributions of <i>Padina</i> Species (Dictyotales, Phaeophyceae): New Insights Based on Molecular and Morphological Analyses. <i>Journal of Phycology</i> , 2021, 57, 454-472.	1.0	4
11427	Population connectivity of fan-shaped sponge holobionts in the deep Cantabrian Sea. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2021, 167, 103427.	0.6	12

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11428	New multilocus phylogeny reorganises the family Macrobiotidae (Eutardigrada) and unveils complex morphological evolution of the Macrobiotus hufelandi group. <i>Molecular Phylogenetics and Evolution</i> , 2021, 160, 106987.	1.2	41
11429	Cryptic diversity in a vagile Hawaiian moth group suggests complex factors drive diversification. <i>Molecular Phylogenetics and Evolution</i> , 2021, 155, 107002.	1.2	3
11430	gcType: a high-quality type strain genome database for microbial phylogenetic and functional research. <i>Nucleic Acids Research</i> , 2021, 49, D694-D705.	6.5	53
11431	Morphological evolution of silica scales in the freshwater genus <i>Synura</i> (Stramenopiles). <i>Journal of Phycology</i> , 2021, 57, 355-369.	1.0	7
11432	Honey as a Functional Food for <i>Apis mellifera</i> . <i>Annual Review of Entomology</i> , 2021, 66, 185-208.	5.7	27
11433	The population genetics of pathogenic <i>Escherichia coli</i> . <i>Nature Reviews Microbiology</i> , 2021, 19, 37-54.	13.6	268
11434	The infestation and habitat of the ambrosia beetle <i>Euwallacea interjectus</i> (Coleoptera: Curculionidae). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 107 Td</i> 104-109.	0.7	12
11435	Phylogenomics of the lepidopteran endoparasitoid wasp subfamily Rogadinae (Hymenoptera). <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 107 Td</i>	1.7	8
11436	Geographical reconstruction of the SARS-CoV-2 outbreak in Lombardy (Italy) during the early phase. <i>Journal of Medical Virology</i> , 2021, 93, 1752-1757.	2.5	17
11437	Phylogenomic Data Reveal Widespread Introgression Across the Range of an Alpine and Arctic Specialist. <i>Systematic Biology</i> , 2021, 70, 527-541.	2.7	4
11438	Origin, extinction and ancient DNA of a new fossil insular viper: molecular clues of overseas immigration. <i>Zoological Journal of the Linnean Society</i> , 2021, 192, 144-168.	1.0	6
11439	Plastome sequencing of a 167-year-old herbarium specimen and classical morphology resolve the systematics of two potentially extinct grass species. <i>Botanical Journal of the Linnean Society</i> , 2021, 195, 115-123.	0.8	9
11440	Eighteen Coral Genomes Reveal the Evolutionary Origin of <i>Acropora</i> Strategies to Accommodate Environmental Changes. <i>Molecular Biology and Evolution</i> , 2021, 38, 16-30.	3.5	75
11441	Scuttling towards monophyly: phylogeny of the mega-diverse genus <i>Megaselia</i> (Diptera: Phoridae). <i>Systematic Entomology</i> , 2021, 46, 71-82.	1.7	3
11442	First report of <i>Neophloeospora maculans</i> causing leaf spots in <i>Morus nigra</i> and <i>M. alba</i> in Brazil. <i>Journal of Plant Diseases and Protection</i> , 2021, 128, 317-321.	1.6	3
11443	<i>Mediocremonas mediterraneus</i> , a New Member within the Developea. <i>Journal of Eukaryotic Microbiology</i> , 2021, 68, e12825.	0.8	2
11444	Morphological evolution and molecular phylogenetics of the <i>Merostachys</i> clade (Poaceae). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 107 Td</i> <i>Journal of the Linnean Society</i> , 2021, 195, 53-76.	0.8	6
11445	Redescriptions of <i>Dussumieria acuta</i> Valenciennes 1847 and <i>Dussumieria albulina</i> (Fowler 1934), two valid species of rainbow sardines (Clupeiformes: Dussumieriidae). <i>Ichthyological Research</i> , 2021, 68, 126-138.	0.5	4

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11446	Morphological variability of choanocyte kinetids supports a novel systematic division within Oscarellidae (Porifera, Homoscleromorpha). <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2021, 59, 31-43.	0.6	1
11447	<i>Oncosaccus</i> : a rare green alga endemic to China belongs to Chaetopeltidales (Chlorophyceae). <i>Tj ETQq1 1 0.784314 rgBT /Oyerlock 10</i>	0.6	2
11448	Genomic Signatures of Coevolution between Nonmodel Mammals and Parasitic Roundworms. <i>Molecular Biology and Evolution</i> , 2021, 38, 531-544.	3.5	10
11449	Discovery and surveillance of viruses from salmon in British Columbia using viral immune-response biomarkers, metatranscriptomics, and high-throughput RT-PCR. <i>Virus Evolution</i> , 2021, 7, veaa069.	2.2	13
11450	New pelagophytes show a novel mode of algal colony development and reveal a perforated theca that may define the class. <i>Journal of Phycology</i> , 2021, 57, 396-411.	1.0	10
11451	Identification of <i>Dermocystidium anguillae</i> Spangenberg, 1975 from the American eel <i>Anguilla rostrata</i> (Lesueur, 1817) and Chinese perch <i>Siniperca chuatsi</i> (Basilewsky, 1855). <i>Aquaculture</i> , 2021, 531, 735793.	1.7	4
11452	Dispersal as a result of asymmetrical hybridization between two closely related oak species in China. <i>Molecular Phylogenetics and Evolution</i> , 2021, 154, 106964.	1.2	4
11453	Evolutionary insights into <i>Rhinolophus episcopus</i> (Chiroptera, Rhinolophidae) in China: Isolation by distance, environment, or sensory system?. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2021, 59, 294-310.	0.6	5
11454	DNA barcoding of <i>Oryza</i> : conventional, specific, and super barcodes. <i>Plant Molecular Biology</i> , 2021, 105, 215-228.	2.0	29
11455	Untangling ITS2 genotypes of algal symbionts in zooxanthellate corals. <i>Molecular Ecology Resources</i> , 2021, 21, 137-152.	2.2	17
11456	Phylogenetic relationships investigation of <i>Mycobacterium caprae</i> strains from sympatric wild boar and goats based on whole genome sequencing. <i>Transboundary and Emerging Diseases</i> , 2021, 68, 1476-1486.	1.3	10
11457	Crystal structure of a S-adenosyl-L-methionine-dependent O-methyltransferase-like enzyme from <i>Aspergillus flavus</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 185-192.	1.5	4
11458	Crop wild phylorelatives (CWPs): phylogenetic distance, cytogenetic compatibility and breeding system data enable estimation of crop wild relative gene pool classification. <i>Botanical Journal of the Linnean Society</i> , 2021, 195, 1-33.	0.8	23
11459	Disparity between morphology and genetics in <i>Urtica dioica</i> (Urticaceae). <i>Botanical Journal of the Linnean Society</i> , 2021, 195, 606-621.	0.8	4
11460	Evolutionary Genomics of Niche-Specific Adaptation to the Cystic Fibrosis Lung in <i>Pseudomonas aeruginosa</i> . <i>Molecular Biology and Evolution</i> , 2021, 38, 663-675.	3.5	18
11461	Characterization of <i>Diaporthe</i> spp. Associated With Spruce Decline on Colorado Blue Spruce in Michigan. <i>Phytopathology</i> , 2021, 111, 509-520.	1.1	5
11462	Too many species: morphometrics, molecular phylogenetics and genome structure of a Brazilian species complex in <i>Epidendrum</i> (Laeliinae; Orchidaceae) reveal fewer species than previously thought. <i>Botanical Journal of the Linnean Society</i> , 2021, 195, 161-188.	0.8	21
11463	Proteome specialization of anaerobic fungi during ruminal degradation of recalcitrant plant fiber. <i>ISME Journal</i> , 2021, 15, 421-434.	4.4	46

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11464	Outbreak of multi-drug-resistant (MDR) <i>Shigella flexneri</i> in northern Australia due to an endemic regional clone acquiring an IncFII plasmid. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2021, 40, 279-286.	1.3	10
11465	Assessing support for <i>Blaberoidea</i> phylogeny suggests optimal locus quality. <i>Systematic Entomology</i> , 2021, 46, 157-171.	1.7	18
11466	Phylogeny, taxonomic reassessment and ecomorph relationship of the <i>Orientallactaga sibirica</i> complex (Rodentia: Dipodidae: Allactaginae). <i>Zoological Journal of the Linnean Society</i> , 2021, 192, 185-205.	1.0	5
11467	Domestic dog origin of Carnivore Protoparvovirus 1 infection in a rescued free-ranging guinea pig (<i>Cavia porcellus</i>). <i>Journal of Virology</i> , 2021, 95, 1-10.	1.3	6
11468	Chromosome-level de novo genome assembly of <i>Sarcophaga peregrina</i> provides insights into the evolutionary adaptation of flesh flies. <i>Molecular Ecology Resources</i> , 2021, 21, 251-262.	2.2	16
11469	The thin red line between species: Genomic differentiation of <i>Gymnosoma</i> Meigen, a taxonomically challenging genus of parasitoid flies (Diptera: Tachinidae). <i>Systematic Entomology</i> , 2021, 46, 96-110.	1.7	4
11470	Suppression of wheat blast resistance by an effector of <i>Pyricularia oryzae</i> is counteracted by a host specificity resistance gene in wheat. <i>New Phytologist</i> , 2021, 229, 488-500.	3.5	13
11471	Origin and spatiotemporal diversification of a fishfly lineage endemic to the islands of East Asia (Megaloptera: Corydalidae). <i>Systematic Entomology</i> , 2021, 46, 124-139.	1.7	8
11472	A Faster Algorithm for Computing the Kernel of Maximum Agreement Subtrees. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 416-430.	1.9	2
11473	Structural characterization and comparative analysis of the chloroplast genome of <i>Ginkgo biloba</i> and other gymnosperms. <i>Journal of Forestry Research</i> , 2021, 32, 765-778.	1.7	19
11474	Congruent spatial patterns of species richness and phylogenetic diversity in karst flora: Case study of <i>Primulina</i> (Gesneriaceae). <i>Journal of Systematics and Evolution</i> , 2021, 59, 251-261.	1.6	15
11475	Comparative phylogenetic analyses of Chinese <i>Horsfieldia</i> (Myristicaceae) using complete chloroplast genome sequences. <i>Journal of Systematics and Evolution</i> , 2021, 59, 504-514.	1.6	14
11476	<i>Gemmatimonas groenlandica</i> sp. nov. Is an Aerobic Anoxygenic Phototroph in the Phylum Gemmatimonadetes. <i>Frontiers in Microbiology</i> , 2020, 11, 606612.	1.5	48
11479	Detection of genes positively selected in Cuban <i>Anolis</i> lizards that naturally inhabit hot and open areas and currently thrive in urban areas. <i>Ecology and Evolution</i> , 2021, 11, 1719-1728.	0.8	7
11480	Integrative taxonomy confirms that <i>Gregarina garnhami</i> and <i>G. acridiorum</i> (Apicomplexa) are distinct species. <i>Parasite</i> , 2021, 28, 12.	0.8	2
11481	Phylogeography of the iconic Australian pink cockatoo, <i>Lophochroa leadbeateri</i> . <i>Biological Journal of the Linnean Society</i> , 2021, 132, 704-723.	0.7	3
11482	The complete plastome sequences of <i>Pseudowintera colorata</i> and <i>Tasmania lanceolata</i> (Winteraceae) are distinct from <i>Canellales</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 104-105.	0.2	0
11483	Tight association of genome rearrangements with gene expression in conifer plastomes. <i>BMC Plant Biology</i> , 2021, 21, 33.	1.6	5

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11484	Rediscovery of <i>Pogostemon dielsianus</i> (Lamiaceae, Lamioideae), a rare endemic species from southwestern China, after one century. <i>PhytoKeys</i> , 2021, 171, 61-73.	0.4	2
11486	Complete chloroplast genome of the grain <i>Chenopodium quinoa</i> Willd., an important economical and dietary plant. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 40-42.	0.2	4
11487	Disentangling species of the genus <i>Limacia</i> O.F. MÅller, 1781, from southern Africa and Europe using integrative taxonomical methods, with the description of four new species. <i>Marine Biodiversity</i> , 2021, 51, 1.	0.3	9
11489	A phylogeny of the subfamily <i>Thiotrichinae</i> (<i>Lepidoptera</i> : <i>Gelechiidae</i>) with a revision of the generic classification based on molecular and morphological analyses. <i>Systematic Entomology</i> , 2021, 46, 357-379.	1.7	4
11490	Gaps in Serologic Immunity against Contemporary Swine-Origin Influenza A Viruses among Healthy Individuals in the United States. <i>Viruses</i> , 2021, 13, 127.	1.5	5
11492	Episodic evolution of coadapted sets of amino acid sites in mitochondrial proteins. <i>PLoS Genetics</i> , 2021, 17, e1008711.	1.5	6
11493	Phylogenetic inferences reveal deep polyphyly of Aongstroemiaceae and Dicranellaceae within the haplolepidous mosses (Dicranidae, Bryophyta). <i>Taxon</i> , 2021, 70, 246-262.	0.4	7
11494	Three complete plastome sequences from the families of Lamiaceae, Mazaceae, and Phrymaceae (Lamiales). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 224-226.	0.2	4
11495	Morphology Characterization, Molecular Phylogeny, and Pathogenicity of <i>Diaporthe passifloricola</i> on <i>Citrus reticulata</i> cv. Nanfengmiju in Jiangxi Province, China. <i>Plants</i> , 2021, 10, 218.	1.6	5
11496	New insights on the distribution and habitat of <i>Ulvella endozoica</i> (Ulvellaceae, Chlorophyta) in the tropical Southwestern Atlantic, based on thallus ontogeny in culture and DNA barcoding. <i>Marine Biodiversity</i> , 2021, 51, 1.	0.3	2
11498	A novel dataset to identify the endemic herpetofauna of the New Caledonia biodiversity hotspot with DNA barcodes. <i>Pacific Conservation Biology</i> , 2022, 28, 36-47.	0.5	6
11499	Rehmannieae or Rehmanniaceae? Evidence from plastome sequences and floral morphology. <i>Botanical Journal of the Linnean Society</i> , 2021, 196, 145-162.	0.8	2
11501	Cytogenetic characterization and mapping of the repetitive DNAs in <i>Cycloramphus bolitoglossus</i> (Werner, 1897): More clues for the chromosome evolution in the genus <i>Cycloramphus</i> (Anura). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 25</i>		
11502	Identification of <i>Lasiodiplodia pseudotheobromae</i> Causing Fruit Rot of Citrus in China. <i>Plants</i> , 2021, 10, 202.	1.6	14
11503	Identifying the true number of specimens of the extinct blue antelope (<i>Hippotragus leucophaeus</i>). <i>Scientific Reports</i> , 2021, 11, 2100.	1.6	9
11504	Genome skimming resolves the giant clam (Bivalvia: Cardiidae: Tridacninae) tree of life. <i>Coral Reefs</i> , 2022, 41, 497-510.	0.9	12
11505	Molecular phylogeny and character mapping support generic adjustments in the Tetrapteroid clade (Malpighiaceae). <i>Nordic Journal of Botany</i> , 2021, 39, .	0.2	11
11506	Life-history traits display strong associations to genome size in annelids. <i>Hydrobiologia</i> , 2021, 848, 799-810.	1.0	3

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11507	<i>Hyalorbilia oviparastica</i> Clade Detected in Field Soils Cropped to Sugar Beets and Enriched in the Presence of <i>Heterodera schachtii</i> and a Host Crop. <i>PhytoFrontiers</i> , 2021, 1, 13-20.	0.8	4
11508	Genome-wide signatures of plastid-nuclear coevolution point to repeated perturbations of plastid proteostasis systems across angiosperms. <i>Plant Cell</i> , 2021, 33, 980-997.	3.1	26
11509	Diversity and phylogeny of Paradiplozoon species (Monogenea: Diplozoidae) parasitising endemic cyprinoids in the peri-Mediterranean area, with a description of three new Paradiplozoon species. <i>Parasitology Research</i> , 2021, 120, 481-496.	0.6	8
11510	<i>Lihengia</i> : A new genus of Asteraceae distinct from <i>Dubyaea</i> . <i>Taxon</i> , 2021, 70, 620-634.	0.4	1
11511	Recovery of freshwater microbial communities after extreme rain events is mediated by cyclic succession. <i>Nature Microbiology</i> , 2021, 6, 479-488.	5.9	42
11512	Chloroplast genome organization and phylogeny of <i>Gynochthodes cochinchinensis</i> (DC.) Razafim. & B. Bremer (Rubiaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 261-262.	0.2	2
11513	Complex History of Aerobic Respiration and Phototrophy in the <i>Chloroflexota</i> Class <i>Anaerolineae</i> ; Revealed by High-Quality Draft Genome of <i>Ca. Roseilinea mizusawaensis</i> AA3_104. <i>Microbes and Environments</i> , 2021, 36, n/a.	0.7	5
11514	Identifying a melanogenesis-related candidate gene by a high-quality genome assembly and population diversity analysis in <i>Hypsizygus marmoreus</i> . <i>Journal of Genetics and Genomics</i> , 2021, 48, 75-87.	1.7	14
11515	Intra-host changes in Kaposi sarcoma-associated herpesvirus genomes in Ugandan adults with Kaposi sarcoma. <i>PLoS Pathogens</i> , 2021, 17, e1008594.	2.1	9
11516	An updated tribal classification of Lamiaceae based on plastome phylogenomics. <i>BMC Biology</i> , 2021, 19, 2.	1.7	126
11517	Systematics of the Neotropical spider genera <i>Jalapyphantes</i> and <i>Selenyphantes</i> and the circumscription of the <i>Pocobletus</i> clade (Araneae: Linyphiidae). <i>Zoological Journal of the Linnean Society</i> , 2021, 192, 896-957.	1.0	3
11519	Delimiting the genera of the <i>Ficinia</i> Clade (Cypereae, Cyperaceae) based on molecular phylogenetic data. <i>PeerJ</i> , 2021, 9, e10737.	0.9	4
11520	The evolutionary history of sedges (Cyperaceae) in Madagascar. <i>Journal of Biogeography</i> , 2021, 48, 917-932.	1.4	16
11521	Physiological and genomic analysis of newly-isolated polysaccharide synthesizing cyanobacterium <i>Chroococcus</i> sp. FPU101 and chemical analysis of the exopolysaccharide. <i>Journal of General and Applied Microbiology</i> , 2021, 67, 207-213.	0.4	3
11522	Evolution of Chi motifs in Proteobacteria. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	5
11524	Unlinking the Speciation Steps: Geographical Factors Drive Changes in Sexual Signals of an Amazonian Nurse-Frog Through Body Size Variation. <i>Evolutionary Biology</i> , 2021, 48, 81-93.	0.5	6
11525	Phanerozoic radiation of ammonia oxidizing bacteria. <i>Scientific Reports</i> , 2021, 11, 2070.	1.6	14
11526	Resolving generic limits in Cyperaceae tribe <i>Abildgaardieae</i> using targeted sequencing. <i>Botanical Journal of the Linnean Society</i> , 2021, 196, 163-187.	0.8	10

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11527	Evolutionary Turnover in Wnt Gene Expression but Conservation of Wnt Signaling during Ovary Determination in a TSD Reptile. <i>Sexual Development</i> , 2021, 15, 47-68.	1.1	4
11528	Extending the fossil record for foliicolous Dothideomycetes: <i>Bleximothyrium ostiolatum</i> gen. et sp. nov., a unique fly-speck fungus from the Lower Cretaceous of Virginia, USA. <i>American Journal of Botany</i> , 2021, 108, 129-144.	0.8	2
11529	More evidence of cryptic diversity in <i>Anatololacerta</i> species complex Arnold, Arribas and Carranza, 2007 (Squamata: Lacertidae) and re-evaluation of its current taxonomy. <i>Amphibia - Reptilia</i> , 2021, 42, 201-216.	0.1	5
11530	Two novel venom proteins underlie divergent parasitic strategies between a generalist and a specialist parasite. <i>Nature Communications</i> , 2021, 12, 234.	5.8	25
11531	De novo genome assembly of the potent medicinal plant <i>Rehmannia glutinosa</i> using nanopore technology. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 3954-3963.	1.9	26
11532	Taxonomic inflation due to inadequate sampling: are girdled lizards (<i>Cordylus minor</i> species) Tj ETQq1 1 0.784314 rgBT /Overl 1-24.	0.7	4
11533	Sequence and Structure-Based Analysis of Specificity Determinants in Eukaryotic Protein Kinases. <i>Cell Reports</i> , 2021, 34, 108602.	2.9	22
11534	Patterns of genetic variation in a prairie wildflower, <i>Silphium integrifolium</i> , suggest a non-prairie origin and locally adaptive variation. <i>American Journal of Botany</i> , 2021, 108, 145-158.	0.8	9
11535	The complete mitochondrial genome of <i>Rhinolophus affinis himalayanus</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 164-165.	0.2	1
11536	<i>Legionella septentrionalis</i> sp. nov., isolated from aquatic environments in the northern PR China. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	8
11537	Identification of microbial signatures linked to oilseed rape yield decline at the landscape scale. <i>Microbiome</i> , 2021, 9, 19.	4.9	31
11538	Augur: a bioinformatics toolkit for phylogenetic analyses of human pathogens. <i>Journal of Open Source Software</i> , 2021, 6, 2906.	2.0	129
11541	ACES: Analysis of Conservation with an Extensive list of Species. <i>Bioinformatics</i> , 2021, 37, 3920-3922.	1.8	0
11542	Learning the language of viral evolution and escape. <i>Science</i> , 2021, 371, 284-288.	6.0	184
11544	Temperature modulates stress response in mainstream anammox reactors. <i>Communications Biology</i> , 2021, 4, 23.	2.0	15
11545	Group 2i Isochrysidales produce characteristic alkenones reflecting sea ice distribution. <i>Nature Communications</i> , 2021, 12, 15.	5.8	33
11546	Differential genetic variability at two mtDNA COI regions does not imply mismatches in Odonata molecular identification performances. , 2021, 88, 425-435.		2
11547	Detection and identification of the large, exotic, crassostreine oyster <i>Magallana bilineata</i> (Rãrding.) Tj ETQq1 1 0.784314 rgBT /Overl 0,2	0,2	6

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11548	Two new species of terrestrial-breeding frogs (Anura: Brachycephaloidea) from Cordillera de Coln, Peru. Neotropical Biodiversity, 2021, 7, 279-296.	0.2	0
11549	New species in Aciculosporium, Shimizuomyces and a new genus Morakotia associated with plants in Clavicipitaceae from Thailand. Fungal Systematics and Evolution, 2021, 8, 27-37.	0.9	2
11550	The complete chloroplast genome sequence of cultivated peach (Prunus persica var. nectarina cv. Rui) Tj ETQq0.0.0 rgBT /Overlock 1	0.2	2
11552	The complete mitochondrial genome of <i>Allonychiurus kimi</i> (Lee, 1973) (Collembola:) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tj	0.2	3
11553	Signatures of conserved and unique molecular features in Afrotheria. Scientific Reports, 2021, 11, 1011.	1.6	2
11554	Additions to Italian Pleosporinae, including Italica heraclei sp. nov.. Biodiversity Data Journal, 2021, 9, e59648.	0.4	1
11555	Molecular, morphological, and toxinological characterizations of an Argentinean strain of Halamphora coffeaeformis with potential biotechnological applications. Journal of Applied Phycology, 2021, 33, 799-806.	1.5	2
11556	Morphological and molecular identification of Diaporthe species in south-western China, with description of eight new species. MycoKeys, 2021, 77, 65-95.	0.8	17
11557	Implications of genome simple sequence repeats signature in 98 Polyomaviridae species. 3 Biotech, 2021, 11, 35.	1.1	7
11558	The Long-Term Evolutionary History of Gradual Reduction of CpG Dinucleotides in the SARS-CoV-2 Lineage. Biology, 2021, 10, 52.	1.3	3
11559	Berberis burruyacuensis O. R. Dantur, S. Radice, E. Giordani, A. Papini sp. nov. (Berberidaceae): a new species. Genetic Resources and Crop Evolution, 2021, 68, 1799-1808.	0.8	0
11562	The complete chloroplast genome of Chinese medicine cultivar species of Rehmannia glutinosa (Orobanchaceae). Mitochondrial DNA Part B: Resources, 2021, 6, 290-292.	0.2	1
11563	<p align="left">A new species with pink lamellae of Amanita section Caesareae from China</p>. Phytotaxa, 2021, 478, 141-150.	0.1	5
11564	Molecular and morphological systematics of the crinoid-parasitic snail genus Goodingia (Mollusca:) Tj ETQq1 1 0.784314 rgBT /Overlock Biodiversity, 2021, 51, 1.	0.3	4
11565	<i>Caulerpa wysorii</i> sp. nov.</i>, a denuded <i>Caulerpa</i> (Chlorophyta) resembling <i>C. sertularioides</i> when dressed™. Phycologia, 2021, 60, 107-119.	0.6	3
11566	Characterization of the complete chloroplast genome sequence of medicinal plant: Potentilla bifurca (Rosaceae). Mitochondrial DNA Part B: Resources, 2021, 6, 143-144.	0.2	3
11568	Characterization and Comparative Analysis of Complete Mitogenomes of Three Cacatua Parrots (Psittaciformes: Cacatuidae). Genes, 2021, 12, 209.	1.0	2
11569	Revision of <i>Xylonaceae</i> (<i>Xylonales</i>, <i>Xylonomycetes</i>) to include Sarea and Tromera. Mycoscience, 2021, 62, 47-63.	0.3	2

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11570	Phylogeography and ecological niche modeling reveal evolutionary history of <i>Leiolepis ocellata</i> (Squamata, Leiolepidae). <i>Ecology and Evolution</i> , 2021, 11, 2221-2233.	0.8	4
11572	Hebeloma in the Malay Peninsula: Masquerading within <i>Psathyrella</i> . <i>MycKeys</i> , 2021, 77, 117-141.	0.8	6
11573	Molecular Placement of an Outbreak-Causing Gall Wasp, <i>Zapatella davisae</i> (Hymenoptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 6 Entomological Science, 2021, 56, 84-95.	0.2	2
11575	Mitochondrial Genome Evolution, Genetic Diversity, and Population Structure in British Water Voles (<i>Arvicola amphibius</i>). <i>Genes</i> , 2021, 12, 138.	1.0	4
11576	Characterization of the complete plastome of <i>Cyperus rotundus</i> L. (Cyperaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 58-59.	0.2	6
11577	A New Dichromatic Species of <i>Myotis</i> (Chiroptera: Vespertilionidae) from the Nimba Mountains, Guinea. <i>American Museum Novitates</i> , 2021, 2020, .	0.2	1
11578	A new nemertean with a branched proboscis, <i>Gorgonorhynchus citrinus</i> sp. nov. (Nemertea: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 502 T	0.5	5
11579	Effects of Sample Size in the Determination of the True Number of Haplogroups or ESUs Within a Species with Phylogeographic and Conservation Purposes: The Case of <i>Cebus albifrons</i> in Ecuador, and the Kinkajous and Coatis Throughout Latin America. , 2021, , 101-148.		0
11580	Ciliate microzooplankton from the Northeastern Gulf of Mexico. <i>ICES Journal of Marine Science</i> , 2021, 78, 3356-3371.	1.2	5
11581	Comparative and Phylogenetic Analysis of Complete Chloroplast Genomes in Eragrostideae (Chloridoideae, Poaceae). <i>Plants</i> , 2021, 10, 109.	1.6	14
11582	Phylogenetic revision of South American Teloschistaceae (lichenized Ascomycota, Teloschistales) reveals three new genera and species. <i>Mycologia</i> , 2021, 113, 278-299.	0.8	11
11583	The evolution of tinamous (Palaeognathae: Tinamidae) in light of molecular and combined analyses. <i>Zoological Journal of the Linnean Society</i> , 2022, 195, 106-124.	1.0	7
11585	A Total-Group Phylogenetic Metatree for Cetacea and the Importance of Fossil Data in Diversification Analyses. <i>Systematic Biology</i> , 2021, 70, 922-939.	2.7	37
11586	Putative ligand binding sites of two functionally characterized bark beetle odorant receptors. <i>BMC Biology</i> , 2021, 19, 16.	1.7	46
11587	Untangling the <i>Lactifluus clarkeae</i> - <i>Lf. flocktoniae</i> (Russulaceae) species complex in Australasia. <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2021, , .	1.6	0
11589	Integrating Different Lines of Evidence to Establish a Novel Ascomycete Genus and Family (<i>Anastomitrabeculia</i> , <i>Anastomitrabeculiaceae</i>) in Pleosporales. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 94.	1.5	10
11590	Comparative analysis of chloroplast genomes indicated different origin for Indian tea (<i>Camellia</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 11	1.6	11
11591	Genome-resolved metagenomics reveals site-specific diversity of episymbiotic CPR bacteria and DPANN archaea in groundwater ecosystems. <i>Nature Microbiology</i> , 2021, 6, 354-365.	5.9	109

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11592	Phenotypic and genomic characterization of <i>Pseudomonas putida</i> ITEM 17297 spoiler of fresh vegetables: Focus on biofilm and antibiotic resistance interaction. <i>Current Research in Food Science</i> , 2021, 4, 74-82.	2.7	12
11593	Granick revisited: Synthesizing evolutionary and ecological evidence for the late origin of bacteriochlorophyll via ghost lineages and horizontal gene transfer. <i>PLoS ONE</i> , 2021, 16, e0239248.	1.1	10
11594	The mitogenomes of two saprophytic Boletales species (<i>Coniophora</i>) reveals intron dynamics and accumulation of plasmid-derived and non-conserved genes. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 401-414.	1.9	23
11595	<i>Leucobacter coleopterorum</i> sp. nov., <i>Leucobacter insecticola</i> sp. nov., and <i>Leucobacter viscericola</i> sp. nov., isolated from the intestine of the diving beetles, <i>Cybister brevis</i> and <i>Cybister lewisianus</i> , and emended description of the genus <i>Leucobacter</i> . <i>Journal of Microbiology</i> , 2021, 59, 360-368.	1.3	21
11596	â€˜Candidatus <i>Phytoplasma stylosanthis</i> â€™™, a novel taxon with a diverse host range in Australia, characterised using multilocus sequence analysis of 16S rRNA, <i>secA</i> , <i>tuf</i> , and <i>rp</i> genes. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	21
11597	Polyphasic study of antibiotic-resistant enterobacteria isolated from fresh produce in Germany and description of <i>Enterobacter vonholyi</i> sp. nov. isolated from marjoram and <i>Enterobacter dykesii</i> sp. nov. isolated from mung bean sprout. <i>Systematic and Applied Microbiology</i> , 2021, 44, 126174.	1.2	18
11598	<i>Sulfurimonas indica</i> sp. nov., a hydrogen- and sulfur-oxidizing chemolithoautotroph isolated from a hydrothermal sulfide chimney in the Northwest Indian Ocean. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	12
11599	Methicillin-Resistant <i>Staphylococcus epidermidis</i> Lineages in the Nasal and Skin Microbiota of Patients Planned for Arthroplasty Surgery. <i>Microorganisms</i> , 2021, 9, 265.	1.6	7
11600	Discovery of a colossal slickhead (<i>Alepocephaliformes</i> : <i>Alepocephalidae</i>): an active-swimming top predator in the deep waters of Suruga Bay, Japan. <i>Scientific Reports</i> , 2021, 11, 2490.	1.6	6
11601	The complete chloroplast genome of <i>Rhododendron platypodum</i> (<i>Ericaceae</i>): an endemic and endangered species from China. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 196-197.	0.2	7
11602	Quantifying fluorescent glycan uptake to elucidate strain-level variability in foraging behaviors of rumen bacteria. <i>Microbiome</i> , 2021, 9, 23.	4.9	16
11603	The First Report for the Presence of <i>Spiroplasma</i> and <i>Rickettsia</i> in Red Palm Weevil <i>Rhynchophorus ferrugineus</i> (<i>Coleoptera</i> : <i>Curculionidae</i>) in Egypt. <i>Acta Parasitologica</i> , 2021, 66, 593-604.	0.4	2
11605	TIPP2: metagenomic taxonomic profiling using phylogenetic markers. <i>Bioinformatics</i> , 2021, 37, 1839-1845.	1.8	18
11606	Taxonomy, Ontogenesis and Evolutionary Relationships of the Algae-Bearing Ciliate <i>Bourlandella viridis</i> (Kahl, 1932) comb. nov., With Establishment of a New Genus and New Family (<i>Protista</i>). <i>Tj ETQq1 1 0.7843 14gBT / Overlock 10</i>		
11607	Phylogenetic placement of <i>Iodosphaeriaceae</i> (<i>Xylariales</i> , <i>Ascomycota</i>), designation of an epitype for the type species of <i>Iodosphaeria</i> , <i>I. phyllophila</i> , and description of <i>I. foliicola</i> sp. nov.. <i>Fungal Systematics and Evolution</i> , 2021, 8, 49-64.	0.9	1
11608	TNet: Transmission Network Inference Using Within-Host Strain Diversity and its Application to Geographical Tracking of COVID-19 Spread. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, 19, 230-242.	1.9	5
11609	Geo-Climatic Changes and Apomixis as Major Drivers of Diversification in the Mediterranean Sea Lavenders (<i>Limonium</i> Mill.). <i>Frontiers in Plant Science</i> , 2020, 11, 612258.	1.7	11
11610	The geographical origin, refugia, and diversification of honey bees (<i>Apis</i> spp.) based on biogeography and niche modeling. <i>Apidologie</i> , 2021, 52, 367-377.	0.9	9

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11611	Multidrug Resistant <i>Klebsiella pneumoniae</i> ST101 Clone Survival Chain From Inpatients to Hospital Effluent After Chlorine Treatment. <i>Frontiers in Microbiology</i> , 2020, 11, 610296.	1.5	28
11612	Analysis of RNA-Seq, DNA Target Enrichment, and Sanger Nucleotide Sequence Data Resolves Deep Splits in the Phylogeny of Cuckoo Wasps (Hymenoptera: Chrysididae). <i>Insect Systematics and Diversity</i> , 2021, 5, .	0.7	8
11613	Genetic diversification of persistent <i>Mycobacterium abscessus</i> within cystic fibrosis patients. <i>Virulence</i> , 2021, 12, 2415-2429.	1.8	14
11614	Comparative Analysis of Core and Accessory Genes in Coexpression Network. <i>Methods in Molecular Biology</i> , 2021, 2242, 45-58.	0.4	2
11616	Comparative Chloroplast Genomics of <i>Corydalis</i> Species (Papaveraceae): Evolutionary Perspectives on Their Unusual Large Scale Rearrangements. <i>Frontiers in Plant Science</i> , 2020, 11, 600354.	1.7	30
11617	Genetic analyses reveal cryptic diversity in the widely distributed. <i>Invertebrate Systematics</i> , 2021, 35, 298-311.	0.5	6
11618	Introduction to COVID-19. , 2021, , 1-32.		1
11619	Knots, spoons, and cloches: DNA barcoding unusual larval forms helps document the diversity of Neotropical marine annelids. <i>Invertebrate Biology</i> , 2021, 140, e12311.	0.3	3
11620	Five Independent Cases of Human Infection with Avian Influenza H5N6 in Sichuan Province, China, 2021. <i>China CDC Weekly</i> , 2021, 3, 751-756.	1.0	13
11621	Cryptic prophages within a <i>Streptococcus pyogenes</i> genotype emm4 lineage. <i>Microbial Genomics</i> , 2021, 7, .	1.0	7
11622	Taxonomy of Three Oxytrichids (Protozoa, Ciliophora, Hypotrichia), With Establishment of the New Species <i>Rubrioxytricha guangzhouensis</i> spec. nov.. <i>Frontiers in Marine Science</i> , 2021, 7, .	1.2	5
11623	Computational Evolutionary Biology. , 2021, , 83-100.		0
11624	Microbiota associated with <i>Mollitrichosiphum</i> aphids (Hemiptera: Aphididae: Greenideinae): diversity, host species specificity and phyllosymbiosis. <i>Environmental Microbiology</i> , 2021, 23, 2184-2198.	1.8	14
11625	Comparative mitogenome analyses uncover mitogenome features and phylogenetic implications of the subfamily Cobitinae. <i>BMC Genomics</i> , 2021, 22, 50.	1.2	11
11626	The role of host promiscuity in the invasion process of a seaweed holobiont. <i>ISME Journal</i> , 2021, 15, 1668-1679.	4.4	13
11627	Three ATP-dependent phosphorylating enzymes in the first committed step of dihydroxyacetone metabolism in <i>Gluconobacter thailandicus</i> NBRC3255. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 1227-1236.	1.7	3
11630	Assessment of mitochondrial genomes for heterobranch gastropod phylogenetics. <i>Bmc Ecology and Evolution</i> , 2021, 21, 6.	0.7	9
11632	Anomalous influenza seasonality in the United States and the emergence of novel influenza B viruses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	10

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11633	Chromoblastomycosis Caused by <i>Phialophora</i> Proven Cases from Mexico. <i>Journal of Fungi (Basel)</i> , 2021, 6, 1-5. Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.5	9
11635	Identification and Characterization of <i>Sphaerulina vaccinii</i> as the Cause of Leaf Spot and Stem Canker in Lowbush Blueberry and its Epidemiology. <i>Phytopathology</i> , 2021, , PHYTO04200143R.	1.1	7
11636	Inferring historical survivals of climate relicts: the effects of climate changes, geography, and population-specific factors on herbaceous hydrangeas. <i>Heredity</i> , 2021, 126, 615-629.	1.2	8
11637	<i>Bodo saltans</i> (Kinetoplastida) is dependent on a novel <i>Paracaedibacter</i> -like endosymbiont that possesses multiple putative toxin-antitoxin systems. <i>ISME Journal</i> , 2021, 15, 1680-1694.	4.4	11
11638	The complete chloroplast genome sequence of <i>Carpinus tibetana</i> (Betulaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 131-132.	0.2	0
11639	Uncovering dynamic evolution in the plastid genome of seven <i>Ligusticum</i> species provides insights into species discrimination and phylogenetic implications. <i>Scientific Reports</i> , 2021, 11, 988.	1.6	10
11640	Lost in a sagebrush sea: comparative genetic assessment of an isolated montane population of <i>Tamias amoenus</i> . <i>Journal of Mammalogy</i> , 2021, 102, 173-187.	0.6	2
11641	Comparative plastid genomics of four <i>Pilea</i> (Urticaceae) species: insight into interspecific plastid genome diversity in <i>Pilea</i> . <i>BMC Plant Biology</i> , 2021, 21, 25.	1.6	20
11642	Multilocus phylogeny suggests a distinct species status for the Nepal population of Assam macaques (&i'Macaca assamensis&i'): implications for evolution and conservation. <i>Zoological Research</i> , 2021, 42, 3-13.	0.9	4
11643	Overlooked cryptic diversity in <i>Muschampia</i> (Lepidoptera: HesperIIDae) adds two species to the European butterfly fauna. <i>Zoological Journal of the Linnean Society</i> , 2021, 193, 847-859.	1.0	9
11644	Refugia within refugium of <i>Geranium yesoense</i> (Geraniaceae) in Japan were driven by recolonization into the southern interglacial refugium. <i>Biological Journal of the Linnean Society</i> , 2021, 132, 552-572.	0.7	6
11646	<i>Natarajania thailandica</i> sp. nov. (Stilbosporaceae, Diaporthales) from Thailand. <i>Phyton</i> , 2021, 90, 677-686.	0.4	0
11647	Bioinformatics resources for SARS-CoV-2 discovery and surveillance. <i>Briefings in Bioinformatics</i> , 2021, 22, 631-641.	3.2	38
11648	<i>Conexivisphaera calida</i> gen. nov., sp. nov., a thermophilic sulfur- and iron-reducing archaeon, and proposal of <i>Conexivisphaeraceae</i> fam. nov., <i>Conexivisphaerales</i> ord. nov., and <i>Conexivisphaeria</i> class. nov. in the phylum Thaumarchaeota. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	19
11649	Spontaneous Emergence of Azithromycin Resistance in Independent Lineages of <i>Salmonella</i> Typhi in Northern India. <i>Clinical Infectious Diseases</i> , 2021, 72, e120-e127.	2.9	39
11650	An Important Afro-Asian Biological Control Agent, <i>Chrysoperla zastrowi sillemi</i> (Neuroptera: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf) 355-364.	1.3	2
11651	Population genomics of a reindeer lichen species from North American lichen woodlands. <i>American Journal of Botany</i> , 2021, 108, 159-171.	0.8	8
11652	The genus <i>Dermoloma</i> is more diverse than expected and forms a monophyletic lineage in the Tricholomataceae. <i>Mycological Progress</i> , 2021, 20, 11-25.	0.5	2

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11653	Detection of Nematophagous Fungi from <i>Heterodera schachtii</i> Females Using a Baiting Experiment with Soils Cropped to Brassica Species from California's Central Coast. PhytoFrontiers, 2021, 1, 4-12.	0.8	4

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#	ARTICLE	IF	CITATIONS
11671	A Global Approach to Estimating the Abundance and Duplication of Polyketide Synthase Domains in Dinoflagellates. <i>Evolutionary Bioinformatics</i> , 2021, 17, 117693432110318.	0.6	3
11672	Whole plastomes are not enough: phylogenomic and morphometric exploration at multiple demographic levels of the bee orchid clade <i>Ophrys</i> sect. <i>Sphegodes</i> . <i>Journal of Experimental Botany</i> , 2021, 72, 654-681.	2.4	15
11673	Diversity of <i>Colletotrichum</i> species causing onion anthracnose in Brazil. <i>European Journal of Plant Pathology</i> , 2021, 159, 339-357.	0.8	12
11674	The Isolate <i>Caproiciproducens</i> sp. 7D4C2 Produces n-Caproate at Mildly Acidic Conditions From Hexoses: Genome and rBOX Comparison With Related Strains and Chain-Elongating Bacteria. <i>Frontiers in Microbiology</i> , 2020, 11, 594524.	1.5	33
11675	<i>Gerricola queenslandensis</i> n. g., n. sp., a new monorchiid trematode from the eastern Australian coast and its life cycle partially elucidated. <i>Journal of Helminthology</i> , 2021, 95, e30.	0.4	4
11676	Wide-Scale Gene Flow, Even in Insects that have Lost their Flight Ability: Presence of Dispersion Due to a Unique Parasitic Ecological Strategy of Piggybacking Hosts. <i>Zoological Science</i> , 2021, 38, 122-139.	0.3	11
11677	Phylogenomics, Origin, and Diversification of Anthozoans (Phylum Cnidaria). <i>Systematic Biology</i> , 2021, 70, 635-647.	2.7	74
11678	Horizontally acquired antibacterial genes associated with adaptive radiation of ladybird beetles. <i>BMC Biology</i> , 2021, 19, 7.	1.7	11
11679	<sc>DNA</sc> barcoding of the German green supralittoral zone indicates the distribution and phenotypic plasticity of <i>Blidingia</i> species and reveals <i>Blidingia cornuta</i> sp. nov.. <i>Taxon</i> , 2021, 70, 229-245.	0.4	7
11680	Ancient evolution of hepadnaviral paleoviruses and their impact on host genomes. <i>Virus Evolution</i> , 2021, 7, veab012.	2.2	8
11681	Chlorinated metabolites from <i>Streptomyces</i> sp. highlight the role of biosynthetic mosaics and superclusters in the evolution of chemical diversity. <i>Organic and Biomolecular Chemistry</i> , 2021, 19, 6147-6159.	1.5	8
11682	TYGS and LPSN:Âa database tandem for fast and reliable genome-based classification and nomenclature of prokaryotes. <i>Nucleic Acids Research</i> , 2022, 50, D801-D807.	6.5	728
11683	Comparative mitogenome phylogeography of two anteater genera (&t;i&t;Tamandua&t;i&t; and) Tj ETQq0 0 0 rgBT /Overlock 10 Tf traits. <i>Zoological Research</i> , 2021, 42, 525-547.	0.9	6
11684	The &t;i&t;Thermosynechococcus&t;i&t; Genus: Wide Environmental Distribution, but a Highly Conserved Genomic Core. <i>Microbes and Environments</i> , 2021, 36, n/a.	0.7	5
11685	The complete plastid genome of <i>Phoenix canariensis</i> Chabaud (Arecaceae) and phylogenetic analysis. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 140-142.	0.2	3
11686	Combined whole cell wall analysis and streamlined in silico carbohydrate-active enzyme discovery to improve biocatalytic conversion of agricultural crop residues. <i>Biotechnology for Biofuels</i> , 2021, 14, 16.	6.2	15
11687	Recurrent mutations promote widespread structural and functional divergence of MULE-derived genes in plants. <i>Nucleic Acids Research</i> , 2021, 49, 11765-11777.	6.5	13
11688	Metagenomic analysis of mother-infant gut microbiome reveals global distinct and shared microbial signatures. <i>Gut Microbes</i> , 2021, 13, 1-24.	4.3	18

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11690	A new genus and species for Chloanthaeae (Lamiaceae). Australian Systematic Botany, 2021, 34, 485.	0.3	1
11691	Fungicidal Activity of Volatile Organic Compounds Emitted by Burkholderia gladioli Strain BBB-01. Molecules, 2021, 26, 745.	1.7	16
11692	Morphology and Molecular Phylogeny of Four Trachelocercid Ciliates (Protozoa, Ciliophora,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 667 T Two New Species and a New Combination. Frontiers in Marine Science, 2021, 7, .	1.2	4
11693	Phylogenomics and biogeography of leptonetid spiders (Araneae Leptonetidae). Invertebrate Systematics, 2021, 35, 332-349.	0.5	15
11694	Evaluation of the taxonomic position of the genus Carinina (Nemertea:Palaeonemertea), with descriptions of two new species. Invertebrate Systematics, 2021, , .	0.5	3
11695	The genus Bilharziella vs. other bird schistosomes in snail hosts from one of the major recreational lakes in Poland. Knowledge and Management of Aquatic Ecosystems, 2021, , 12.	0.5	1
11696	Characterization of the prion protein gene in axis deer (Axis axis) and implications for susceptibility to chronic wasting disease. Prion, 2021, 15, 44-52.	0.9	2
11698	The complete chloroplast genome of <i>Syzygium acuminatissimum</i>. Mitochondrial DNA Part B: Resources, 2021, 6, 127-128.	0.2	1
11699	Contribution to the taxonomy of the genus <i>Lycodon</i> H. Boie in Fitzinger, 1827 (Reptilia:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 42 of <i>Dinodon septentrionale chapaense</i> Angel, Bourret, 1933. Zoological Research, 2021, 42, 62-86.	0.9	3
11700	Transcriptomic analysis of s-methoprene resistance in the lesser grain borer, Rhyzopertha dominica, and evaluation of piperonyl butoxide as a resistance breaker. BMC Genomics, 2021, 22, 65.	1.2	3
11702	The complete chloroplast genome of <i>Chenopodium acuminatum</i> Willd. (Amaranthaceae). Mitochondrial DNA Part B: Resources, 2021, 6, 174-175.	0.2	2
11703	The seasonal changes of the gut microbiome of the population living in traditional lifestyles are represented by characteristic species-level and functional-level SNP enrichment patterns. BMC Genomics, 2021, 22, 83.	1.2	4
11704	Taxonomic Evaluation of the Heyndrickxia (Basonym Bacillus) sporothermodurans Group (H.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 267 246.	1.6	2
11705	Complete chloroplast genome sequence and phylogenetic analysis of a wild species of abiu fruit, Pouteria caimito (Ruiz & Pavon.) Radlk. Mitochondrial DNA Part B: Resources, 2021, 6, 138-139.	0.2	1
11706	Ä#EÄžÄ°TLÄ° SUCUL HÄ°PERSALÄ°N HABÄ°TATLARDAKÄ° (TÄ°RKÄ°YE) PROKARYOTÄ°K TOPLULUKLARIN VE NANOHALOARKEAL SOYLARIN Ä#EÄžÄ°TLÄ°LÄ°ÄžÄ°NÄ°N YÄ°KSEK-VERÄ°MLÄ° DÄ°ZÄ°LEME VE KLONLAMA KULLANILARAK DEÄžERLENDÄ°RÄ°MESÄ°. Es Ä°niversitesi Bilim Ve Teknoloji Dergisi - C YaÄ°m Bilimleri Ve Biyoteknoloji, 2021, 10, 57-68.		
11708	Analysis of Rice Transcriptome Reveals the LncRNA/CircRNA Regulation in Tissue Development. Rice, 2021, 14, 14.	1.7	26
11709	Revisiting the phylogenetic predicament of the genus <i>Huia</i> (Amphibia: Ranidae) using molecular data and tadpole morphology. Zoological Journal of the Linnean Society, 2021, 193, 673-699.	1.0	5
11710	Type <sc>IV</sc> pili are widespread among nonâ€pathogenic Gramâ€positive gut bacteria with diverse carbohydrate utilization patterns. Environmental Microbiology, 2021, 23, 1527-1540.	1.8	3

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11711	Chemoreceptor Diversity in Apoid Wasps and Its Reduction during the Evolution of the Pollen-Collecting Lifestyle of Bees (Hymenoptera: Apoidea). <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	11
11712	Emergence and Transmission of Daptomycin and Vancomycin-Resistant Enterococci Between Patients and Hospital Rooms. <i>Clinical Infectious Diseases</i> , 2021, 73, 2306-2313.	2.9	12
11713	The genomic characterisation and comparison of <i>Bacillus cereus</i> strains isolated from indoor air. <i>Gut Pathogens</i> , 2021, 13, 6.	1.6	9
11715	Polymorphism of genetic ambigrams. <i>Virus Evolution</i> , 2021, 7, veab038.	2.2	5
11716	Identification and Characterization of Mycobacterial Species Using Whole-Genome Sequences. <i>Methods in Molecular Biology</i> , 2021, 2314, 399-457.	0.4	0
11717	Haplotype diversity in the mitochondrial genome of the Egyptian river buffalo (<i>Bubalus bubalis</i>). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 145-147.	0.2	3
11718	Fungal Wound Healing through Instantaneous Protoplasmic Gelation. <i>Current Biology</i> , 2021, 31, 271-282.e5.	1.8	7
11719	Evaluating species in Botryosphaerales. <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2021, , .	1.6	45
11720	The pineapple MADS-box gene family and the evolution of early monocot flower. <i>Scientific Reports</i> , 2021, 11, 849.	1.6	13
11721	Whole-Genome Assemblies of 16 <i>Burkholderia pseudomallei</i> Isolates from Rivers in Laos. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	3
11722	White pupae phenotype of tephritids is caused by parallel mutations of a MFS transporter. <i>Nature Communications</i> , 2021, 12, 491.	5.8	25
11723	Chromosome-level genome assembly of the Chinese longsnout catfish <i>Leiocassis longirostris</i>. <i>Zoological Research</i> , 2021, 42, 417-422.	0.9	14
11724	Reorganized Genomic Taxonomy of Francisellaceae Enables Design of Robust Environmental PCR Assays for Detection of <i>Francisella tularensis</i> . <i>Microorganisms</i> , 2021, 9, 146.	1.6	19
11725	Fungal Planet description sheets: 1182â€“1283. <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2021, , .	1.6	40
11726	<i>Tessaracoccus coleopterorum</i> sp. nov., isolated from the intestine of the dark diving beetle, <i>Hydrophilus acuminatus</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	7
11727	<i>Pseudoceanicola algae</i> sp. nov., isolated from the marine macroalga <i>Fucus spiralis</i> , shows genomic and physiological adaptations for an algae-associated lifestyle. <i>Systematic and Applied Microbiology</i> , 2021, 44, 126166.	1.2	18
11728	Taxonomic revision of <i>Amolops</i> <i>chunganensis</i> (Pope, 1929) (Amphibia): Tj ETQq0 0 0 rgBT /Overlock <i>Amolops monticola</i> group and assignment of species groups of the genus <i>Amolops</i>. <i>Zoological Research</i> , 2021, 42, 574-591.	0.9	9
11729	Visualizing the superfamily of metallo- β -lactamases through sequence similarity network neighborhood connectivity analysis. <i>Heliyon</i> , 2021, 7, e05867.	1.4	18

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11730	Leuconostoc falkenbergense sp. nov., isolated from a lactic culture, fermentating string beans and traditional yogurt. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	13
11732	Chromosome-level genome assembly of Ophiorrhiza pumila reveals the evolution of camptothecin biosynthesis. Nature Communications, 2021, 12, 405.	5.8	77
11733	Historical biogeography of a neglected family of armoured harvestmen (Opiliones: Laniatores: Calceptidae) with the first record and a new genus for tropical Mesoamerica. Invertebrate Systematics, 2021, 35, 493-513.	0.5	2
11734	Heme-binding enables allosteric modulation in an ancient TIM-barrel glycosidase. Nature Communications, 2021, 12, 380.	5.8	20
11735	Gene Duplications Are At Least 50 Times Less Frequent than Gene Transfers in Prokaryotic Genomes. Genome Biology and Evolution, 2021, 13, .	1.1	22
11736	The genus <i>Jorunna</i> (Nudibranchia: Discodorididae) in Europe: a new species and a possible case of incipient speciation. Journal of Molluscan Studies, 2021, 87, .	0.4	6
11737	Molecular data support the Atelurinae and Coletiniinae as sister groups: a second Lepidospora (Brinckina) species (Zygentoma: Nicoletiidae: Coletiniinae) from the Pilbara. Records of the Western Australian Museum, 2021, 36, 1.	0.8	0
11738	Phylogenetic Methods for Genome-Wide Association Studies in Bacteria. Methods in Molecular Biology, 2021, 2242, 205-220.	0.4	5
11739	Unexpected diversity in the sponge-associated shrimps. Invertebrate Systematics, 2021, 35, 361-393.	0.5	1
11740	Phylogeny of Viruses. , 2021, , 116-123.		0
11741	Ancient balancing selection maintains incompatible versions of the galactose pathway in yeast. Science, 2021, 371, 415-419.	6.0	27
11742	The Scientific View of the Origin of Life. , 2021, , 11-33.		0
11743	Three independent evolutionary events of sequestrate Lactifluus species in Australasia. Fungal Systematics and Evolution, 2021, 8, 9-25.	0.9	0
11744	Markers for genetic change. Heliyon, 2021, 7, e05583.	1.4	5
11746	The complete plastid genome of Cotinus coggygia and phylogenetic analysis of the Anacardiaceae. Genetics and Molecular Biology, 2021, 44, e20210006.	0.6	1
11747	Comparative mitochondrial genome analysis reveals intron dynamics and gene rearrangements in two Trametes species. Scientific Reports, 2021, 11, 2569.	1.6	13
11749	A new cryptic species of yellow-eared bat <i>Vampyressa melissa</i> species complex (Chiroptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.6	9
11750	Inferring the Phylogenetic Positions of Two Fig Wasp Subfamilies of Epichrysomallinae and Sycophaginae Using Transcriptomes and Mitochondrial Data. Life, 2021, 11, 40.	1.1	4

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11751	Variable Release of Lipoteichoic Acid From <i>Staphylococcus aureus</i> Bloodstream Isolates Relates to Distinct Clinical Phenotypes, Strain Background, and Antibiotic Exposure. <i>Frontiers in Microbiology</i> , 2020, 11, 609280.	1.5	1
11752	Demographic History and Genomic Response to Environmental Changes in a Rapid Radiation of Wild Rats. <i>Molecular Biology and Evolution</i> , 2021, 38, 1905-1923.	3.5	7
11753	Whole genomic comparative analysis of <i>Streptococcus pneumoniae</i> serotype 1 isolates causing invasive and non-invasive infections among children under 5 years in Casablanca, Morocco. <i>BMC Genomics</i> , 2021, 22, 39.	1.2	2
11754	Determining the position of <i>Diomocoris</i> , <i>Micromimetes</i> and <i>Taylorilygus</i> in the <i>Lygus</i> -complex based on molecular data and first records of <i>Diomocoris</i> and <i>Micromimetes</i> from Australia, including four new species (Insecta : Hemiptera : Miridae : Mirinae). <i>Invertebrate Systematics</i> , 2021, , .	0.5	1
11755	Genomic Characterization of Multidrug-Resistant <i>Escherichia coli</i> BH100 Sub-strains. <i>Frontiers in Microbiology</i> , 2020, 11, 549254.	1.5	5
11756	Genome Assembly and Transcriptome Analysis of the Fungus <i>Coniella diplodiella</i> During Infection on Grapevine (<i>Vitis vinifera</i> L.). <i>Frontiers in Microbiology</i> , 2020, 11, 599150.	1.5	7
11757	Taxonomic status of nominal species of the anchovy genus <i>Stolephorus</i> previously regarded as synonyms of <i>Stolephorus commersonii</i> Lacepède 1803 and <i>Stolephorus indicus</i> (van Hasselt 1823), and descriptions of three new species (Clupeiformes: Engraulidae). <i>Ichthyological Research</i> , 2021, 68, 327.	0.5	11
11758	Local adaptation in populations of <i>Mycobacterium tuberculosis</i> endemic to the Indian Ocean Rim. <i>F1000Research</i> , 2021, 10, 60.	0.8	13
11759	Pathogenomic analyses of <i>Mycobacterium microti</i> , an ESX-1-deleted member of the <i>Mycobacterium tuberculosis</i> complex causing disease in various hosts. <i>Microbial Genomics</i> , 2021, 7, .	1.0	11
11760	Measurable Genomic Changes in <i>Mycobacterium avium</i> subsp. <i>hominissuis</i> after Long-Term Adaptation in <i>Acanthamoeba lenticulata</i> and Reduced Persistence in Macrophages. <i>Journal of Bacteriology</i> , 2021, 203, .	1.0	5
11761	Dengue Virus Serotype 2 Intra-host Diversity in Patients with Different Clinical Outcomes. <i>Viruses</i> , 2021, 13, 349.	1.5	11
11762	Global Phylogeny and Taxonomy of the Wood-Decaying Fungal Genus <i>Phlebiopsis</i> (Polyporales.) Tj ETQq1 1 0.784314 rgBT /Qyerlock 11	1.5	11
11763	Ash Trees (<i>Fraxinus</i> spp.) in Urban Greenery as Possible Invasion Gates of Non-Native <i>Phyllactinia</i> Species. <i>Forests</i> , 2021, 12, 183.	0.9	1
11764	Pollen <i>Streptomyces</i> Produce Antibiotic That Inhibits the Honey Bee Pathogen <i>Paenibacillus</i> larvae. <i>Frontiers in Microbiology</i> , 2021, 12, 632637.	1.5	15
11765	Phylogenetic relations and mitogenome-wide similarity metrics reveal monophyly of <i>Penaeus</i> sensu lato. <i>Ecology and Evolution</i> , 2021, 11, 2040-2049.	0.8	6
11769	Ecological features of <i>Telmatobius chusmisensis</i> (Anura: Telmatobiidae), a poorly known species from northern Chile. <i>South American Journal of Herpetology</i> , 2021, 20, .	0.5	0
11772	Chromosome-Level Genome Assembly and Annotation of a Sciaenid Fish, <i>Argyrosomus japonicus</i> . <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	6
11773	Systematic errors in orthology inference and their effects on evolutionary analyses. <i>IScience</i> , 2021, 24, 102110.	1.9	27

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11774	Characterization of Two <i>Zygnema</i> Strains (<i>Zygnema circumcarinatum</i> SAG 698-1a and SAG 698-1b) and a Rapid Method to Estimate Nuclear Genome Size of Zygnematophycean Green Algae. <i>Frontiers in Plant Science</i> , 2021, 12, 610381.	1.7	10
11775	<i>Ophiocordyceps salganeicola</i> , a parasite of social cockroaches in Japan and insights into the evolution of other closely-related Blattodea-associated lineages. <i>IMA Fungus</i> , 2021, 12, 3.	1.7	8
11776	Biogeography and genome size evolution of the oldest extant vascular plant genus, <i>Equisetum</i> (Equisetaceae). <i>Annals of Botany</i> , 2021, 127, 681-695.	1.4	9
11777	Gastronautidae Deroux, 1994 and Trithigmostoma Jankowski, 1967: Evolutionary Links Among Cyrtophorian Ciliates (Protista, Ciliophora, and Phyllopharyngea). <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	3
11778	<i>Grappleria corona</i> gen. et sp. nov. (Platyhelminthes: Rhabdocoela: Jenseniidae fam. nov.) and an updated molecular phylogeny of <i>dalyelliid</i> ™ and temnocephalid microturbellarians. <i>Systematics and Biodiversity</i> , 2021, 19, 261-272.	0.5	4
11779	Comparative plastome genomics and phylogenetic analyses of Liliaceae. <i>Botanical Journal of the Linnean Society</i> , 2021, 196, 279-293.	0.8	19
11782	Parallel Genomic Changes Drive Repeated Evolution of Placentas in Live-Bearing Fish. <i>Molecular Biology and Evolution</i> , 2021, 38, 2627-2638.	3.5	11
11783	Essential Amino Acid Enrichment and Positive Selection Highlight Endosymbiont's Role in a Global Virus-Vectoring Pest. <i>MSystems</i> , 2021, 6, .	1.7	3
11784	Orange is the new white: taxonomic revision of <i>Tritonia</i> species (Gastropoda: Nudibranchia) from the Weddell Sea and Bouvet Island. <i>Polar Biology</i> , 2021, 44, 559-573.	0.5	3
11785	Endophytic <i>Diaporthe</i> Associated With <i>Citrus grandis</i> cv. <i>Tomentosa</i> in China. <i>Frontiers in Microbiology</i> , 2020, 11, 609387.	1.5	24
11786	Complete plastid genome sequence of <i>Oberonioides microtatantha</i> (Schltr.) Szlach. (Orchidaceae), an endemic herb in China. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 703-704.	0.2	0
11787	The complete chloroplast genome of <i>Lemmaphyllum intermedium</i> , a valuable medicinal fern. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 423-424.	0.2	1
11788	FASTRAL: improving scalability of phylogenomic analysis. <i>Bioinformatics</i> , 2021, 37, 2317-2324.	1.8	13
11790	Impact of Pleistocene Eustatic Fluctuations on Evolutionary Dynamics in Southeast Asian Biodiversity Hotspots. <i>Systematic Biology</i> , 2021, 70, 940-960.	2.7	25
11792	Gene family amplification facilitates adaptation in freshwater unionid bivalve <i>Megaloniais nervosa</i> . <i>Molecular Ecology</i> , 2021, 30, 1155-1173.	2.0	19
11793	Development of qPCR Detection Assay for Potato Pathogen <i>Pectobacterium atrosepticum</i> Based on a Unique Target Sequence. <i>Plants</i> , 2021, 10, 355.	1.6	4
11794	Evolutionary analyses of the major variant surface antigen-encoding genes reveal population structure of <i>Plasmodium falciparum</i> within and between continents. <i>PLoS Genetics</i> , 2021, 17, e1009269.	1.5	20
11795	Comparative Genomics Analysis Demonstrated a Link Between Staphylococci Isolated From Different Sources: A Possible Public Health Risk. <i>Frontiers in Microbiology</i> , 2021, 12, 576696.	1.5	4

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11796	Comparative Mitogenomic Analysis Reveals Dynamics of Intron Within and Between <i>Tricholoma</i> Species and Phylogeny of Basidiomycota. <i>Frontiers in Genetics</i> , 2021, 12, 534871.	1.1	13
11797	Genomic data from the Brazilian sibilator frog reveal contrasting pleistocene dynamics and regionalism in two South American dry biomes. <i>Journal of Biogeography</i> , 2021, 48, 1112-1123.	1.4	13
11798	Diel transcriptional oscillations of light-sensitive regulatory elements in open-ocean eukaryotic plankton communities. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	24
11799	Mitochondrial Coevolution, but not Nuclear Compensation, Drives Evolution of OXPHOS Complexes in Bivalves. <i>Molecular Biology and Evolution</i> , 2021, 38, 2597-2614.	3.5	21
11800	Panorama of intron dynamics and gene rearrangements in the phylum Basidiomycota as revealed by the complete mitochondrial genome of <i>Turbinellus floccosus</i> . <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 2017-2032.	1.7	20
11803	Beyond <i>Drosophila</i> : resolving the rapid radiation of schizophoran flies with phylotranscriptomics. <i>BMC Biology</i> , 2021, 19, 23.	1.7	22
11804	<i>Aethionema arabicum</i> genome annotation using PacBio full-length transcripts provides a valuable resource for seed dormancy and Brassicaceae evolution research. <i>Plant Journal</i> , 2021, 106, 275-293.	2.8	20
11805	Roles of host small RNAs in the evolution and host tropism of coronaviruses. <i>Briefings in Bioinformatics</i> , 2021, 22, 1096-1105.	3.2	2
11806	Quantification and evolution of mitochondrial genome rearrangement in Amphibians. <i>Bmc Ecology and Evolution</i> , 2021, 21, 19.	0.7	6
11810	Diversity of Root Nodule-Associated Bacteria of Diverse Legumes Along an Elevation Gradient in the Kunlun Mountains, China. <i>Frontiers in Microbiology</i> , 2021, 12, 633141.	1.5	9
11812	<i>Legionella</i> spp. All Ears? The Broad Occurrence of Quorum Sensing Elements outside <i>Legionella pneumophila</i> . <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	6
11813	Structure and functional properties of the cold-adapted catalase from <i>Acinetobacter</i> sp. Ver3 native to the Atacama plateau in northern Argentina. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 369-379.	1.1	4
11816	Genome announcement of <i>Steinernema khuongi</i> and its associated symbiont from Florida. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	6
11817	Hierarchical spatial sampling reveals factors influencing arbuscular mycorrhizal fungus diversity in Côte d'Ivoire cocoa plantations. <i>Mycorrhiza</i> , 2021, 31, 289-300.	1.3	7
11818	Two new species and one new record of <i>Xenosporium</i> with ellipsoidal or ovoid conidia from Taiwan. <i>Mycologia</i> , 2021, 113, 434-449.	0.8	4
11819	Broad and narrow host ranges in resolved species of <i>Cintractia limitata</i> s. lat. (Anthracoideaceae.) <i>Tj ETQq1 1 0.784314 rgBT 2 Overloc</i>	0.5	2
11820	Genome-Scale Phylogenetic and Population Genetic Studies Provide Insight Into Introgression and Adaptive Evolution of <i>Takifugu</i> Species in East Asia. <i>Frontiers in Genetics</i> , 2021, 12, 625600.	1.1	5
11821	Comparative genomics of <i>Staphylococcus epidermidis</i> from prosthetic-joint infections and nares highlights genetic traits associated with antimicrobial resistance, not virulence. <i>Microbial Genomics</i> , 2021, 7, .	1.0	19

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11822	Expansion and Accelerated Evolution of 9-Exon Odorant Receptors in <i>Polistes</i> Paper Wasps. <i>Molecular Biology and Evolution</i> , 2021, 38, 3832-3846.	3.5	22
11823	Genome-wide analysis of pseudogenes reveals HBBP1's human-specific essentiality in erythropoiesis and implication in β -thalassemia. <i>Developmental Cell</i> , 2021, 56, 478-493.e11.	3.1	22
11824	Phylogenomic analysis of <i>Anabaenopsis elenkinii</i> (Nostocales, Cyanobacteria). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	3
11825	An integrated approach to re-evaluate the validity of the family Leptobathynellidae (Crustacea: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	1.0	5
11826	Genome of <i>Superficieibacter maynardsmithii</i> , a novel, antibiotic susceptible representative of Enterobacteriaceae. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	3
11827	Diversity of the green macroalgal genus <i>Ulva</i> (Ulvothyxales, Chlorophyta) from the east and gulf coast of the United States based on molecular data. <i>Journal of Phycology</i> , 2021, 57, 551-568.	1.0	18
11828	Progressing diversification and biogeography of the mesopelagic <i>Nematoscelis</i> (Crustacea: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.2	10
11829	<i>Kulikovia alborostrata</i> and <i>Kulikovia fulva</i> comb. nov. (Nemertea: Heteronemertea) are Sister Species with Prezygotic Isolating Barriers. <i>Zoological Science</i> , 2021, 38, 193-202.	0.3	3
11830	<i>Aeromicrobium terrae</i> sp. nov., isolated from a maize field. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	7
11831	<i>Kibdelosporangium persicum</i> sp. nov., a new member of the Actinomycetes from a hot desert in Iran. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	9
11832	<i>Teredinibacter haidensis</i> sp. nov., <i>Teredinibacter purpureus</i> sp. nov. and <i>Teredinibacter frankisiae</i> sp. nov., marine, cellulolytic endosymbiotic bacteria isolated from the gills of the wood-boring mollusc <i>Bankia setacea</i> (Bivalvia: Teredinidae) and emended description of the genus <i>Teredinibacter</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	20
11833	Identifying Potentially Beneficial Genetic Mutations Associated with Monophyletic Selective Sweep and a Proof-of-Concept Study with Viral Genetic Data. <i>MSystems</i> , 2021, 6, .	1.7	2
11834	Bridgehead effect and multiple introductions shape the global invasion history of a termite. <i>Communications Biology</i> , 2021, 4, 196.	2.0	42
11835	<i>Saccharomycomorpha psychra</i> n. g., n. sp., a Novel Member of Glissmonadida (Cercozoa) Isolated from Arctic and Antarctica. <i>Journal of Eukaryotic Microbiology</i> , 2021, 68, e12840.	0.8	2
11836	The Genomes of Two Billfishes Provide Insights into the Evolution of Endothermy in Teleosts. <i>Molecular Biology and Evolution</i> , 2021, 38, 2413-2427.	3.5	15
11837	Glycine acylation and trafficking of a new class of bacterial lipoprotein by a composite secretion system. <i>ELife</i> , 2021, 10, .	2.8	7
11838	The complete chloroplast genome of <i>Geum macrophyllum</i> (Rosaceae: Colurieae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 297-298.	0.2	3
11839	The complete plastid genome sequence of <i>Quercus acuta</i> (Fagaceae), an evergreen broad-leaved oak endemic to East Asia. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 320-322.	0.2	2

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11840	Characteristic and phylogenetic analyses of chloroplast genome for <i>Ephedra monosperma</i> (Ephedraceae), an important medicinal species. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 483-484.	0.2	0
11841	The complete chloroplast genome and phylogenetic analysis of <i>Nephelium lappaceum</i> (rambutan). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 485-487.	0.2	0
11842	The complete chloroplast genome sequence of medicinal plant: <i>Dianthus chinensis</i> (Caryophyllaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 327-328.	0.2	1
11843	The complete chloroplast genome of <i>Passiflora caerulea</i> , a tropical fruit with a distinctive aroma. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 488-490.	0.2	4
11844	Comparative genomics of a novel clade shed light on the evolution of the genus <i>Erysipelothrix</i> and characterise an emerging species. <i>Scientific Reports</i> , 2021, 11, 3383.	1.6	10
11845	Identification of drug resistance mutations among <i>Mycobacterium bovis</i> lineages in the Americas. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009145.	1.3	7
11846	Crop type exerts greater influence upon rhizosphere phosphohydrolase gene abundance and phylogenetic diversity than phosphorus fertilization. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	8
11847	Size Variation of the Nonrecombining Region on the Mating-Type Chromosomes in the Fungal <i>Podospira anserina</i> Species Complex. <i>Molecular Biology and Evolution</i> , 2021, 38, 2475-2492.	3.5	13
11849	Ancient and recent introgression shape the evolutionary history of pollinator adaptation and speciation in a model monkeyflower radiation (<i>Mimulus</i> section <i>Erythranthe</i>). <i>PLoS Genetics</i> , 2021, 17, e1009095.	1.5	56
11850	SARS-CoV-2 genomic diversity and the implications for qRT-PCR diagnostics and transmission. <i>Genome Research</i> , 2021, 31, 635-644.	2.4	39
11851	Complete minicircle genome of <i>Leptomonas pyrrocoris</i> reveals sources of its non-canonical mitochondrial RNA editing events. <i>Nucleic Acids Research</i> , 2021, 49, 3354-3370.	6.5	9
11852	Xylariales (Sordariomycetes, Ascomycota) of the Boston Harbor Islands. <i>Northeastern Naturalist</i> , 2021, 25, .	0.1	2
11853	National Prevalence of <i>Salmonella enterica</i> Serotype Kentucky ST198 with High-Level Resistance to Ciprofloxacin and Extended-Spectrum Cephalosporins in China, 2013 to 2017. <i>MSystems</i> , 2021, 6, .	1.7	19
11856	Systematic positions and taxonomy of two new ciliates found in China: <i>Euplotes tuffraui</i> sp. nov. and <i>E. shii</i> sp. nov. (Alveolata, Ciliophora, Euplotida). <i>Systematics and Biodiversity</i> , 2021, 19, 359-374.	0.5	6
11857	Two new species of Chytriomycetaceae: Morphological, phylogenetic, and ultrastructural characterization. <i>Mycologia</i> , 2021, 113, 312-325.	0.8	1
11858	Methodological synthesis of Bayesian phylodynamics, HIV-TRACE, and GEE: HIV-1 transmission epidemiology in a racially/ethnically diverse Southern U.S. context. <i>Scientific Reports</i> , 2021, 11, 3325.	1.6	8
11859	Chloroplast genome sequence of the wild <i>Ziziphus jujuba</i> Mill. var <i>spinosa</i> from North China. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 666-667.	0.2	3
11860	The complete chloroplast genome sequence of <i>Ficus beipeiensis</i> (Moraceae), an endemic and endangered plant in China. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 604-605.	0.2	1

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11861	The complete plastid genome sequence of <i>Dracaena fragrans</i> (L.) Ker Gawl. (Asparagaceae). Mitochondrial DNA Part B: Resources, 2021, 6, 653-655.	0.2	0
11862	Analysis of complete mitochondrial genome sequence of bar-tailed Treecreeper <i>certhia himalayana</i> (psittaciformes: Certhiidae). Mitochondrial DNA Part B: Resources, 2021, 6, 578-580.	0.2	0
11863	Complete chloroplast genome sequence and phylogenetic analysis of <i>Populus deltoides</i> Caihong. Mitochondrial DNA Part B: Resources, 2021, 6, 389-390.	0.2	2
11864	Complete mitochondrial genome of a cave dwelling <i>Desmopachria</i> (Insecta: Coleoptera: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	0.2	1
11865	Complete mitochondrial genome of <i>Mollitrichosiphum tenuicorpus</i> (Okajima, 1908) (Hemiptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.2	1
11866	The complete chloroplast genome of <i>Bupleurum marginatum</i> var. <i>stenophyllum</i> (H. Wolff) Shan & Yin Li (Apiaceae), a new substitution for Chinese medicinal material, <i>Bupleuri Radix</i> (Chai hu). Mitochondrial DNA Part B: Resources, 2021, 6, 441-443.	0.2	3
11867	The complete chloroplast genome of an endangered species <i>Apostasia ramifera</i> (Orchidaceae). Mitochondrial DNA Part B: Resources, 2021, 6, 470-471.	0.2	1
11868	A New Record of <i>Oxytricha granulifera granulifera</i> Foissner and Adam, 1983 (Protozoa, Ciliophora,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 Frontiers in Marine Science, 2021, 8, .	1.2	4
11869	Phylogenetic analysis of the distribution of deadly amatoxins among the little brown mushrooms of the genus <i>Galerina</i> . PLoS ONE, 2021, 16, e0246575.	1.1	7
11870	Complex Historical Biogeography of the Eastern Japanese Skink, <i>Plestiodon finitimus</i> (Scincidae,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 Science, 2021, 38, 148-161.	0.3	0
11871	Morphological and phylogenetic analyses reveal three new species of <i>Diaporthe</i> from Yunnan, China. MycoKeys, 2021, 78, 49-77.	0.8	17
11874	Developmental hourglass and heterochronic shifts in fin and limb development. ELife, 2021, 10, .	2.8	10
11875	Analysis of the Global Population Structure of <i>Paenibacillus</i> larvae and Outbreak Investigation of American Foulbrood Using a Stable wgMLST Scheme. Frontiers in Veterinary Science, 2021, 8, 582677.	0.9	10
11876	Approaches for characterizing and tracking hospital-associated multidrug-resistant bacteria. Cellular and Molecular Life Sciences, 2021, 78, 2585-2606.	2.4	21
11877	Extremely low nucleotide diversity among thirty-six new chloroplast genome sequences from <i>Aldama</i> (Heliantheae, Asteraceae) and comparative chloroplast genomics analyses with closely related genera. PeerJ, 2021, 9, e10886.	0.9	15
11878	Integrating morphology and DNA barcoding to assess cetacean diversity in Brazil. Mammal Research, 2021, 66, 349-369.	0.6	7
11879	Patterns of genetic divergence and demographic history shed light on islandâ€mainland population dynamics and melanic plumage evolution in the whiteâ€winged Fairywren*. Evolution; International Journal of Organic Evolution, 2021, 75, 1348-1360.	1.1	8
11880	Two new stygobiotic species of <i>Horatia</i> Bourguignat, 1887 (Hydrobiidae) from Croatia. Subterranean Biology, 0, 37, 89-104.	5.0	4

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11882	Eucalyptus scab and shoot malformation: A new and serious foliar disease of <i>Eucalyptus</i> caused by <i>Elsinoe necatrix</i> sp. nov.. <i>Plant Pathology</i> , 2021, 70, 1230-1242.	1.2	11
11883	Effects of Seasonal Anoxia on the Microbial Community Structure in Demosponges in a Marine Lake in Lough Hyne, Ireland. <i>MSphere</i> , 2021, 6, .	1.3	7
11884	<i>Hildenbrandia</i> (Hildenbrandiales, Florideophyceae) from Japan and taxonomic lumping of <i>H. jigongshanensis</i> and <i>H. japananensis</i> . <i>Phycological Research</i> , 2021, 69, 166-170.	0.8	4
11885	PPIT: an R package for inferring microbial taxonomy from <i>nifH</i> sequences. <i>Bioinformatics</i> , 2021, 37, 2289-2298.	1.8	13
11886	<i>Gobius xoriguer</i> , a new offshore Mediterranean goby (Gobiidae), and phylogenetic relationships within the genus <i>Gobius</i> . <i>Ichthyological Research</i> , 2021, 68, 445-459.	0.5	10
11887	Integrating Sequence Capture and Restriction Site-Associated DNA Sequencing to Resolve Recent Radiations of Pelagic Seabirds. <i>Systematic Biology</i> , 2021, 70, 976-996.	2.7	12
11888	By Animal, Water, or Wind: Can Dispersal Mode Predict Genetic Connectivity in Riverine Plant Species?. <i>Frontiers in Plant Science</i> , 2021, 12, 626405.	1.7	16
11889	Tracking the Emergence of Azithromycin Resistance in Multiple Genotypes of Typhoidal <i>Salmonella</i> . <i>MBio</i> , 2021, 12, .	1.8	39
11890	Biorefinery Platform for <i>Spathaspora passalidarum</i> NRRL Y-27907 in the Production of Ethanol, Xylitol, and Single Cell Protein from Sugarcane Bagasse. <i>Bioenergy Research</i> , 2022, 15, 1169-1181.	2.2	21
11891	Genome-scale phylogenetic analyses confirm <i>Olpidium</i> as the closest living zoosporic fungus to the non-flagellated, terrestrial fungi. <i>Scientific Reports</i> , 2021, 11, 3217.	1.6	24
11892	An epidemiological surveillance of hand foot and mouth disease in paediatric patients and in community: A Singapore retrospective cohort study, 2013–2018. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0008885.	1.3	17
11893	Gulf of Mexico blue hole harbors high levels of novel microbial lineages. <i>ISME Journal</i> , 2021, 15, 2206-2232.	4.4	13
11894	The Evolution of <i>euAPETALA2</i> Genes in Vascular Plants: From Plesiomorphic Roles in Sporangia to Acquired Functions in Ovules and Fruits. <i>Molecular Biology and Evolution</i> , 2021, 38, 2319-2336.	3.5	13
11895	Five Novel Freshwater Ascomycetes Indicate High Undiscovered Diversity in Lotic Habitats in Thailand. <i>Journal of Fungi</i> (Basel, Switzerland), 2021, 7, 117.	1.5	18
11896	Decreased coevolutionary potential and increased symbiont fecundity during the biological invasion of a legume–rhizobium mutualism. <i>Evolution; International Journal of Organic Evolution</i> , 2021, 75, 731-747.	1.1	9
11897	A comprehensive and high-quality collection of <i>Escherichia coli</i> genomes and their genes. <i>Microbial Genomics</i> , 2021, 7, .	1.0	38
11898	Continental-Scale Gene Flow Prevents Allopatric Divergence of Pelagic Freshwater Bacteria. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	50
11899	Simple sequence repeats drive genome plasticity and promote adaptive evolution in penaeid shrimp. <i>Communications Biology</i> , 2021, 4, 186.	2.0	37

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11900	<i>Brassica carinata</i> genome characterization clarifies Uâ€™s triangle model of evolution and polyploidy in <i>Brassica</i>. <i>Plant Physiology</i> , 2021, 186, 388-406.	2.3	75
11901	Host apoplastic cysteine protease activity is suppressed during the mutualistic association of <i>Lolium perenne</i> and <i>Epichloa festucae</i>. <i>Journal of Experimental Botany</i> , 2021, 72, 3410-3426.	2.4	6
11902	Association of T2/S-RNase With Self-Incompatibility of Japanese Citrus Accessions Examined by Transcriptomic, Phylogenetic, and Genetic Approaches. <i>Frontiers in Plant Science</i> , 2021, 12, 638321.	1.7	10
11903	Phylogenetic analyses of Macaronesian turf-forming species reveal cryptic diversity and resolve <i>Stichothamnion</i> in the <i>Vertebrata</i> clade (Rhodomelaceae, Rhodophyta). <i>European Journal of Phycology</i> , 2021, 56, 444-454.	0.9	13
11904	Delimitation and phylogeny of <i>Dictyochaeta</i>, and introduction of <i>Achrochaeta</i> and <i>Tubulicolla</i>, genera nova. <i>Mycologia</i> , 2021, 113, 390-433.	0.8	13
11905	A drought-driven model for the evolution of obligate apomixis in ferns: evidence from pellaids (Pteridaceae). <i>American Journal of Botany</i> , 2021, 108, 263-283.	0.8	13
11906	Pathogenic Determinants of the Mycobacterium kansasii Complex: An Unsuspected Role for Distributive Conjugal Transfer. <i>Microorganisms</i> , 2021, 9, 348.	1.6	5
11908	The late pleistocene cave bear fauna of the Torneer BÃrenhÃhle in the northern alps (Salzburg.) Tj ETQq1 1 0.784314 rgBT 0 Overlooked	0.7	0
11909	Integrating coalescent-based species delimitation with ecological niche modeling delimited two species within the <i>Stewartia sinensis</i> complex (Theaceae). <i>Journal of Systematics and Evolution</i> , 2022, 60, 1037-1048.	1.6	9
11910	Performance comparison of two reduced-representation based genome-wide marker-discovery strategies in a multi-taxon phylogeographic framework. <i>Scientific Reports</i> , 2021, 11, 3978.	1.6	7
11911	Evolutionary relationships, biogeography and morphological characters of Glinus (Molluginaceae), with special emphasis on the genus composition in Sub-Saharan Africa. <i>PhytoKeys</i> , 2021, 173, 1-92.	0.4	2
11912	Cryptic speciation in the <i>Marshallora nigrocincta</i>-species complex (Gastropoda, Triphoridae) from the Western Atlantic. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2021, 59, 819-838.	0.6	2
11916	Genomic characterization and probiotic potential of <i>Lactobacillus casei</i> IDCC 3451 isolated from infant faeces. <i>Letters in Applied Microbiology</i> , 2021, 72, 578-588.	1.0	7
11917	Diet Diversity in Carnivorous Terebrid Snails Is Tied to the Presence and Absence of a Venom Gland. <i>Toxins</i> , 2021, 13, 108.	1.5	2
11918	Extrinsically reinforced hybrid speciation within Holarctic ermine (<i>Mustela</i> spp.) produces an insular endemic. <i>Diversity and Distributions</i> , 2021, 27, 747-762.	1.9	8
11919	Comprehensive genomic analysis of Bacillus subtilis 9407 reveals its biocontrol potential against bacterial fruit blotch. <i>Phytopathology Research</i> , 2021, 3, .	0.9	18
11921	The taxonomic status of Myotis nesopolus larensis (Chiroptera, Vespertilionidae) and new insights on the diversity of Caribbean Myotis. <i>ZooKeys</i> , 2021, 1015, 145-167.	0.5	8
11922	Phylogeny of Salmonella enterica subspecies arizonae by whole-genome sequencing reveals high incidence of polyphyly and low phase 1 H antigen variability. <i>Microbial Genomics</i> , 2021, 7, .	1.0	3

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11923	First report of <i>Septoria steviae</i> causing stevia leaf spot in Thailand. <i>Journal of Phytopathology</i> , 2021, 169, 260-268.	0.5	3
11924	Epidemiological analysis of pneumococcal strains isolated at Yangon Children's Hospital in Myanmar via whole-genome sequencing-based methods. <i>Microbial Genomics</i> , 2021, 7, .	1.0	2
11926	Fossil palm reading: using fruits to reveal the deep roots of palm diversity. <i>American Journal of Botany</i> , 2021, 108, 472-494.	0.8	14
11927	Unique niche-specific adaptation of fructophilic lactic acid bacteria and proposal of three <i>Apilactobacillus</i> species as novel members of the group. <i>BMC Microbiology</i> , 2021, 21, 41.	1.3	19
11929	Molecular systematics and biogeography of an Australian soil-dwelling cockroach with polymorphic males, <i>Geoscapheus dilatatus</i> (Blattodea: Blaberidae). <i>Austral Entomology</i> , 2021, 60, 317-329.	0.8	0
11930	High-Resolution Typing of <i>Staphylococcus epidermidis</i> Based on Core Genome Multilocus Sequence Typing To Investigate the Hospital Spread of Multidrug-Resistant Clones. <i>Journal of Clinical Microbiology</i> , 2021, 59, .	1.8	4
11931	Comparative Phylogeography of <i>Veronica spicata</i> and <i>V. longifolia</i> (Plantaginaceae) Across Europe: Integrating Hybridization and Polyploidy in Phylogeography. <i>Frontiers in Plant Science</i> , 2020, 11, 588354.	1.7	7
11932	The <i>Pharus latifolius</i> genome bridges the gap of early grass evolution. <i>Plant Cell</i> , 2021, 33, 846-864.	3.1	32
11933	Assessing the sensitivity of divergence time estimates to locus sampling, calibration points, and model priors in a RAD-seq phylogeny of <i>Carex</i> section <i>Schoenoxiphium</i> . <i>Journal of Systematics and Evolution</i> , 2021, 59, 687-697.	1.6	12
11934	Applications of Machine Learning in Human Microbiome Studies: A Review on Feature Selection, Biomarker Identification, Disease Prediction and Treatment. <i>Frontiers in Microbiology</i> , 2021, 12, 634511.	1.5	157
11935	The complete chloroplast genome of <i>Lonicera hypoglauca</i> Miq (Caprifoliaceae: Dipsacales) from Guangxi, China. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 450-451.	0.2	4
11936	The complete chloroplast genome of <i>Torreya parvifolia</i> , a species with extremely small population in China. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 387-388.	0.2	1
11937	Characterization of the complete mitochondrial genome of <i>Cottiusculus nihonkaiensis</i> (Scorpaeniformes, Cottidae) and phylogenetic studies of Scorpaeniformes. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 358-360.	0.2	1
11938	The complete chloroplast genome sequence of <i>Potentilla tanacetifolia</i> Willd. ex Schldl.. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 478-479.	0.2	1
11939	The complete chloroplast genome of a distylous-homostylous species, <i>Primula homogama</i> (Primulaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 393-394.	0.2	2
11940	Characterization of the complete chloroplast genome of <i>Bupleurum hamiltonii</i> N. P. Balakr. (Apiaceae) and its phylogenetic implications. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 447-449.	0.2	1
11941	Complete chloroplast genome sequences of two <i>Alloteropsis</i> species (Poaceae) from China. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 365-367.	0.2	0
11942	Evolution at two time frames: ancient structural variants involved in post-glacial divergence of the European plaice (<i>Pleuronectes platessa</i>). <i>Heredity</i> , 2021, 126, 668-683.	1.2	15

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11943	Microbiota restoration reduces antibiotic-resistant bacteria gut colonization in patients with recurrent <i>Clostridioides difficile</i> infection from the open-label PUNCH CD study. <i>Genome Medicine</i> , 2021, 13, 28.	3.6	51
11944	Ancient mitogenomics elucidates diversity of extinct West Indian tortoises. <i>Scientific Reports</i> , 2021, 11, 3224.	1.6	13
11945	Dissemination of Extended-Spectrum-β-Lactamase-Producing <i>Enterobacter cloacae</i> Complex from a Hospital to the Nearby Environment in Guadeloupe (French West Indies): ST114 Lineage Coding for a Successful IncHI2/ST1 Plasmid. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, .	1.4	9
11946	Molecular phylogeny of the Mammilloid clade (Cactaceae) resolves the monophyly of <i>Mammillaria</i> . <i>Taxon</i> , 2021, 70, 308-323.	0.4	22
11947	North American Fireflies Host Low Bacterial Diversity. <i>Microbial Ecology</i> , 2021, 82, 793-804.	1.4	3
11948	New <i>Phytophthora</i> species in clade 2a from the Asia-Pacific region including a re-examination of <i>P. colocasiae</i> and <i>P. meadii</i> . <i>Mycological Progress</i> , 2021, 20, 111-129.	0.5	11
11949	Verification of a pseudocryptic species in the commercially important tiger prawn <i>Penaeus monodon</i> Fabricius, 1798 (Decapoda: Penaeidae) from Aceh Province, Indonesia. <i>Journal of Crustacean Biology</i> , 2021, 41, .	0.3	5
11950	<i>Salmonella</i> Genomics and Population Analyses Reveal High Inter- and Intraserovar Diversity in Freshwater. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	18
11951	A chromosome-level assembly of the harlequin ladybird <i>Harmonia axyridis</i> as a genomic resource to study beetle and invasion biology. <i>Molecular Ecology Resources</i> , 2021, 21, 1318-1332.	2.2	17
11952	High-Resolution Differentiation of Enteric Bacteria in Premature Infant Fecal Microbiomes Using a Novel rRNA Amplicon. <i>MBio</i> , 2021, 12, .	1.8	23
11953	Chloroplast genomes and phylogenetic analysis of two species of <i>Oedocladium</i> (Oedogoniales). <i>Tj ETQq0 0 0 rgBT /Overlock_10 Tf 50 3</i>	0.9	5
11954	Mitochondrial genomes of eight Scelimeninae species (Orthoptera) and their phylogenetic implications within Tetrigoidea. <i>PeerJ</i> , 2021, 9, e10523.	0.9	7
11956	The Brief Case: A Maggot Mystery— <i>Ignatzschineria</i> larvae Sepsis Secondary to an Infested Wound. <i>Journal of Clinical Microbiology</i> , 2021, 59, .	1.8	1
11957	The bacterial communities of Alaskan mosses and their contributions to N ₂ -fixation. <i>Microbiome</i> , 2021, 9, 53.	4.9	34
11958	Chronological Incongruences between Mitochondrial and Nuclear Phylogenies of <i>Aedes</i> Mosquitoes. <i>Life</i> , 2021, 11, 181.	1.1	14
11959	Sequence characterisation and novel insights into bovine mastitis-associated <i>Streptococcus uberis</i> in dairy herds. <i>Scientific Reports</i> , 2021, 11, 3046.	1.6	16
11961	Application of phylogenomic tools to unravel anthozoan evolution. <i>Coral Reefs</i> , 2022, 41, 475-495.	0.9	11
11962	Characterization of the complete chloroplast genome of <i>Farfugium japonicum</i> (Asteraceae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 678-679.	0.2	2

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11963	The complete chloroplast genome of <i>Keteleeria davidiana</i> var. <i>calcareo</i> (Pinaceae), an endangered species endemic to China. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 693-695.	0.2	2
11964	The complete chloroplast genome sequence of <i>Camellia sinensis</i> var. <i>sinensis</i> cultivar Tieguanyin (Theaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 395-396.	0.2	5
11965	Pleistocene aridification underlies the evolutionary history of the Caribbean endemic, insular, giant <i>Consolea</i> (Opuntioideae). <i>American Journal of Botany</i> , 2021, 108, 200-215.	0.8	21
11967	Evaluating DNA Barcoding for Species Identification and Discovery in European Gracillariid Moths. <i>Frontiers in Ecology and Evolution</i> , 2021, 9, .	1.1	40
11968	<i>Streptomyces</i> sp. M54: an actinobacteria associated with a neotropical social wasp with high potential for antibiotic production. <i>Antonie Van Leeuwenhoek</i> , 2021, 114, 379-398.	0.7	9
11969	A new species of <i>Rhagomys</i> (Rodentia, Sigmodontinae) from southeastern Ecuador. <i>Journal of Mammalogy</i> , 2021, 102, 123-138.	0.6	5
11970	Two Haplotypes of <i>Aedes aegypti</i> Detected by ND4 Mitochondrial Marker in Three Regions of Ecuador. <i>Insects</i> , 2021, 12, 200.	1.0	2
11972	The first record of genus <i>Neocystis</i> from Kamchatka volcano soils, confirmed by genetic data. <i>IOP Conference Series: Earth and Environmental Science</i> , 2021, 663, 012009.	0.2	1
11973	Phylogenetic Relationships and Adaptation in Deep-Sea Mussels: Insights from Mitochondrial Genomes. <i>International Journal of Molecular Sciences</i> , 2021, 22, 1900.	1.8	20
11974	Resolving Recalcitrant Clades in the Pantropical Ochnaceae: Insights From Comparative Phylogenomics of Plastome and Nuclear Genomic Data Derived From Targeted Sequencing. <i>Frontiers in Plant Science</i> , 2021, 12, 638650.	1.7	18
11975	Evolutionary Analysis of Cystatins of Early-Emerging Metazoans Reveals a Novel Subtype in Parasitic Cnidarians. <i>Biology</i> , 2021, 10, 110.	1.3	6
11976	Ecological and spatial patterns associated with diversification of South American Physaria (Brassicaceae) through the general concept of species. <i>Organisms Diversity and Evolution</i> , 2021, 21, 161-188.	0.7	3
11977	The Genome of Banana Leaf Blight Pathogen <i>Fusarium sacchari</i> str. FS66 Harbors Widespread Gene Transfer From <i>Fusarium oxysporum</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 629859.	1.7	5
11978	<i>Novakomyces olei</i> sp. nov., the First Member of a Novel Taphrinomycotina Lineage. <i>Microorganisms</i> , 2021, 9, 301.	1.6	3
11982	<i>Xylaria necrophora</i> , sp. nov., is an emerging root-associated pathogen responsible for taproot decline of soybean in the southern United States. <i>Mycologia</i> , 2021, 113, 326-347.	0.8	7
11983	A new terraranan genus from the Brazilian Atlantic Forest with comments on the systematics of Brachycephaloidea (Amphibia: Anura). <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2021, 59, 663-679.	0.6	5
11984	Molecular bases of an alternative dual-enzyme system for light color acclimation of marine <i>Synechococcus</i> cyanobacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	16
11985	The Pediatric Obesity Microbiome and Metabolism Study (POMMS): Methods, Baseline Data, and Early Insights. <i>Obesity</i> , 2021, 29, 569-578.	1.5	19

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11986	GalaxyTrakr: a distributed analysis tool for public health whole genome sequence data accessible to non-bioinformaticians. <i>BMC Genomics</i> , 2021, 22, 114.	1.2	38
11987	Colonization with <i>Staphylococcus aureus</i> and <i>Klebsiella pneumoniae</i> causes infections in a Vietnamese intensive care unit. <i>Microbial Genomics</i> , 2021, 7, .	1.0	10
11988	The genomic content and context of auxiliary metabolic genes in roseophages. <i>Environmental Microbiology</i> , 2021, 23, 3743-3757.	1.8	18
11989	<i>Lunatibacter salilacus</i> gen. nov., sp. nov., a member of the family Cyclobacteriaceae, isolated from a saline and alkaline lake sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	9
11990	<i>Siccirubicoccus phaeus</i> sp. nov., isolated from oil reservoir water and emended description of the genus <i>Siccirubicoccus</i> . <i>Antonie Van Leeuwenhoek</i> , 2021, 114, 355-364.	0.7	11
11991	<i>Crateriforma spongiae</i> sp. nov., isolated from a marine sponge and emended description of the genus "Crateriforma". <i>Antonie Van Leeuwenhoek</i> , 2021, 114, 341-353.	0.7	19
11992	The Majority of Typhoid Toxin-Positive <i>Salmonella</i> Serovars Encode ArtB, an Alternate Binding Subunit. <i>MSphere</i> , 2021, 6, .	1.3	10
11993	Ethanol Production from Wheat Straw Hydrolysate by <i>Issatchenkia Orientalis</i> Isolated from Waste Cooking Oil. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 121.	1.5	5
11994	Species delimitation and hybridization history of a hazel species complex. <i>Annals of Botany</i> , 2021, 127, 875-886.	1.4	6
11995	Genomic evidence of prevalent hybridization throughout the evolutionary history of the fig-wasp pollination mutualism. <i>Nature Communications</i> , 2021, 12, 718.	5.8	31
11996	Environmental palaeogenomic reconstruction of an Ice Age algal population. <i>Communications Biology</i> , 2021, 4, 220.	2.0	24
11997	Microbial production and consumption of hydrocarbons in the global ocean. <i>Nature Microbiology</i> , 2021, 6, 489-498.	5.9	56
11998	Phylogenetic placement of enigmatic <i>Astianthus</i> (Bignoniaceae) based on molecular data, wood and bark anatomy. <i>Botanical Sciences</i> , 2021, 99, 398-412.	0.3	0
11999	<i>Pyricularia oryzae</i> incites gray leaf spot disease on hard fescue (<i>Festuca brevipila</i>). <i>Itsrsj</i> , 2022, 14, 997-1002.	0.1	2
12000	A Case Report of Avian Malaria (<i>Plasmodium</i> spp.) in Pen-Reared Pigeons (<i>Columba livia</i>). <i>Avian Diseases</i> , 2021, 65, 213-218.	0.4	1
12001	The Mitochondrial Genome of Nematodontous Moss <i>Polytrichum commune</i> and Analysis of Intergenic Repeats Distribution Among Bryophyta. <i>Diversity</i> , 2021, 13, 54.	0.7	4
12002	Diversification, disparification and hybridization in the desert shrubs <i>Encelia</i> . <i>New Phytologist</i> , 2021, 230, 1228-1241.	3.5	10
12003	Towards a new classification of Muscidae (Diptera): a comparison of hypotheses based on multiple molecular phylogenetic approaches. <i>Systematic Entomology</i> , 2021, 46, 508-525.	1.7	20

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12005	A large genome with chromosome-scale assembly sheds light on the evolutionary success of a true toad (<i>Bufo gargarizans</i>). <i>Molecular Ecology Resources</i> , 2021, 21, 1256-1273.	2.2	32
12006	Population genomic structure of Eurasian and African foxtail millet landrace accessions inferred from genotyping-by-sequencing. <i>Plant Genome</i> , 2021, 14, e20081.	1.6	14
12007	The complete chloroplast genome sequence of <i>Alniphyllum fortunei</i> (Styracaceae) from Fujian, China. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 439-440.	0.2	0
12008	The complete chloroplast genome of <i>Lilium rosthornii</i> Diels (Liliopsida: Liliaceae) from Hunan, China. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 553-554.	0.2	2
12009	The mitochondrial genome of one "twisted-wing parasite" <i>Xenos cf. moutoni</i> (Insecta, Strepsiptera). <i>Tj ETQq0 0 0 rgBT /Overlock</i> 6, 512-514.	0.2	2
12010	The complete chloroplast genome sequence of <i>Anemone reflexa</i> (Ranunculaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 304-305.	0.2	1
12011	The complete chloroplast genome of Chinese medicinal herb <i>Belamcanda chinensis</i> (L.) Redouté (Iridaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 331-332.	0.2	2
12012	Characterization and phylogenetic analysis of the complete chloroplast genome of <i>Actinidia latifolia</i> (Actinidiaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 672-673.	0.2	2
12013	The complete chloroplast genome of <i>Zanthoxylum piasezkii</i> Maxim. (Rutaceae) and its phylogenetic analysis. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 306-307.	0.2	1
12014	Pharaoh Cuttlefish, <i>Sepia pharaonis</i> , Genome Reveals Unique Reflectin Camouflage Gene Set. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	10
12015	<i>Dominikia bonfanteae</i> and <i>Glomus atlanticum</i> , two new species in the Glomeraceae (phylum). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 347</i> <i>Progress</i> , 2021, 20, 131-148.	0.5	7
12016	Two new <i>Morinia</i> species from palms (Arecaceae) in Portugal. <i>Mycological Progress</i> , 2021, 20, 83-94.	0.5	1
12017	Cytochrome P450 monooxygenase genes in the wild silkworm, <i>Bombyx mandarina</i> . <i>PeerJ</i> , 2021, 9, e10818.	0.9	6
12018	Evidence for reduced immune gene diversity and activity during the evolution of termites. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2021, 288, 20203168.	1.2	9
12019	Defining a novel domain that provides an essential contribution to site-specific interaction of Rep protein with DNA. <i>Nucleic Acids Research</i> , 2021, 49, 3394-3408.	6.5	8
12020	The pedomorphic lateral line system in <i>Pseudamiops</i> and <i>Gymnapogon</i> (Percomorpha, Apogonidae), with morphological and molecular-based phylogenetic considerations. <i>Journal of Morphology</i> , 2021, 282, 652-678.	0.6	4
12022	Sequencing of Organellar Genomes of <i>Nowellia curvifolia</i> (Cephaloziaceae Jungermanniales) Revealed the Smallest Plastome with Complete Gene Set and High Intraspecific Variation Suggesting Cryptic Speciation. <i>Diversity</i> , 2021, 13, 81.	0.7	3
12023	Comparative Mitogenomic Analysis of Heptageniid Mayflies (Insecta: Ephemeroptera): Conserved Intergenic Spacer and tRNA Gene Duplication. <i>Insects</i> , 2021, 12, 170.	1.0	14

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12025	Phylogeny and biogeography of the genus <i>Hesperis</i> (Brassicaceae, tribe Hesperideae) inferred from nuclear ribosomal DNA sequence data. <i>Plant Systematics and Evolution</i> , 2021, 307, 1.	0.3	2
12026	Genome-wide identification and gene-editing of pigment transporter genes in the swallowtail butterfly <i>Papilio xuthus</i> . <i>BMC Genomics</i> , 2021, 22, 120.	1.2	7
12027	Malvaviscus yellow mosaic virus, a divergent begomovirus carrying a nanovirus-like nonanucleotide and a modified stem-loop structure. <i>Annals of Applied Biology</i> , 2021, 179, 96-107.	1.3	0
12028	Identification of Closely Related <i>Listeria monocytogenes</i> Isolates with No Apparent Evidence for a Common Source or Location: A Retrospective Whole Genome Sequencing Analysis. <i>Journal of Food Protection</i> , 2021, 84, 1104-1113.	0.8	6
12029	Dissecting Incongruence between Concatenation- and Quartet-Based Approaches in Phylogenomic Data. <i>Systematic Biology</i> , 2021, 70, 997-1014.	2.7	28
12031	New insights into the phylogeny of <i>Spyridia</i> (Ceramiales, Rhodophyta) species with uncinata spines, focusing on the structure of determinate branches. <i>European Journal of Phycology</i> , 0, , 1-14.	0.9	1
12032	Quaternary diversification of a columnar cactus in the driest place on earth. <i>American Journal of Botany</i> , 2021, 108, 184-199.	0.8	22
12033	Insights into triterpene synthesis and unsaturated fatty-acid accumulation provided by chromosomal-level genome analysis of <i>Akebia trifoliata</i> subsp. <i>australis</i> . <i>Horticulture Research</i> , 2021, 8, 33.	2.9	23
12034	Draft genome of a novel methanotrophic <i>Methylobacter</i> sp. from the volcanic soils of Pantelleria Island. <i>Antonie Van Leeuwenhoek</i> , 2021, 114, 313-324.	0.7	12
12035	A switch to feeding on cycads generates parallel accelerated evolution of toxin tolerance in two clades of <i>Eumaeus</i> caterpillars (Lepidoptera: Lycaenidae). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	7
12036	Genome sequences reveal global dispersal routes and suggest convergent genetic adaptations in seahorse evolution. <i>Nature Communications</i> , 2021, 12, 1094.	5.8	29
12037	Convergent antibody evolution and clonotype expansion following influenza virus vaccination. <i>PLoS ONE</i> , 2021, 16, e0247253.	1.1	19
12038	Systematic Detection of Large-Scale Multigene Horizontal Transfer in Prokaryotes. <i>Molecular Biology and Evolution</i> , 2021, 38, 2639-2659.	3.5	10
12039	Genome-wide characterization of PEBP family genes in nine Rosaceae tree species and their expression analysis in <i>P. mume</i> . <i>Bmc Ecology and Evolution</i> , 2021, 21, 32.	0.7	10
12040	Characterization of <i>Sulfurimonas hydrogeniphila</i> sp. nov., a Novel Bacterium Predominant in Deep-Sea Hydrothermal Vents and Comparative Genomic Analyses of the Genus <i>Sulfurimonas</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 626705.	1.5	18
12041	Genetic Diversity and Potential Paths of Transmission of <i>Mycobacterium bovis</i> in the Amazon: The Discovery of <i>M. bovis</i> Lineage Lb1 Circulating in South America. <i>Frontiers in Veterinary Science</i> , 2021, 8, 630989.	0.9	3
12042	<i>Limosilactobacillus balticus</i> sp. nov., <i>Limosilactobacillus agrestis</i> sp. nov., <i>Limosilactobacillus albertensis</i> sp. nov., <i>Limosilactobacillus rudii</i> sp. nov. and <i>Limosilactobacillus fastidiosus</i> sp. nov., five novel <i>Limosilactobacillus</i> species isolated from the vertebrate gastrointestinal tract, and proposal of six subspecies of <i>Limosilactobacillus reuteri</i> adapted to the gastrointestinal tract of specific vertebrate hosts. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	60
12043	Molecular investigation of an outbreak associated with total parenteral nutrition contaminated with NDM-producing <i>Leclercia adecarboxylata</i> . <i>BMC Infectious Diseases</i> , 2021, 21, 235.	1.3	10

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12044	Phylogeographic Origin of California Slender Salamanders (<i>Batrachoseps attenuatus</i>) in the Sutter Buttes. <i>Journal of Herpetology</i> , 2021, 55, .	0.2	2
12045	An early dog from southeast Alaska supports a coastal route for the first dog migration into the Americas. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2021, 288, 20203103.	1.2	17
12046	Reconstructing the nonadaptive radiation of an ancient lineage of ground-dwelling stick insects (Phasmatodea: Heteropterygidae). <i>Systematic Entomology</i> , 2021, 46, 487-507.	1.7	23
12049	Classification of a Texan wild grapevine population within the genus <i>Vitis</i> . <i>Acta Horticulturae</i> , 2021, , 131-140.	0.1	1
12051	Location, but not defensive genotype, determines ectomycorrhizal community composition in Scots pine (<i>Pinus sylvestris</i> L.) seedlings. <i>Ecology and Evolution</i> , 2021, 11, 4826-4842.	0.8	3
12053	In situ recordings of large gelatinous spheres from NE Atlantic, and the first genetic confirmation of egg mass of <i>Illex coindetii</i> (Vérany, 1839) (Cephalopoda, Mollusca). <i>Scientific Reports</i> , 2021, 11, 7168.	1.6	6
12054	The complete chloroplast genome of <i>Achyranthes bidentata</i> Blume. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 782-783.	0.2	1
12055	Structural and functional diversity of asparaginases: Overview and recommendations for a revised nomenclature. <i>Biotechnology and Applied Biochemistry</i> , 2022, 69, 503-513.	1.4	14
12056	Triclosan Tolerance Is Driven by a Conserved Mechanism in Diverse <i>Pseudomonas</i> Species. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	8
12057	Genome editing reveals fitness effects of a gene for sexual dichromatism in Sulawesian fishes. <i>Nature Communications</i> , 2021, 12, 1350.	5.8	36
12058	Cytochrome c oxidase subunit I barcode species delineation methods imply critically underestimated diversity in "common" <i>Hermeuptychia</i> butterflies (Lepidoptera: Nymphalidae: Tj ETQq0.00 rgBT\$Overlock		
12059	The first genomic resources for <i>Phymatotrichopsis omnivora</i> , a soil-borne pezizomycete pathogen with a broad host range. <i>Phytopathology</i> , 2021, , PHYTO01210014A.	1.1	3
12060	Phylogenomic Framework for Taxonomic Delineation of <i>Paracoccus</i> spp. and Exploration of Core-Pan Genome. <i>Indian Journal of Microbiology</i> , 2021, 61, 180-194.	1.5	3
12062	New insights into the phylogeny and taxonomy of Chinese <i>Physospermopsis</i> (Apiaceae). <i>PhytoKeys</i> , 2021, 175, 67-88.	0.4	4
12063	The myxozoan minicollagen gene repertoire was not simplified by the parasitic lifestyle: computational identification of a novel myxozoan minicollagen gene. <i>BMC Genomics</i> , 2021, 22, 198.	1.2	4
12064	Deciphering the transcriptomic regulation of heat stress responses in <i>Nothofagus pumilio</i> . <i>PLoS ONE</i> , 2021, 16, e0246615.	1.1	6
12065	Phylogenetic placement of <i>Cailliella praeupticola</i> (Melastomataceae), a rare, monospecific lineage from Guinea, West Africa. <i>Willdenowia</i> , 2021, 51, .	0.5	6
12067	Marine sediments harbor diverse archaea and bacteria with the potential for anaerobic hydrocarbon degradation via fumarate addition. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	13

#	ARTICLE	IF	CITATIONS
12068	Allophoma species (Pleosporales: Didymellaceae) associated with Thunbergia grandiflora in Guangxi Province, China. Biodiversity Data Journal, 2021, 9, e63643.	0.4	5
12069	Two Archaeal Metagenome-Assembled Genomes from El Tatio Provide New Insights into the Crenarchaeota Phylum. Genes, 2021, 12, 391.	1.0	5
12070	Investigating pollination strategies in disturbed habitats: the case of the narrow-endemic toadflax Linaria tonzigii (Plantaginaceae) on mountain screes. Plant Ecology, 2021, 222, 511-523.	0.7	5
12071	<i>Stigonema</i> associated with boreal <i>Stereocaulon</i> possesses the alternative vanadium nitrogenase. Lichenologist, 2021, 53, 215-220.	0.5	6
12072	The "evil tribe" spreads across the land: A dated molecular phylogeny provides insight into dispersal, expansion, and biogeographic relationships within one of the largest tribes of the sunflower family (Vernonieae: Compositae). American Journal of Botany, 2021, 108, 505-519.	0.8	10
12073	Aestuariimicrobium ganzense sp. nov., a new Gram-positive bacterium isolated from soil in the Ganzi Tibetan autonomous prefecture, China. Archives of Microbiology, 2021, 203, 2653-2658.	1.0	1
12074	Deep sea sediments associated with cold seeps are a subsurface reservoir of viral diversity. ISME Journal, 2021, 15, 2366-2378.	4.4	93
12075	Foliar fungi of the enigmatic desert plant Welwitschia mirabilis show little adaptation to their unique host plant. South African Journal of Science, 2021, 117, .	0.3	2
12076	Characterization of the complete chloroplast genome of Homalomena occulta (Lour.) Schott. Mitochondrial DNA Part B: Resources, 2021, 6, 1018-1019.	0.2	0
12077	The complete mitochondrial genome of Yuukianura szeptyckii Deharveng & Weiner 1984 (Collembola): Tj ETQq1 1 0,784314,rgBT /Ove 0,2 1	0.2	1
12078	The complete chloroplast genome sequence of Nicotiana debneyi (Solanaceae). Mitochondrial DNA Part B: Resources, 2021, 6, 1042-1043.	0.2	0
12079	The complete chloroplast genome of Hippeastrum rutilum (Ker-Gawl.) Herb.. Mitochondrial DNA Part B: Resources, 2021, 6, 1141-1143.	0.2	0
12080	The complete chloroplast genome sequence of <i>Achimenes cettoana</i> (Gesneriaceae). Mitochondrial DNA Part B: Resources, 2021, 6, 705-707.	0.2	1
12081	Mitogenomics of the endemic Ethiopian rats: looking for footprints of adaptive evolution in sky islands. Mitochondrion, 2021, 57, 182-191.	1.6	7
12082	Chromosome-level assembly of the mangrove plant <i>Aegiceras corniculatum</i> genome generated through Illumina, PacBio and Hi-C sequencing technologies. Molecular Ecology Resources, 2021, 21, 1593-1607.	2.2	16
12083	Morpho-Phylo Taxonomy of Novel Dothideomycetous Fungi Associated With Dead Woody Twigs in Yunnan Province, China. Frontiers in Microbiology, 2021, 12, 654683.	1.5	21
12084	"More than meets the eye" phylogeographic inferences and remarkable cryptic diversity and in endemic catfish Parotocinclus (Loricariidae: Hypoptopomatinae) from neglected and impacted basins in South America. Conservation Genetics, 2021, 22, 411-425.	0.8	4
12085	Genomic plasticity and antibody response of <i>Bordetella bronchiseptica</i> strain HT200, a natural variant from a thermal spring. FEMS Microbiology Letters, 2021, 368, .	0.7	4

#	ARTICLE	IF	CITATIONS
12086	Characterization of the complete plastome of <i>Aster pekinensis</i> (Asteraceae), a perennial herb. Mitochondrial DNA Part B: Resources, 2021, 6, 1064-1065.	0.2	2
12087	Integrative systematics of the scleractinian coral genera <i>Caulastraea</i> , <i>Erythrastrea</i> and <i>Oulophyllia</i> . Zoologica Scripta, 2021, 50, 509-527.	0.7	6
12088	A Test for the Rapid Detection of the Cefazolin Inoculum Effect in Methicillin-Susceptible <i>Staphylococcus aureus</i> . Journal of Clinical Microbiology, 2021, 59, .	1.8	6
12089	Two New Species in the Family Cunninghamellaceae from China. Mycobiology, 2021, 49, 142-150.	0.6	12
12090	Molecular and morphological analyses reveal new taxa additions to the tribe Streblocladiae (Rhodomelaceae, Rhodophyta). Journal of Phycology, 2021, 57, 817-830.	1.0	2
12091	Market Chickens as a Source of Antibiotic-Resistant <i>Escherichia coli</i> in a Peri-Urban Community in Lima, Peru. Frontiers in Microbiology, 2021, 12, 635871.	1.5	27
12092	Hagenia from the early Miocene of Ethiopia: Evidence for possible niche evolution?. Ecology and Evolution, 2021, 11, 5164-5186.	0.8	6
12093	Systematics and biogeography of the <i>Boana albopunctata</i> species group (Anura, Hylidae), with the description of two new species from Amazonia. Systematics and Biodiversity, 2021, 19, 375-399.	0.5	20
12095	First report of powdery mildew of rainforest spinach (<i>Elatostema reticulatum</i>), native to Australia, caused by <i>Podosphaera xanthii</i> . Australasian Plant Disease Notes, 2021, 16, 1.	0.4	4
12096	Computational design of enzymes for biotechnological applications. Biotechnology Advances, 2021, 47, 107696.	6.0	51
12097	Deep-sea microbes as tools to refine the rules of innate immune pattern recognition. Science Immunology, 2021, 6, .	5.6	21
12098	Phylogenetic relationships in <i>Brachyotum</i> and allies (Melastomataceae, Melastomataceae): a reassessment of the limits of the genera. Botanical Journal of the Linnean Society, 2021, 197, 170-189.	0.8	8
12099	Evolution and biogeography of <i>Memecylon</i> . American Journal of Botany, 2021, 108, 628-646.	0.8	14
12100	A Persistent Giant Algal Virus, with a Unique Morphology, Encodes an Unprecedented Number of Genes Involved in Energy Metabolism. Journal of Virology, 2021, 95, .	1.5	31
12101	<i>Phytophthora theobromicola</i> sp. nov.: A New Species Causing Black Pod Disease on Cacao in Brazil. Frontiers in Microbiology, 2021, 12, 537399.	1.5	14
12102	Novel Endosymbionts in Rhizarian Amoebae Imply Universal Infection of Unrelated Free-Living Amoebae by Legionellales. Frontiers in Cellular and Infection Microbiology, 2021, 11, 642216.	1.8	9
12103	Analysis of Fungal Genomes Reveals Commonalities of Intron Gain or Loss and Functions in Intron-Poor Species. Molecular Biology and Evolution, 2021, 38, 4166-4186.	3.5	19
12104	The mitochondrial genome of a leaf insect <i>Phyllium westwoodii</i> (Phasmatodea: Phylliidae) in Southeast Asia. Mitochondrial DNA Part B: Resources, 2021, 6, 888-890.	0.2	2

#	ARTICLE	IF	CITATIONS
12105	Genetic characterisation of a subset of <i>Campylobacter jejuni</i> isolates from clinical and poultry sources in Ireland. <i>PLoS ONE</i> , 2021, 16, e0246843.	1.1	8
12106	The first eleven mitochondrial genomes from the ectomycorrhizal fungal genus (<i>Boletus</i>) reveal intron loss and gene rearrangement. <i>International Journal of Biological Macromolecules</i> , 2021, 172, 560-572.	3.6	38
12107	Genomic insights into the host specific adaptation of the <i>Pneumocystis</i> genus. <i>Communications Biology</i> , 2021, 4, 305.	2.0	23
12108	Systematic revision of <i>Platevindex</i> Baker, 1938 (Gastropoda: Euthyneura: Onchidiidae). <i>European Journal of Taxonomy</i> , 0, 737, 1-133.	0.6	3
12111	The History of Lentil (<i>Lens culinaris</i> subsp. <i>culinaris</i>) Domestication and Spread as Revealed by Genotyping-by-Sequencing of Wild and Landrace Accessions. <i>Frontiers in Plant Science</i> , 2021, 12, 628439.	1.7	25
12112	Genomic analysis of <i>Medicago ruthenica</i> provides insights into its tolerance to abiotic stress and demographic history. <i>Molecular Ecology Resources</i> , 2021, 21, 1641-1657.	2.2	17
12113	Phylogenetic study and taxonomic update of <i>Chondrina</i> (Gastropoda, Pulmonata). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 507 Td</i> 2021, 19, 218-236.	0.5	3
12114	Most Genomic Loci Misrepresent the Phylogeny of an Avian Radiation Because of Ancient Gene Flow. <i>Systematic Biology</i> , 2021, 70, 961-975.	2.7	45
12115	Genomic surveillance of <i>Neisseria gonorrhoeae</i> in the Philippines, 2013–2014. <i>Western Pacific Surveillance and Response Journal: WPSAR</i> , 2021, 12, 17-25.	0.3	3
12116	Genome assembly and annotation at the chromosomal level of first <i>Pleuronectidae</i> : <i>Verasper variegatus</i> provides a basis for phylogenetic study of <i>Pleuronectiformes</i> . <i>Genomics</i> , 2021, 113, 717-726.	1.3	8
12117	The Roles of Protein Structure, Taxon Sampling, and Model Complexity in Phylogenomics: A Case Study Focused on Early Animal Divergences. <i>Biophysica</i> , 2021, 1, 87-105.	0.6	2
12119	<i>Ophiocordyceps asiana</i> and <i>Ophiocordyceps tessaratomidarum</i> (Ophiocordycipitaceae, Hypocreales), two new species on stink bugs from Thailand. <i>Mycological Progress</i> , 2021, 20, 341-353.	0.5	7
12120	<i>Zebrus pallaoroi</i> sp. nov.: a new species of goby (Actinopterygii: Gobiidae) from the Mediterranean Sea with a dna-based phylogenetic analysis of the <i>Gobius</i> -lineage. <i>Contributions To Zoology</i> , 2021, 90, 1-33.	0.2	3
12122	Morphological and phylogenetic analyses of <i>Toniniopsis subincompta</i> s. lat. (<i>Ramalinaceae</i> , <i>Lecanorales</i>) in Eurasia. <i>Lichenologist</i> , 2021, 53, 171-183.	0.5	4
12123	<i>Catillaria flexuosa</i> (Catillariaceae), a new lichen species described from the Netherlands. <i>Lichenologist</i> , 2021, 53, 193-202.	0.5	0
12124	Additional description and genome analyses of <i>Caenorhabditis auriculariae</i> representing the basal lineage of genus <i>Caenorhabditis</i> . <i>Scientific Reports</i> , 2021, 11, 6720.	1.6	10
12125	<i>Lasioloma antillarum</i> (Ascomycota: Pilocarpaceae), a new lichenized fungus from the Antilles, and the importance of posterior annotations of sequence data in public repositories. <i>Willdenowia</i> , 2021, 51, .	0.5	1
12126	Characterization of the Complete Chloroplast Genome of <i>Meconopsis punicea</i> (Papaveraceae), an Endemic Species from the Qinghai-Tibet Plateau in China. <i>Cytology and Genetics</i> , 2021, 55, 183-187.	0.2	2

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12127	Altered Expression of Chemosensory and Odorant Binding Proteins in Response to Fungal Infection in the Red Imported Fire Ant, <i>Solenopsis invicta</i> . <i>Frontiers in Physiology</i> , 2021, 12, 596571.	1.3	8
12128	A review of the diagnosis and geographical distribution of the recently described flea toad <i>Brachycephalus sulfuratus</i> in relation to <i>B. hermogenesi</i> (Anura: Brachycephalidae). <i>PeerJ</i> , 2021, 9, e10983.	0.9	4
12129	Non-breeding season records of the Alpine Leaf Warbler <i>Phylloscopus occisinensis</i> . <i>Bulletin of the British Ornithologists' Club</i> , 2021, 141, .	0.1	0
12130	Systematic review of the polychromatic ground snakes <i>Atractus snethlageae</i> complex reveals four new species from threatened environments. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2021, 59, 718-747.	0.6	8
12131	Phylogenetic and Haplotype Network Analyses of <i>Diaporthe eres</i> Species in China Based on Sequences of Multiple Loci. <i>Biology</i> , 2021, 10, 179.	1.3	16
12132	Extensive Genome-Wide Phylogenetic Discordance Is Due to Incomplete Lineage Sorting and Not Ongoing Introgression in a Rapidly Radiated Bryophyte Genus. <i>Molecular Biology and Evolution</i> , 2021, 38, 2750-2766.	3.5	54
12133	When morphology does not match phylogeny: The puzzling case of two sibling nudibranchs (Gastropoda). <i>Zoologica Scripta</i> , 2021, 50, 439-454.	0.7	12
12134	Going with the flow? Diversification of gastropods reflects drainage evolution in Africa. <i>Journal of Biogeography</i> , 2021, 48, 1579-1593.	1.4	3
12135	The Rufous Sengi is not <i>Elephantulus</i> – Multilocus reconstruction of evolutionary history of sengis from the subfamily Macroscelidinae. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2021, 59, 918-932.	0.6	6
12136	Phylogeny of cercosporoid fungi (Mycosphaerellaceae, Mycosphaerellales) from Hawaii and New York reveals novel species within the <i>Cercospora beticola</i> complex. <i>Mycological Progress</i> , 2021, 20, 261-287.	0.5	6
12137	A molecular timescale for eukaryote evolution with implications for the origin of red algal-derived plastids. <i>Nature Communications</i> , 2021, 12, 1879.	5.8	124
12138	Pre-Cambrian roots of novel Antarctic cryptoendolithic bacterial lineages. <i>Microbiome</i> , 2021, 9, 63.	4.9	17
12139	Neotypification of <i>Rhipsalis rhombea</i> (Rhipsalideae, Cactaceae) and Its Taxonomic History. <i>Haseltonia</i> , 2021, 27, .	0.3	1
12140	Gorgocephalidae (Digenea: Lepocreadioidea) in the Indo-West Pacific: new species, life-cycle data and perspectives on species delineation over geographic range. <i>Zoological Journal of the Linnean Society</i> , 2021, 193, 1416-1455.	1.0	18
12141	<i>Paenibacillus glycinis</i> sp. nov., an Endophytic Bacterium Isolated from the Nodules of Soybean (Glycine) Tj ETQqO 0,0rgBT /Oyerlock 10	1.0	10
12142	<i>Tamlana haliotis</i> sp. nov., isolated from the gut of the abalone <i>Haliotis rubra</i> . <i>Archives of Microbiology</i> , 2021, 203, 2357-2364.	1.0	8
12143	Heat-acclimatised strains of <i>Rhodospseudomonas palustris</i> reveal higher temperature optima with concomitantly enhanced biohydrogen production rates. <i>International Journal of Hydrogen Energy</i> , 2021, 46, 11564-11572.	3.8	26
12144	ESBL-producing strains isolated from imported cases of enteric fever in England and Wales reveal multiple chromosomal integrations of <i>bla</i> CTX-M-15 in XDR <i>Salmonella</i> Typhi. <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 76, 1459-1466.	1.3	27

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12145	The complete chloroplast genome of <i>Toona sinensis</i> , an important economic and medicinal plant endemic in China. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1025-1027.	0.2	3
12146	The complete chloroplast genome of <i>Ottelia acuminata</i> var. <i>crispa</i> , an endangered aquatic herb with extremely narrow distribution. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1071-1072.	0.2	1
12147	The complete chloroplast genome of <i>Ophiopogon bodinieri</i> Levl. and its phylogenetic position. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1022-1024.	0.2	0
12148	The complete chloroplast genome of <i>Lonicera fulvotomentosa</i> Hsu et S. C. Cheng and its phylogenetic analysis. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 842-843.	0.2	4
12149	The complete mitochondrial genome of <i>Scyra compressipes</i> Stimpson, 1857 (Decapoda: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 5	0.2	1
12150	Characterization of the complete plastome of <i>Eleusine coracana</i> (Gramineae), an annual crop. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1089-1090.	0.2	1
12151	The complete chloroplast genome sequences and phylogenetic analysis of <i>Crotalaria pallida</i> (Leguminosae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1231-1232.	0.2	0
12152	The complete mitochondrial genome of <i>Chaetodon speculum</i> (Chaetodontiformes,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 5	0.2	2
12156	<i>Tremella macrobasidiata</i> and <i>Tremella varia</i> have abundant and widespread yeast stages in <i>Lecanora</i> lichens. <i>Environmental Microbiology</i> , 2021, 23, 2484-2498.	1.8	16
12157	<i>Pigmentibacter ruber</i> gen. nov., sp. nov., a novel bacterium of the family Silvanigrellaceae isolated from human blood. <i>Antonie Van Leeuwenhoek</i> , 2021, 114, 731-739.	0.7	4
12158	Limited Multidrug Resistance Efflux Pump Overexpression among Multidrug-Resistant <i>Escherichia coli</i> Strains of ST131. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, .	1.4	12
12159	Genomics and transcriptomics of the green mussel explain the durability of its byssus. <i>Scientific Reports</i> , 2021, 11, 5992.	1.6	14
12160	Genetic assessment of captive red pandas (<i>Ailurus fulgens</i>) in American zoos to address management separation by putative subspecies. <i>Zoo Biology</i> , 2021, 40, 238-251.	0.5	5
12161	Apparent nosocomial adaptation of <i>Enterococcus faecalis</i> predates the modern hospital era. <i>Nature Communications</i> , 2021, 12, 1523.	5.8	69
12162	Chloroplast genome sequence of Chongming lima bean (<i>Phaseolus lunatus</i> L.) and comparative analyses with other legume chloroplast genomes. <i>BMC Genomics</i> , 2021, 22, 194.	1.2	26
12163	<i>Fusarium</i> : more than a node or a foot-shaped basal cell. <i>Studies in Mycology</i> , 2021, 98, 100116.	4.5	134
12164	Elucidation of Japanese pepper (<i>Zanthoxylum piperitum</i> De Candolle) domestication using RAD-Seq. <i>Scientific Reports</i> , 2021, 11, 6464.	1.6	7
12165	Molecular data reveals two new species of <i>Hypnea</i> (Cystocloniaceae, Rhodophyta) from India: <i>Hypnea indica</i> sp. nov. and <i>Hypnea bullata</i> sp. nov.. <i>Botanica Marina</i> , 2021, 64, 139-148.	0.6	4

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12166	Adaptation and convergence in circadian-related genes in Iberian freshwater fish. <i>Bmc Ecology and Evolution</i> , 2021, 21, 38.	0.7	3
12168	The diversity of stomatal development regulation in <i>Callitriche</i> is related to the intrageneric diversity in lifestyles. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	14
12169	Analysis of a small outbreak of Shiga toxin-producing <i>Escherichia coli</i> O157:H7 using long-read sequencing. <i>Microbial Genomics</i> , 2021, 7, .	1.0	9
12170	Genome Sequencing of five <i>Lactocaseibacillus</i> Strains and Analysis of Type I and II Toxin-Antitoxin System Distribution. <i>Microorganisms</i> , 2021, 9, 648.	1.6	7
12172	Phylogeography of a gypsum endemic plant across its entire distribution range in the western Mediterranean. <i>American Journal of Botany</i> , 2021, 108, 443-460.	0.8	3
12174	Comparative Plastomes and Phylogenetic Analysis of <i>Cleistogenes</i> and Closely Related Genera (Poaceae). <i>Frontiers in Plant Science</i> , 2021, 12, 638597.	1.7	5
12175	<i>Cladophora rigida</i> sp. nov., a new freshwater species within Cladophoraceae (Ulvophyceae,). <i>Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50</i>	0.6	4
12176	Gill microbiome structure and function in the chemosymbiotic coastal lucinid <i>Stewartia floridana</i> . <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	2
12177	The mango seed weevil <i>Sternochetus mangiferae</i> (Fabricius) (Coleoptera: Curculionidae) is characterized by low genetic diversity and lack of genetic structure. <i>Agricultural and Forest Entomology</i> , 2021, 23, 353.	0.7	2
12178	Comparison of Brassica Genomes reveals asymmetrical gene retention between functional groups of genes in recurrent polyploidizations. <i>Plant Molecular Biology</i> , 2021, 106, 193-206.	2.0	6
12179	Evolutionary histories and antimicrobial resistance in <i>Shigella flexneri</i> and <i>Shigella sonnei</i> in Southeast Asia. <i>Communications Biology</i> , 2021, 4, 353.	2.0	17
12182	Phylogeny and Systematics of <i>Crescentieae</i> (Bignoniaceae), a Neotropical Clade of Cauliflorous and Bat-Pollinated Trees. <i>Systematic Botany</i> , 2021, 46, 218-228.	0.2	2
12183	Genetic variation in aneuploidy prevalence and tolerance across <i>Saccharomyces cerevisiae</i> lineages. <i>Genetics</i> , 2021, 217, .	1.2	25
12186	The complete mitochondrial genome of <i>Sanghuangporus vaninii</i> Zhehuang-1 (Hymenochaetales,). <i>Tj ETQq1 1 0,784314 rgBT/Overlock 10 Tf 50</i>	0.2	2
12187	Complete plastid genome characterization and phylogenetic analysis of <i>Pentasachme caudatum</i> Wallich ex Wight (Gentianales: Apocynaceae) from Guangdong, China. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 858-859.	0.2	0
12188	The complete mitochondrial genome sequences of Japanese earthworms <i>Metaphire hilgendorfi</i> and <i>Amyntas yunoshimensis</i> (Clitellata: Megascolecidae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 965-967.	0.2	3
12189	Complete chloroplast genome of a novel chlorophyll-deficient mutant (<i>clm</i>) in sweetpotato (<i>Ipomoea batatas</i> L.). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 968-969.	0.2	4
12190	The complete chloroplast genome of <i>Bupleurum euphorbioides</i> , a traditional medicinal plant. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 870-871.	0.2	0

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12191	The complete chloroplast genome sequence of <i>Sinolimprichtia alpina</i> var. <i>dissecta</i> (Apiaceae). Mitochondrial DNA Part B: Resources, 2021, 6, 1162-1163.	0.2	0
12192	Using neural networks to mine text and predict metabolic traits for thousands of microbes. PLoS Computational Biology, 2021, 17, e1008757.	1.5	4
12193	Expansion and Diversification of Fluorescent Protein Genes in Fifteen Acropora Species during the Evolution of Acroporid Corals. Genes, 2021, 12, 397.	1.0	4
12194	DNA-SIP and repeated isolation corroborate <i>Variovorax</i> as a key organism in maintaining the genetic memory for linuron biodegradation in an agricultural soil. FEMS Microbiology Ecology, 2021, 97, .	1.3	0
12195	Review of the Genus <i>Pseudiberus</i> Ancey, 1887 (Eupulmonata: Camaenidae) in Shandong Province, China. Malacologia, 2021, 63, .	0.2	3
12196	Metabolic Capacity of the Antarctic Cyanobacterium <i>Phormidium pseudopriestleyi</i> That Sustains Oxygenic Photosynthesis in the Presence of Hydrogen Sulfide. Genes, 2021, 12, 426.	1.0	12
12197	Localization of Bacterial Communities within Gut Compartments across <i>Cephalotes</i> Turtle Ants. Applied and Environmental Microbiology, 2021, 87, .	1.4	14
12198	Structural and functional characterization of a putative de novo gene in <i>Drosophila</i> . Nature Communications, 2021, 12, 1667.	5.8	40
12199	Genetic Diversity and Pathogenicity of Botryosphaeriaceae Species Associated with Symptomatic Citrus Plants in Europe. Plants, 2021, 10, 492.	1.6	28
12200	Exact mapping of Illumina blind spots in the <i>Mycobacterium tuberculosis</i> genome reveals platform-wide and workflow-specific biases. Microbial Genomics, 2021, 7, .	1.0	13
12201	<i>Peronospora kuewa</i> , sp. nov., a new downy mildew species infecting the endangered Hawaiian plant <i>Plantago princeps</i> var. <i>princeps</i> . Mycologia, 2021, 113, 643-652.	0.8	1
12202	The complete mitochondrial genome of the New Zealand parasitic blowfly <i>Lucilia sericata</i> (Insecta: Diptera: Calliphoridae). Mitochondrial DNA Part B: Resources, 2021, 6, 1267-1269.	0.2	7
12203	Morphological, ecological and geographical evolution of the Neotropical genus <i>Nasa</i> (Loasaceae subfamily Loasoideae). Botanical Journal of the Linnean Society, 2021, 196, 480-505.	0.8	3
12204	Reinstatement and recircumscription of <i>Jupunba</i> and <i>Punjuba</i> (Fabaceae) based on phylogenetic evidence. Botanical Journal of the Linnean Society, 2021, 196, 456-479.	0.8	6
12205	Targeted sequencing supports morphology and embryo features in resolving the classification of Cyperaceae tribe Fuireneae s.l.. Journal of Systematics and Evolution, 2021, 59, 809-832.	1.6	10
12206	Fine-scale metabolic discontinuity in a stratified prokaryote microbiome of a Red Sea deep halocline. ISME Journal, 2021, 15, 2351-2365.	4.4	11
12208	Evolution of Bird and Insect Flower Traits in <i>Fritillaria</i> L. (Liliaceae). Frontiers in Plant Science, 2021, 12, 656783.	1.7	6
12209	Whole-genome resequencing reveals persistence of forest-associated mammals in Late Pleistocene refugia along North America's North Pacific Coast. Journal of Biogeography, 2021, 48, 1153-1169.	1.4	7

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12210	Genome-wide DNA and phenotypic information supports recent colonization of South American grasslands by <i>Correndera Pipit</i> (Aves, Motacillidae). <i>Zoologica Scripta</i> , 2021, 50, 397-410.	0.7	1
12211	Identification of the type locality of the South Island Brown Kiwi <i>Apteryx australis</i> . <i>Conservation Genetics</i> , 2021, 22, 645-652.	0.8	1
12212	Reproductive character displacement and potential underlying drivers in a species-rich and florally diverse lineage of tropical angiosperms (<i>Ruellia</i> ; Acanthaceae). <i>Ecology and Evolution</i> , 2021, 11, 4719-4730.	0.8	4
12213	The metabolic network of the last bacterial common ancestor. <i>Communications Biology</i> , 2021, 4, 413.	2.0	33
12214	Resolving the Early Divergence Pattern of Teleost Fish Using Genome-Scale Data. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	7
12215	<i>Paraeutypella guizhouensis</i> gen. et sp. nov. and <i>Diatrypella longiasca</i> sp. nov. (Diatrypaceae) from China. <i>Biodiversity Data Journal</i> , 2021, 9, e63864.	0.4	13
12216	Genomic consequences of human-mediated translocations in margin populations of an endangered amphibian. <i>Evolutionary Applications</i> , 2021, 14, 1623-1634.	1.5	2
12217	A story from the Miocene: Clock-dated phylogeny of <i>Sisymbrium</i> L. (Sisymbrieae, Brassicaceae). <i>Ecology and Evolution</i> , 2021, 11, 2573-2595.	0.8	7
12218	Long-insert clone experimental evidence for assembly improvement and chimeric chromosomes detection in an allopolyploid beer yeast. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	2
12219	Signatures of north-eastern expansion and multiple refugia: genomic phylogeography of the Pine Barrens tree frog, <i>Hyla andersonii</i> (Anura: Hylidae). <i>Biological Journal of the Linnean Society</i> , 2021, 133, 120-134.	0.7	3
12220	EZmito: a simple and fast tool for multiple mitogenome analyses. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1101-1109.	0.2	23
12222	Phylogenetic structure of Shiga toxin-producing <i>Escherichia coli</i> O157:H7 from sub-lineage to SNPs. <i>Microbial Genomics</i> , 2021, 7, .	1.0	14
12223	Characterization of the complete mitochondrial genome of the New Zealand parasitic blowfly <i>Calliphora vicina</i> (Insecta: Diptera: Calliphoridae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1270-1272.	0.2	5
12224	Coordinative mediation of the response to alarm pheromones by three odorant binding proteins in the green peach aphid <i>Myzus persicae</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2021, 130, 103528.	1.2	33
12225	What drives species' distributions along elevational gradients? Macroecological and evolutionary insights from Brassicaceae of the central Alps. <i>Global Ecology and Biogeography</i> , 2021, 30, 1030-1042.	2.7	7
12226	Identification of Novel Sensitive and Reliable Serovar-Specific Targets for PCR Detection of <i>Salmonella</i> Serovars Hadar and Albany by Pan-Genome Analysis. <i>Frontiers in Microbiology</i> , 2021, 12, 605984.	1.5	8
12227	Local adaptation in populations of <i>Mycobacterium tuberculosis</i> endemic to the Indian Ocean Rim. <i>F1000Research</i> , 2021, 10, 60.	0.8	21
12228	Complex evolutionary history of two ecologically significant grass genera, <i>Themeda</i> and <i>Heteropogon</i> (Poaceae: Panicoideae: Andropogoneae). <i>Botanical Journal of the Linnean Society</i> , 2021, 196, 437-455.	0.8	10

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12229	Multidrug Resistance Dissemination in <i>Escherichia coli</i> Isolated from Wild Animals: Bacterial Clones and Plasmid Complicity. <i>Microbiology Research</i> , 2021, 12, 123-137.	0.8	4
12230	Reanalysis of the apoid wasp phylogeny with additional taxa and sequence data confirms the placement of <i>Ammoplanidae</i> as sister to bees. <i>Systematic Entomology</i> , 2021, 46, 558-569.	1.7	16
12231	Recurrent deletions in the SARS-CoV-2 spike glycoprotein drive antibody escape. <i>Science</i> , 2021, 371, 1139-1142.	6.0	475
12232	Phylogenomics of Tick Inward Rectifier Potassium Channels and Their Potential as Targets to Innovate Control Technologies. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 647020.	1.8	3
12233	Comparative in silico genome analysis of <i>Clostridium perfringens</i> unravels stable phylogroups with different genome characteristics and pathogenic potential. <i>Scientific Reports</i> , 2021, 11, 6756.	1.6	16
12234	Anaerobic endosymbiont generates energy for ciliate host by denitrification. <i>Nature</i> , 2021, 591, 445-450.	13.7	53
12235	Plastid phylogenomics resolves ambiguous relationships within the orchid family and provides a solid timeframe for biogeography and macroevolution. <i>Scientific Reports</i> , 2021, 11, 6858.	1.6	30
12236	A multi-omic characterization of temperature stress in a halotolerant <i>Scenedesmus</i> strain for algal biotechnology. <i>Communications Biology</i> , 2021, 4, 333.	2.0	22
12238	Isolation and Characterisation of Bacteriophages with Activity against Invasive Non-Typhoidal <i>Salmonella</i> Causing Bloodstream Infection in Malawi. <i>Viruses</i> , 2021, 13, 478.	1.5	8
12240	Complete chloroplast genome and phylogenetic analysis of a wild grass, <i>Hordeum roshevitzii</i> Bowden. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1219-1221.	0.2	1
12241	Characterization and phylogenetic analysis of the complete plastome of <i>Maclura tricuspidata</i> (Moraceae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 993-994.	0.2	0
12242	Complete mitochondrial genome of the hybrid grouper <i>Hyporthodus septemfasciatus</i> (â™)â— <i>Epinephelus moara</i> (â™,) (Perciformes, Serranidae) and results of a phylogenetic analysis. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 771-773.	0.2	0
12243	The complete chloroplast genome of <i>Berberis weiningensis</i> (Berberidaceae), an endemic and traditional Chinese medicinal herb. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1175-1177.	0.2	1
12244	Complete chloroplast genome sequence and phylogenetic analysis of <i>Chimonobambusa sichuanensis</i> (Bambusoideae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 824-825.	0.2	2
12245	The complete chloroplast genome of <i>Callicarpa bodinieri</i> (Lamiales, Lamiaceae), an ornamental and medicinal plant from Chongqing, China. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1229-1230.	0.2	3
12246	The complete chloroplast genome sequence of <i>Prunus salicina</i> â€Wushan plumâ™. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1243-1244.	0.2	2
12247	Low dispersal and ploidy differences in a grass maintain photosynthetic diversity despite gene flow and habitat overlap. <i>Molecular Ecology</i> , 2021, 30, 2116-2130.	2.0	12
12248	Effector Profiles of Endophytic <i>Fusarium</i> Associated with Asymptomatic Banana (<i>Musa</i> sp.) Hosts. <i>International Journal of Molecular Sciences</i> , 2021, 22, 2508.	1.8	11

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12249	WOODIV, a database of occurrences, functional traits, and phylogenetic data for all Euro-Mediterranean trees. <i>Scientific Data</i> , 2021, 8, 89.	2.4	7
12250	A chromosome level genome assembly of <i>Propiloscerus akamusi</i> to understand its response to heavy metal exposure. <i>Molecular Ecology Resources</i> , 2021, 21, 1996-2012.	2.2	11
12251	Four new species of sequestrate <i>Inocybe</i> from Chilean Nothofagaceae forests. <i>Mycologia</i> , 2021, 113, 629-642.	0.8	6
12252	Phylogeny, biogeography and systematics of Dysphanieae (Amaranthaceae). <i>Taxon</i> , 2021, 70, 526-551.	0.4	6
12255	Genome Sequence Analysis of First Ross River Virus Isolate from Papua New Guinea Indicates Long-Term, Local Evolution. <i>Viruses</i> , 2021, 13, 482.	1.5	4
12256	Host specialization and molecular evidence support a distinct species of smut fungus, <i>Anthracoidea halleriana</i> (Anthracoideaceae), on <i>Carex halleriana</i> (Cyperaceae). <i>Willdenowia</i> , 2021, 51, .	0.5	4
12257	Taxonomy and phylogeny of <i>Aphanomyopsis bacillariacearum</i> , a holocarpic oomycete parasitoid of the freshwater diatom genus <i>Pinnularia</i> . <i>Mycological Progress</i> , 2021, 20, 289-298.	0.5	5
12260	<i>Phaeonawawia</i> , a novel chaetosphaeriaceous anamorph from submerged wood in Malaysia. <i>Mycological Progress</i> , 2021, 20, 227-245.	0.5	2
12261	Seed Banks as Incidental Fungi Banks: Fungal Endophyte Diversity in Stored Seeds of Banana Wild Relatives. <i>Frontiers in Microbiology</i> , 2021, 12, 643731.	1.5	12
12262	Phylogeny of the Styracaceae Revisited Based on Whole Plastome Sequences, Including Novel Plastome Data from <i>Parastyrax</i> . <i>Systematic Botany</i> , 2021, 46, 162-174.	0.2	1
12263	Insights into the individual evolutionary origins of <i>Yersinia</i> virulence factor effector proteins. <i>Plasmid</i> , 2021, 114, 102562.	0.4	5
12264	Runes from Lány (Czech Republic) - The oldest inscription among Slavs. A new standard for multidisciplinary analysis of runic bones. <i>Journal of Archaeological Science</i> , 2021, 127, 105333.	1.2	5
12265	Evolutionary Rates are Correlated Between <i>Buchnera</i> Endosymbionts and the Mitochondrial Genomes of Their Aphid Hosts. <i>Journal of Molecular Evolution</i> , 2021, 89, 238-248.	0.8	5
12266	A first insight into the genome of <i>Prototheca wickerhamii</i> , a major causative agent of human protothecosis. <i>BMC Genomics</i> , 2021, 22, 168.	1.2	9
12267	Coagulase-negative staphylococci release a purine analog that inhibits <i>Staphylococcus aureus</i> virulence. <i>Nature Communications</i> , 2021, 12, 1887.	5.8	27
12268	Harnessing machine learning to guide phylogenetic-tree search algorithms. <i>Nature Communications</i> , 2021, 12, 1983.	5.8	20
12270	Investigating species boundaries in <i>Colletotrichum</i> . <i>Fungal Diversity</i> , 2021, 107, 107-127.	4.7	71
12272	Delayed Adaptive Radiation among New Zealand Stream Fishes: Joint Estimation of Divergence Time and Trait Evolution in a Newly Delineated Island Species Flock. <i>Systematic Biology</i> , 2021, 71, 13-23.	2.7	7

#	ARTICLE	IF	CITATIONS
12273	Structure and movement of the hybrid zone between two divergent lineages of the Japanese newt <i>Cynops pyrrhogaster</i> (Amphibia: Urodela) in central Japan. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2021, 59, 1097-1112.	0.6	6
12274	A New SNP-Based Genotyping Method for <i>C. psittaci</i> : Application to Field Samples for Quick Identification. <i>Microorganisms</i> , 2021, 9, 625.	1.6	15
12275	Rapid speciation via the evolution of pre-mating isolation in the Iberian Seedeater. <i>Science</i> , 2021, 371, .	6.0	44
12276	The McdAB system positions $\hat{\pm}$ carboxysomes in proteobacteria. <i>Molecular Microbiology</i> , 2021, 116, 277-297.	1.2	22
12277	Estimating maximal microbial growth rates from cultures, metagenomes, and single cells via codon usage patterns. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	130
12278	Diversity of the insect pathogenic fungi in the genus <i>Metarhizium</i> in New Zealand. <i>New Zealand Journal of Botany</i> , 2021, 59, 440-456.	0.8	7
12279	Multiple Reassortants of H5N8 Clade 2.3.4.4b Highly Pathogenic Avian Influenza Viruses Detected in South Korea during the Winter of 2020–2021. <i>Viruses</i> , 2021, 13, 490.	1.5	46
12280	Tracing the genetic footprints of vertebrate landing in non-teleost ray-finned fishes. <i>Cell</i> , 2021, 184, 1377-1391.e14.	13.5	66
12281	Complete chloroplast genome of <i>Eurya alata</i> : a nectar shrub that blossoms in winter. <i>Pakistan Journal of Botany</i> , 2021, 53, .	0.2	0
12282	A New Remarkable Dwarf Sedge (<i>Carex phylloscirpoides</i> , Cyperaceae) from Northern Chile, with Insights on the Evolution of Austral <i>Carex</i> section <i>Racemosae</i> . <i>Systematic Botany</i> , 2021, 46, 34-47.	0.2	4
12283	Phylogenetic Relationships of <i>Tovomita</i> (Clusiaceae): Carpel Number and Geographic Distribution Speak Louder than Venation Pattern. <i>Systematic Botany</i> , 2021, 46, 102-108.	0.2	1
12284	Genomic Epidemiology of CC30 Methicillin-Resistant <i>Staphylococcus aureus</i> Strains from Argentina Reveals Four Major Clades with Distinctive Genetic Features. <i>MSphere</i> , 2021, 6, .	1.3	11
12285	Signal, bias, and the role of transcriptome assembly quality in phylogenomic inference. <i>Bmc Ecology and Evolution</i> , 2021, 21, 43.	0.7	8
12286	Comparative genome analyses suggest a hemibiotrophic lifestyle and virulence differences for the beech bark disease fungal pathogens <i>Neonectria faginata</i> and <i>Neonectria coccinea</i> . <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	2
12287	Phylogeny and historical biogeography analysis support Caucasian and Mediterranean centres of origin of key holoparasitic Orobanchaeae (Orobanchaceae) lineages. <i>PhytoKeys</i> , 2021, 174, 165-194.	0.4	17
12288	VERSO: A comprehensive framework for the inference of robust phylogenies and the quantification of intra-host genomic diversity of viral samples. <i>Patterns</i> , 2021, 2, 100212.	3.1	26
12290	Genomic surveillance of methicillin-resistant <i>Staphylococcus aureus</i> in the Philippines, 2013–2014. <i>Western Pacific Surveillance and Response Journal: WPSAR</i> , 2021, 12, 6-16.	0.3	5
12291	The Evolution of Sox Gene Repertoires and Regulation of Segmentation in Arachnids. <i>Molecular Biology and Evolution</i> , 2021, 38, 3153-3169.	3.5	10

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12292	Parallel evolution of placental calcium transfer in the lizard <i>Mabuya</i> and eutherian mammals. <i>Journal of Experimental Biology</i> , 2021, 224, .	0.8	2
12293	The <i>Corylus mandshurica</i> genome provides insights into the evolution of Betulaceae genomes and hazelnut breeding. <i>Horticulture Research</i> , 2021, 8, 54.	2.9	20
12294	Emerging carbapenem-resistant <i>Klebsiella pneumoniae</i> sequence type 16 causing multiple outbreaks in a tertiary hospital in southern Vietnam. <i>Microbial Genomics</i> , 2021, 7, .	1.0	14
12295	Comparative analysis of the complete chloroplast genome of seven <i>Nymphaea</i> species. <i>Aquatic Botany</i> , 2021, 170, 103353.	0.8	13
12296	<i>Cocconeis vaiamanuensis</i> sp. nov. (Bacillariophyceae) from Raivavae (South Pacific) and allied taxa: ultrastructural specificities and remarks about the polyphyletic genus <i>Cocconeis</i> Ehrenberg. <i>Marine Biodiversity</i> , 2021, 51, 1.	0.3	2
12297	Population Genomics of the <i>Arcanum</i> Species Group in Wild Tomatoes: Evidence for Separate Origins of Two Self-Compatible Lineages. <i>Frontiers in Plant Science</i> , 2021, 12, 624442.	1.7	3
12300	Molecular phylogeny, historical biogeography and revised classification of andrenine bees (Hymenoptera: Andrenidae). <i>Molecular Phylogenetics and Evolution</i> , 2022, 170, 107151.	1.2	37
12301	Multiple lines of evidence indicate ongoing allopatric and parapatric diversification in an Afromontane sunbird (<i>Cinnyris reichenowi</i>). <i>Auk</i> , 2021, 138, .	0.7	7
12302	Emergence of a <i>Neisseria gonorrhoeae</i> clone with reduced cephalosporin susceptibility between 2014 and 2019 in Amsterdam, The Netherlands, revealed by genomic population analysis. <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 76, 1759-1768.	1.3	17
12303	Disentangling <i>Antirhea</i> (Rubiaceae): resurrection of <i>Guettardella</i> and description of the new genus <i>Achilleanthus</i> . <i>Botanical Journal of the Linnean Society</i> , 2021, 197, 85-103.	0.8	0
12304	Integrative taxonomy of herbaceous plants with narrow fragmented distributions: A case study on <i>Primula merrilliana</i> species complex. <i>Journal of Systematics and Evolution</i> , 2022, 60, 859-875.	1.6	9
12305	Multilocus phylogeny and historical biogeography of <i>Hypostomus</i> shed light on the processes of fish diversification in La Plata Basin. <i>Scientific Reports</i> , 2021, 11, 5073.	1.6	11
12306	Phylogeny, Global Biogeography and Pleomorphism of <i>Zanclospora</i> . <i>Microorganisms</i> , 2021, 9, 706.	1.6	10
12307	Phylogeny, evolution and ecological speciation analyses of <i>Imperata</i> (Poaceae: Andropogoneae) in the Neotropics. <i>Systematics and Biodiversity</i> , 2021, 19, 526-543.	0.5	3
12308	Population genomics of the pathogenic yeast <i>Candida tropicalis</i> identifies hybrid isolates in environmental samples. <i>PLoS Pathogens</i> , 2021, 17, e1009138.	2.1	36
12309	Chromosome-scale genome assembly of <i>Cucumis hystrix</i> a wild species interspecifically cross-compatible with cultivated cucumber. <i>Horticulture Research</i> , 2021, 8, 40.	2.9	18
12310	Characteration and comparative analysis of the whole chloroplast genomes of five common millet (<i>Panicum miliaceum</i>). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 738-744.	0.2	2
12311	Characterization of the complete chloroplast genome of <i>Polyspora tiantangensis</i> (Theaceae), an endemic and endangered species in southwestern China. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 814-815.	0.2	2

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12312	The complete chloroplast genome of <i>Castanea sativa</i> Mill. (Fagaceae). Mitochondrial DNA Part B: Resources, 2021, 6, 1249-1250.	0.2	0
12313	The complete chloroplast genome of <i>Pterospermum menglunense</i> (Sterculiaceae), an endangered species. Mitochondrial DNA Part B: Resources, 2021, 6, 1276-1278.	0.2	0
12314	The complete chloroplast genome of <i>Castanea mollissima</i> "Chuizhili". Mitochondrial DNA Part B: Resources, 2021, 6, 1160-1161.	0.2	1
12315	The complete chloroplast genome of <i>Phlomoides younghusbandii</i> (Lamiaceae), a traditional Tibetan medicinal herb. Mitochondrial DNA Part B: Resources, 2021, 6, 1186-1188.	0.2	3
12316	Draft Genome Sequences of Three Penicillin-Resistant <i>Neisseria gonorrhoeae</i> Strains Isolated in Cincinnati, Ohio, in 1994. Microbiology Resource Announcements, 2021, 10, .	0.3	1
12317	The complete plastome sequence of <i>Tanakaea radicans</i> (Saxifragaceae) and its phylogenetic analysis. Mitochondrial DNA Part B: Resources, 2021, 6, 946-947.	0.2	2
12318	Insight into the Systematics of Microfungi Colonizing Dead Woody Twigs of <i>Dodonaea viscosa</i> in Honghe (China). Journal of Fungi (Basel, Switzerland), 2021, 7, 180.	1.5	25
12319	The complete chloroplast genome of <i>Damnacanthus indicus</i> C.F.Gaertn. (Rubiaceae). Mitochondrial DNA Part B: Resources, 2021, 6, 1251-1252.	0.2	2
12320	The phylogeographic history of <i>Krascheninnikovia</i> reflects the development of dry steppes and semi-deserts in Eurasia. Scientific Reports, 2021, 11, 6645.	1.6	10
12321	Comparative Analysis of Plastid Genomes in the Non-photosynthetic Genus <i>Thismia</i> Reveals Ongoing Gene Set Reduction. Frontiers in Plant Science, 2021, 12, 602598.	1.7	13
12322	A synopsis of the androgynous species of <i>Carex</i> subgenus <i>Vignea</i> (Cyperaceae) in South America. Botanical Journal of the Linnean Society, 2021, 196, 188-220.	0.8	4
12323	Description of a new species of Southeast Asian reed snake from northern Laos (Squamata): <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10</i> 1962. Journal of Natural History, 2021, 55, 531-560.	0.2	2
12324	First complete mitogenomes of three mayflies in the genus <i>Afronurus</i> (Ephemeroptera: Heptageniidae) and their implications for phylogenetic reconstruction. Biologia (Poland), 2021, 76, 2291-2302.	0.8	4
12325	Neonatal hyperoxia induces gut dysbiosis and behavioral changes in adolescent mice. Journal of the Chinese Medical Association, 2021, 84, 290-298.	0.6	11
12326	Global phylogeography of a pantropical mangrove genus <i>Rhizophora</i> . Scientific Reports, 2021, 11, 7228.	1.6	16
12328	Biosystematic studies on the status of <i>Solanum chilense</i> . American Journal of Botany, 2021, 108, 520-537.	0.8	11
12329	Systematics of Lobelioideae (Campanulaceae): review, phylogenetic and biogeographic analyses. PhytoKeys, 2021, 174, 13-45.	0.4	5
12330	New insights into the phylogeny and evolution of lady beetles (Coleoptera: Coccinellidae) by extensive sampling of genes and species. Molecular Phylogenetics and Evolution, 2021, 156, 107045.	1.2	36

#	ARTICLE	IF	CITATIONS
12331	Natural selection in the evolution of SARS-CoV-2 in bats created a generalist virus and highly capable human pathogen. <i>PLoS Biology</i> , 2021, 19, e3001115.	2.6	172
12332	Three New Derivatives of Zopfinol from <i>Pseudorhizophila Mangenotii</i> gen. et comb. nov.. <i>Journal of Fungi</i> (Basel, Switzerland), 2021, 7, 181.	1.5	6
12333	Biogeography and Independent Diversification in the Protist Symbiont Community of <i>Heterotermes tenuis</i> . <i>Frontiers in Ecology and Evolution</i> , 2021, 9, .	1.1	3
12334	IMA genome - F14. <i>IMA Fungus</i> , 2021, 12, 5.	1.7	5
12335	Range and niche expansion through multiple interspecific hybridization: a genotyping by sequencing analysis of <i>Cherleria</i> (Caryophyllaceae). <i>Bmc Ecology and Evolution</i> , 2021, 21, 40.	0.7	2
12336	Complete Genome Sequence, Genome Stability and Phylogeny of the Vaccine Strain <i>Mycobacterium bovis</i> BCG SL222 Sofia. <i>Vaccines</i> , 2021, 9, 237.	2.1	5
12338	The Mitochondrial Genome of a Plant Fungal Pathogen <i>Pseudocercospora fijiensis</i> (Mycosphaerellaceae), Comparative Analysis and Diversification Times of the Sigatoka Disease Complex Using Fossil Calibrated Phylogenies. <i>Life</i> , 2021, 11, 215.	1.1	8
12339	Multiple lines of evidence reveal a new species of Krait (Squamata, Elapidae, <i>Bungarus</i>) from Southwestern China and Northern Myanmar. <i>ZooKeys</i> , 2021, 1025, 35-71.	0.5	10
12340	Filling the Gaps in the Cyanobacterial Tree of Life—Metagenome Analysis of <i>Stigonema ocellatum</i> DSM 106950, <i>Chlorogloea purpurea</i> SAG 13.99 and <i>Gomphosphaeria aponina</i> DSM 107014. <i>Genes</i> , 2021, 12, 389.	1.0	5
12341	Detection of subgenome bias using an anchored syntenic approach in <i>Eleusine coracana</i> (finger) Tj ETQq1 1 0.784314 rgBT /Overlock 1.2 2		
12344	Evidence of gene nucleotide composition favoring replication and growth in a fastidious plant pathogen. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	5
12345	The highly conserved <i>rps12</i> gene in ferns provides strong evidence for decreased substitution rates in the inverted repeat region. <i>Plant Systematics and Evolution</i> , 2021, 307, 1.	0.3	4
12351	Whole-Genome Enrichment and Sequencing of <i>Chlamydia trachomatis</i> Directly from Patient Clinical Vaginal and Rectal Swabs. <i>MSphere</i> , 2021, 6, .	1.3	9
12354	Insights into <i>Acinetobacter baumannii</i> fatty acid synthesis 3-oxoacyl-ACP reductases. <i>Scientific Reports</i> , 2021, 11, 7050.	1.6	9
12355	Pactacin is a novel digestive enzyme in teleosts. <i>Scientific Reports</i> , 2021, 11, 7230.	1.6	4
12356	Comparative Analysis of Complete Chloroplast Genome Sequences in <i>Edgeworthia</i> (Thymelaeaceae) and New Insights Into Phylogenetic Relationships. <i>Frontiers in Genetics</i> , 2021, 12, 643552.	1.1	11
12357	Complex histories of gene flow and a mitochondrial capture event in a nonsister pair of birds. <i>Molecular Ecology</i> , 2021, 30, 2087-2103.	2.0	25
12358	Integrating morphological and molecular approaches for characterizing four species of <i>Dactylogyrus</i> (Monogenea: Dactylogyridae) from Moroccan cyprinids, with comments on their host specificity and phylogenetic relationships. <i>PeerJ</i> , 2021, 9, e10867.	0.9	8

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12359	Diversity of <i>Weissella confusa</i> in Pozol and Its Carbohydrate Metabolism. <i>Frontiers in Microbiology</i> , 2021, 12, 629449.	1.5	6
12360	Transmission and Antibiotic Resistance of <i>Achromobacter</i> in Cystic Fibrosis. <i>Journal of Clinical Microbiology</i> , 2021, 59, .	1.8	30
12361	Allopatric Plant Pathogen Population Divergence following Disease Emergence. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	14
12362	Comparative analysis of complete plastid genomes from <i>Lilium lankongense</i> Franchet and its closely related species and screening of <i>Lilium</i> -specific primers. <i>PeerJ</i> , 2021, 9, e10964.	0.9	1
12364	Recent divergence and lack of shared phylogeographic history characterize the diversification of neotropical savanna birds. <i>Journal of Biogeography</i> , 2021, 48, 1124-1137.	1.4	13
12365	Predicted Input of Uncultured Fungal Symbionts to a Lichen Symbiosis from Metagenome-Assembled Genomes. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	19
12366	Genera specific distribution of DEAD-box RNA helicases in cyanobacteria. <i>Microbial Genomics</i> , 2021, 7, .	1.0	4
12367	The limits of Quediini at last (Staphylinidae: Staphylininae): a rove beetle mega-radiation resolved by comprehensive sampling and anchored phylogenomics. <i>Systematic Entomology</i> , 2021, 46, 396-421.	1.7	16
12368	Epidemiology and Genomic Analysis of Equine Encephalosis Virus Detected in Horses with Clinical Signs in South Africa, 2010–2017. <i>Viruses</i> , 2021, 13, 398.	1.5	6
12369	Molecular evolution and SSRs analysis based on the chloroplast genome of <i>Callitropsis funebris</i> . <i>Ecology and Evolution</i> , 2021, 11, 4786-4802.	0.8	19
12370	Taxonomic turnover and northward phylogenetic clustering reveal evidence for environmental filtering in structuring Trichoptera communities across Europe. <i>Freshwater Biology</i> , 2021, 66, 1060-1073.	1.2	4
12371	The complete chloroplast genome and phylogenetic analysis of <i>Bupleurum yinchowense</i> Shan & Yin Li. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1233-1235.	0.2	0
12372	The complete chloroplast genome of <i>Phyllostachys edulis</i> f. <i>curculmis</i> (Bambusoideae): a newly ornamental bamboo endemic to China. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 941-942.	0.2	1
12373	The complete chloroplast genome sequence of <i>Vernonia amygdalina</i> Delile. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1134-1135.	0.2	2
12374	Complete chloroplast genome sequence and phylogenetic analysis of dragon fruit (<i>Selenicereus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.2	2
12375	Characterization and phylogenetic analysis of the complete plastome of <i>Ipomoea aquatica</i> (Convolvulaceae), an edible vegetable. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 990-992.	0.2	0
12376	The chromosome-level genome of dragon fruit reveals whole-genome duplication and chromosomal co-localization of betacyanin biosynthetic genes. <i>Horticulture Research</i> , 2021, 8, 63.	2.9	25
12377	African lungfish genome sheds light on the vertebrate water-to-land transition. <i>Cell</i> , 2021, 184, 1362-1376.e18.	13.5	99

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12378	Genome-guided investigation of secondary metabolites produced by a potential new strain <i>Streptomyces</i> BA2 isolated from an endemic plant rhizosphere in Turkey. <i>Archives of Microbiology</i> , 2021, 203, 2431-2438.	1.0	12
12379	CD4 receptor diversity represents an ancient protection mechanism against primate lentiviruses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	9
12380	A novel <i>Arabidopsis</i> phyllosphere resident <i>Protomyces</i> species and a re-examination of genus <i>Protomyces</i> based on genome sequence data. <i>IMA Fungus</i> , 2021, 12, 8.	1.7	11
12381	Ancient DNA from the extinct Haitian cave-rail (<i>Nesotrochis steganinos</i>) suggests a biogeographic connection between the Caribbean and Old World. <i>Biology Letters</i> , 2021, 17, 20200760.	1.0	11
12383	Activity of imipenem/relebactam against a Spanish nationwide collection of carbapenemase-producing Enterobacterales. <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 76, 1498-1510.	1.3	27
12384	Pheromone receptor of the globally invasive quarantine pest of the palm tree, the red palm weevil (<i>Rhynchophorus ferrugineus</i>). <i>Molecular Ecology</i> , 2021, 30, 2025-2039.	2.0	30
12385	Parallel and Intertwining Threads of Domestication in Allopolyploid Cotton. <i>Advanced Science</i> , 2021, 8, 2003634.	5.6	45
12386	Identification, subtyping, and tracking of dairy spoilage-associated <i>Pseudomonas</i> by sequencing the ileS gene. <i>Journal of Dairy Science</i> , 2021, 104, 2668-2683.	1.4	7
12387	Isolation and Characterization of <i>Klebsiella</i> Phages for Phage Therapy. <i>Phage</i> , 2021, 2, 26-42.	0.8	36
12388	<i>Micromelanconis kaihuiae</i> gen. et sp. nov., a new diaporthealean fungus from Chinese chestnut branches in southern China. <i>MycKeys</i> , 2021, 79, 1-16.	0.8	2
12390	Unexpected genomic, biosynthetic and species diversity of <i>Streptomyces</i> bacteria from bats in Arizona and New Mexico, USA. <i>BMC Genomics</i> , 2021, 22, 247.	1.2	2
12391	Beginning the quest: phylogenetic hypothesis and identification of evolutionary lineages in bats of the genus <i>Micronycteris</i> (Chiroptera, Phyllostomidae). <i>ZooKeys</i> , 2021, 1028, 135-159.	0.5	3
12392	Molecular Signatures of Reticulate Evolution within the Complex of European Pine Taxa. <i>Forests</i> , 2021, 12, 489.	0.9	1
12393	Species composition and infection levels of <i>Anisakis</i> (Nematoda: Anisakidae) in the skipjack tuna <i>Katsuwonus pelamis</i> (Linnaeus) in the Northwest Pacific. <i>Parasitology Research</i> , 2021, 120, 1605-1615.	0.6	11
12394	Roles of three putative salmon louse (<i>Lepeophtheirus salmonis</i>) prostaglandin E2 synthases in physiology and host-parasite interactions. <i>Parasites and Vectors</i> , 2021, 14, 206.	1.0	10
12395	Museomics and phylogenomics with protein-encoding ultraconserved elements illuminate the evolution of life history and phallic morphology of flesh flies (Diptera: Sarcophagidae). <i>Bmc Ecology and Evolution</i> , 2021, 21, 70.	0.7	9
12396	Biotechnological and Ecological Potential of <i>Micromonospora provocatoris</i> sp. nov., a Gifted Strain Isolated from the Challenger Deep of the Mariana Trench. <i>Marine Drugs</i> , 2021, 19, 243.	2.2	10
12398	Genomic and phenotypic diversity of <i>Enterococcus faecalis</i> isolated from endophthalmitis. <i>PLoS ONE</i> , 2021, 16, e0250084.	1.1	8

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12400	An introgressed gene causes meiotic drive in <i>Neurospora sitophila</i> . Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	26
12402	Molecular Epidemiology of Clinical and Colonizing Methicillin-Resistant Staphylococcus Isolates in Companion Animals. Frontiers in Veterinary Science, 2021, 8, 620491.	0.9	9
12403	Morpho-molecular characterization of <i>Discosia ravennica</i> sp. nov. and a new host record for <i>Sporocadus rosigena</i> . MycoKeys, 2021, 79, 173-192.	0.8	4
12405	<i>Craterellus atrobrunneolus</i> sp. nov. from southwestern China. Mycotaxon, 2021, 136, 59-71.	0.1	4
12406	Lizards of a different stripe: phylogenetics of the <i>Pedioplanis undata</i> species complex (Squamata, Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 262	0.4	2
12407	High Rates of Genome Rearrangements and Pathogenicity of <i>Shigella</i> spp.. Frontiers in Microbiology, 2021, 12, 628622.	1.5	13
12408	The chromosome-level <i>Hemerocallis citrina</i> Borani genome provides new insights into the rutin biosynthesis and the lack of colchicine. Horticulture Research, 2021, 8, 89.	2.9	25
12409	Genetic diversity and population structure of razor clam <i>Sinonovacula constricta</i> in Ariake Bay, Japan, revealed using RAD-Seq SNP markers. Scientific Reports, 2021, 11, 7761.	1.6	6
12410	Systematics of <i>lithistid</i> ™ tetractinellid demosponges from the Tropical Western Atlanticâ€”implications for phylodiversity and bathymetric distribution. PeerJ, 2021, 9, e10775.	0.9	9
12411	Microstructures amplify carotenoid plumage signals in tanagers. Scientific Reports, 2021, 11, 8582.	1.6	17
12412	Middle Pleistocene genome calibrates a revised evolutionary history of extinct cave bears. Current Biology, 2021, 31, 1771-1779.e7.	1.8	27
12413	<i>Opium Poppy Mosaic Virus</i> Has an Xrn-Resistant, Translated Subgenomic RNA and a BTE 3â€² CITE. Journal of Virology, 2021, 95, .	1.5	17
12414	Complete mitochondrial genomes of <i>Epeorus carinatus</i> and <i>E. dayongensis</i> (Ephemeroptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 262	1.0	6
12415	Exploring the industrial potential of <i>Lactobacillus delbrueckii</i> ssp. <i>bulgaricus</i> by population genomics and genome-wide association study analysis. Journal of Dairy Science, 2021, 104, 4044-4055.	1.4	10
12416	Effect of temperature and salinity on the growth and cell size of the first cultures of <i>Gymnodinium aureolum</i> from the Black Sea. Botanica Marina, 2021, 64, 201-210.	0.6	1
12417	Phylogenetics of <i>Piresia</i> (Poaceae: Bambusoideae) reveals unexpected generic relationships within Olyreae with taxonomic and biogeographic implications. Taxon, 2021, 70, 492-514.	0.4	2
12418	Complex interactions underlie the correlated evolution of floral traits and their association with pollinators in a clade with diverse pollination systems. Evolution; International Journal of Organic Evolution, 2021, 75, 1431-1449.	1.1	9
12419	Presence of Broad-Spectrum Beta-Lactamase-Producing Enterobacteriaceae in Zoo Mammals. Microorganisms, 2021, 9, 834.	1.6	9

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12420	Unique Duplication of trnN in <i>Odontoptilum angulatum</i> (Lepidoptera: Pyrginae) and Phylogeny within HesperIIDae. <i>Insects</i> , 2021, 12, 348.	1.0	5
12421	Phylogenomics Reveals that <i>Asaia</i> Symbionts from Insects Underwent Convergent Genome Reduction, Preserving an Insecticide-Degrading Gene. <i>MBio</i> , 2021, 12, .	1.8	10
12422	Repeated evolution of a reproductive polyphenism in plants is strongly associated with bilateral flower symmetry. <i>Current Biology</i> , 2021, 31, 1515-1520.e3.	1.8	13
12423	The full mitochondrial genome sequence of the greater argonaut <i>Argonauta argo</i> (Cephalopoda,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 54 Resources, 2021, 6, 1451-1453.	0.2	5
12424	The complete chloroplast genome of <i>Viburnum sargentii</i> Koehne (Adoxaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1328-1329.	0.2	1
12425	The complete chloroplast genome of <i>Chimonobambusa hejiangensis</i> (Poaceae:) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 54 1285-1286.	0.2	2
12426	The first complete mitochondrial genome of the Northern Pacific deep-sea goniasterid sea star <i>Ceramaster japonicus</i> (Sladen, 1889) determined using NGS-based shotgun sequencing. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1406-1408.	0.2	0
12427	Complete chloroplast genome of <i>Clematis taeguensis</i> (Ranunculaceae), an endemic species from South Korea. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1496-1497.	0.2	3
12428	Genomic insights into the origin, domestication and genetic basis of agronomic traits of castor bean. <i>Genome Biology</i> , 2021, 22, 113.	3.8	32
12430	Molecular characterization of <i>Neisseria gonorrhoeae</i> isolates collected through a national surveillance programme in Japan, 2013: evidence of the emergence of a ceftriaxone-resistant strain from a ceftriaxone-susceptible lineage. <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 76, 1769-1775.	1.3	8
12431	Evolution and genomic insight into methicillin-resistant <i>Staphylococcus aureus</i> ST9 in China. <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 76, 1703-1711.	1.3	11
12432	Antarctic <i>Rahnella inusitata</i> : A Producer of Cold-Stable Î²-Galactosidase Enzymes. <i>International Journal of Molecular Sciences</i> , 2021, 22, 4144.	1.8	8
12433	Historical diversification and biogeography of the endemic southern African dung beetle genus, <i>Epirinus</i> (Scarabaeidae: Scarabaeinae). <i>Biological Journal of the Linnean Society</i> , 2021, 133, 751-765.	0.7	3
12435	Population Genomics of <i>Mycobacterium abscessus</i> from U.S. Cystic Fibrosis Care Centers. <i>Annals of the American Thoracic Society</i> , 2021, 18, 1960-1969.	1.5	42
12436	The chromosome-scale reference genome of safflower (<i>Carthamus tinctorius</i>) provides insights into linoleic acid and flavonoid biosynthesis. <i>Plant Biotechnology Journal</i> , 2021, 19, 1725-1742.	4.1	60
12437	A New, Morphologically Cryptic Species of Fanged Frog, Genus <i>Limnonectes</i> (Amphibia: Anura:) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 54 0,3 2	0.3	2
12438	The Evolution of Calcification in Reef-Building Corals. <i>Molecular Biology and Evolution</i> , 2021, 38, 3543-3555.	3.5	19
12439	Phylogenomic inference of species and subspecies diversity in the Palearctic salamander genus <i>Salamandra</i> . <i>Molecular Phylogenetics and Evolution</i> , 2021, 157, 107063.	1.2	22

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12440	Complete genome sequences of three newly discovered cacao mild mosaic virus isolates from <i>Theobroma cacao</i> L. in Brazil and Puerto Rico and evidence for recombination. <i>Archives of Virology</i> , 2021, 166, 2027-2031.	0.9	7
12441	Reclassification of <i>Catabacter hongkongensis</i> as <i>Christensenella hongkongensis</i> comb. nov. based on whole genome analysis. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	11
12442	Phylogenetic relationship of phototrophic heliobacteria and systematic reconsideration of species and genus assignments based on genome sequences of eight species. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	29
12443	New observations on the large hemidiscoid diatom <i>Palmerina ostenfeldii</i> and its symbiotic ciliate <i>Vaginicola collariforma</i> sp. nov. from subtropical Australian waters. <i>Diatom Research</i> , 2021, 36, 75-91.	0.5	1
12444	Improved de novo chromosome-level genome assembly of the vulnerable walnut tree <i>Juglans mandshurica</i> reveals gene family evolution and possible genome basis of resistance to lesion nematode. <i>Molecular Ecology Resources</i> , 2021, 21, 2063-2076.	2.2	20
12445	Duration of SARS-CoV-2 positive in quarantine room environments: A perspective analysis. <i>International Journal of Infectious Diseases</i> , 2021, 105, 68-74.	1.5	22
12446	Comparative genome analyses of four rice-infecting <i>Rhizoctonia solani</i> isolates reveal extensive enrichment of homogalacturonan modification genes. <i>BMC Genomics</i> , 2021, 22, 242.	1.2	18
12447	Host barriers to SARS-CoV-2 demonstrated by ferrets in a high-exposure domestic setting. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	28
12448	Novel <i>Fusarium</i> mutualists of two <i>Euwallacea</i> species infesting <i>Acacia crassicarpa</i> in Indonesia. <i>Mycologia</i> , 2021, 113, 536-558.	0.8	9
12449	Identification of Bloodmeals from Sand Flies (Diptera: Psychodidae) Collected in the Parque Nacional do Viruã, State of Roraima, Brazil. <i>Journal of Medical Entomology</i> , 2021, 58, 2488-2494.	0.9	4
12450	Simultaneous diversification of Polytopiales and angiosperms in the Mesozoic. <i>Cladistics</i> , 2021, 37, 518-539.	1.5	38
12451	Detection of newly introduced Y280 lineage H9N2 avian influenza viruses in live bird markets in Korea. <i>Transboundary and Emerging Diseases</i> , 2022, 69, 881-885.	1.3	6
12452	Long-term evolution and short-term adaptation of microbiota strains and sub-strains in mice. <i>Cell Host and Microbe</i> , 2021, 29, 650-663.e9.	5.1	58
12453	Ultraconserved elements reconstruct the evolution of Chagas disease vectoring kissing bugs (Reduviidae: Triatominae). <i>Systematic Entomology</i> , 2021, 46, 725-740.	1.7	24
12454	Description of <i>Candidatus Mesopelagibacter carboxydoxydans</i> and <i>Candidatus Anoxipelagibacter denitrificans</i> : Nitrate-reducing SAR11 genera that dominate mesopelagic and anoxic marine zones. <i>Systematic and Applied Microbiology</i> , 2021, 44, 126185.	1.2	14
12455	Genomic analysis uncovers functional variation in the C-terminus of anthocyanin-activating MYB transcription factors. <i>Horticulture Research</i> , 2021, 8, 77.	2.9	28
12457	<i>Plasmodium vinckei</i> genomes provide insights into the pan-genome and evolution of rodent malaria parasites. <i>BMC Biology</i> , 2021, 19, 69.	1.7	10
12458	Genome and Pangenome Analysis of <i>Lactobacillus hilgardii</i> FLUB A New Strain Isolated from Mead. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3780.	1.8	2

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12459	Genomic and acoustic differences separate Lilianâ€™s Meadowlark (<i>Sturnella magna lilianae</i>) from Eastern (<i>S. magna</i>) and Western (<i>S. neglecta</i>) meadowlarks. <i>Auk</i> , 2021, 138, .	0.7	1
12460	Out of the Qinghaiâ€™ Tibetan Plateau and rapid radiation across Eurasia for <i>Allium</i> section <i>Daghestanica</i> (Amaryllidaceae). <i>AoB PLANTS</i> , 2021, 13, plab017.	1.2	7
12461	Mining and evaluating novel serovar-specific <i>Salmonella</i> C1 serogroup genes by polymerase chain reaction analysis. <i>LWT - Food Science and Technology</i> , 2021, 141, 110821.	2.5	5
12463	An integrative approach to address species limits in the southernmost members of the <i>Liolaemus kingii</i> group (Squamata: Liolaemini). <i>Molecular Phylogenetics and Evolution</i> , 2021, 157, 107046.	1.2	5
12464	Phylogeny, divergence times, and diversification in Calophyllaceae: Linking key characters and habitat changes to the evolution of Neotropical Calophylleae. <i>Molecular Phylogenetics and Evolution</i> , 2021, 157, 107041.	1.2	7
12465	Epidemiological Characterization of <i>Listeria monocytogenes</i> Infections in Pavia Province in 2017 Reveals the Presence of Multiple Concurrently Circulating Strains. <i>Foodborne Pathogens and Disease</i> , 2021, 18, 267-275.	0.8	1
12466	Two new species of Neofoleyellides (Nematoda: Onchocercidae) parasitising anuran amphibians in South Africa. <i>International Journal for Parasitology: Parasites and Wildlife</i> , 2021, 14, 298-307.	0.6	4
12467	Genomic Surveillance of a Globally Circulating Distinct Group W Clonal Complex 11 Meningococcal Variant, New Zealand, 2013â€™2018. <i>Emerging Infectious Diseases</i> , 2021, 27, 1087-1097.	2.0	4
12468	Elucidation of Early Evolution of HIV-1 Group M in the Congo Basin Using Computational Methods. <i>Genes</i> , 2021, 12, 517.	1.0	0
12469	Safety and Modulatory Effects of Humanized Galacto-Oligosaccharides on the Gut Microbiome. <i>Frontiers in Nutrition</i> , 2021, 8, 640100.	1.6	9
12471	Host-Switching Events in <i>Litomosoides</i> Chandler, 1931 (Filarioidea: Onchocercidae) are Not Rampant But Clade Dependent. <i>Journal of Parasitology</i> , 2021, 107, 320-335.	0.3	4
12474	Unexpected distribution of the 4-formylaminoxyvinylglycine (FVG) biosynthetic pathway in <i>Pseudomonas</i> and beyond. <i>PLoS ONE</i> , 2021, 16, e0247348.	1.1	8
12477	Mucoralean Fungi in Thailand: Novel Species of <i>Absidia</i> from Tropical Forest Soil. <i>Cryptogamie, Mycologie</i> , 2021, 42, .	0.2	6
12480	DNA-based diversity assessment reveals a new coral barnacle, <i>Cantellius alveopora</i> sp. nov. (Balanomorpha: Pyrgomatidae) exclusively associated with the high latitude coral <i>Alveopora japonica</i> in the waters of southern Korea. <i>PeerJ</i> , 2021, 9, e11284.	0.9	2
12481	Taxonomy, phylogeny, and geographical distribution of the little-known <i>Helicoprordon multinucleatum</i> Dragesco, 1960 (Ciliophora, Haptorida) and key to species within the genus. <i>European Journal of Protistology</i> , 2021, 78, 125769.	0.5	18
12483	Plantâ€™caterpillar food web: Integrating leaf stoichiometry and phylogeny. <i>Ecological Entomology</i> , 2021, 46, 1026-1035.	1.1	2
12485	Nuclear phylogenomics, but not mitogenomics, resolves the most successful Late Miocene radiation of African mammals (Rodentia: Muridae: Arvicanthini). <i>Molecular Phylogenetics and Evolution</i> , 2021, 157, 107069.	1.2	15
12486	A cross-border outbreak of <i>Salmonella</i> Bareilly cases confirmed by whole genome sequencing, Czech Republic and Slovakia, 2017 to 2018. <i>Eurosurveillance</i> , 2021, 26, .	3.9	6

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12487	Genome of a citrus rootstock and global DNA demethylation caused by heterografting. <i>Horticulture Research</i> , 2021, 8, 69.	2.9	45
12488	<i>Aphanomyces astaci</i> mtDNA: insights into the pathogen's differentiation and its genetic diversity from other closely related oomycetes. <i>Fungal Biology</i> , 2021, 125, 316-325.	1.1	10
12489	Phylogeny of true ladybird beetles (Coccinellidae: Coccinellini) reveals pervasive convergent evolution and a rapid Cenozoic radiation. <i>Systematic Entomology</i> , 2021, 46, 611-631.	1.7	13
12490	A global phylogenetic analysis of trapjaw ants, <i>Anochetus</i> Mayr and <i>Odontomachus</i> Latreille (Hymenoptera: Formicidae: Ponerinae). <i>Systematic Entomology</i> , 2021, 46, 685-703.	1.7	9
12491	Genomic insights into persistence of <i>Listeria</i> species in the food processing environment. <i>Journal of Applied Microbiology</i> , 2021, 131, 2082-2094.	1.4	35
12492	Whitefly hijacks a plant detoxification gene that neutralizes plant toxins. <i>Cell</i> , 2021, 184, 1693-1705.e17.	13.5	161
12493	A robust phylogenetic framework for members of the order Legionellales and its main genera (<i>Legionella</i> , <i>Aquicella</i> , <i>Coxiella</i> and <i>Rickettsiella</i>) based on phylogenomic analyses and identification of molecular markers demarcating different clades. <i>Antonie Van Leeuwenhoek</i> , 2021, 114, 957-982.	0.7	20
12494	Seasonal shifts of microbial methane oxidation in Arctic shelf waters above gas seeps. <i>Limnology and Oceanography</i> , 2021, 66, 1896-1914.	1.6	12
12495	Two new lichen species of the genus <i>Ramalina</i> (Ramalinaceae) from China. <i>Bryologist</i> , 2021, 124, .	0.1	0
12496	Composition and temporal dynamics of sand-dwelling dinoflagellate communities from three Mediterranean beaches. <i>Aquatic Microbial Ecology</i> , 2021, 86, 85-98.	0.9	6
12497	Reassortment and Persistence of Influenza A Viruses from Diverse Geographic Origins within Australian Wild Birds: Evidence from a Small, Isolated Population of Ruddy Turnstones. <i>Journal of Virology</i> , 2021, 95, .	1.5	6
12499	An endangered flightless grasshopper with strong genetic structure maintains population genetic variation despite extensive habitat loss. <i>Ecology and Evolution</i> , 2021, 11, 5364-5380.	0.8	18
12500	âœKankashaâœ in Kassala: A prospective observational cohort study of the clinical characteristics, epidemiology, genetic origin, and chronic impact of the 2018 epidemic of Chikungunya virus infection in Kassala, Sudan. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009387.	1.3	13
12501	Phylogenetic and Selection Analysis of an Expanded Family of Putatively Pore-Forming Jellyfish Toxins (Cnidaria: Medusozoa). <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	8
12502	Strain-Resolved Dynamics of the Lung Microbiome in Patients with Cystic Fibrosis. <i>MBio</i> , 2021, 12, .	1.8	13
12503	Description of <i>Nocardioides piscis</i> sp. nov., <i>Sphingomonas piscis</i> sp. nov. and <i>Sphingomonas sinipercae</i> sp. nov., isolated from the intestine of fish species <i>Odontobutis interrupta</i> (Korean spotted sleeper) and <i>Siniperca scherzeri</i> (leopard mandarin fish). <i>Journal of Microbiology</i> , 2021, 59, 552-562.	1.3	23
12504	<i>Etelis boweni</i> sp. nov., a new cryptic deepwater eteline snapper from the Indo-Pacific (Perciformes: Lutjanidae). <i>Journal of Fish Biology</i> , 2021, 99, 335-344.	0.7	2
12505	An approach using ddRADseq and machine learning for understanding speciation in Antarctic Antarctophilinidae gastropods. <i>Scientific Reports</i> , 2021, 11, 8473.	1.6	8

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12506	Genomic features underlying the evolutionary transitions of <i>Apibacter</i> to honey bee gut symbionts. <i>Insect Science</i> , 2022, 29, 259-275.	1.5	13
12507	Phylogenetically diverse diets favor more complex venoms in North American pitvipers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	48
12508	A decadal perspective on north water microbial eukaryotes as Arctic Ocean sentinels. <i>Scientific Reports</i> , 2021, 11, 8413.	1.6	10
12509	Paleogenomics illuminates the evolutionary history of the extinct Holocene "horned" crocodile of Madagascar, <i>Voay robustus</i> . <i>Communications Biology</i> , 2021, 4, 505.	2.0	16
12510	Evolutionary genomics of endangered Hawaiian tree snails (Achatinellidae: Achatinellinae) for conservation of adaptive capacity. <i>PeerJ</i> , 2021, 9, e10993.	0.9	7
12512	Connectivity of Edaphic and Endolithic Microbial Niches in Cold Mountain Desert of Eastern Pamir (Tajikistan). <i>Biology</i> , 2021, 10, 314.	1.3	6
12513	<i>Ophiocordyceps flavida</i> sp. nov. (Ophiocordycipitaceae), a new species from Thailand associated with <i>Pseudogibbellula formicarum</i> (Cordycipitaceae), and their bioactive secondary metabolites. <i>Mycological Progress</i> , 2021, 20, 477-492.	0.5	8
12514	The smallest known heliozoans are the Erebor lineage (nom. clad. n.) inside <i>Microheliella maris</i> (Eukaryota, Diaphoretickes), with the amendment of <i>M. maris</i> diagnosis and description of <i>Berkeleyaesol magnus</i> gen. nov., comb. nov. (Eukaryota, incertae sedis). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	0
12515	The Evolution of Molybdenum Dependent Nitrogenase in Cyanobacteria. <i>Biology</i> , 2021, 10, 329.	1.3	11
12516	Genomic and transcriptomic insights into the habitat adaptation of the diazotrophic paddy field cyanobacterium <i>Nostoc sphaeroides</i> . <i>Environmental Microbiology</i> , 2021, 23, 5802-5822.	1.8	5
12517	Resolved phylogenetic relationships in the <i>Ocotea</i> complex (<i>Supraocotea</i>) facilitate phylogenetic classification and studies of character evolution. <i>American Journal of Botany</i> , 2021, 108, 664-679.	0.8	10
12518	An Investigation of the Variations in Complete Mitochondrial Genomes of <i>Lingula anatina</i> in the Western Pacific Region. <i>Biology</i> , 2021, 10, 367.	1.3	2
12519	The Asian plethodontid salamander preserves historical genetic imprints of recent northern expansion. <i>Scientific Reports</i> , 2021, 11, 9193.	1.6	6
12521	Assessing Temporal Patterns and Species Composition of Glass Eel (<i>Anguilla</i> spp.) Cohorts in Sumatra and Java Using DNA Barcodes. <i>Diversity</i> , 2021, 13, 193.	0.7	2
12523	The efficacy of DNA barcoding in the classification, genetic differentiation, and biodiversity assessment of benthic macroinvertebrates. <i>Ecology and Evolution</i> , 2021, 11, 5669-5681.	0.8	14
12524	Population and subspecies diversity at mouse centromere satellites. <i>BMC Genomics</i> , 2021, 22, 279.	1.2	15
12527	The complete chloroplast genome sequence of <i>Styrax wuyuanensis</i> S. M. Hwang (Styracaceae) from Jiangxi Province, China. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1395-1396.	0.2	0
12528	The complete mitochondrial genome of sea slug <i>Phyllidiopsis krempfi</i> Pruvot-Fol, 1957 (Nudibranchia, Phyllidiidae) from Pacific Ocean. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1523-1524.	0.2	3

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12529	Genetic and morphological relationships of fieldwrens (<i>Calamanthus</i>): implications for conservation status and management. <i>Emu</i> , 2021, 121, 75-89.	0.2	2
12530	Helminth communities of endemic cyprinoids of the Apennine Peninsula, with remarks on ectoparasitic monogeneans, and a description of four new <i>Dactylogyrus</i> species. <i>Parasitology</i> , 2021, 148, 1003-1018.	0.7	5
12531	Molecular Evolutionary Analyses of <i>Euplotes</i> Species Living in Freshwater and Marine Habitats: A Mitogenomic Perspective. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	2
12532	Genome sequencing and comparative genomic analysis of highly and weakly aggressive strains of <i>Sclerotium rolfsii</i> , the causal agent of peanut stem rot. <i>BMC Genomics</i> , 2021, 22, 276.	1.2	20
12533	Phylogenomic analyses reveal a Gondwanan origin and repeated out of India colonizations into Asia by tarantulas (Araneae: Theraphosidae). <i>PeerJ</i> , 2021, 9, e11162.	0.9	5
12535	Geography is more important than life history in the recent diversification of the tiger salamander complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	13
12537	Biogeographic diversification of <i>Eranthis</i> (<i>Ranunculaceae</i>) reflects the geological history of the three great Asian plateaus. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2021, 288, 20210281.	1.2	17
12538	Novelties in <i>Lactifluus</i> subg. <i>Gymnocarpi</i> (<i>Russulales</i> , <i>Basidiomycota</i>) from Brazilian tropical forests. <i>Mycological Progress</i> , 2021, 20, 549-565.	0.5	4
12539	Habitat influences skeletal morphology and density in the snailfishes (family <i>Liparidae</i>). <i>Frontiers in Zoology</i> , 2021, 18, 16.	0.9	13
12540	Diversification in Qinghai-Tibet Plateau: <i>Orchidinae</i> (<i>Orchidaceae</i>) clades exhibiting pre-adaptations play critical role. <i>Molecular Phylogenetics and Evolution</i> , 2021, 157, 107062.	1.2	10
12541	Reacquisition of light-harvesting genes in a marine cyanobacterium confers a broader solar niche. <i>Current Biology</i> , 2021, 31, 1539-1546.e4.	1.8	7
12542	Assessment of <i>Erythrobacter</i> Species Diversity through Pan-Genome Analysis with Newly Isolated <i>Erythrobacter</i> sp. 3-20A1M. <i>Journal of Microbiology and Biotechnology</i> , 2021, 31, 601-609.	0.9	3
12543	Anaerobic gut fungi are an untapped reservoir of natural products. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	35
12544	Large-Scale Phylogenomic Analyses Reveal the Monophyly of Bryophytes and Neoproterozoic Origin of Land Plants. <i>Molecular Biology and Evolution</i> , 2021, 38, 3332-3344.	3.5	56
12545	<i>Litoribacterium kuwaitense</i> gen. nov., sp. nov., isolated from a Kuwait tidal flat. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	8
12546	Vestiges of the Bacterial Signal Recognition Particle-Based Protein Targeting in Mitochondria. <i>Molecular Biology and Evolution</i> , 2021, 38, 3170-3187.	3.5	8
12547	Genetic diversity analysis of Chinese plum (<i>Prunus salicina</i> L.) based on whole-genome resequencing. <i>Tree Genetics and Genomes</i> , 2021, 17, 1.	0.6	12
12548	Molecular evidence for hybridization in the aquatic plant <i>Limosella</i> on sub-Antarctic Marion Island. <i>Antarctic Science</i> , 2021, 33, 243-251.	0.5	2

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12549	Impaired viral infection and reduced mortality of diatoms in iron-limited oceanic regions. <i>Nature Geoscience</i> , 2021, 14, 231-237.	5.4	17
12550	The complete chloroplast genome of <i>Photinia davidsoniae</i> : molecular structures and comparative analysis. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1431-1439.	0.2	3
12551	Antimicrobial Resistance in Porcine Enterococci in Australia and the Ramifications for Human Health. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	13
12552	<i>Colletotrichum gloeosporioides sensu lato</i> associated with anthracnose in <i>Bauhinia forficata</i> . <i>European Journal of Plant Pathology</i> , 2021, 160, 745-751.	0.8	1
12553	<i>Cysteiniphilum marinum</i> sp. nov., isolated from coastal seawater. <i>Antonie Van Leeuwenhoek</i> , 2021, 114, 1079-1089.	0.7	11
12554	A third purine biosynthetic pathway encoded by aminoadenine-based viral DNA genomes. <i>Science</i> , 2021, 372, 516-520.	6.0	40
12555	Chloroplast acquisition without the gene transfer in kleptoplastic sea slugs, <i>Plakobranchus ocellatus</i> . <i>ELife</i> , 2021, 10, .	2.8	29
12556	Systematic Revision of the Sand Scorpions, Genus <i>Buthacus</i> Birula, 1908 (<i>Buthidae</i> C.L. Koch, 1837) of the Levant, with Redescription of <i>Buthacus arenicola</i> (Simon, 1885) from Algeria and Tunisia. <i>Bulletin of the American Museum of Natural History</i> , 2021, 450, .	1.2	5
12557	On the origin of the widespread self-compatible allotetraploid <i>Capsella bursa-pastoris</i> (Brassicaceae). <i>Heredity</i> , 2021, 127, 124-134.	1.2	12
12558	Draft Genome of the Sea Cucumber <i>Holothuria glaberrima</i> , a Model for the Study of Regeneration. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	14
12559	Chromosome-level genome reference and genome editing of the tea geometrid. <i>Molecular Ecology Resources</i> , 2021, 21, 2034-2049.	2.2	8
12560	Chromosome-level genome assembly of burbot (<i>Lota lota</i>) provides insights into the evolutionary adaptations in freshwater. <i>Molecular Ecology Resources</i> , 2021, 21, 2022-2033.	2.2	8
12561	Morphology and molecular phylogeny of three <i>Epistylis</i> species found in freshwater habitats in China, including the description of <i>E. foissneri</i> n. sp. (Ciliophora, Peritrichia). <i>European Journal of Protistology</i> , 2021, 78, 125767.	0.5	16
12562	Phylotranscriptomics reveals the complex evolutionary and biogeographic history of the genus <i>Tsuga</i> with an East Asian-North American disjunct distribution. <i>Molecular Phylogenetics and Evolution</i> , 2021, 157, 107066.	1.2	18
12563	Addressing widespread misidentifications of traditional medicinal mushrooms in <i>Sanghuangporus</i> (Basidiomycota) through ITS barcoding and designation of reference sequences. <i>IMA Fungus</i> , 2021, 12, 10.	1.7	18
12564	Genome-wide identification of sucrose nonfermenting-1-related protein kinase (SnRK) genes in barley and RNA-seq analyses of their expression in response to abscisic acid treatment. <i>BMC Genomics</i> , 2021, 22, 300.	1.2	12
12565	Sequence Analysis and Ontogenetic Expression Patterns of Cone Opsin Genes in the Bluefin Killifish (<i>Lucania goodei</i>). <i>Journal of Heredity</i> , 2021, 112, 357-366.	1.0	11
12566	Evolution of specialization in a plant-microbial mutualism is explained by the oscillation theory of speciation. <i>Evolution; International Journal of Organic Evolution</i> , 2021, 75, 1070-1086.	1.1	11

#	ARTICLE	IF	CITATIONS
12567	Fossil pollen from early Palaeogene sediments in western India provides phylogenetic insights into divergence history and pollen character evolution in the pantropical family Ebenaceae. <i>Botanical Journal of the Linnean Society</i> , 2021, 197, 147-169.	0.8	3
12568	SARS-CoV-2 ORF6 Disrupts Bidirectional Nucleocytoplasmic Transport through Interactions with Rae1 and Nup98. <i>MBio</i> , 2021, 12, .	1.8	92
12569	Tracing the origin of the crayfish plague pathogen, <i>Aphanomyces astaci</i> , to the Southeastern United States. <i>Scientific Reports</i> , 2021, 11, 9332.	1.6	28
12570	Interspecies Genomic Variation and Transcriptional Activeness of Secondary Metabolism-Related Genes in <i>Aspergillus Section Fumigati</i> . <i>Frontiers in Fungal Biology</i> , 2021, 2, .	0.9	5
12571	Universal nomenclature for oxytocinâ€“vasotocin ligand and receptor families. <i>Nature</i> , 2021, 592, 747-755.	13.7	73
12572	BEEExact: a Metataxonomic Database Tool for High-Resolution Inference of Bee-Associated Microbial Communities. <i>MSystems</i> , 2021, 6, .	1.7	20
12573	The complete chloroplast genome sequence of <i>Oxalis corniculata</i> (L.). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1346-1347.	0.2	1
12574	The complete chloroplast genome of <i>Pollia japonica</i> (Commelinaceae) from Southeast China. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1486-1487.	0.2	0
12575	Comparative and phylogenetic analysis of the complete chloroplast genome sequences of <i>Lactuca raddeana</i> and <i>Lactuca sativa</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1498-1506.	0.2	2
12576	Genome-based classification of the <i>Streptomyces violaceusniger</i> clade and description of <i>Streptomyces sabulosicollis</i> sp. nov. from an Indonesian sand dune. <i>Antonie Van Leeuwenhoek</i> , 2021, 114, 859-873.	0.7	12
12577	An integrative taxonomic review of the <i>N</i> -atal mountain catfish, <i>Amphilius natalensis</i> Boulenger 1917 (<i>S</i> -iluriformes, <i>A</i> -mphiliidae), with description of four new species. <i>Journal of Fish Biology</i> , 2021, 99, 219-239.	0.7	8
12578	Lepiotaceous fungi of West Bengal, India: two new species of <i>Leucoagaricus</i> . <i>Mycological Progress</i> , 2021, 20, 493-507.	0.5	4
12579	A comprehensive species sampling sheds light on the molecular phylogenetics of Calothecinae (Poaceae, Pooideae, Poeae): evidence for a new subtribe and multiple genera within the <i>Chascolytrum</i> clade. <i>Journal of Systematics and Evolution</i> , 0, , .	1.6	5
12581	Multiple concurrent and convergent stages of genome reduction in bacterial symbionts across a stink bug family. <i>Scientific Reports</i> , 2021, 11, 7731.	1.6	7
12582	Population genomics and antimicrobial resistance dynamics of <i>Escherichia coli</i> in wastewater and river environments. <i>Communications Biology</i> , 2021, 4, 457.	2.0	20
12583	Genome Characterization of <i>Lactiplantibacillus plantarum</i> Strain UTNGt2 Originated from <i>Theobroma grandiflorum</i> (White Cacao) of Ecuadorian Amazon: Antimicrobial Peptides from Safety to Potential Applications. <i>Antibiotics</i> , 2021, 10, 383.	1.5	22
12585	<i>Saussurea talungensis</i> (Asteraceae), a new species from Humla, Nepal Himalayas. <i>PhytoKeys</i> , 2021, 176, 55-66.	0.4	1
12586	<i>Clitocybula azurea</i> in Argentina: redescription and phylogenetic position. <i>Mycotaxon</i> , 2021, 136, 235-247.	0.1	0

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12587	Systematic Placement of the Enigmatic Southeast Asian Genus <i>Paralamium</i> and an Updated Phylogeny of Tribe Pogostemoneae (Lamiaceae Subfamily Lamioideae). <i>Frontiers in Plant Science</i> , 2021, 12, 646133.	1.7	3
12588	Multi-omics analysis provides insights into lignocellulosic biomass degradation by <i>Laetiporus sulphureus</i> ATCC 52600. <i>Biotechnology for Biofuels</i> , 2021, 14, 96.	6.2	15
12589	Phylogenomic Insights into Distribution and Adaptation of Bdellovibrionota in Marine Waters. <i>Microorganisms</i> , 2021, 9, 757.	1.6	14
12590	Molecular characterization and phylogenetic analyses of <i>Tripartiella macrosoma</i> Basson and Van As, 1987 and <i>Tripartiella obtusa</i> Ergens and Lom, 1970 based on 18S rRNA gene sequence data. <i>Parasitology Research</i> , 2021, 120, 2391-2399.	0.6	1
12591	The genus <i>Agaricus</i> in the Caribbean II. Refined phylogeny of <i>Agaricus</i> subg. <i>Spissicaules</i> with description of two new sections and eight new species. <i>Mycological Progress</i> , 2021, 20, 381-411.	0.5	8
12592	MALDI-TOF mass spectrometry-based identification of Eurotiales from different substrates and locations in Brazil. <i>Mycological Progress</i> , 2021, 20, 539-548.	0.5	1
12593	Mitochondrial phylogeny and taxonomic revision of Italian and Slovenian fluvio-lacustrine barbels, <i>Barbus</i> sp. (Cypriniformes, Cyprinidae). <i>BMC Zoology</i> , 2021, 6, .	0.3	1
12594	Multiple-marker phylogeny and morphological evidence reveal two new species in Steccherinaceae (Polyporales, Basidiomycota) from Asia. <i>MycKeys</i> , 2021, 78, 169-186.	0.8	3
12595	Genome-Wide Analysis of the Temporal Genetic Changes in <i>Streptococcus pneumoniae</i> Isolates of Genotype ST320 and Serotype 19A from South Korea. <i>Microorganisms</i> , 2021, 9, 795.	1.6	2
12598	Diversity of Batrachospermales (Rhodophyta) in the Iberian Peninsula. <i>Fottea</i> , 2021, 21, 73-81.	0.4	1
12599	Evaluating the monophyly of <i>Mammillaria</i> series <i>Supertextae</i> (Cactaceae). <i>PhytoKeys</i> , 2021, 177, 25-42.	0.4	5
12600	ITN-VIROINF: Understanding (Harmful) Virus-Host Interactions by Linking Virology and Bioinformatics. <i>Viruses</i> , 2021, 13, 766.	1.5	5
12603	Grincamycins P-T: Rearranged Angucyclines from the Marine Sediment-Derived <i>Streptomyces</i> sp. CNZ-748 Inhibit Cell Lines of the Rare Cancer Pseudomyxoma Peritonei. <i>Journal of Natural Products</i> , 2021, 84, 1638-1648.	1.5	9
12604	A double-edged sword: Unrecognized cryptic diversity and taxonomic impediment in <i>Eois</i> (Lepidoptera, Geometridae). <i>Zoologica Scripta</i> , 2021, 50, 633-646.	0.7	3
12605	Morphology, ontogenesis and molecular phylogeny of a new saline soil ciliate, <i>Uroleptoides salina</i> nov. spec. (Ciliophora, Hypotrichia). <i>European Journal of Protistology</i> , 2021, 78, 125766.	0.5	12
12606	Large-scale diversity reassessment, evolutionary history, and taxonomic revision of the green macroalgae family Udoteaceae (Bryopsidales, Chlorophyta). <i>Journal of Systematics and Evolution</i> , 2022, 60, 101-127.	1.6	3
12607	Mitochondrial genome of <i>Scutogyrus longicornis</i> (Monogenea: Dactylogyridea), a parasite of Nile tilapia <i>Oreochromis niloticus</i> . <i>Parasitology International</i> , 2021, 81, 102281.	0.6	11
12608	Genome-Wide Analysis of PL7 Alginate Lyases in the Genus <i>Zobellia</i> . <i>Molecules</i> , 2021, 26, 2387.	1.7	8

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12609	Recommendations for epitypification of dinophytes exemplified by <i>Lingulodinium polyedra</i> and molecular phylogenetics of the Gonyaulacales based on curated rRNA sequence data. <i>Harmful Algae</i> , 2021, 104, 101956.	2.2	19
12610	CAZymes in <i>Maribacter dokdonensis</i> 62â€“1 From the Patagonian Shelf: Genomics and Physiology Compared to Related Flavobacteria and a Co-occurring <i>Alteromonas</i> Strain. <i>Frontiers in Microbiology</i> , 2021, 12, 628055.	1.5	13
12611	Complex evolution of novel red floral color in <i>Petunia</i> . <i>Plant Cell</i> , 2021, 33, 2273-2295.	3.1	44
12612	Unraveling microbiomes associated with decomposition of needles of two <i>Pinus</i> species with contrasting fire-adaptive strategies. <i>Biology and Fertility of Soils</i> , 2021, 57, 715-729.	2.3	2
12613	A robust phylogenomic framework for the calamoid palms. <i>Molecular Phylogenetics and Evolution</i> , 2021, 157, 107067.	1.2	13
12614	A new species of <i>Picrasma</i> , <i>P. nanophylla</i> (Simaroubaceae), from the Dominican Republic. <i>Brittonia</i> , 2020, 73, 334.	0.8	3
12615	Characterisation of the Viral Community Associated with the Alfalfa Weevil (<i>Hypera postica</i>) and Its Host Plant, Alfalfa (<i>Medicago sativa</i>). <i>Viruses</i> , 2021, 13, 791.	1.5	10
12616	The diversification of the northern temperate woody flora â€“ A case study of the Elm family (Ulmaceae) based on phylogenomic and paleobotanical evidence. <i>Journal of Systematics and Evolution</i> , 2022, 60, 728-746.	1.6	16
12617	<i>Ruegeria haliotis</i> sp. nov., Isolated from the Gut of the Abalone <i>Haliotis rubra</i> . <i>Current Microbiology</i> , 2021, 78, 2151-2159.	1.0	7
12618	Complete chloroplast genome sequence of a Chinese traditional cultivar in <i>Chrysanthemum morifolium</i> â€“ Anhuishiliuyeâ€™. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1281-1282.	0.2	5
12619	Taxonomy of <i>Ctenomys</i> (Rodentia: Ctenomyidae) in northwestern Patagonia, Argentina: the occurrence of the â€œ <i>mendocinus</i> â€•lineage. <i>Mammalia</i> , 2021, 85, 482-486.	0.3	4
12620	Phylogenomic and morphological relationships among the botryllid ascidians (Subphylum Tunicata,) Tj ETQq1 1 0.784314 rgBT /Overbo	1.6	14
12621	Host-Diet Effect on the Metabolism of <i>Bifidobacterium</i> . <i>Genes</i> , 2021, 12, 609.	1.0	17
12622	Chromosome-scale assembly and analysis of biomass crop <i>Miscanthus lutarioriparius</i> genome. <i>Nature Communications</i> , 2021, 12, 2458.	5.8	25
12623	Phylogenomics and Historical Biogeography of Seahorses, Dragonets, Goatfishes, and Allies (Teleostei: Syngnatharia): Assessing Factors Driving Uncertainty in Biogeographic Inferences. <i>Systematic Biology</i> , 2021, 70, 1145-1162.	2.7	24
12624	Multiple independent recombinations led to hermaphroditism in grapevine. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	32
12625	Large-scale sequencing of flatfish genomes provides insights into the polyphyletic origin of their specialized body plan. <i>Nature Genetics</i> , 2021, 53, 742-751.	9.4	30
12626	Six-State Amino Acid Recoding is not an Effective Strategy to Offset Compositional Heterogeneity and Saturation in Phylogenetic Analyses. <i>Systematic Biology</i> , 2021, 70, 1200-1212.	2.7	31

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12627	Assessing the taxonomy of <i>Heterometra</i> -like feather stars (Echinodermata: Crinoidea). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 747</i> 632-647.	0.5	2
12628	A review of the taxonomy of spiny-backed orb-weaving spiders of the subfamily Gasteracanthinae (Araneae, Araneidae) in Thailand. <i>ZooKeys</i> , 2021, 1032, 17-62.	0.5	2
12629	Seagrass (<i>Zostera marina</i>) promotes nitrification potential and selects specific ammonia oxidizers in coastal sediments. <i>Journal of Soils and Sediments</i> , 2021, 21, 3259-3273.	1.5	12
12630	Complete Mitochondrial Genomes of <i>Paedocypris micromegethes</i> and <i>Paedocypris carbunculus</i> Reveal Conserved Gene Order and Phylogenetic Relationships of Miniaturized Cyprinids. <i>Frontiers in Ecology and Evolution</i> , 2021, 9, .	1.1	5
12631	High drug resistance levels could compromise the control of HIV infection in paediatric and adolescent population in Kinshasa, the Democratic Republic of Congo. <i>PLoS ONE</i> , 2021, 16, e0248835.	1.1	4
12632	A new synonym of <i>Polygonatum</i> in China, based on morphological and molecular evidence. <i>PhytoKeys</i> , 2021, 175, 137-149.	0.4	4
12633	Evolutionary diversification of cytokinin-specific glucosyltransferases in angiosperms and enigma of missing cis-zeatin O-glucosyltransferase gene in Brassicaceae. <i>Scientific Reports</i> , 2021, 11, 7885.	1.6	5
12636	Molecular and Phylogenetic Characterization of Novel Papillomaviruses Isolated from Oral and Anogenital Neoplasms of Japanese Macaques (<i>Macaca fuscata</i>). <i>Viruses</i> , 2021, 13, 630.	1.5	0
12637	Multi-Drug Resistant Plasmids with ESBL/AmpC and mcr-5.1 in Paraguayan Poultry Farms: The Linkage of Antibiotic Resistance and Hatcheries. <i>Microorganisms</i> , 2021, 9, 866.	1.6	6
12638	Morphological and genetic differentiation in the anguid lizard <i>Pseudopus apodus</i> supports the existence of an endemic subspecies in the Levant. <i>Vertebrate Zoology</i> , 0, 71, 175-200.	2.0	7
12642	Comparative analysis of the complete chloroplast genomes of <i>Cirsium japonicum</i> from China and Korea. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1468-1470.	0.2	3
12643	Genetic variation of staphylococcal LukAB toxin determines receptor tropism. <i>Nature Microbiology</i> , 2021, 6, 731-745.	5.9	14
12644	A New Geometrid Genus from the Southwestern United States (Lepidoptera: Geometridae). <i>Proceedings of the Entomological Society of Washington</i> , 2021, 123, .	0.0	0
12645	Predictive Models of Genetic Redundancy in <i>Arabidopsis thaliana</i> . <i>Molecular Biology and Evolution</i> , 2021, 38, 3397-3414.	3.5	16
12646	Toxic effects in <i>Aphanomyces brasiliensis</i> and zebrafish embryos caused by oomycetocides. <i>Diseases of Aquatic Organisms</i> , 2021, 144, 75-87.	0.5	3
12647	Hidden Evolutionary Units and Its Implications on Conservation in a Vulnerable Species of a Freshwater Fish. <i>Zebrafish</i> , 2021, 18, 149-161.	0.5	1
12648	The piggyBac-derived protein 5 (PGBD5) transposes both the closely and the distantly related piggyBac-like elements Tcr-pble and Ifp2. <i>Journal of Molecular Biology</i> , 2021, 433, 166839.	2.0	5
12649	The origin and subgenome dynamics of the octoploid strawberries. <i>Acta Horticulturae</i> , 2021, , 107-118.	0.1	2

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12650	Molecular characterisation of <i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i> in Australia. <i>BMC Microbiology</i> , 2021, 21, 101.	1.3	6
12651	Diversity of Kallymeniaceae (Gigartinales, Rhodophyta) associated with Hawaiian mesophotic reefs. <i>European Journal of Phycology</i> , 2022, 57, 68-78.	0.9	6
12652	Mix and match: Patchwork domain evolution of the land plant-specific Ca ²⁺ -permeable mechanosensitive channel MCA. <i>PLoS ONE</i> , 2021, 16, e0249735.	1.1	10
12653	A functional bacteria-derived restriction modification system in the mitochondrion of a heterotrophic protist. <i>PLoS Biology</i> , 2021, 19, e3001126.	2.6	6
12654	Molecular phylogeny and new light microscopic data of <i>Metchnikovella spiralis</i> (Microsporidia) in <i>T. ETQq0 0 0 rgBT /Overlock 10 Tf 50 58</i> <i>elegans</i> . <i>Parasitology</i> , 2021, 148, 779-786.	0.7	2
12656	A Primer on the Analysis of High-Throughput Sequencing Data for Detection of Plant Viruses. <i>Microorganisms</i> , 2021, 9, 841.	1.6	36
12657	Rapid detection and differentiation of mobile colistin resistance (<i>mcr-1</i> to <i>mcr-10</i>) genes by real-time PCR and melt-curve analysis. <i>Journal of Hospital Infection</i> , 2021, 110, 148-155.	1.4	13
12658	The complete mitochondrial genome sequences of <i>Brassica napus</i> varieties NY18 and O88018. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1429-1430.	0.2	0
12659	Peculiarities of the inverted repeats in the complete chloroplast genome of <i>Strobilanthes bantonensis</i> Lindau. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1440-1447.	0.2	1
12660	The complete chloroplast genome of <i>Bupleurum euphorbioides</i> , a traditional medicinal plant. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1332-1334.	0.2	0
12661	Phylogeny and divergence dating of the ladybird beetle tribe Coccinellini Latreille (Coleoptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 34	1.7	8
12662	High-throughput sequencing of the kelp <i>Alaria</i> (Phaeophyceae) reveals epi-endobiotic associations, including a likely phaeophycean parasite. <i>European Journal of Phycology</i> , 2021, 56, 494-504.	0.9	7
12663	Complex reticulate evolution of speckled brush-furred rats (<i>Lophuromys</i>) in the Ethiopian centre of endemism. <i>Molecular Ecology</i> , 2021, 30, 2349-2365.	2.0	21
12664	Asexuality Associated with Marked Genomic Expansion of Tandemly Repeated rRNA and Histone Genes. <i>Molecular Biology and Evolution</i> , 2021, 38, 3581-3592.	3.5	9
12665	Molecular phylogenetics and premating isolation in the punctoid land snails of Belau (Republic of Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.7	3
12666	A multilocus phylogeny of the moss genus <i>Didymodon</i> and allied genera (Pottiaceae): Generic delimitations and their implications for systematics. <i>Journal of Systematics and Evolution</i> , 2022, 60, 281-304.	1.6	16
12667	Olive anthracnose caused by <i>Colletotrichum</i> in Uruguay: symptoms, species diversity and pathogenicity on flowers and fruits. <i>European Journal of Plant Pathology</i> , 2021, 160, 663-681.	0.8	13
12668	Stepwise pathogenic evolution of <i>Mycobacterium abscessus</i> . <i>Science</i> , 2021, 372, .	6.0	91

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12669	Morphology, ontogeny and molecular phylogeny of a new urostyleid ciliate, <i>Bakuella</i> (<i>Pseudobakuella</i>) <i>guangdongica</i> n. sp. (Ciliophora, Hypotrichia) from southern China. <i>European Journal of Protistology</i> , 2021, 81, 125795.	0.5	6
12670	Cycad-Weevil Pollination Symbiosis Is Characterized by Rapidly Evolving and Highly Specific Plant-Insect Chemical Communication. <i>Frontiers in Plant Science</i> , 2021, 12, 639368.	1.7	8
12671	First Report of Fruit Canker Caused by <i>Nothophoma quercina</i> on Chinese Quince in South Korea. <i>Plant Disease</i> , 2021, 105, 3760.	0.7	5
12672	<i>Stachybotrys musae</i> sp. nov., <i>S. microsporus</i> , and <i>Memnoniella levispora</i> (Stachybotryaceae.) Tj ETQq1 1 0.784314 rgBT /Overlock 10 1.1 P 5		
12673	New lineages of photobionts in Bolivian lichens expand our knowledge on habitat preferences and distribution of <i>Asterochloris</i> algae. <i>Scientific Reports</i> , 2021, 11, 8701.	1.6	15
12674	Discriminating arboviral species. <i>Journal of General Virology</i> , 2021, 102, .	1.3	1
12675	Taxonomy and species diversity of <i>Padina</i> (Dictyotales, Phaeophyceae) from the Indo-Pacific with the description of two new species. <i>European Journal of Phycology</i> , 2022, 57, 1-17.	0.9	2
12676	New species and a new record of <i>Phylloporia</i> from Benin. <i>Scientific Reports</i> , 2021, 11, 8879.	1.6	1
12677	A Novel Microbial Zearalenone Transformation through Phosphorylation. <i>Toxins</i> , 2021, 13, 294.	1.5	9
12678	A survey of <i>Hebeloma</i> (Hymenogastraceae) in Greenland. <i>MycKeys</i> , 2021, 79, 17-118.	0.8	8
12679	<i>Rhodolitica</i> on rhodoliths: a new stoloniferan genus (Anthozoa, Octocorallia, Alcyonacea). <i>ZooKeys</i> , 2021, 1032, 63-77.	0.5	3
12684	Genomics reveals the novel species placement of industrial contaminant isolates incorrectly identified as <i>Burkholderia lata</i> . <i>Microbial Genomics</i> , 2021, 7, .	1.0	2
12685	<i>Tigridiopalma exalata</i> , a new and endangered species of Melastomataceae from China. <i>PhytoKeys</i> , 2021, 176, 33-42.	0.4	2
12686	Discordant Phylogenomic Placement of Hydnoraceae and Lactoridaceae Within Piperales Using Data From All Three Genomes. <i>Frontiers in Plant Science</i> , 2021, 12, 642598.	1.7	19
12687	Frequency, Local Dynamics, and Genomic Characteristics of ESBL-Producing <i>Escherichia coli</i> Isolated From Specimens of Hospitalized Horses. <i>Frontiers in Microbiology</i> , 2021, 12, 671676.	1.5	10
12688	New Glomeromycotan Taxa, <i>Dominikia glomerocarpica</i> sp. nov. and <i>Epigeocarpum crypticum</i> gen. nov. et sp. nov. From Brazil, and <i>Silvaspora</i> gen. nov. From New Caledonia. <i>Frontiers in Microbiology</i> , 2021, 12, 655910.	1.5	12
12690	Genetic Analysis of Formosan Subterranean Termite (Blattodea: Rhinotermitidae) Populations in California. <i>Journal of Economic Entomology</i> , 2021, 114, 1264-1269.	0.8	7
12691	Discovery of the first Amazonian <i>Thomasomys</i> (Rodentia, Cricetidae, Sigmodontinae): a new species from the remote Cordilleras del C�ndor and Kutuk� in Ecuador. <i>Journal of Mammalogy</i> , 2021, 102, 615-635.	0.6	11

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12692	<i>Brassica rapa</i> Domestication: Untangling Wild and Feral Forms and Convergence of Crop Morphotypes. <i>Molecular Biology and Evolution</i> , 2021, 38, 3358-3372.	3.5	30
12693	An Alternative and Conserved Cell Wall Enzyme That Can Substitute for the Lipid II Synthase MurG. <i>MBio</i> , 2021, 12, .	1.8	6
12694	Diverse phylogenomic datasets uncover a concordant scenario of laurasiatherian interordinal relationships. <i>Molecular Phylogenetics and Evolution</i> , 2021, 157, 107065.	1.2	4
12695	Phylogenomics of <i>Fargesia</i> and <i>Yushania</i> reveals a history of reticulate evolution. <i>Journal of Systematics and Evolution</i> , 2021, 59, 1183-1197.	1.6	9
12696	MolluscDB: a genome and transcriptome database for molluscs. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2021, 376, 20200157.	1.8	17
12697	Redescription of <i>Emplectonema viride</i> – a ubiquitous intertidal hoplonemertean found along the West Coast of North America. <i>ZooKeys</i> , 2021, 1031, 1-17.	0.5	7
12698	Evolutionary history of Heptapteridae catfishes using ultraconserved elements (Teleostei,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 502 Td	0.7	18
12700	<i>Haslea silbo</i> , A Novel Cosmopolitan Species of Blue Diatoms. <i>Biology</i> , 2021, 10, 328.	1.3	12
12701	Gregarine single-cell transcriptomics reveals differential mitochondrial remodeling and adaptation in apicomplexans. <i>BMC Biology</i> , 2021, 19, 77.	1.7	30
12702	Phylogeography of <i>Mytilisepta virgata</i> (Mytilidae: Bivalvia) in the northwestern Pacific: Cryptic mitochondrial lineages and mito-nuclear discordance. <i>Molecular Phylogenetics and Evolution</i> , 2021, 157, 107037.	1.2	11
12703	Phylogenomics of Gesneriaceae using targeted capture of nuclear genes. <i>Molecular Phylogenetics and Evolution</i> , 2021, 157, 107068.	1.2	46
12704	High-Fiber, Whole-Food Dietary Intervention Alters the Human Gut Microbiome but Not Fecal Short-Chain Fatty Acids. <i>MSystems</i> , 2021, 6, .	1.7	69
12705	Characterization of the complete chloroplast genome of China <i>Viburnum burejaeticum</i> Regel et Herd and intra-species diversity. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1353-1354.	0.2	2
12706	Characterization of the complete chloroplast genome of <i>Pterocarya macroptera</i> var. <i>delavayi</i> (Juglandaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1344-1345.	0.2	1
12707	<i>Rhodocybe cistetorum</i> (Basidiomycota, Entolomataceae), a new species from the Colchic ecoregion of Turkey. <i>Nordic Journal of Botany</i> , 2021, 39, .	0.2	1
12708	Western Tethys origin, tropical Asia and tropical America disjunction in <i>Berchemia</i> and reinstatement of <i>Phyllogeiton</i> (Rhamnaceae, Rhamnaceae). <i>Taxon</i> , 2021, 70, 515-525.	0.4	1
12709	Systematics of <i>Brucepattersonius</i> Hershkovitz, 1998 (Rodentia, Sigmodontinae): molecular species delimitation and morphological analyses suggest an overestimation in species diversity. <i>Systematics and Biodiversity</i> , 2021, 19, 544-570.	0.5	0
12710	Spatial phylogenetics of butterflies in relation to environmental drivers and angiosperm diversity across North America. <i>IScience</i> , 2021, 24, 102239.	1.9	22

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12711	Detection of <i>Gambierdiscus</i> and <i>Fukuyoa</i> single cells using recombinase polymerase amplification combined with a sandwich hybridization assay. <i>Journal of Applied Phycology</i> , 2021, 33, 2273-2282.	1.5	7
12712	Extensive microbial diversity within the chicken gut microbiome revealed by metagenomics and culture. <i>PeerJ</i> , 2021, 9, e10941.	0.9	79
12713	<i>Brevilactibacter coleopterorum</i> sp. nov., isolated from the intestine of the dark diving beetle <i>Hydrophilus acuminatus</i> , and <i>Weissella coleopterorum</i> sp. nov., isolated from the intestine of the diving beetle <i>Cybister lewisianus</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	17
12714	Mobile Type VI secretion system loci of the gut Bacteroidales display extensive intra-ecosystem transfer, multi-species spread and geographical clustering. <i>PLoS Genetics</i> , 2021, 17, e1009541.	1.5	32
12715	Widespread lateral gene transfer among grasses. <i>New Phytologist</i> , 2021, 230, 2474-2486.	3.5	24
12716	Structural Insights into the Interaction of the Intrinsically Disordered Co-activator TIF2 with Retinoic Acid Receptor Heterodimer (RXR/RAR). <i>Journal of Molecular Biology</i> , 2021, 433, 166899.	2.0	14
12717	Integrative descriptions of two new species of <i>Dugesia</i> from Hainan Island, China (Platyhelminthes,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.5	9
12719	Genomic epidemiological analysis identifies high relapse among individuals with recurring tuberculosis and provides evidence of recent household-related transmission of tuberculosis in Ghana. <i>International Journal of Infectious Diseases</i> , 2021, 106, 13-22.	1.5	3
12720	Characterization of the complete chloroplast genome of <i>Centranthera grandiflora</i> Benth (Orobanchaceae), an important species of medicinal herb. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1784-1785.	0.2	2
12721	Complete chloroplast genome sequences of <i>Lagotis brevituba</i> (Plantaginaceae): a famous Tibetan medicine plant. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1638-1639.	0.2	0
12722	Complete mitogenome of the entomopathogenic fungus <i>Metarhizium album</i> and phylogenetic analysis of Hypocreales. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1689-1690.	0.2	1
12723	Integration of early disease-resistance phenotyping, histological characterization, and transcriptome sequencing reveals insights into downy mildew resistance in <i>Impatiens</i> . <i>Horticulture Research</i> , 2021, 8, 108.	2.9	5
12724	<i>Gorgorhynchoides pseudocarangis</i> n. sp. (Acanthocephala: Isthmosacanthidae) from <i>Pseudocarax dentex</i> (Carangidae) in southeast Queensland, Australia, with comments on the Isthmosacanthidae. <i>Systematic Parasitology</i> , 2021, 98, 399-412.	0.5	2
12725	Exploring parallel MPI fault tolerance mechanisms for phylogenetic inference with RAxML-NG. <i>Bioinformatics</i> , 2021, 37, 4056-4063.	1.8	4
12726	Common bacterial blight of bean: a model of seed transmission and pathological convergence. <i>Molecular Plant Pathology</i> , 2021, 22, 1464-1480.	2.0	16
12727	Revisiting the hyperdominance of Neotropical tree species under a taxonomic, functional and evolutionary perspective. <i>Scientific Reports</i> , 2021, 11, 9585.	1.6	13
12728	Decreased soil moisture due to warming drives phylogenetic diversity and community transitions in the tundra. <i>Environmental Research Letters</i> , 2021, 16, 064031.	2.2	10
12732	Distribution of Merlin in eukaryotes and first report of DNA transposons in kinetoplastid protists. <i>PLoS ONE</i> , 2021, 16, e0251133.	1.1	1

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12733	Investigating the Circulation of Ebola Viruses in Bats during the Ebola Virus Disease Outbreaks in the Equateur and North Kivu Provinces of the Democratic Republic of Congo from 2018. <i>Pathogens</i> , 2021, 10, 557.	1.2	13
12734	A new species, phylogeny, and a worldwide key of the edible wood decay <i>Fistulina</i> (Agaricales). <i>Mycological Progress</i> , 2021, 20, 733-746.	0.5	7
12735	Horizontal transfer and evolution of wall teichoic acid gene cassettes in <i>Bacillus subtilis</i> . <i>F1000Research</i> , 2021, 10, 354.	0.8	4
12736	Diversity, Distribution and Phylogenetic Relationships of Deep-Sea Lithistids (Porifera). <i>TJ ETQq1 1 0.784314 rgBT / Overlock 10 Tf 50 62</i>	1.2	5
12739	A high-quality carabid genome assembly provides insights into beetle genome evolution and cold adaptation. <i>Molecular Ecology Resources</i> , 2021, 21, 2145-2165.	2.2	13
12740	The Presence of Ancient Core Genes Reveals Endogenization from Diverse Viral Ancestors in Parasitoid Wasps. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	14
12741	Base-substitution mutation rate across the nuclear genome of <i>Alpheus</i> snapping shrimp and the timing of isolation by the Isthmus of Panama. <i>Bmc Ecology and Evolution</i> , 2021, 21, 104.	0.7	6
12742	Comparative genome sequencing reveals insights into the dynamics of <i>Wolbachia</i> in native and invasive cherry fruit flies. <i>Molecular Ecology</i> , 2021, 30, 6259-6272.	2.0	17
12745	<i>Pseudomonas aeruginosa</i> infection in augmented care: the molecular ecology and transmission dynamics in four large UK hospitals. <i>Journal of Hospital Infection</i> , 2021, 111, 162-168.	1.4	12
12746	Long- and short-read metabarcoding technologies reveal similar spatiotemporal structures in fungal communities. <i>Molecular Ecology Resources</i> , 2021, 21, 1833-1849.	2.2	16
12747	Ecological niche divergence between the brown recluse spiders <i>Loxosceles laeta</i> and <i>L. surca</i> (Sicariidae) in Chile. <i>Journal of Natural History</i> , 2021, 55, 1177-1193.	0.2	4
12748	Prisons as ecological drivers of fitness-compensated multidrug-resistant <i>Mycobacterium tuberculosis</i> . <i>Nature Medicine</i> , 2021, 27, 1171-1177.	15.2	43
12749	A Novel Broad Host Range Phage Infecting <i>Alteromonas</i> . <i>Viruses</i> , 2021, 13, 987.	1.5	9
12750	Modular Molecular Weaponry Plays a Key Role in Competition Within an Environmental <i>Vibrio cholerae</i> Population. <i>Frontiers in Microbiology</i> , 2021, 12, 671092.	1.5	15
12751	Phylogenetic relatedness drives protist assembly in marine and terrestrial environments. <i>Global Ecology and Biogeography</i> , 2021, 30, 1532-1544.	2.7	9
12752	Chromosomal-Level Reference Genome of the Neotropical Tree <i>Jacaranda mimosifolia</i> D. Don. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	7
12753	Demographic history and local adaptation of <i>Myriopholis dioica</i> (Asteraceae) provide insight on plant evolution in northern China flora. <i>Ecology and Evolution</i> , 2021, 11, 8000-8013.	0.8	8
12754	Plastid genome sequencing, identification of nuclear SNP markers, and quality assessment of medicinal rhizomatous herb <i>Polygonatum odoratum</i> (Asparagaceae) cultivars. <i>Ecology and Evolution</i> , 2021, 11, 7660-7676.	0.8	4

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12755	Phylogenomic conflict coincides with rapid morphological innovation. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	40
12756	Type II Photosynthetic Reaction Center Genes of Avocado (<i>Persea americana</i> Mill.) Bark Microbial Communities are Dominated by Aerobic Anoxygenic Alphaproteobacteria. Current Microbiology, 2021, 78, 2623-2630.	1.0	2
12758	Evolutionary drivers of sexual signal variation in Amazon Slender Anoles. Evolution; International Journal of Organic Evolution, 2021, 75, 1361-1376.	1.1	2
12759	Aquaculture mediates global transmission of a viral pathogen to wild salmon. Science Advances, 2021, 7, .	4.7	24
12760	Population transcriptomic sequencing reveals allopatric divergence and local adaptation in <i>Pseudotaxus chienii</i> (Taxaceae). BMC Genomics, 2021, 22, 388.	1.2	11
12761	Highly rearranged mitochondrial genome in <i>Falcolipeurus</i> lice (Phthiraptera: Philopteridae) from endangered eagles. Parasites and Vectors, 2021, 14, 269.	1.0	6
12763	Prevalence, genomic characteristics, and transmission dynamics of mcr-1-positive <i>Salmonella enterica</i> Typhimurium from patients with infectious diarrhea. International Journal of Medical Microbiology, 2021, 311, 151501.	1.5	8
12764	Myoglobin primary structure reveals multiple convergent transitions to semi-aquatic life in the world's smallest mammalian divers. ELife, 2021, 10, .	2.8	8
12765	<i>Ampelomyces</i> strains isolated from diverse powdery mildew hosts in Japan: Their phylogeny and mycoparasitic activity, including timing and quantifying mycoparasitism of <i>Pseudoidium neolycopersici</i> on tomato. PLoS ONE, 2021, 16, e0251444.	1.1	9
12766	The identification of a transposon affecting the asexual reproduction of the wheat pathogen <i>Zymoseptoria tritici</i> . Molecular Plant Pathology, 2021, 22, 800-816.	2.0	17
12767	Robustness of Phylogenetic Inference to Model Misspecification Caused by Pairwise Epistasis. Molecular Biology and Evolution, 2021, 38, 4603-4615.	3.5	3
12768	Population genomics provides insights into the evolution and adaptation to humans of the waterborne pathogen <i>Mycobacterium kansasii</i> . Nature Communications, 2021, 12, 2491.	5.8	20
12769	Collapsing dubiously resolved gene-tree branches in phylogenomic coalescent analyses. Molecular Phylogenetics and Evolution, 2021, 158, 107092.	1.2	24
12770	<i>Aquiluna borgnonia</i> gen. nov., sp. nov., a member of a Microbacteriaceae lineage of freshwater bacteria with small genome sizes. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	16
12771	SARS-CoV-2 Infections and Viral Isolations among Serially Tested Cats and Dogs in Households with Infected Owners in Texas, USA. Viruses, 2021, 13, 938.	1.5	123
12772	The cytochrome P450 (CYP) superfamily in cnidarians. Scientific Reports, 2021, 11, 9834.	1.6	7
12773	Use of unbiased metagenomic and transcriptomic analyses to investigate the association between feline calicivirus and feline chronic gingivostomatitis in domestic cats. American Journal of Veterinary Research, 2021, 82, 381-394.	0.3	18
12774	New Coelomycetous Fungi from Freshwater in Spain. Journal of Fungi (Basel, Switzerland), 2021, 7, 368.	1.5	9

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12775	Evaluation of the S-locus in <i>Prunus domestica</i> , characterization, phylogeny and 3D modelling. <i>PLoS ONE</i> , 2021, 16, e0251305.	1.1	7
12776	First complete mitogenomes of Diamesinae, Orthoclaadiinae, Prodiamesinae, Tanytopodinae (Diptera): Tj ETQq1 1 0.784314 rgBT /Overlo	0.9	18
12777	A phylogeny for the <i>Drosophila montium</i> species group: A model clade for comparative analyses. <i>Molecular Phylogenetics and Evolution</i> , 2021, 158, 107061.	1.2	19
12778	Fossil-Informed Models Reveal a Boreotropical Origin and Divergent Evolutionary Trajectories in the Walnut Family (Juglandaceae). <i>Systematic Biology</i> , 2021, 71, 242-258.	2.7	37
12779	The Evolution Pathway of Ammonia-Oxidizing Archaea Shaped by Major Geological Events. <i>Molecular Biology and Evolution</i> , 2021, 38, 3637-3648.	3.5	33
12780	The demographic and ecological factors shaping diversification among rare <i>Astragalus</i> species. <i>Diversity and Distributions</i> , 2021, 27, 1407-1421.	1.9	11
12781	Genome of the butterfly hillstream loach provides insights into adaptations to torrential mountain stream life. <i>Molecular Ecology Resources</i> , 2021, 21, 1922-1935.	2.2	1
12782	The genome of the European estuarine calanoid copepod <i>Eurytemora affinis</i> : Potential use in molecular ecotoxicology. <i>Marine Pollution Bulletin</i> , 2021, 166, 112190.	2.3	14
12783	A new species of <i>Sakuraeolis</i> from Mozambique, described using 3D reconstruction of anatomy and phylogenetic analysis. <i>Journal of Molluscan Studies</i> , 2021, 87, .	0.4	4
12784	Low diversity of a key phytoplankton group along the West Antarctic Peninsula. <i>Limnology and Oceanography</i> , 2021, 66, 2470-2480.	1.6	13
12787	A Machine Learning Approach to Prioritizing Functionally Active F-box Members in <i>Arabidopsis thaliana</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 639253.	1.7	3
12788	The Evolution of Rag Gene Enhancers and Transcription Factor E and Id Proteins in the Adaptive Immune System. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5888.	1.8	7
12790	First detection of porcine respirovirus 1 in Germany and the Netherlands. <i>Transboundary and Emerging Diseases</i> , 2021, 68, 3120-3125.	1.3	15
12791	Coadaptation between host genome and microbiome under long-term xenobiotic-induced selection. <i>Science Advances</i> , 2021, 7, .	4.7	14
12792	Genealogical relationship inference to identify areas of intensive poaching of the Orange-fronted Parakeet (<i>Eupsittula canicularis</i>). <i>BMC Zoology</i> , 2021, 6, .	0.3	0
12794	Disjoint Tree Mergers for Large-Scale Maximum Likelihood Tree Estimation. <i>Algorithms</i> , 2021, 14, 148.	1.2	7
12795	Genes Encoding Microbial Acyl Coenzyme A Binding Protein/Diazepam-Binding Inhibitor Orthologs Are Rare in the Human Gut Microbiome and Show No Links to Obesity. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0047121.	1.4	7
12796	Hercide Atrazine Alters the Microbiota of the Filamentous Green Alga <i>Cladophora</i> sp. Cultured from Thailand. <i>Sains Malaysiana</i> , 2021, 50, 1255-1265.	0.3	1

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12797	Novel <i>Acinetobacter baumannii</i> Myovirus TaPaz Encoding Two Tailspike Depolymerases: Characterization and Host-Recognition Strategy. <i>Viruses</i> , 2021, 13, 978.	1.5	7
12798	Development and evaluation of a target enrichment bait set for phylogenetic analysis of oomycetes. <i>Mycologia</i> , 2021, 113, 856-867.	0.8	5
12799	Revealing two centuries of confusion: new insights on nomenclature and systematic position of <i>Argyrogena fasciolata</i> (Shaw, 1802) (auctt.), with description of a new species from India (Reptilia: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.8	5
12800	Pathogenic potential assessment of the Shiga toxin-producing <i>Escherichia coli</i> by a source attribution—considered machine learning model. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	8
12801	Disease management in two sympatric <i>Apterostigma</i> fungus-growing ants for controlling the parasitic fungus <i>Escovopsis</i> . <i>Ecology and Evolution</i> , 2021, 11, 6041-6052.	0.8	3
12802	The complete chloroplast genome sequence of <i>Heteropolygonatum ginfushanicum</i> (Asparagaceae) and phylogenetic analysis. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1799-1802.	0.2	2
12803	Eukaryotic Biodiversity and Spatial Patterns in the Clarion-Clipperton Zone and Other Abyssal Regions: Insights From Sediment DNA and RNA Metabarcoding. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	33
12804	Integrated omics analyses reveal differential gene expression and potential for cooperation between denitrifying polyphosphate and glycogen accumulating organisms. <i>Environmental Microbiology</i> , 2021, 23, 3274-3293.	1.8	17
12805	Genomic variation of an endosymbiotic dinoflagellate (<i>Symbiodinium fitti</i>) among closely related coral hosts. <i>Molecular Ecology</i> , 2021, 30, 3500-3514.	2.0	21
12806	<i>Massilia horti</i> sp. nov. and <i>Noviherbaspirillum arenae</i> sp. nov., two novel soil bacteria of the Oxalobacteraceae. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	12
12808	Prevalence and relationship of endosymbiotic <i>Wolbachia</i> in the butterfly genus <i>Erebia</i> . <i>Bmc Ecology and Evolution</i> , 2021, 21, 95.	0.7	9
12810	Microbiome characterization of defensive tissues in the model anemone <i>Exaiptasia diaphana</i> . <i>BMC Microbiology</i> , 2021, 21, 152.	1.3	14
12811	Genome Reduction and Secondary Metabolism of the Marine Sponge-Associated Cyanobacterium <i>Leptothoe</i> . <i>Marine Drugs</i> , 2021, 19, 298.	2.2	4
12812	<i>Radula subacuminata</i> , a new epiphyllous species of <i>Radula</i> (Marchantiophyta) from China and Vietnam. <i>Bryologist</i> , 2021, 124, .	0.1	1
12813	Visibility and attractiveness of <i>Fritillaria</i> (Liliaceae) flowers to potential pollinators. <i>Scientific Reports</i> , 2021, 11, 11006.	1.6	8
12814	Pan-Genome Analysis Reveals Host-Specific Functional Divergences in <i>Burkholderia gladioli</i> . <i>Microorganisms</i> , 2021, 9, 1123.	1.6	13
12816	Oral Microbiome in Relation to Periodontitis Severity and Systemic Inflammation. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5876.	1.8	38
12817	Two new invasive bark beetles (Coleoptera: Curculionidae) in mainland China and their potential distribution in Asia. <i>Pest Management Science</i> , 2021, 77, 4000-4008.	1.7	12

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12819	Genomic Analysis of Avian Infectious Bronchitis Viruses Recently Isolated in South Korea Reveals Multiple Introductions of GI-19 Lineage (QX Genotype). <i>Viruses</i> , 2021, 13, 1045.	1.5	9
12820	Comparative phylogenetics of repetitive elements in a diverse order of flowering plants (Brassicales). <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	15
12821	The complete chloroplast genome of <i>Zanthoxylum bungeanum</i> var. <i>pubescens</i> with distinct leaf shapes. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1768-1769.	0.2	0
12822	Root Digger: a root placement program for phylogenetic trees. <i>BMC Bioinformatics</i> , 2021, 22, 225.	1.2	20
12823	Phylogeny and temporal diversification of mosquitoes (Diptera: Culicidae) with an emphasis on the Neotropical fauna. <i>Systematic Entomology</i> , 2021, 46, 798-811.	1.7	20
12824	Anchored Phylogenomics, Evolution and Systematics of Elateridae: Are All Bioluminescent Elateroidea Derived Click Beetles?. <i>Biology</i> , 2021, 10, 451.	1.3	39
12825	<i>Listeria cossartiae</i> sp. nov., <i>Listeria immobilis</i> sp. nov., <i>Listeria portnoyi</i> sp. nov. and <i>Listeria rustica</i> sp. nov., isolated from agricultural water and natural environments. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	54
12826	Plastome structure and phylogenetic relationships of Styracaceae (Ericales). <i>Bmc Ecology and Evolution</i> , 2021, 21, 103.	0.7	13
12827	Identification and characterization of andalusicin: N-terminally dimethylated class III lantibiotic from <i>Bacillus thuringiensis</i> sv. <i>andalousiensis</i> . <i>IScience</i> , 2021, 24, 102480.	1.9	18
12828	Positive selection plays a major role in shaping signatures of differentiation across the genomic landscape of two independent <i>Ficedula</i> flycatcher species pairs*. <i>Evolution; International Journal of Organic Evolution</i> , 2021, 75, 2179-2196.	1.1	18
12829	SARS-CoV-2 gene content and COVID-19 mutation impact by comparing 44 Sarbecovirus genomes. <i>Nature Communications</i> , 2021, 12, 2642.	5.8	136
12830	Rampant Genome-Wide Admixture across the <i>Heliconius</i> Radiation. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	31
12831	Characterization of an Infectious Bronchitis Virus Isolated from Commercial Layers Suffering from False Layer Syndrome. <i>Avian Diseases</i> , 2021, 65, 373-380.	0.4	7
12832	<i>Azohydromonas caseinilytica</i> sp. nov., a Nitrogen-Fixing Bacterium Isolated From Forest Soil by Using Optimized Culture Method. <i>Frontiers in Microbiology</i> , 2021, 12, 647132.	1.5	14
12833	Evidence for Glacial Refugia of the Forest Understorey Species <i>Helleborus niger</i> (Ranunculaceae) in the Southern as Well as in the Northern Limestone Alps. <i>Frontiers in Plant Science</i> , 2021, 12, 683043.	1.7	9
12835	Plastid phylogenomics provides novel insights into the infrafamilial relationship of Polypodiaceae. <i>Cladistics</i> , 2021, 37, 717-727.	1.5	12
12836	Extensive Comparative Genomic Analysis of <i>Enterococcus faecalis</i> and <i>Enterococcus faecium</i> Reveals a Direct Association between the Absence of CRISPR-Cas Systems, the Presence of Anti-Endonuclease (<i>ardA</i>) and the Acquisition of Vancomycin Resistance in <i>E. faecium</i> . <i>Microorganisms</i> , 2021, 9, 1118.	1.6	6
12837	Metagenomic Characterization of Soil Microbial Communities in the Luquillo Experimental Forest (Puerto Rico) and Implications for Nitrogen Cycling. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0054621.	1.4	8

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12838	Molecular Analysis of SARS-CoV-2 Circulating in Bangladesh during 2020 Revealed Lineage Diversity and Potential Mutations. <i>Microorganisms</i> , 2021, 9, 1035.	1.6	7
12839	African and Asian leopards are highly differentiated at the genomic level. <i>Current Biology</i> , 2021, 31, 1872-1882.e5.	1.8	20
12840	Mulching has negative impact on fungal and plant diversity in Slovak oligotrophic grasslands. <i>Basic and Applied Ecology</i> , 2021, 52, 24-37.	1.2	5
12841	Taxonomic and phylogenetic contributions to <i>Celtis formosana</i> , <i>Ficus ampelas</i> , <i>F. septica</i> , <i>Macaranga tanarius</i> and <i>Morus australis</i> leaf litter inhabiting microfungi. <i>Fungal Diversity</i> , 2021, 108, 1-215.	4.7	48
12842	Macroecological diversification and convergence in a clade of keystone symbionts. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	14
12843	HERMES: An improved method to test mitochondrial genome molecular synapomorphies among clades. <i>Mitochondrion</i> , 2021, 58, 285-295.	1.6	2
12844	Recent developments of HDAC inhibitors: Emerging indications and novel molecules. <i>British Journal of Clinical Pharmacology</i> , 2021, 87, 4577-4597.	1.1	168
12845	<i>Natronoglycomyces albus</i> gen. nov., sp. nov, a haloalkaliphilic actinobacterium from a soda solonchak soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	12
12846	To lump, to split or to maintain? Molecular taxonomy of the spotted barb <i>Barbodes binotatus</i> (<i>Cyprinidae</i>) and closely related species in <i>Peninsular Malaysia</i> . <i>Journal of Fish Biology</i> , 2021, 99, 656-668.	0.7	3
12847	<i>In Vivo</i> Generation of BK and JC Polyomavirus Defective Viral Genomes in Human Urine Samples Associated with Higher Viral Loads. <i>Journal of Virology</i> , 2021, 95, .	1.5	9
12848	A phylogenomic supermatrix of Galliformes (Landfowl) reveals biased branch lengths. <i>Molecular Phylogenetics and Evolution</i> , 2021, 158, 107091.	1.2	26
12850	The pseudodichotomous <i>Dasya sylviae</i> sp. nov. (Delesseriaceae, Ceramiales) from 60–90 m mesophotic reefs off Bermuda. <i>European Journal of Taxonomy</i> , 0, 751, 24-37.	0.6	3
12853	Disruption of the odorant coreceptor Orco impairs foraging and host finding behaviors in the New World screwworm fly. <i>Scientific Reports</i> , 2021, 11, 11379.	1.6	7
12855	Reflections on <i>Menisporopsis</i> , <i>Multiguttulispora</i> and <i>Tainosphaeria</i> Using Molecular and Morphological Data. <i>Journal of Fungi</i> (Basel, Switzerland), 2021, 7, 438.	1.5	7
12856	The evolution of hard tick-borne relapsing fever borreliae is correlated with vector species rather than geographical distance. <i>Bmc Ecology and Evolution</i> , 2021, 21, 105.	0.7	10
12857	Evolution of the “world’s only alpine parrot”: Genomic adaptation or phenotypic plasticity, behaviour and ecology?. <i>Molecular Ecology</i> , 2021, 30, 6370-6386.	2.0	11
12858	Impacts of allopolyploidization and structural variation on intraspecific diversification in <i>Brassica rapa</i> . <i>Genome Biology</i> , 2021, 22, 166.	3.8	80
12859	Uncovering hidden species diversity of alopoglossid lizards in Amazonia, with the description of three new species of <i>Alopoglossus</i> (Squamata: Gymnophthalmoidae). <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2021, 59, 1322-1356.	0.6	3

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12861	Whole mitogenome analysis and phylogeny of freshwater fish red-finned catopra (<i>Pristolepis</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 742	0.4	3
12862	Four Species Linked by Three Hybrid Zones: Two Instances of Repeated Hybridization in One Species Group (Genus <i>Liolaemus</i>). <i>Frontiers in Ecology and Evolution</i> , 2021, 9, .	1.1	6
12863	Nuclear phylotranscriptomics and phylogenomics support numerous polyploidization events and hypotheses for the evolution of rhizobial nitrogen-fixing symbiosis in Fabaceae. <i>Molecular Plant</i> , 2021, 14, 748-773.	3.9	86
12864	Whole-genome sequencing and phylogenetic analysis of rabies viruses from Jordan. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009431.	1.3	6
12865	HIV Drug Resistance and Transmission Networks Among a Justice-Involved Population at the Time of Community Reentry in Washington, D.C.. <i>AIDS Research and Human Retroviruses</i> , 2021, 37, 903-912.	0.5	2
12867	Historical biogeography of <i>Pomaderris</i> (Rhamnaceae): Continental vicariance in Australia and repeated independent dispersals to New Zealand. <i>Molecular Phylogenetics and Evolution</i> , 2021, 158, 107085.	1.2	15
12868	Metagenomics and Culture-Based Diversity Analysis of the Bacterial Community in the Zharkent Geothermal Spring in Kazakhstan. <i>Current Microbiology</i> , 2021, 78, 2926-2934.	1.0	7
12869	The complete chloroplast genome sequence of <i>Dryobalanops aromatica</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1687-1688.	0.2	2
12870	The complete mitochondrial genome of <i>Microconidiobolus nodosus</i> (<i>Entomophthorales</i> : <i>Ancylistaceae</i>). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1743-1744.	0.2	4
12871	The complete chloroplast genome of <i>Gaultheria fragrantissima</i> Wall. (Ericaceae) from Yunnan, China, an aromatic medicinal plant in the wintergreens. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1761-1762.	0.2	1
12872	The complete mitochondrial genome of <i>Nothochrysa sinica</i> (Neuroptera: Chrysopidae) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 347 Td (N 2021, 6, 1632-1633.	0.2	1
12873	The complete chloroplast genome of <i>Walla Patta</i> , <i>Gyrinops walla</i> (Thymelaeaceae), an agarwood-producing tree species from Sri Lanka. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1699-1701.	0.2	2
12874	The complete chloroplast genome of <i>Pluchea pteropoda</i> Hemsl, a mangrove associate plant. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1729-1731.	0.2	2
12875	Molecular and morphological clocks for estimating evolutionary divergence times. <i>Bmc Ecology and Evolution</i> , 2021, 21, 83.	0.7	7
12876	Warts Galore “ on Three New <i>Lamprospora</i> De Not. Species (Pezizales) from Southern Europe and Macaronesia and a Type Revision of Three Species Described from the US by F. J. Seaver in the 1910s. <i>Cryptogamie, Mycologie</i> , 2021, 42, .	0.2	1
12877	Geographical vs. ecological diversification in <i>Carex</i> section <i>Phacocystis</i> (Cyperaceae): Patterns hidden behind a twisted taxonomy. <i>Journal of Systematics and Evolution</i> , 2021, 59, 642-667.	1.6	17
12878	Interdomain horizontal gene transfer of nickel-binding superoxide dismutase. <i>Geobiology</i> , 2021, 19, 450-459.	1.1	11
12879	Phylogenetic assessment and taxonomic revision of <i>Halobyssothecium</i> and <i>Lentithecium</i> (Lentitheciaceae, Pleosporales). <i>Mycological Progress</i> , 2021, 20, 701-720.	0.5	12

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12880	Phylogenomic Insights into the Origin of Primary Plastids. <i>Systematic Biology</i> , 2021, 71, 105-120.	2.7	22
12881	Reflections on <i>Canalisporium</i> , with descriptions of new species and records from Taiwan. <i>Mycological Progress</i> , 2021, 20, 647-680.	0.5	7
12882	Peripheral taste detection in honey bees: What do taste receptors respond to?. <i>European Journal of Neuroscience</i> , 2021, 54, 4417-4444.	1.2	22
12884	Exploring the vertebrate fauna of the Bird's Head Peninsula (Indonesia, West Papua) through DNA barcodes. <i>Molecular Ecology Resources</i> , 2021, 21, 2369-2387.	2.2	10
12886	The pESI mega-plasmid conferring virulence and multiple-drug resistance is detected in <i>Salmonella Infantis</i> genome from Brazil. <i>Infection, Genetics and Evolution</i> , 2021, 95, 104934.	1.0	10
12887	Reconstruction of ancient microbial genomes from the human gut. <i>Nature</i> , 2021, 594, 234-239.	13.7	139
12888	The genome of <i>Nautilus pompilius</i> illuminates eye evolution and biomineralization. <i>Nature Ecology and Evolution</i> , 2021, 5, 927-938.	3.4	40
12889	Two repeated motifs enriched within some enhancers and origins of replication are bound by SETMAR isoforms in human colon cells. <i>Genomics</i> , 2021, 113, 1589-1604.	1.3	5
12891	Comparative Analysis of Mitochondrial Genome Features among Four <i>Clonostachys</i> Species and Insight into Their Systematic Positions in the Order Hypocreales. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5530.	1.8	7
12893	Unravelling the Symbiotic Microalgal Diversity in <i>Buellia zoharyi</i> (Lichenized Ascomycota) from the Iberian Peninsula and Balearic Islands Using DNA Metabarcoding. <i>Diversity</i> , 2021, 13, 220.	0.7	10
12894	An Integrative Bioinformatic Analysis for Keratinase Detection in Marine-Derived <i>Streptomyces</i> . <i>Marine Drugs</i> , 2021, 19, 286.	2.2	2
12895	Transcriptome Analysis Identifies a Gene Cluster for the Biosynthesis of Biruloquinone, a Rare Phenanthraquinone, in a Lichen-Forming Fungus <i>Cladonia macilenta</i> . <i>Journal of Fungi (Basel)</i> , 2021, 7, 1077.	0.7	1
12899	An overview of <i>Favolus</i> from the Neotropics, including four new species. <i>Mycologia</i> , 2021, 113, 759-775.	0.8	3
12900	Analysis of Paralogs in Target Enrichment Data Pinpoints Multiple Ancient Polyploidy Events in <i>Alchemilla</i> s.l. (Rosaceae). <i>Systematic Biology</i> , 2021, 71, 190-207.	2.7	26
12901	Genome Skimming Reveals Widespread Hybridization in a Neotropical Flowering Plant Radiation. <i>Frontiers in Ecology and Evolution</i> , 2021, 9, .	1.1	15
12902	Unraveling a Lignocellulose-Decomposing Bacterial Consortium from Soil Associated with Dry Sugarcane Straw by Genomic-Centered Metagenomics. <i>Microorganisms</i> , 2021, 9, 995.	1.6	17
12904	Whole-genome resequencing of <i>Osmanthus fragrans</i> provides insights into flower color evolution. <i>Horticulture Research</i> , 2021, 8, 98.	2.9	35
12905	The complete chloroplast genome of <i>Strobilanthes biocullata</i> (Acanthaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1668-1669.	0.2	2

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12906	The complete mitochondrial genome of <i>Anneissia intermedia</i> (Crinoidea: Comatulida: Comatulidae). Mitochondrial DNA Part B: Resources, 2021, 6, 1777-1778.	0.2	1
12907	Genomic reconstruction of fossil and living microorganisms in ancient Siberian permafrost. Microbiome, 2021, 9, 110.	4.9	17
12908	Evolution of reproductive strategies in the species-rich land snail subfamily Phaedusinae (Stylommatophora: Clausiliidae). Molecular Phylogenetics and Evolution, 2021, 158, 107060.	1.2	10
12909	Phylogenetic analysis of the salinipostin $\hat{1}^3$ -butyrolactone gene cluster uncovers new potential for bacterial signalling-molecule diversity. Microbial Genomics, 2021, 7, .	1.0	8
12910	The Eastern Nebraska Salt Marsh Microbiome Is Well Adapted to an Alkaline and Extreme Saline Environment. Life, 2021, 11, 446.	1.1	5
12912	Mitochondrial Phylogenomics of Tenthredinidae (Hymenoptera: Tenthredinoidea) Supports the Monophyly of Megabelesesinae as a Subfamily. Insects, 2021, 12, 495.	1.0	7
12913	Revisited Molecular Phylogeny of the Genus <i>Sphaerotheca</i> (Anura: Dicroglossidae): The Biogeographic Status of Northernmost Populations and Further Taxonomic Changes. Diversity, 2021, 13, 216.	0.7	6
12914	Genome of the fatal tapeworm <i>Sparganum proliferum</i> uncovers mechanisms for cryptic life cycle and aberrant larval proliferation. Communications Biology, 2021, 4, 649.	2.0	9
12915	A revised multilocus phylogeny of Old World sparrows (Aves: Passeridae). Vertebrate Zoology, 0, 71, 353-366.	2.0	2
12916	Complete Mitochondrial Genome of <i>Bubo bubo</i> (Aves, Strigiformes, Strigidae), a National Protected Wildlife Bird in China. Cytology and Genetics, 2021, 55, 270-273.	0.2	0
12917	Reassessment of Suitable Markers for Taxonomy of Chaetophorales (Chlorophyceae, Chlorophyta) based on Chloroplast Genomes. Journal of Eukaryotic Microbiology, 2021, 68, e12858.	0.8	3
12918	Role of Phylogenetic Structure in the Dynamics of Coastal Viral Assemblages. Applied and Environmental Microbiology, 2021, 87, .	1.4	6
12920	Molecular Identification of Plerocercoids of <i>Clistobothrium montaukensis</i> (Cestoda: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 267 Td (Phyll 1586-1592.	0.4	2
12921	Warts Galore “ on Three New <i>Lamprospora</i> De Not. Species (Pezizales) from Southern Europe and Macaronesia and a Type Revision of Three Species Described from the US by F. J. Seaver in the 1910s. Cryptogamie, Mycologie, 2021, 42, .	0.2	5
12922	Update of seagrass cover and species diversity in Southern Viet Nam using remote sensing data and molecular analyses. Regional Studies in Marine Science, 2021, 44, 101803.	0.4	4
12924	The Subcellular Proteome of a Planctomycetes Bacterium Shows That Newly Evolved Proteins Have Distinct Fractionation Patterns. Frontiers in Microbiology, 2021, 12, 643045.	1.5	8
12925	<i>Fomitiporia punicata</i> and <i>Phaeoacremonium minimum</i> associated with Esca complex of grapevine in China. Phytopathology Research, 2021, 3, .	0.9	5
12926	<i>Coxiella burnetii</i> and Related Tick Endosymbionts Evolved from Pathogenic Ancestors. Genome Biology and Evolution, 2021, 13, .	1.1	27

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12928	New insight to the role of microbes in the methane exchange in trees: evidence from metagenomic sequencing. <i>New Phytologist</i> , 2021, 231, 524-536.	3.5	23
12929	Early embryogenesis and organogenesis in the annelid <i>Owenia fusiformis</i> . <i>EvoDevo</i> , 2021, 12, 5.	1.3	42
12930	A chromosome-level genome of a Kordofan melon illuminates the origin of domesticated watermelons. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	37
12931	Sample Sequence Analysis Uncovers Recurrent Horizontal Transfers of Transposable Elements among Grasses. <i>Molecular Biology and Evolution</i> , 2021, 38, 3664-3675.	3.5	10
12932	Phylogenetic placement of the enigmatic longhorned beetle <i>Vesperoctenus flohri</i> Bates (Vesperidae) and a first description of its female internal structures. <i>Arthropod Systematics and Phylogeny</i> , 0, 79, 99-114.	5.5	6
12933	Phylogenomics and biogeography of <i>Wisteria</i> : Implications on plastome evolution among inverted repeat-lacking clade (IRLC) legumes. <i>Journal of Systematics and Evolution</i> , 2022, 60, 253-265.	1.6	10
12934	Characterization of the Complete Mitochondrial Genome of Basidiomycete Yeast <i>Hannaella oryzae</i> : Intron Evolution, Gene Rearrangement, and Its Phylogeny. <i>Frontiers in Microbiology</i> , 2021, 12, 646567.	1.5	25
12935	Two new <i>Nothophytophthora</i> species from streams in Ireland and Northern Ireland: <i>Nothophytophthora irlandica</i> and <i>N. lirii</i> sp. nov.. <i>PLoS ONE</i> , 2021, 16, e0250527.	1.1	6
12936	Target sequence capture in orchids: Developing a kit to sequence hundreds of single-copy loci. <i>Applications in Plant Sciences</i> , 2021, 9, e11416.	0.8	21
12937	Gut Microbial SNPs Induced by High-Fiber Diet Dominate Nutrition Metabolism and Environmental Adaption of <i>Faecalibacterium prausnitzii</i> in Obese Children. <i>Frontiers in Microbiology</i> , 2021, 12, 683714.	1.5	8
12938	Evidence from oyster suggests an ancient role for Pdx in regulating insulin gene expression in animals. <i>Nature Communications</i> , 2021, 12, 3117.	5.8	10
12939	Hidden diversity of <i>Macrophomina</i> associated with broadacre and horticultural crops in Australia. <i>European Journal of Plant Pathology</i> , 2021, 161, 1-23.	0.8	23
12940	Identifying potential candidate <i>Culicoides</i> spp. for the study of interactions with <i>Candidatus Cardinium hertigii</i> . <i>Medical and Veterinary Entomology</i> , 2021, 35, 501-506.	0.7	0
12941	Toward a Stable Global Noctuidae (Lepidoptera) Taxonomy. <i>Insect Systematics and Diversity</i> , 2021, 5, .	0.7	24
12943	Ancient horse genomes reveal the timing and extent of dispersals across the Bering Land Bridge. <i>Molecular Ecology</i> , 2021, 30, 6144-6161.	2.0	30
12944	<i>Melanothamnus macaronensis</i> Rodr�guez-Buj�n & D�az-Tapia, sp. nov. (Rhodomelaceae,) <i>Tj ETQq1 1 0.784314 rgBT /Overlock</i> <i>Algologie</i> , 2021, 42, .	0.3	3
12945	Comprehensive phylogeny of <i>Konosirus punctatus</i> (Clupeiformes: Clupeidae) based on transcriptomic data. <i>Bioscience Reports</i> , 2021, 41, .	1.1	2
12946	Genomic Analysis of the Yet-Uncultured <i>Binatota</i> Reveals Broad Methylotrophic, Alkane-Degradation, and Pigment Production Capacities. <i>MBio</i> , 2021, 12, .	1.8	13

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12947	Kelp-associated Microbiota are Structured by Host Anatomy. Journal of Phycology, 2021, 57, 1119-1130.	1.0	22
12948	The new genus Pulvinora (Lecanoraceae) for species of the <i>Lecanora pringlei</i> group, including the new species <i>Pulvinora stereothallina</i> . Bryologist, 2021, 124, .	0.1	6
12949	Revision of the phylogeny of Placididea (Stramenopiles): Molecular and morphological diversity of novel placidid protists from extreme aquatic environments. European Journal of Protistology, 2021, 81, 125809.	0.5	9
12950	Molecular Characterization of 4/91 Infectious Bronchitis Virus Leading to Studies of Pathogenesis and Host Responses in Laying Hens. Pathogens, 2021, 10, 624.	1.2	10
12953	Integrative genomic analysis of blood pressure and related phenotypes in rats. DMM Disease Models and Mechanisms, 2021, 14, .	1.2	6
12954	The mitogenome of <i>Phytophthora agathidicida</i> : Evidence for a not so recent arrival of the <i>œkauri</i> killing <i>Phytophthora</i> in New Zealand. PLoS ONE, 2021, 16, e0250422.	1.1	8
12955	Fungal communities of submerged fine detritus from temperate peatland and stream habitats. Aquatic Microbial Ecology, 2021, 86, 191-207.	0.9	2
12956	Genetic variation, environment and demography intersect to shape <i>Arabidopsis</i> defense metabolite variation across Europe. ELife, 2021, 10, .	2.8	33
12957	The complete chloroplast genome sequence of <i>Strobilanthes tonkinensis</i> Lindau. Mitochondrial DNA Part B: Resources, 2021, 6, 1786-1787.	0.2	0
12958	The complete chloroplast genome sequence of <i>Bambusa vulgaris</i> cv. Wamin. Mitochondrial DNA Part B: Resources, 2021, 6, 1704-1705.	0.2	0
12959	The genome of the Pyrenean desman and the effects of bottlenecks and inbreeding on the genomic landscape of an endangered species. Evolutionary Applications, 2021, 14, 1898-1913.	1.5	11
12960	Population genomics and phylogeography of the boll weevil, <i>Anthonomus grandis</i> Boheman (Coleoptera: Curculionidae), in the United States, northern Mexico, and Argentina. Evolutionary Applications, 2021, 14, 1778-1793.	1.5	10
12961	Digging deep: a revised phylogeny of Australian burrowing cockroaches (Blaberidae: Panesthiinae.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 evolution of burrowing. Systematic Entomology, 2021, 46, 767-783.	1.7	9
12962	Comparative analysis of chloroplast genome structure and molecular dating in Myrtales. BMC Plant Biology, 2021, 21, 219.	1.6	25
12963	Evolution of an Epidermal Differentiation Complex (EDC) Gene Family in Birds. Genes, 2021, 12, 767.	1.0	10
12964	Sweet spheres: succession and <i>CAZyme</i> expression of marine bacterial communities colonizing a mix of alginate and pectin particles. Environmental Microbiology, 2021, 23, 3130-3148.	1.8	17
12965	The Plot Thickens: Haploid and Triploid-Like Thalli, Hybridization, and Biased Mating Type Ratios in <i>Letharia</i> . Frontiers in Fungal Biology, 2021, 2, .	0.9	6
12967	Polyploidy underlies co-option and diversification of biosynthetic triterpene pathways in the apple tribe. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	37

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12968	A phase-separated nuclear GBPL circuit controls immunity in plants. <i>Nature</i> , 2021, 594, 424-429.	13.7	79
12969	Integrating taxonomic, functional, and strain-level profiling of diverse microbial communities with bioBakery 3. <i>ELife</i> , 2021, 10, .	2.8	808
12970	Incorporating mitogenome sequencing into integrative taxonomy: The multidisciplinary redescription of the ciliate <i>Thuricola similis</i> (Peritrichia, Vaginicolidae) provides new insights into the evolutionary relationships among Oligohymenophorea subclasses. <i>Molecular Phylogenetics and Evolution</i> , 2021, 158, 107089.	1.2	6
12971	Reducing Data Deficiencies: Preliminary Elasmobranch Fisheries Surveys in India, Identify Range Extensions and Large Proportions of Female and Juvenile Landings. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	3
12972	Schistosomiasis Drug Discovery in the Era of Automation and Artificial Intelligence. <i>Frontiers in Immunology</i> , 2021, 12, 642383.	2.2	10
12973	Community composition and functional prediction of prokaryotes associated with sympatric sponge species of southwestern Atlantic coast. <i>Scientific Reports</i> , 2021, 11, 9576.	1.6	9
12974	Diversity and function of rhizosphere microorganisms between wild and cultivated medicinal plant <i>Glycyrrhiza uralensis</i> Fisch under different soil conditions. <i>Archives of Microbiology</i> , 2021, 203, 3657-3665.	1.0	12
12975	An integrative monograph of <i>Carex</i> section <i>Schoenoxiphium</i> (Cyperaceae). <i>PeerJ</i> , 2021, 9, e11336.	0.9	4
12976	<i>Bacillus pumilus</i> Group Comparative Genomics: Toward Pangenome Features, Diversity, and Marine Environmental Adaptation. <i>Frontiers in Microbiology</i> , 2021, 12, 571212.	1.5	9
12977	<i>Ornithobacterium rhinotracheale</i> : MALDI-TOF MS and Whole Genome Sequencing Confirm That Serotypes K, L and M Deviate from Well-Known Reference Strains and Numerous Field Isolates. <i>Microorganisms</i> , 2021, 9, 1006.	1.6	7
12978	Integrative taxonomy reveals a rare and new cusk-eel species of <i>Luciobrotula</i> (Teleostei, Ophidiidae) from the Solomon Sea, West Pacific. <i>European Journal of Taxonomy</i> , 0, 750, 52-69.	0.6	1
12979	Description of three new species of Geometridae (Lepidoptera) using species delimitation in an integrative taxonomy approach for a cryptic species complex. <i>PeerJ</i> , 2021, 9, e11304.	0.9	9
12980	Expanded Genomic Sampling Refines Current Understanding of the Distribution and Evolution of Sulfur Metabolisms in the Desulfobulbales. <i>Frontiers in Microbiology</i> , 2021, 12, 666052.	1.5	15
12982	The Genomic Signature of Allopatric Speciation in a Songbird Is Shaped by Genome Architecture (Aves: <i>Turdus philomelos</i>). <i>Genome Biology and Evolution</i> , 2021, 13, e24211.	1.1	10
12983	Enhanced Mutation Rate, Relaxed Selection, and the "Domino Effect" are associated with Gene Loss in <i>Blattabacterium</i> , A Cockroach Endosymbiont. <i>Molecular Biology and Evolution</i> , 2021, 38, 3820-3831.	3.5	13
12984	Longitudinal typing of molecular HIV clusters in a statewide epidemic. <i>Aids</i> , 2021, 35, 1711-1722.	1.0	4
12985	Genomic Analyses Unveil Helmeted Guinea Fowl (<i>Numida meleagris</i>) Domestication in West Africa. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	6
12987	Return of the walking dead: First verified record of the shrew <i>Crocidura leucodon</i> (Hermann, 1780) in Hamburg, Germany. <i>Evolutionary Systematics</i> , 2021, 5, 121-128.	0.2	1

#	ARTICLE	IF	CITATIONS
12989	Repeat proliferation and partial endoreplication jointly shape the patterns of genome size evolution in orchids. <i>Plant Journal</i> , 2021, 107, 511-524.	2.8	10
12990	Testing the Utility of Alternative Metrics of Branch Support to Address the Ancient Evolutionary Radiation of Tunas, Stromateoids, and Allies (Teleostei: Pelagiaria). <i>Systematic Biology</i> , 2021, 70, 1123-1144.	2.7	19
12991	Biogeography and diversification of Old World buntings (Aves: Emberizidae): radiation in open habitats. <i>Journal of Avian Biology</i> , 2021, 52, .	0.6	8
12992	Mitochondrial substitution rates estimation for divergence time analyses in modern birds based on full mitochondrial genomes. <i>Ibis</i> , 2021, 163, 1463-1471.	1.0	5
12993	Characterization of the complete chloroplast genome of <i>Hippophae salicifolia</i> D. Don (Elaeagnaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1818-1820.	0.2	1
12994	Phylogenomic analyses reveal non-monophyly of the antbird genera <i>Herpsilochmus</i> and <i>Sakesphorus</i> (Thamnophilidae), with description of a new genus for <i>Herpsilochmus sellowi</i> . <i>Auk</i> , 2021, 138, .	0.7	3
12995	Chromosome-level assembly of southern catfish (<i>Silurus meridionalis</i>) provides insights into visual adaptation to nocturnal and benthic lifestyles. <i>Molecular Ecology Resources</i> , 2021, 21, 1575-1592.	2.2	20
12996	Viruses infecting a warm water picoeukaryote shed light on spatial co-occurrence dynamics of marine viruses and their hosts. <i>ISME Journal</i> , 2021, 15, 3129-3147.	4.4	10
12997	Morphological and genetic diversification of <i>Russula floriformis</i> , sp. nov., along the Isthmus of Panama. <i>Mycologia</i> , 2021, 113, 807-827.	0.8	11
12998	Geological and paleoclimatic events reflected in phylogeographic patterns of intertidal arthropods (Acari, Oribatida, Selenoribatidae) from southern Japanese islands. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2021, 59, 1273-1296.	0.6	5
12999	Mitogenome Analysis of Four Lamiinae Species (Coleoptera: Cerambycidae) and Gene Expression Responses by <i>Monochamus alternatus</i> When Infected with the Parasitic Nematode, <i>Bursaphelenchus mucronatus</i> . <i>Insects</i> , 2021, 12, 453.	1.0	9
13000	Sexual deception of a beetle pollinator through floral mimicry. <i>Current Biology</i> , 2021, 31, 1962-1969.e6.	1.8	30
13001	UBCG2: Up-to-date bacterial core genes and pipeline for phylogenomic analysis. <i>Journal of Microbiology</i> , 2021, 59, 609-615.	1.3	83
13002	<i>Amazonocrinis nigriterrae</i> gen. nov., sp. nov., <i>Atlanticothrix silvestris</i> gen. nov., sp. nov. and <i>Dendronalium phyllosphericum</i> gen. nov., sp. nov., nostocacean cyanobacteria from Brazilian environments. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	30
13003	<i>Peteryoungia</i> gen. nov. with four new species combinations and description of <i>Peteryoungia desertarenae</i> sp. nov., and taxonomic revision of the genus <i>Ciceribacter</i> based on phylogenomics of Rhizobiaceae. <i>Archives of Microbiology</i> , 2021, 203, 3591-3604.	1.0	51
13005	Genome-wide insights into population structure and host specificity of <i>Campylobacter jejuni</i> . <i>Scientific Reports</i> , 2021, 11, 10358.	1.6	18
13006	The first complete mitochondrial genome of <i>Zoodes fulguratus</i> (Gahan 1906) (Coleoptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 102 T	0.2	0
13007	The complete chloroplast genome sequence of <i>Veratrum oxyspalum</i> and phylogenetic analysis. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2015-2016.	0.2	0

#	ARTICLE	IF	CITATIONS
13009	Comparative genomic insights into culturable symbiotic cyanobacteria from the water fern <i>Azolla</i> . <i>Microbial Genomics</i> , 2021, 7, .	1.0	19
13010	Physcraper: a Python package for continually updated phylogenetic trees using the Open Tree of Life. <i>BMC Bioinformatics</i> , 2021, 22, 355.	1.2	2
13011	<i>Schizocorticium</i> gen. nov. (Hymenochaetales, Basidiomycota) with three new species. <i>Mycological Progress</i> , 2021, 20, 769-779.	0.5	0
13012	Molecular phylogenetics of the <i>Dissochaeta</i> alliance (Melastomataceae): Redefining tribe <i>Dissochaeteae</i> . <i>Taxon</i> , 2021, 70, 793-825.	0.4	19
13013	Molecular Epidemiology, Genetic Diversity, and Antifungal Susceptibility of Major Pathogenic Dermatophytes Isolated From Human Dermatophytosis. <i>Frontiers in Microbiology</i> , 2021, 12, 643509.	1.5	8
13014	<i>Heterocapsa busanensis</i> sp. nov. (Peridinales, Dinophyceae): A new marine thecate dinoflagellate from Korean coastal waters. <i>European Journal of Protistology</i> , 2021, 79, 125797.	0.5	8
13015	The Chromosome-Level Genome of <i>Triplophysa dalaica</i> (Cypriniformes: Cobitidae) Provides Insights into Its Survival in Extremely Alkaline Environment. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	7
13016	Morphological stasis masks ecologically divergent coral species on tropical reefs. <i>Current Biology</i> , 2021, 31, 2286-2298.e8.	1.8	39
13017	<i>Neglectella glomerata</i> sp. nov., a new species and implications for the systematics of the genus <i>Neglectella</i> (Oocystaceae, Trebouxiophyceae, Chlorophyta). <i>Journal of Oceanology and Limnology</i> , 2021, 39, 2370-2379.	0.6	1
13018	Resurrection and characterization of ancestral CYP11A1 enzymes. <i>FEBS Journal</i> , 2021, 288, 6510-6527.	2.2	10
13019	Identification of sequence changes in myosin II that adjust muscle contraction velocity. <i>PLoS Biology</i> , 2021, 19, e3001248.	2.6	9
13020	Bacteria Isolated From the Antarctic Sponge <i>Iophon</i> sp. Reveals Mechanisms of Symbiosis in <i>Sporosarcina</i> , <i>Cellulophaga</i> , and <i>Nesterenkonia</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 660779.	1.5	5
13021	Genomic signatures of adaptation to natural settings in non-typhoidal <i>Salmonella enterica</i> Serovars Saintpaul, Thompson and Weltevreden. <i>Infection, Genetics and Evolution</i> , 2021, 90, 104771.	1.0	5
13022	Inter- and Intra-Continental Genetic Variation in the Generalist Conifer Wood Saprobiic Fungus <i>Phlebiopsis gigantea</i> . <i>Forests</i> , 2021, 12, 751.	0.9	5
13023	Comparative Genomics of Eight <i>Fusarium graminearum</i> Strains with Contrasting Aggressiveness Reveals an Expanded Open Pangenome and Extended Effector Content Signatures. <i>International Journal of Molecular Sciences</i> , 2021, 22, 6257.	1.8	12
13024	Phylogenetic relationships, infrageneric classification and species limits in the Neotropical genus <i>Faramea</i> (Coussareeae: Rubiaceae). <i>Botanical Journal of the Linnean Society</i> , 2021, 197, 478-497.	0.8	0
13025	Heterotrophic euglenid <i>Rhodomonas costata</i> resembles its phototrophic relatives in many aspects of molecular and cell biology. <i>Scientific Reports</i> , 2021, 11, 13070.	1.6	5
13026	<i>Lithothamnion</i> (Hapalidiales, Rhodophyta) in the changing Arctic and Subarctic: DNA sequencing of type and recent specimens provides a systematics foundation*. <i>European Journal of Phycology</i> , 2021, 56, 468-493.	0.9	13

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13027	Donadinia echinacea and Plectania sichuanensis, two novel species of Sarcosomataceae from southwestern China. <i>Phytotaxa</i> , 2021, 508, .	0.1	1
13028	Population-scale peach genome analyses unravel selection patterns and biochemical basis underlying fruit flavor. <i>Nature Communications</i> , 2021, 12, 3604.	5.8	31
13029	Detection of the widespread presence of the genus <i>Ansanella</i> along the Catalan coast (NW) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 <i>Journal of Phycology</i> , 2022, 57, 125-142.	0.9	3
13030	Expression of Wnt and TGF-Beta Pathway Components during Whole-Body Regeneration from Cell Aggregates in Demosponge <i>Halisarca dujardini</i> . <i>Genes</i> , 2021, 12, 944.	1.0	8
13031	Dispersal ability, habitat characteristics, and sea-surface circulation shape population structure of <i>Cingula trifasciata</i> (Gastropoda: Rissoidae) in the remote Azores Archipelago. <i>Bmc Ecology and Evolution</i> , 2021, 21, 128.	0.7	5
13032	18S rRNA variability maps reveal three highly divergent, conserved motifs within Rotifera. <i>Bmc Ecology and Evolution</i> , 2021, 21, 118.	0.7	6
13033	Genetic changes and evolutionary analysis of canine circovirus. <i>Archives of Virology</i> , 2021, 166, 2235-2247.	0.9	6
13034	SARS-CoV-2 infection and transmission in the North American deer mouse. <i>Nature Communications</i> , 2021, 12, 3612.	5.8	96
13035	Comparison among the chloroplast genomes of five species of <i>Chamaerhodos</i> (Rosaceae:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.2	3
13036	Four new species and a new record of Orchidinae (Orchidaceae: Orchideae) from China. <i>Plant Diversity</i> , 2021, 43, 390-400.	1.8	5
13037	Gene-rich UV sex chromosomes harbor conserved regulators of sexual development. <i>Science Advances</i> , 2021, 7, .	4.7	53
13038	Empirical and Methodological Challenges to the Model-Based Inference of Diversification Rates in Extinct Clades. <i>Systematic Biology</i> , 2021, 71, 153-171.	2.7	13
13039	<i>Alkalibacillus aidingensis</i> sp. nov., an Bacterium Isolated from Aiding Lake in Xinjiang Province, North-West China. <i>Current Microbiology</i> , 2021, 78, 3307-3312.	1.0	7
13040	Large-scale phylogenomic analysis provides new insights into the phylogeny of the class Oligohymenophorea (Protista, Ciliophora) with establishment of a new subclass Urocentria nov. subcl. <i>Molecular Phylogenetics and Evolution</i> , 2021, 159, 107112.	1.2	23
13041	Investigation of Tick-Borne Pathogens in <i>Ixodes ricinus</i> in a Peri-Urban Park in Lombardy (Italy) Reveals the Presence of Emerging Pathogens. <i>Pathogens</i> , 2021, 10, 732.	1.2	9
13042	The complete chloroplast genome sequence of <i>Bambusa contracta</i> L.C.Chia & H.L.Fung (Bambusodae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2123-2125.	0.2	0
13043	<i>Corynebacterium rouxii</i> , a recently described member of the <i>C. diphtheriae</i> group isolated from three dogs with ulcerative skin lesions. <i>Antonie Van Leeuwenhoek</i> , 2021, 114, 1361-1371.	0.7	8
13044	Disparate origins for endemic bird taxa from the "Gondwana Rainforests"™ of Central Eastern Australia. <i>Biological Journal of the Linnean Society</i> , 2021, 134, 40-56.	0.7	3

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13045	Endosymbiont Capture, a Repeated Process of Endosymbiont Transfer with Replacement in Trypanosomatids <i>Angomonas</i> spp.. <i>Pathogens</i> , 2021, 10, 702.	1.2	2
13046	Genomic analysis of <i>Neisseria elongata</i> isolate from a patient with infective endocarditis. <i>FEBS Open Bio</i> , 2021, 11, 1987-1996.	1.0	1
13047	Understanding introduction history: Genetic structure and diversity of the edible ectomycorrhizal fungus, <i>Suillus luteus</i> , in Patagonia (Argentina). <i>Mycologia</i> , 2021, 113, 715-724.	0.8	5
13048	Distinctive genetic signatures of two fairy shrimp species with overlapping ranges in Iberian temporary ponds. <i>Freshwater Biology</i> , 2021, 66, 1680-1697.	1.2	1
13049	MicroRNA-Mediated Regulation of Initial Host Responses in a Symbiotic Organ. <i>MSystems</i> , 2021, 6, .	1.7	3
13050	Genomic surveillance of <i>Pseudomonas aeruginosa</i> in the Philippines, 2013–2014. <i>Western Pacific Surveillance and Response Journal: WPSAR</i> , 2021, 12, 4-18.	0.3	3
13051	Roseobacters in a Sea of Poly- and Paraphyly: Whole Genome-Based Taxonomy of the Family Rhodobacteraceae and the Proposal for the Split of the ‘‘Roseobacter Clade’’ Into a Novel Family, Roseobacteraceae fam. nov.. <i>Frontiers in Microbiology</i> , 2021, 12, 683109.	1.5	263
13052	Genetic diversity and expanded host range of astroviruses detected in small mammals in Singapore. <i>One Health</i> , 2021, 12, 100218.	1.5	3
13053	Subtle environmental variation affects phenotypic differentiation of shallow divergent treefrog lineages in Amazonia. <i>Biological Journal of the Linnean Society</i> , 2021, 134, 177-197.	0.7	3
13054	Integrating Genetics, Morphology, and Fungal Host Specificity in Conservation Studies of a Vulnerable, Selfing, Mycoheterotrophic Orchid (<i>Corallorhiza bentleyi</i> Freudenst.). <i>Castanea</i> , 2021, 86, .	0.2	2
13055	A chromosome-level <i>Camptotheca acuminata</i> genome assembly provides insights into the evolutionary origin of camptothecin biosynthesis. <i>Nature Communications</i> , 2021, 12, 3531.	5.8	66
13056	Extended divergence estimates and species descriptions of new craspedid choanoflagellates from the Atacama Desert, Northern Chile. <i>European Journal of Protistology</i> , 2021, 79, 125798.	0.5	5
13058	The global emergence of a novel <i>Streptococcus suis</i> clade associated with human infections. <i>EMBO Molecular Medicine</i> , 2021, 13, e13810.	3.3	33
13059	Lineage-specific vs. universal: A comparison of the Compositae1061 and Angiosperms353 enrichment panels in the sunflower family. <i>Applications in Plant Sciences</i> , 2021, 9, .	0.8	19
13060	Genetic diversity of <i>Colletotrichum lupini</i> and its virulence on white and Andean lupin. <i>Scientific Reports</i> , 2021, 11, 13547.	1.6	16
13061	PDR Transporter ABC1 Is Involved in the Innate Azole Resistance of the Human Fungal Pathogen <i>Fusarium keratoplasticum</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 673206.	1.5	7
13062	Identification and Characterization of Genes for the Allo A Lectins in Japanese Rhinoceros Beetle (<i>Trypoxylus dichotomus</i> [<i>Allomyrina dichotoma</i>]). <i>Biochemical Genetics</i> , 2022, 60, 94-105.	0.8	0
13063	Microscopic and Metagenomic Evidence for Eukaryotic Microorganisms Associated with Atacama Desert Populations of Giant Equisetum. <i>American Fern Journal</i> , 2021, 111, .	0.2	3

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13065	Using Robinson-Foulds supertrees in divide-and-conquer phylogeny estimation. <i>Algorithms for Molecular Biology</i> , 2021, 16, 12.	0.3	0
13066	A New Species of the Genus <i>Adelophryne</i> (Anura: Eleutherodactylidae: Phyzelaphryninae) from the Atlantic Forest of Northeastern Brazil. <i>Herpetologica</i> , 2021, 77, .	0.2	2
13067	Coxsackievirus B4: an underestimated pathogen associated with a hand, foot, and mouth disease outbreak. <i>Archives of Virology</i> , 2021, 166, 2225-2234.	0.9	7
13068	Comparative analysis of mite genomes reveals positive selection for diet adaptation. <i>Communications Biology</i> , 2021, 4, 668.	2.0	6
13069	Systematics and phylogeography of the Brazilian Atlantic Forest endemic harvestmen <i>Neosadocus Mello-Leitão</i> , 1926 (Arachnida: Opiliones: Gonyleptidae). <i>PLoS ONE</i> , 2021, 16, e0249746.	1.1	3
13070	Historical biogeography of <i>Tetrastigma</i> (Vitaceae): Insights into floristic exchange patterns between Asia and Australia. <i>Cladistics</i> , 2021, 37, 803-815.	1.5	7
13071	Exploring the functional composition of the human microbiome using a hand-curated microbial trait database. <i>BMC Bioinformatics</i> , 2021, 22, 306.	1.2	8
13072	Discovery of Viral Myosin Genes With Complex Evolutionary History Within Plankton. <i>Frontiers in Microbiology</i> , 2021, 12, 683294.	1.5	17
13073	A real-time multiplex PCR assay for detection of the causative agents of rat bite fever, <i>Streptobacillus moniliformis</i> and zoonotic <i>Streptobacillus</i> species. <i>Diagnostic Microbiology and Infectious Disease</i> , 2021, 100, 115335.	0.8	4
13074	Genetic Divergence and Population Structure in Weedy and Cultivated Broomcorn Millets (<i>Panicum</i>) Tj ETQq1 1 0.784314 rgBT /Over Science, 2021, 12, 688444.	1.7	13
13075	A Molecular Analysis of Microalgae from Around the Globe to Revise <i>Raphidonema</i> (Trebouxiophyceae, Chlorophyta). <i>Journal of Phycology</i> , 2021, 57, 1419-1432.	1.0	6
13076	Comparative genomics of the chitinase gene family in lodgepole and jack pines: contrasting responses to biotic threats and landscape level investigation of genetic differentiation. <i>Botany</i> , 2021, 99, 355-378.	0.5	4
13077	Molecular Taxonomy and Diversification of Atlantic Skates (Chondrichthyes, Rajiformes): Adding More Pieces to the Puzzle of Their Evolutionary History. <i>Life</i> , 2021, 11, 596.	1.1	6
13078	Temporal variation in community structure of zoosporic fungi in Lake Biwa, Japan. <i>Aquatic Microbial Ecology</i> , 2021, 87, 17-28.	0.9	2
13079	Thermal Performance Curves of Multiple Isolates of <i>Batrachochytrium dendrobatidis</i> , a Lethal Pathogen of Amphibians. <i>Frontiers in Veterinary Science</i> , 2021, 8, 687084.	0.9	9
13080	Antifungal Peptides from a <i>Burkholderia</i> Strain Suppress Basal Stem Rot Disease of Oil Palm. <i>Phytopathology</i> , 2022, 112, 238-248.	1.1	2
13081	Comparative Genomics of Closely Related <i>Tetragenococcus halophilus</i> Strains Elucidate the Diversity and Microevolution of CRISPR Elements. <i>Frontiers in Microbiology</i> , 2021, 12, 687985.	1.5	5
13082	Iron and sulfate reduction structure microbial communities in (sub-)Antarctic sediments. <i>ISME Journal</i> , 2021, 15, 3587-3604.	4.4	29

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13083	Limited dispersal and in situ diversification drive the evolutionary history of Rasborinae fishes in Sundaland. <i>Journal of Biogeography</i> , 2021, 48, 2153-2173.	1.4	8
13084	<i>Fensomea setacea</i> , gen. & sp. nov. (Cladopyxidaceae, Dinophyceae), is neither gonyaulacoid nor peridinioid as inferred from morphological and molecular data. <i>Scientific Reports</i> , 2021, 11, 12824.	1.6	6
13085	The complete chloroplast genome of <i>Hydrangea strigosa</i> Rehder (Hydrangeaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1877-1879.	0.2	0
13086	The complete chloroplast genome of <i>Androsace erecta</i> (Primulaceae) and its phylogenetic implication. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1987-1989.	0.2	0
13087	The complete mitochondrial genome sequence of <i>Fragaria orientalis</i> (Rosaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1951-1952.	0.2	1
13088	Complete mitochondrial genome of the Pacific limpet <i>Cellana nigrolineata</i> (Gastropoda: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1857-1859.	0.2	1
13089	Molecular phylogeny and historical biogeography of Apicotermitinae (Blattodea: Termitidae). <i>Systematic Entomology</i> , 2021, 46, 741-756.	1.7	10
13090	Distribution of methionine sulfoxide reductases in fungi and conservation of the free-methionine-R-sulfoxide reductase in multicellular eukaryotes. <i>Free Radical Biology and Medicine</i> , 2021, 169, 187-215.	1.3	9
13091	Gene duplication and adaptive evolution of Toll-like receptor genes in birds. <i>Developmental and Comparative Immunology</i> , 2021, 119, 103990.	1.0	8
13092	<i>Lecidea soledioatrobrunnea</i> sp. nov. from Turkey, the first saxicolous true <i>Lecidea</i> with soredia. <i>Herzogia</i> , 2021, 34, .	0.1	0
13094	Evaluating Species Delimitation Methods in Radiations: The Land Snail <i>Albinaria cretensis</i> Complex on Crete. <i>Systematic Biology</i> , 2022, 71, 439-460.	2.7	13
13095	Description of <i>Acinetobacter kanungonis</i> sp. nov., based on phylogenomic analysis. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	14
13096	Genomic Aromatic Compound Degradation Potential of Novel Paraburkholderia Species: <i>Paraburkholderia domus</i> sp. nov., <i>Paraburkholderia haematera</i> sp. nov. and <i>Paraburkholderia nemoris</i> sp. nov.. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7003.	1.8	22
13098	The wall lizards of the Balkan peninsula: Tackling questions at the interface of phylogenomics and population genomics. <i>Molecular Phylogenetics and Evolution</i> , 2021, 159, 107121.	1.2	6
13099	A New Host Record for <i>Clinostomum</i> cf. <i>marginatum</i> (Trematoda: Digenea: Clinostomidae) from the Endemic Salado Salamander, <i>Eurycea chisholmensis</i> (Caudata: Plethodontidae), from the Edwards Plateau, Texas, U.S.A.. <i>Comparative Parasitology</i> , 2021, 88, .	0.0	0
13100	The complete chloroplast genome sequence of <i>Bambusa lapidea</i> (Bambusodae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2046-2047.	0.2	0
13101	The complete mitochondrial genome and phylogenetic analysis of the deep-sea limpet <i>Bathycyba lactea</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2090-2091.	0.2	2
13102	The complete chloroplast genome of <i>Atractylodes japonica</i> Koidz. ex Kitam. and its phylogenetic inference. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2038-2040.	0.2	2

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13103	Molecular phylogeny of Elmidae (Coleoptera: Byrrhoidea) with a focus on Japanese species: implications for intrafamilial classification. <i>Systematic Entomology</i> , 2021, 46, 870-886.	1.7	9
13104	Patterns of transmission and horizontal gene transfer in the <i>Dioscorea sansibarensis</i> leaf symbiosis revealed by whole-genome sequencing. <i>Current Biology</i> , 2021, 31, 2666-2673.e4.	1.8	6
13105	Phylogenetic delimitation of <i>Apiospora</i> and <i>Arthrinium</i> . <i>Fungal Systematics and Evolution</i> , 2021, 7, 197-221.	0.9	31
13106	Genomic Analysis of Antibiotic-Resistant and -Susceptible <i>Escherichia coli</i> Isolated from Bovine Sources in Maputo, Mozambique. <i>Foodborne Pathogens and Disease</i> , 2021, 18, 426-435.	0.8	2
13107	Taxonomy and Molecular Phylogeny of Two New Species of Prostomatean Ciliates With Establishment of <i>Foissnerophrys</i> gen. n. (Alveolata, Ciliophora). <i>Frontiers in Microbiology</i> , 2021, 12, 686929.	1.5	6
13109	Large-scale genome sampling reveals unique immunity and metabolic adaptations in bats. <i>Molecular Ecology</i> , 2021, 30, 6449-6467.	2.0	40
13111	Contribution to Chaetosphaeriaceae— <i>Kionochaeta setosimplicia</i> sp. nov. from Thailand. <i>Phytotaxa</i> , 2021, 508, .	0.1	1
13112	Engineering yeast metabolism for the discovery and production of polyamines and polyamine analogues. <i>Nature Catalysis</i> , 2021, 4, 498-509.	16.1	26
13113	Phylogeny of terraranan frogs based on 2,665 loci and impacts of missing data on phylogenomic analyses. <i>Systematics and Biodiversity</i> , 2021, 19, 818-833.	0.5	10
13114	Evolutionary origins and species delineation of the two Pyrenean endemics <i>Campanula jaubertiana</i> and <i>C. andorrana</i> (Campanulaceae): evidence for transverse alpine speciation. <i>Alpine Botany</i> , 2022, 132, 51-64.	1.1	4
13115	Cytological Study of <i>Begonia</i> Sect. <i>Baryandra</i> (Begoniaceae). <i>Cytologia</i> , 2021, 86, 133-141.	0.2	7
13116	Horizontal Gene Transfer of Genes Encoding Copper-Containing Membrane-Bound Monooxygenase (CuMMO) and Soluble Di-iron Monooxygenase (SDIMO) in Ethane- and Propane-Oxidizing <i>Rhodococcus</i> Bacteria. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0022721.	1.4	5
13117	Variation and Diagnostic Power of the Internal Transcribed Spacer 2 in Mediterranean and Atlantic Eolid Nudibranchs (Mollusca, Gastropoda). <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	1
13118	Systematics of the shrimp genus <i>Atya</i> (Decapoda, Atyidae) in the light of multigene-based phylogenetic and species delimitation inference. <i>Zoologica Scripta</i> , 2021, 50, 780-794.	0.7	2
13119	Diversity and taxonomic revision of tribes Rhipileae and Rhipiliopsidae (Halimedaceae, Chlorophyta) based on molecular and morphological data. <i>Journal of Phycology</i> , 2021, 57, 1450-1471.	1.0	3
13120	The complete chloroplast genome sequence of <i>Ficus formosana</i> Maxim (Moraceae) from Guangzhou, China. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1895-1896.	0.2	2
13121	Complete chloroplast genome sequence of a Dutch cultivar of <i>Chrysanthemum</i> , <i>Chrysanthemum morifolium</i> "Orizaba" (Asteraceae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1937-1938.	0.2	2
13122	The complete chloroplast genome of <i>Semenovia thomsonii</i> (Tordylieae: Apiaceae), a new record from Xizang, China. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1911-1913.	0.2	1

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13123	Complete chloroplast genome of a semi-mangrove plant <i>Hibiscus tiliaceus</i> (Malvaceae). Mitochondrial DNA Part B: Resources, 2021, 6, 1904-1905.	0.2	1
13124	The complete chloroplast genome of the desert shrub <i>Nitraria sphaerocarpa</i> (Nitrariaceae) and phylogenetic analysis. Mitochondrial DNA Part B: Resources, 2021, 6, 1901-1903.	0.2	0
13125	Tightening the girdle: phylotranscriptomics of Polyplacophora. Journal of Molluscan Studies, 2021, 87, .	0.4	6
13126	The complete mitochondrial genome of <i>Taxoblenus sinicus</i> Wei & Nie, 1999 (Hymenoptera: Tj ETQq1 1 0.784314 0.2 / Overlock 10	0.2	1
13127	Complete mitochondrial genome sequence of Tosa-Jidori sheds light on the origin and evolution of Japanese native chickens. Animal Bioscience, 2021, 34, 941-948.	0.8	3
13128	<i>Myxobdella socotrensis</i> sp. nov., a new parasitic leech from Socotra Island, with comments on the phylogeny of Praobdellidae (Hirudinida: Arhynchobdellida). Parasitology International, 2021, 82, 102310.	0.6	4
13129	First report on Mermithidae (Mermithida) infection in <i>Ligidium</i> sp. (Isopoda, Ligiidae). Parasitology International, 2021, 82, 102304.	0.6	3
13130	Description of two new <i>Cisticola</i> species endemic to the marshes of the Kilombero floodplain of southwestern Tanzania. Ibis, 2021, 163, 1330-1354.	1.0	2
13131	Microbiome Aggregated Traits and Assembly Are More Sensitive to Soil Management than Diversity. MSystems, 2021, 6, e0105620.	1.7	17
13132	Analysis of the <i>Coptis chinensis</i> genome reveals the diversification of protoberberine-type alkaloids. Nature Communications, 2021, 12, 3276.	5.8	68
13133	The response of tartary buckwheat and 19 bZIP genes to abscisic acid (ABA). Molecular Biology Reports, 2021, 48, 4341-4350.	1.0	5
13134	Genomic Analysis of <i>Pasteurella atlantica</i> Provides Insight on Its Virulence Factors and Phylogeny and Highlights the Potential of Reverse Vaccinology in Aquaculture. Microorganisms, 2021, 9, 1215.	1.6	4
13135	Three new species of <i>Trichoderma</i> in the Harzianum and Longibrachiatum lineages from Peruvian cacao crop soils based on an integrative approach. Mycologia, 2021, 113, 1-17.	0.8	10
13136	Monograph of <i>Carex</i> section <i>Schiedeanae</i> (Cyperaceae): Unexpected taxonomic and ecological diversity in a Mexican sedge clade. Journal of Systematics and Evolution, 2021, 59, 698-725.	1.6	7
13137	Biogeographical patterns and speciation of the genus <i>Pinguicula</i> (Lentibulariaceae) inferred by phylogenetic analyses. PLoS ONE, 2021, 16, e0252581.	1.1	6
13139	Inhibition of Fibrinolysis by Streptococcal Phage Lysin _{SM1} . MBio, 2021, 12, e0074621.	1.8	0
13140	Revisiting the Diversity of <i>Barbonymus</i> (Cypriniformes, Cyprinidae) in Sundaland Using DNA-Based Species Delimitation Methods. Diversity, 2021, 13, 283.	0.7	5
13141	Characterization of the complete chloroplast genome of <i>Lonicera tatarica</i> L. (Caprifoliaceae). Mitochondrial DNA Part B: Resources, 2021, 6, 1871-1872.	0.2	3

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13142	First Report of Domoic Acid Production from <i>Pseudo-nitzschia multistriata</i> in Paracas Bay (Peru). <i>Toxins</i> , 2021, 13, 408.	1.5	6
13144	Longitudinal Changes in Diet Cause Repeatable and Largely Reversible Shifts in Gut Microbial Communities of Laboratory Mice and Are Observed across Segments of the Entire Intestinal Tract. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5981.	1.8	10
13145	Complete mitochondrial genome sequencing of <i>Lutra lutra</i> (Linnaeus, 1758) (Carnivora). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 60 2066-2068</i> .	0.2	5
13146	The complete chloroplast genome of <i>Lithocarpus hancei</i> (Benth.) Rehd (Fagaceae) from Zhejiang, China. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2022-2023.	0.2	4
13147	The complete chloroplast genome of <i>Wurfbainia neaurantiaca</i> (Zingiberaceae: Zingiberea) from Yunnan Province, China. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2114-2116.	0.2	0
13148	Two <i>Fusarium</i> copper radical oxidases with high activity on aryl alcohols. <i>Biotechnology for Biofuels</i> , 2021, 14, 138.	6.2	12
13149	Mitogenomics and Evolutionary History of Rodent Whipworms (<i>Trichuris</i> spp.) Originating from Three Biogeographic Regions. <i>Life</i> , 2021, 11, 540.	1.1	2
13150	Social network analysis and whole-genome sequencing to evaluate disease transmission in a large, dynamic population: A study of avian mycobacteriosis in zoo birds. <i>PLoS ONE</i> , 2021, 16, e0252152.	1.1	2
13151	<i>Cyperus prophyllatus</i> : An endangered aquatic new species of <i>Cyperus</i> L. (Cyperaceae) with a exceptional spikelet disarticulation pattern among about 950 species, including molecular phylogenetic, anatomical and (micro)morphological data. <i>PLoS ONE</i> , 2021, 16, e0249737.	1.1	2
13152	Five new species of <i>Moelleriella</i> infecting scale insects (Coccidae) in Thailand. <i>Mycological Progress</i> , 2021, 20, 847.	0.5	1
13153	Genomic Rearrangements and Sequence Evolution across Brown Algal Organelles. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	12
13154	Two new species of the Balkan genus <i>Paladilhropsis</i> Pavlovič, 1913 (Caenogastropoda, Moitessieriidae). <i>ZooKeys</i> , 2021, 1046, 157-176.	0.5	2
13155	Phylogenomics of flavobacterial insect nutritional endosymbionts with implications for Auchenorrhyncha phylogeny. <i>Cladistics</i> , 2022, 38, 38-58.	1.5	13
13157	<i>Helvellosebacina granulata</i> sp. nov. (Basidiomycota: Sebacinaceae) from the East Black Sea Region of Turkey. <i>Nordic Journal of Botany</i> , 2021, 39, .	0.2	0
13158	X-ray microtomography and phylogenomics provide insights into the morphology and evolution of an enigmatic Mesozoic insect larva. <i>Systematic Entomology</i> , 2021, 46, 672-684.	1.7	27
13159	Molecular Clocks and Archeogenomics of a Late Period Egyptian Date Palm Leaf Reveal Introgression from Wild Relatives and Add Timestamps on the Domestication. <i>Molecular Biology and Evolution</i> , 2021, 38, 4475-4492.	3.5	14
13160	Gastropod first intermediate hosts for two species of Monorchidae Odhner, 1911 (Trematoda): I can't believe it's not bivalves!. <i>International Journal for Parasitology</i> , 2021, 51, 1035-1046.	1.3	9
13161	An acquired acyltransferase promotes <i>Klebsiella pneumoniae</i> ST258 respiratory infection. <i>Cell Reports</i> , 2021, 35, 109196.	2.9	15

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13162	Looking at the Nudibranch Family Myrrhinidae (Gastropoda, Heterobranchia) from a Mitochondrial 2D Folding Structure™ Point of View. <i>Life</i> , 2021, 11, 583.	1.1	3
13163	The riverine thruway hypothesis: rivers as a key mediator of gene flow for the aquatic paradoxical frog <i>Pseudis tocantins</i> (Anura, Hylidae). <i>Landscape Ecology</i> , 2021, 36, 3049-3060.	1.9	11
13164	Patterns of host tree use within a lineage of saproxylic snout-less weevils (Coleoptera: Curculionidae: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.2	6
13165	Integrative taxonomy and molecular phylogeny of three poorly known tintinnine ciliates, with the establishment of a new genus (Protista; Ciliophora; Oligotrichea). <i>Bmc Ecology and Evolution</i> , 2021, 21, 115.	0.7	7
13166	Wide Distribution and Specific Resistance Pattern to Third-Generation Cephalosporins of <i>Enterobacter cloacae</i> Complex Members in Humans and in the Environment in Guadeloupe (French) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.5	6
13167	Fifty million years of beetle evolution along the Antarctic Polar Front. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	21
13168	Morphological and molecular characterization of <i>Neopestalotiopsis vitis</i> associated with leaf blight disease of <i>Manilkara zapota</i> – a new record from India. <i>Letters in Applied Microbiology</i> , 2021, 73, 352-362.	1.0	2
13169	A new species of pikeblenny (Blenniiformes: Chaenopsidae: <i>Chaenopsis</i>) from the tropical eastern Pacific and a key to all species. <i>Journal of Fish Biology</i> , 2021, 99, 888-895.	0.7	0
13170	Multilocus phylogenies reveal three new truffle-like taxa and the traces of interspecific hybridization in Octaviania (Boletaceae, Boletales). <i>IMA Fungus</i> , 2021, 12, 14.	1.7	8
13171	A 5,000-year-old hunter-gatherer already plagued by <i>Yersinia pestis</i> . <i>Cell Reports</i> , 2021, 35, 109278.	2.9	42
13172	Whole-Genome Sequencing Investigation of a Large Nosocomial Outbreak Caused by ST131 H30Rx KPC-Producing <i>Escherichia coli</i> in Italy. <i>Antibiotics</i> , 2021, 10, 718.	1.5	7
13175	Insights into evolution and coexistence of the colibactin- and yersiniabactin secondary metabolite determinants in enterobacterial populations. <i>Microbial Genomics</i> , 2021, 7, .	1.0	13
13176	Relict from the Jurassic: new family of brittle-stars from a New Caledonian seamount. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2021, 288, 20210684.	1.2	1
13177	Genomic and Phenotypic Characterization of <i>Chloracidobacterium</i> Isolates Provides Evidence for Multiple Species. <i>Frontiers in Microbiology</i> , 2021, 12, 704168.	1.5	3
13178	Molecular and Functional Evolution of the Spermatophyte Sesquiterpene Synthases. <i>International Journal of Molecular Sciences</i> , 2021, 22, 6348.	1.8	6
13179	Genomic diversity of 39 samples of <i>Pyropia</i> species grown in Japan. <i>PLoS ONE</i> , 2021, 16, e0252207.	1.1	6
13181	<i>Tima nigroannulata</i> (Cnidaria: Hydrozoa: Eirenidae), a New Species of Hydrozoan from Japan. <i>Zoological Science</i> , 2021, 38, 370-382.	0.3	1
13182	The complete chloroplast genome of <i>Tibetia liangshanensis</i> P. C. Li (Leguminosae: Papilionoideae), an endemic species of China. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1917-1918.	0.2	0

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13183	The first complete mitochondrial genome of <i>Euroleon coreanus</i> (Okamoto, 1926) (Neuroptera: Tj ETQq0 0 0 rgBT /Overlock 1 Tf 50 74	0.2	1
13184	Phylogenomic Analysis Reveals Dispersal-Driven Speciation and Divergence with Gene Flow in Lesser Sunda Flying Lizards (Genus <i>Draco</i>). <i>Systematic Biology</i> , 2021, 71, 221-241.	2.7	11
13185	Genomic, karyological and morphological changes of South American garlics (<i>Ipheion</i>) provide insights into mechanisms of speciation in the Pampean region. <i>Molecular Ecology</i> , 2021, 30, 3716-3729.	2.0	3
13186	Additions to the knowledge of hydroid Steccherinaceae: <i>Cabalodontia</i> , <i>Etheirodon</i> , <i>Metuloidea</i> , and <i>Steccherinum</i> . <i>Mycologia</i> , 2021, 113, 791-806.	0.8	10
13187	Investigation of the prevalence and catalytic activity of rubredoxin-fused alkane monooxygenases (AlkB). <i>Journal of Inorganic Biochemistry</i> , 2021, 219, 111409.	1.5	11
13188	Comparative mitogenomics and phylogenetics of the stinging wasps (Hymenoptera: Aculeata). <i>Molecular Phylogenetics and Evolution</i> , 2021, 159, 107119.	1.2	13
13189	Diversity and substrate-specificity of green algae and other micro-eukaryotes colonizing amphibian clutches in Germany, revealed by DNA metabarcoding. <i>Die Naturwissenschaften</i> , 2021, 108, 29.	0.6	6
13190	The complete chloroplast genome of <i>Yulinglong</i> ™ (<i>Narcissus tazetta</i> var. <i>chinensis</i>) with double-petaled in southeast of China. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1765-1767.	0.2	0
13191	Protein Family Content Uncovers Lineage Relationships and Bacterial Pathway Maintenance Mechanisms in DPANN Archaea. <i>Frontiers in Microbiology</i> , 2021, 12, 660052.	1.5	20
13192	Systematics and conservation of an endemic radiation of <i>Accipiter</i> hawks in the Caribbean islands. <i>Auk</i> , 2021, 138, .	0.7	9
13193	Bioinformatics tools used for whole-genome sequencing analysis of <i>Neisseria gonorrhoeae</i> : a literature review. <i>Briefings in Functional Genomics</i> , 2022, 21, 78-89.	1.3	3
13194	Genomic evolution and virulence association of <i>Clostridioides difficile</i> sequence type 37 (ribotype 017) in China. <i>Emerging Microbes and Infections</i> , 2021, 10, 1331-1345.	3.0	12
13196	Comparative Chloroplast Genomics of <i>Litsea</i> Lam. (Lauraceae) and Its Phylogenetic Implications. <i>Forests</i> , 2021, 12, 744.	0.9	13
13198	Precise Species Identification for <i>Acinetobacter</i> : a Genome-Based Study with Description of Two Novel <i>Acinetobacter</i> Species. <i>MSystems</i> , 2021, 6, e0023721.	1.7	13
13201	Comparative chloroplast genome analysis of medicinally important <i>Veratrum</i> (Melanthiaceae) in China: Insights into genomic characterization and phylogenetic relationships. <i>Plant Diversity</i> , 2022, 44, 70-82.	1.8	15
13202	Parasite and Host Erythrocyte Kinomics of <i>Plasmodium</i> Infection. <i>Trends in Parasitology</i> , 2021, 37, 508-524.	1.5	14
13203	Accelerated Diversification Explains the Exceptional Species Richness of Tropical Characoid Fishes. <i>Systematic Biology</i> , 2021, 71, 78-92.	2.7	42
13204	Ubiquity of <i>Euglena mutabilis</i> Population in Three Ecologically Distinct Acidic Habitats in Southwestern Japan. <i>Water (Switzerland)</i> , 2021, 13, 1570.	1.2	9

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13205	A 313 plastome phylogenomic analysis of Pooideae: Exploring relationships among the largest subfamily of grasses. <i>Molecular Phylogenetics and Evolution</i> , 2021, 159, 107110.	1.2	16
13206	Phylogenomic reconstruction addressing the Peltigeralean backbone (Lecanoromycetes, Ascomycota). <i>Fungal Diversity</i> , 2021, 110, 59.	4.7	3
13207	Freshwater hyphomycetes in Sordariomycetes: two new species of <i>Tainosphaeria</i> (Chaetosphaeriaceae, Tj ETQq0 0.0 rgBT /Qverlock 10	0.1	5
13209	<i>Leucogaster solidus</i> sp. nov. (Albatrellaceae, Russulales) from China. <i>Phytotaxa</i> , 2021, 508, .	0.1	0
13210	Comparative Analysis of the Complete Chloroplast Genomes of Four Chestnut Species (<i>Castanea</i>). <i>Forests</i> , 2021, 12, 861.	0.9	8
13211	An overview of <i>Agaricus</i> section <i>Hondenses</i> and <i>Agaricus</i> section <i>Xanthodermatei</i> with description of eight new species from Pakistan. <i>Scientific Reports</i> , 2021, 11, 12905.	1.6	5
13212	<i>Staphylococcus saprophyticus</i> From Clinical and Environmental Origins Have Distinct Biofilm Composition. <i>Frontiers in Microbiology</i> , 2021, 12, 663768.	1.5	12
13213	GRINS: Genetic elements that recode assembly-line polyketide synthases and accelerate their diversification. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	13
13214	Resolving species boundaries in a recent radiation with the Angiosperms353 probe set: the <i>Lomatium packardiae</i> / <i>L. anomalum</i> clade of the <i>L. triternatum</i> (<i>Apiaceae</i>) complex. <i>American Journal of Botany</i> , 2021, 108, 1217-1233.	0.8	12
13215	Genetic, but Not Behavioral, Evidence Supports the Distinctiveness of the Mealy Amazon Parrot in the Brazilian Atlantic Forest. <i>Diversity</i> , 2021, 13, 273.	0.7	2
13216	Chromosome-Scale Genome Assembly of the Resurrection Plant <i>Acanthochlamys bracteata</i> (<i>Velloziaceae</i>). <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	6
13217	<i>Paradictyocheirospora tectonae</i> , a novel genus in the family <i>Dictyosporiaceae</i> from India. <i>Phytotaxa</i> , 2021, 509, .	0.1	4
13218	Population matched (pm) germline allelic variants of immunoglobulin (IG) loci: Relevance in infectious diseases and vaccination studies in human populations. <i>Genes and Immunity</i> , 2021, 22, 172-186.	2.2	14
13219	Reclassification of <i>Facklamia ignava</i> , <i>Facklamia sourekii</i> and <i>Facklamia tabacinasalis</i> as <i>Falseniella ignava</i> gen. nov., comb. nov., <i>Hutsoniella sourekii</i> gen. nov., comb. nov., and <i>Ruoffia tabacinasalis</i> gen. nov., comb. nov., and description of <i>Ruoffia halotolerans</i> sp. nov., isolated from hypersaline Inland Sea of Qatar. <i>Antonie Van Leeuwenhoek</i> , 2021, 114, 1181-1193.	0.7	28
13220	Genomic analyses provide comprehensive insights into the domestication of bast fiber crop ramie (<i>Boehmeria nivea</i>). <i>Plant Journal</i> , 2021, 107, 787-800.	2.8	18
13222	A deep-sea bacterium related to coastal marine pathogens. <i>Environmental Microbiology</i> , 2021, 23, 5349-5363.	1.8	4
13223	The quorum-sensing systems of <i>Vibrio campbellii</i> and <i>V. DS40M4</i> and <i>V. BB120</i> are genetically and functionally distinct. <i>Environmental Microbiology</i> , 2021, 23, 5412-5432.	1.8	11
13224	Clary Sage Cultivation and Mycorrhizal Inoculation Influence the Rhizosphere Fungal Community of an Aged Trace-Element Polluted Soil. <i>Microorganisms</i> , 2021, 9, 1333.	1.6	3

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13225	Genetic variation in neotropical butterflies is associated with sampling scale, species distributions, and historical forest dynamics. <i>Molecular Ecology Resources</i> , 2021, 21, 2333-2349.	2.2	4
13226	Environmental genomics of Late Pleistocene black bears and giant short-faced bears. <i>Current Biology</i> , 2021, 31, 2728-2736.e8.	1.8	42
13227	A population specific mitochondrial intron from the sponge <i>Phakellia robusta</i> in the North-East Atlantic. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2021, 172, 103534.	0.6	2
13228	Day and night regulation of the HO-1/HSP32 synthesis in the harmful dinoflagellate <i>Prorocentrum minimum</i> : response to salinity stress. <i>Journal of Experimental Marine Biology and Ecology</i> , 2021, 539, 151545.	0.7	1
13232	Molecular Phylogeny, Character Evolution, and Biogeography of <i>Hydrangea</i> Section <i>Cornidia</i> , <i>Hydrangeaceae</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 661522.	1.7	1
13233	New Insight into Taxonomy of European Mountain Pines, <i>Pinus mugo</i> Complex, Based on Complete Chloroplast Genomes Sequencing. <i>Plants</i> , 2021, 10, 1331.	1.6	10
13234	The nearly complete genome of <i>Ginkgo biloba</i> illuminates gymnosperm evolution. <i>Nature Plants</i> , 2021, 7, 748-756.	4.7	98
13235	The Evolution of Interdependence in a Four-Way Mealybug Symbiosis. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	9
13236	Comparative analyses of transcriptional responses of <i>Dectes texanus</i> LeConte (Coleoptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 427 T 11448.	1.6	6
13237	Two new <i>Penicillium</i> section <i>Sclerotiorum</i> species from sugarcane soil in Brazil. <i>Mycological Progress</i> , 2021, 20, 823-835.	0.5	6
13238	The effect of recombination on the evolution of a population of <i>Neisseria meningitidis</i> . <i>Genome Research</i> , 2021, 31, 1258-1268.	2.4	4
13239	Comparative analyses of <i>Mikania</i> (Asteraceae: Eupatorieae) plastomes and impact of data partitioning and inference methods on phylogenetic relationships. <i>Scientific Reports</i> , 2021, 11, 13267.	1.6	6
13240	Evolutionary and phylogenetic insights from a nuclear genome sequence of the extinct, giant, subfossil koala lemur <i>Megaladapis edwardsi</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	12
13241	The Evolutionary Patterns of Genome Size in <i>Ensifera</i> (Insecta: Orthoptera). <i>Frontiers in Genetics</i> , 2021, 12, 693541.	1.1	19
13242	Mitochondrial Genetic Diversity among Farmed Stocks of <i>Oreochromis</i> spp. (Perciformes, Cichlidae) in Madagascar. <i>Diversity</i> , 2021, 13, 281.	0.7	2
13243	Crenobiont, stygophile and stygobiont molluscs in the hydrographic area of the Trebišnjica River Basin. <i>ZooKeys</i> , 2021, 1047, 61-89.	0.5	6
13244	Triple RNA-Seq characterizes aphid gene expression in response to infection with unequally virulent strains of the endosymbiont <i>Hamiltonella defensa</i> . <i>BMC Genomics</i> , 2021, 22, 449.	1.2	10
13246	The complete chloroplast genome of <i>Atractylodes koreana</i> (Nakai) Kitam and its phylogenetic analysis. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2041-2043.	0.2	1

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13247	Genomic characterization of three novel Desulfobacterota classes expand the metabolic and phylogenetic diversity of the phylum. <i>Environmental Microbiology</i> , 2021, 23, 4326-4343.	1.8	65
13248	Using phylogenetic diversity to explore the socioeconomic and ecological drivers of a tropical, coastal urban forest. <i>Urban Forestry and Urban Greening</i> , 2021, 61, 127111.	2.3	6
13249	Identification of new serovar-specific detection targets against salmonella B serogroup using large-scale comparative genomics. <i>Food Control</i> , 2021, 124, 107862.	2.8	5
13250	Genotyping-by-sequencing resolves relationships in Polygonaceae tribe Eriogoneae. <i>Taxon</i> , 2021, 70, 826-841.	0.4	2
13254	Revision of the Genus <i>Sirodotia</i> Kylin (Batrachospermales, Rhodophyta) with Description of Four New Species. <i>Cryptogamie, Algologie</i> , 2021, 42, .	0.3	1
13255	Phylogeny and taxonomy of <i>Catenularia</i> and similar fungi with catenate conidia. <i>MycKeys</i> , 2021, 81, 1-44.	0.8	11
13256	Analysis of Unusual Sulfated Constituents and Anti-infective Properties of Two Indonesian Mangroves, <i>Lumnitzera littorea</i> and <i>Lumnitzera racemosa</i> (Combretaceae). <i>Separations</i> , 2021, 8, 82.	1.1	9
13257	Novel clades of soil biphenyl degraders revealed by integrating isotope probing, multi-omics, and single-cell analyses. <i>ISME Journal</i> , 2021, 15, 3508-3521.	4.4	14
13258	First Report of the Marine Benthic Dinoflagellate <i>Bysmatrum subsalsum</i> from Korean Tidal Pools. <i>Journal of Marine Science and Engineering</i> , 2021, 9, 649.	1.2	1
13259	Delimiting cryptic species within the brown-banded bamboo shark, <i>Chiloscyllium punctatum</i> in the Indo-Australian region with mitochondrial DNA and genome-wide SNP approaches. <i>Bmc Ecology and Evolution</i> , 2021, 21, 121.	0.7	6
13260	Mitochondrial DNA Data Support the Recognition of the Mud Turtle, <i>Kinosternon vogti</i> (Cryptodira: Testudinata). <i>Journal of Herpetology</i> , 2021, 55, 107-114.	0.1	0
13261	<i>Siroplidium bryopsisidis</i> , a parasite of green algae, is probably conspecific with <i>Pontisma lagenidioides</i> , a parasite of red algae. <i>Fungal Systematics and Evolution</i> , 2021, 7, 223-231.	0.9	6
13262	An overview of current population genomics methods for the analysis of whole-genome resequencing data in eukaryotes. <i>Molecular Ecology</i> , 2021, 30, 6036-6071.	2.0	38
13264	A New Pathway for Forming Acetate and Synthesizing ATP during Fermentation in Bacteria. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0295920.	1.4	19
13265	The complete plastid genome sequence of <i>Vaccinium japonicum</i> (Ericales: Ericaceae), a deciduous broad-leaved shrub endemic to East Asia. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1926-1928.	0.2	4
13266	The complete mitochondrial genome of <i>Micromus paganus</i> (Linnaeus, 1767) (Neuroptera: Megaloptera). <i>Journal of Herpetology</i> , 2021, 55, 1842-1843.	0.2	0
13267	Evaluation of Virulence Determinants Using Whole-Genome Sequencing and Phenotypic Biofilm Analysis of Outbreak-Linked <i>Staphylococcus aureus</i> Isolates. <i>Frontiers in Microbiology</i> , 2021, 12, 687625.	1.5	10
13268	<i>Staphylococcus saprophyticus</i> Causing Infections in Humans Is Associated with High Resistance to Heavy Metals. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, e0268520.	1.4	9

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13269	The complete chloroplast genome of <i>Euphorbia hirta</i> (Euphorbiaceae), a commonly used medicinal plant in China. Mitochondrial DNA Part B: Resources, 2021, 6, 2166-2168.	0.2	0
13270	Individual recognition and individual identity signals in <i>Polistes fuscatus</i> wasps vary geographically. Animal Behaviour, 2021, 176, 87-98.	0.8	7
13271	Heterogeneous Histories of Recombination Suppression on Stickleback Sex Chromosomes. Molecular Biology and Evolution, 2021, 38, 4403-4418.	3.5	26
13272	Gene Conversion Facilitates the Adaptive Evolution of Self-Resistance in Highly Toxic Newts. Molecular Biology and Evolution, 2021, 38, 4077-4094.	3.5	12
13273	Evolutionary and Ecological Drivers Shape the Emergence and Extinction of Foot-and-Mouth Disease Virus Lineages. Molecular Biology and Evolution, 2021, 38, 4346-4361.	3.5	14
13274	Rapid radiation of angraecoids (Orchidaceae, Angraecinae) in tropical Africa characterised by multiple karyotypic shifts under major environmental instability. Molecular Phylogenetics and Evolution, 2021, 159, 107105.	1.2	7
13275	New genetic evidences for distinct populations of the common minke whale (Balaenoptera) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 502 T	0.5	4
13276	Genomic insights into diverse bacterial taxa that degrade extracellular DNA in marine sediments. Nature Microbiology, 2021, 6, 885-898.	5.9	29
13277	Evolution of the cytochrome <i>bd</i> oxygen reductase superfamily and the function of CydAA [™] in Archaea. ISME Journal, 2021, 15, 3534-3548.	4.4	18
13279	The queen conch mitogenome: intra- and interspecific mitogenomic variability in Strombidae and phylogenetic considerations within the Hypsogastropoda. Scientific Reports, 2021, 11, 11972.	1.6	6
13280	Natal origin of Namibian grey whale implies new distance record for in-water migration. Biology Letters, 2021, 17, 20210136.	1.0	4
13281	New epiphytic sooty molds: <i>Alloscorias syngonii</i> (Readeriellipsoidaceae) from Thailand. Phytotaxa, 2021, 507, .	0.1	3
13282	The reduced genome of a heritable symbiont from an ectoparasitic feather feeding louse. BMC Ecology and Evolution, 2021, 21, 108.	0.7	7
13283	<i>Cladophialophora bromeliacearum</i> (Herpotrichiellaceae, Chaetothyriales), a novel endophytic species from the Brazilian tropical dry forest. Phytotaxa, 2021, 509, .	0.1	2
13284	Niche adaptation promoted the evolutionary diversification of tiny ocean predators. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	12
13286	<i>Gastrum dolomiticum</i> , a new earthstar species from Central Europe. Plant Systematics and Evolution, 2021, 307, 1.	0.3	2
13287	Somatic variations led to the selection of acidic and acidless orange cultivars. Nature Plants, 2021, 7, 954-965.	4.7	48
13288	Chloroplast phylogenomics and divergence times of <i>Lagerstroemia</i> (Lythraceae). BMC Genomics, 2021, 22, 434.	1.2	29

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13289	The ocular pyogranulomatous lesion in a Gentoo penguin (<i>Pygoscelis papua</i>) from the Antarctic Peninsula: evaluation of microbiological and histopathological analysis outcomes. <i>Veterinary Research Communications</i> , 2021, 45, 143-158.	0.6	9
13290	A near comprehensive phylogenetic framework gives new insights toward a natural classification of the African genus <i>Cyrtorchis</i> (Angraecinae, Orchidaceae). <i>Taxon</i> , 2021, 70, 720.	0.4	1
13291	Structural and immunogenicity analysis of reconstructed ancestral and consensus P48/45 for cross-species anti malaria transmission-blocking vaccine. <i>Computational Biology and Chemistry</i> , 2021, 92, 107495.	1.1	1
13292	Immunogenicity and structural efficacy of P41 of <i>Plasmodium</i> sp. as potential cross-species blood-stage malaria vaccine. <i>Computational Biology and Chemistry</i> , 2021, 92, 107493.	1.1	0
13293	A horizontally acquired <i>Legionella</i> genomic island encoding a LuxR type regulator and effector proteins displays variation in gene content and regulation. <i>Molecular Microbiology</i> , 2021, 116, 766-782.	1.2	3
13294	Comparative Genomics Reveals Potential Mechanisms of Plant Beneficial Effects of a Novel Bamboo-Endophytic Bacterial Isolate <i>Paraburkholderia sacchari</i> Suichang626. <i>Frontiers in Microbiology</i> , 2021, 12, 686998.	1.5	5
13295	Morphological groupings within <i>Euphlyctis</i> (Anura: Dicroglossidae) and description of a new species from the surroundings of Thattekad Bird Sanctuary, Kerala, India. <i>Zootaxa</i> , 2021, 4990, 329353.	0.2	5
13297	Unravelling unexplored diversity of cercosporoid fungi (<i>Mycosphaerellaceae</i> , <i>Mycosphaerellales</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 4	0.8	4
13298	The complete mitochondrial genome of an endangered minnow <i>Aphyocypris lini</i> (Cypriniformes:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 4 3311-3321.	0.8	3
13299	A preliminary phylogenetic study of <i>Paraphlomis</i> (Lamiaceae) based on molecular and morphological evidence. <i>Plant Diversity</i> , 2021, 43, 206-215.	1.8	9
13300	<i>Corollospora mediterranea</i> : A Novel Species Complex in the Mediterranean Sea. <i>Applied Sciences (Switzerland)</i> , 2021, 11, 5452.	1.3	9
13301	Total Evidence Phylogenetic Analysis Supports New Morphological Synapomorphies for Bovidae (Mammalia, Artiodactyla). <i>American Museum Novitates</i> , 2021, 2021, .	0.2	1
13303	Revision of the <i>Merodon bombiformis</i> group (Diptera: Syrphidae) – rare and endemic African hoverflies. <i>European Journal of Taxonomy</i> , 0, 755, .	0.6	3
13304	Satellitome Analysis of <i>Rhodnius prolixus</i> , One of the Main Chagas Disease Vector Species. <i>International Journal of Molecular Sciences</i> , 2021, 22, 6052.	1.8	19
13305	Phylogeny of the supertribe <i>Nebriiinae</i> (Coleoptera, Carabidae) based on analyses of DNA sequence data. <i>ZooKeys</i> , 2021, 1044, 41-152.	0.5	6
13306	Integration of genetic structure into conservation of an endangered, endemic lizard, <i>Ceratophora aspera</i> : A case study from Sri Lanka. <i>Biotropica</i> , 2021, 53, 1301-1315.	0.8	1
13307	The complete chloroplast genome of <i>Alsophila latebrosa</i> , a common and widespread tree fern (Cyatheaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2084-2085.	0.2	0
13308	The complete chloroplast genome of <i>Sparganium fallax</i> (Typhaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2097-2098.	0.2	2

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13309	<i>Brucella</i> sp. sequence-type 27 associated with abortion in dwarf sperm whale <i>Kogia sima</i> . <i>European Journal of Wildlife Research</i> , 2021, 67, 1.	0.7	6
13310	Long-distance dispersal events rather than growth habit and life-history traits affect diversification rate in tribe Apieae (Apiaceae). <i>Botanical Journal of the Linnean Society</i> , 2022, 198, 1-25.	0.8	7
13313	Linking a Gene Cluster to Atranorin, a Major Cortical Substance of Lichens, through Genetic Dereplication and Heterologous Expression. <i>MBio</i> , 2021, 12, e0111121.	1.8	33
13315	Genomic and Phenotypic Evolution of <i>Achromobacter xylosoxidans</i> during Chronic Airway Infections of Patients with Cystic Fibrosis. <i>MSystems</i> , 2021, 6, e0052321.	1.7	13
13316	A new Amaryllidaceae genus, <i>Shoubiaonia</i> , from Yunnan Province, China. <i>Nordic Journal of Botany</i> , 2021, 39, .	0.2	3
13317	Phylogenetic relationships among false truffle genera of Paxillaceae— <i>Alpova</i> , <i>Melanogaster</i> , <i>Nealpova</i> , and <i>Paralpova</i> , gen. nov. <i>Mycologia</i> , 2021, 113, 828-841.	0.8	4
13318	Biochemical and molecular responses of the Mediterranean mussel (<i>Mytilus galloprovincialis</i>) to short-term exposure to three commonly prescribed drugs. <i>Marine Environmental Research</i> , 2021, 168, 105309.	1.1	10
13320	A chromosome-level genome assembly of rugged rose (<i>Rosa rugosa</i>) provides insights into its evolution, ecology, and floral characteristics. <i>Horticulture Research</i> , 2021, 8, 141.	2.9	29
13321	Genome-Wide Association Analysis for Triazole Resistance in <i>Aspergillus fumigatus</i> . <i>Pathogens</i> , 2021, 10, 701.	1.2	17
13322	De Novo SNP Discovery and Genotyping of Iranian <i>Pimpinella</i> Species Using ddRAD Sequencing. <i>Agronomy</i> , 2021, 11, 1342.	1.3	6
13323	<i>Fluviispira sanaruensis</i> sp., nov., Isolated from a Brackish Lake in Hamamatsu, Japan. <i>Current Microbiology</i> , 2021, 78, 3268-3276.	1.0	7
13324	<i>Cellulosimicrobium fucosivorans</i> sp. nov., isolated from San Elijo Lagoon, contains a fucose metabolic pathway linked to carotenoid production. <i>Archives of Microbiology</i> , 2021, 203, 4525-4538.	1.0	8
13325	Phenotypic and genomic differences among <i>S. cerevisiae</i> strains in nitrogen requirements during wine fermentations. <i>Food Microbiology</i> , 2021, 96, 103685.	2.1	5
13326	Stochasticity overrides deterministic processes in structuring macroinvertebrate communities in a plateau aquatic system. <i>Ecosphere</i> , 2021, 12, e03675.	1.0	12
13327	The complete chloroplast genome sequence of <i>Camellia rostrata</i> S. X. Yang & S. F. Chai (Theaceae), a critically endangered yellow camellia from southwest China. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2427-2429.	0.2	2
13328	Characterization of the complete chloroplast genome of <i>Dracocephalum heterophyllum</i> (Lamiaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2169-2170.	0.2	1
13329	Complete mitochondrial genome of the giant root-rat (<i>Tachyoryctes macrocephalus</i>). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2191-2193.	0.2	2
13330	Bayesian-Weighted Triplet and Quartet Methods for Species Tree Inference. <i>Bulletin of Mathematical Biology</i> , 2021, 83, 93.	0.9	9

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13331	The complete chloroplast genome of <i>Pleione maculata</i> , an orchid with important ornamental value and medicinal value. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2263-2265.	0.2	3
13332	A 180 Myr-old female-specific genome region in sturgeon reveals the oldest known vertebrate sex determining system with undifferentiated sex chromosomes. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2021, 376, 20200089.	1.8	41
13333	Intercontinental distributions, phylogenetic position and life cycles of species of <i>Apharyngostrigea</i> (Digenea, Diplostomoidea) illuminated with morphological, experimental, molecular and genomic data. <i>International Journal for Parasitology</i> , 2021, 51, 667-683.	1.3	11
13334	Genomic methods reveal independent demographic histories despite strong morphological conservatism in fish species. <i>Heredity</i> , 2021, 127, 323-333.	1.2	2
13335	Ovulate Cones of <i>Schizolepidopsis ediae</i> sp. nov. Provide Insights into the Evolution of Pinaceae. <i>International Journal of Plant Sciences</i> , 2021, 182, 490-507.	0.6	12
13336	Phylogeny and classification of Odonata using targeted genomics. <i>Molecular Phylogenetics and Evolution</i> , 2021, 160, 107115.	1.2	36
13337	Diatom Genus <i>Hyalosira</i> (Rhabdonematales emend.) and Resolution of its Polyphyly in Grammatophoraceae and Rhabdonemataceae with a New Genus, <i>Placosira</i> , and Five New <i>Hyalosira</i> Species. <i>Protist</i> , 2021, 172, 125816.	0.6	10
13338	Revisiting of <i>Carex</i> sect. <i>Confertiflorae</i> s.l. (Cyperaceae): New data from molecular and morphological evidence and first insights on <i>Carex</i> biogeography in East Asia. <i>Journal of Systematics and Evolution</i> , 2021, 59, 668-686.	1.6	5
13340	Comparative Analysis of the Chloroplast Genome for Four <i>Pennisetum</i> Species: Molecular Structure and Phylogenetic Relationships. <i>Frontiers in Genetics</i> , 2021, 12, 687844.	1.1	11
13344	Molecular characterization of a <i>Bacillus thuringiensis</i> strain from Argentina, toxic against Lepidoptera and Coleoptera, based on its whole-genome and Cry protein analysis. <i>Journal of Invertebrate Pathology</i> , 2021, 183, 107563.	1.5	8
13346	Expression Patterns and Functional Characterization of Arabidopsis <i>Galactose Oxidase-Like</i> Genes Suggest Specialized Roles for Galactose Oxidases in Plants. <i>Plant and Cell Physiology</i> , 2021, 62, 1927-1943.	1.5	8
13347	Nanopore metagenomic sequencing of influenza virus directly from respiratory samples: diagnosis, drug resistance and nosocomial transmission, United Kingdom, 2018/19 influenza season. <i>Eurosurveillance</i> , 2021, 26, .	3.9	17
13348	Molecular and morphological evidence for a unified, inclusive <i>Sinotaia quadrata</i> (Caenogastropoda: Viviparidae: Bellamyinae). <i>Journal of Molluscan Studies</i> , 2021, 87, .	0.4	2
13349	Total evidence phylogeny of the coastal <i>Cafius</i> complex (Coleoptera: Staphylinidae) and its new generic concepts. <i>Zoologica Scripta</i> , 2021, 50, 734-751.	0.7	8
13351	Evolutionary history of <i>Hemerocallis</i> in Japan inferred from chloroplast and nuclear phylogenies and levels of interspecific gene flow. <i>Molecular Phylogenetics and Evolution</i> , 2021, 164, 107264.	1.2	14
13352	Comparison of sand fly trapping approaches for vector surveillance of <i>Leishmania</i> and <i>Bartonella</i> species in ecologically distinct, endemic regions of Peru. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009517.	1.3	3
13354	Comparison of Two <i>Aspergillus oryzae</i> Genomes From Different Clades Reveals Independent Evolution of Alpha-Amylase Duplication, Variation in Secondary Metabolism Genes, and Differences in Primary Metabolism. <i>Frontiers in Microbiology</i> , 2021, 12, 691296.	1.5	7
13355	DNA transposons mediate duplications via transposition-independent and -dependent mechanisms in metazoans. <i>Nature Communications</i> , 2021, 12, 4280.	5.8	9

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13356	The super repertoire of type IV effectors in the pangenome of Ehrlichia spp. provides insights into host-specificity and pathogenesis. PLoS Computational Biology, 2021, 17, e1008788.	1.5	7
13357	Molecular Identification and Antimicrobial Activity of Foliar Endophytic Fungi on the Brazilian Pepper Tree (<i>Schinus terebinthifolius</i>) Reveal New Species of Diaporthe. Current Microbiology, 2021, 78, 3218-3229.	1.0	13
13359	The complete mitochondrial genome of the wood tiger moth (<i>Arctia plantaginis</i>) and phylogenetic analyses within Arctiinae. Mitochondrial DNA Part B: Resources, 2021, 6, 2171-2173.	0.2	0
13360	Phylogeography and resistome of pneumococcal meningitis in West Africa before and after vaccine introduction. Microbial Genomics, 2021, 7, .	1.0	0
13361	Identification of Three Clf-Sdr Subfamily Proteins in <i>Staphylococcus warneri</i> , and Comparative Genomics Analysis of a Locus Encoding CWA Proteins in <i>Staphylococcus</i> Species. Frontiers in Microbiology, 2021, 12, 691087.	1.5	0
13362	Evolutionary models of amino acid substitutions based on the tertiary structure of their neighborhoods. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1565-1576.	1.5	0
13364	Molecular Systematics of the Native Seagrass, <i>Ruppia</i> cf. <i>Maritima</i> (Ruppiales, Alismatales), on Hawai'i Island. Pacific Science, 2021, 75, .	0.2	1
13365	<i>Entyloma eranthis</i> sp. nov. on <i>Eranthis longistipitata</i> from Uzbekistan. Mycotaxon, 2021, 136, 373-385.	0.1	1
13366	Accurate large-scale phylogeny-aware alignment using BALi-Phy. Bioinformatics, 2021, 37, 4677-4683.	1.8	2
13367	Identification and host response interaction study of SARS-CoV-2 encoded miRNA-like sequences: an in silico approach. Computers in Biology and Medicine, 2021, 134, 104451.	3.9	10
13368	<i>Yersinia pestis</i> strains isolated in natural plague foci of Caucasus and Transcaucasia in the context of the global evolution of species. Genomics, 2021, 113, 1952-1961.	1.3	9
13369	Phormidepistatin from the Cyanobacterium UIC 10484: Assessing the Phylogenetic Distribution of the Statine Pharmacophore. Journal of Natural Products, 2021, 84, 2256-2264.	1.5	2
13370	Identification and characterization of <i>Colletotrichum</i> species associated with anthracnose disease of banana. Plant Pathology, 2021, 70, 1827-1837.	1.2	10
13371	Patterns of protist distribution and diversification in alpine lakes across Europe. MicrobiologyOpen, 2021, 10, e1216.	1.2	6
13372	Targeted conservation management of white pines in China: Integrating phylogeographic structure, niche modeling, and conservation gap analyses. Forest Ecology and Management, 2021, 492, 119211.	1.4	7
13373	Reduction in antimicrobial resistance prevalence in <i>Escherichia coli</i> from a pig farm following withdrawal of group antimicrobial treatment. Veterinary Microbiology, 2021, 258, 109125.	0.8	18
13374	The spatial-temporal dynamics of respiratory syncytial virus infections across the east-west coasts of Australia during 2016-17. Virus Evolution, 2021, 7, veab068.	2.2	11
13375	Phylogeographic analysis delimits three evolutionary significant units of least chipmunks in North America and identifies unique genetic diversity within the imperiled <i>Peromyscus</i> population. Ecology and Evolution, 2021, 11, 12114-12128.	0.8	3

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13376	Invasion at the population level: a story of the freshwater snails <i>Gyraulus parvus</i> and <i>G. laevis</i> . <i>Hydrobiologia</i> , 2021, 848, 4661-4671.	1.0	9
13377	A new, undescribed species of <i>Melanocharis</i> berrypecker from western New Guinea and the evolutionary history of the family Melanocharitidae. <i>Ibis</i> , 2021, 163, 1310-1329.	1.0	7
13378	Description of <i>Devosia faecipullorum</i> sp. nov., harboring antibiotic- and toxic compound-resistant genes, isolated from poultry manure. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	8
13379	Detailed characterization of the UMAMIT proteins provides insight into their evolution, amino acid transport properties, and role in the plant. <i>Journal of Experimental Botany</i> , 2021, 72, 6400-6417.	2.4	17
13380	Unravelling hybridization in <i>Phytophthora</i> using phylogenomics and genome size estimation. <i>IMA Fungus</i> , 2021, 12, 16.	1.7	22
13381	An updated infrafamilial classification of Sapindaceae based on targeted enrichment data. <i>American Journal of Botany</i> , 2021, 108, 1234-1251.	0.8	20
13382	Improved genome assembly of Chinese shrimp (<i>Fenneropenaeus chinensis</i>) suggests adaptation to the environment during evolution and domestication. <i>Molecular Ecology Resources</i> , 2022, 22, 334-344.	2.2	14
13383	A new cave-dwelling genus and species of Nerillidae (Annelida) from the Ryukyu Islands, Japan. <i>Marine Biodiversity</i> , 2021, 51, 1.	0.3	3
13385	<i>Mallocybe heimii</i> ectomycorrhizae with <i>Cistus creticus</i> and <i>Pinus halepensis</i> in Mediterranean littoral sand dunes—assessment of phylogenetic relationships to <i>M. arenaria</i> and <i>M. agardhii</i> . <i>Mycorrhiza</i> , 2021, 31, 497-510.	1.3	4
13386	Adaptive divergence and post-zygotic barriers to gene flow between sympatric populations of a herbivorous mite. <i>Communications Biology</i> , 2021, 4, 853.	2.0	12
13387	Multiple Introductions of the Pestiferous Land Snail <i>Theba pisana</i> (Müller, 1774) (Gastropoda: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 3	1.0	3
13388	A Novel Family of RNA-Binding Proteins Regulate Polysaccharide Metabolism in <i>Bacteroides thetaiotaomicron</i> . <i>Journal of Bacteriology</i> , 2021, 203, e0021721.	1.0	6
13390	A nuclear phylogenomic study of the angiosperm order Myrtales, exploring the potential and limitations of the universal Angiosperms353 probe set. <i>American Journal of Botany</i> , 2021, 108, 1087-1111.	0.8	53
13392	Chromosome-level genome assembly of an agricultural pest, the rice leaffolder <i>Cnaphalocrocis exigua</i> (Crambidae, Lepidoptera). <i>Molecular Ecology Resources</i> , 2022, 22, 307-318.	2.2	7
13393	<i>Clypifer cribrifer</i> gen. nov., sp. nov. (Clypiferidae fam. nov., Pterocystida, Centroplasthelida), with notes on evolution of centrohelid siliceous coverings. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	6
13394	Genomic Analysis of <i>Sarcomyxa edulis</i> Reveals the Basis of Its Medicinal Properties and Evolutionary Relationships. <i>Frontiers in Microbiology</i> , 2021, 12, 652324.	1.5	6
13395	Copy number analyses of DNA repair genes reveal the role of poly(ADP-ribose) polymerase (PARP) in tree longevity. <i>IScience</i> , 2021, 24, 102779.	1.9	12
13396	Biodiversity of Hawaiian Peyssonneliales (Rhodophyta). 1. Two New Species in the Genus <i>Ramicrusta</i> from Lehua Island1. <i>Pacific Science</i> , 2021, 75, .	0.2	9

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13397	Evolution of Toll, Spatzle and MyD88 in insects: the problem of the Diptera bias. <i>BMC Genomics</i> , 2021, 22, 562.	1.2	13
13398	Successful Dissemination of Plasmid-Mediated Extended-Spectrum β -Lactamases in Enterobacterales over Humans to Wild Fauna. <i>Microorganisms</i> , 2021, 9, 1471.	1.6	2
13399	A SWEET surprise: Anaerobic fungal sugar transporters and chimeras enhance sugar uptake in yeast. <i>Metabolic Engineering</i> , 2021, 66, 137-147.	3.6	19
13400	Legacy effects of pre-crop plant functional group on fungal root symbionts of barley. <i>Ecological Applications</i> , 2021, 31, e02378.	1.8	6
13401	Two Reference-Quality Sea Snake Genomes Reveal Their Divergent Evolution of Adaptive Traits and Venom Systems. <i>Molecular Biology and Evolution</i> , 2021, 38, 4867-4883.	3.5	20
13402	The first mitochondrial genome of a South America parthenogenetic lizard (Squamata: Tj ETQq1 1 0.784314 rgBT /Overlock 1 Tf 505	0.2	1
13403	The complete chloroplast genome sequence of <i>Prunus simonii</i> Weiwang TM . <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2353-2354.	0.2	0
13404	Target enrichment improves phylogenetic resolution in the genus <i>Zanthoxylum</i> (Rutaceae) and indicates both incomplete lineage sorting and hybridization events. <i>Annals of Botany</i> , 2021, 128, 497-510.	1.4	12
13405	The complete mitochondrial genome of <i>Atypus karschi</i> (Araneae, Atypidae) with phylogenetic consideration. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2523-2525.	0.2	3
13406	Evolution, systematics and historical biogeography of sand flies of the subgenus <i>Paraphlebotomus</i> (Diptera, Psychodidae, Phlebotomus) inferred using restriction-site associated DNA markers. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009479.	1.3	7
13407	Cattle connection: molecular epidemiology of BVDV outbreaks via rapid nanopore whole-genome sequencing of clinical samples. <i>BMC Veterinary Research</i> , 2021, 17, 242.	0.7	4
13408	Genotype-Specific Expression and NLR Repertoire Contribute to Phenotypic Resistance Diversity in <i>Plantago lanceolata</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 675760.	1.7	4
13409	<i>Watanabea</i> green microalgae (Trebouxiophyceae) inhabiting lichen holobiomes: <i>Watanabea lichenicola</i> sp. nova. <i>Phycological Research</i> , 2021, 69, 226-236.	0.8	7
13410	Complete Genome Sequence of <i>Streptococcus oralis</i> SF100, Isolated from Blood Cultures from a Patient with Infective Endocarditis. <i>Microbiology Resource Announcements</i> , 2021, 10, e0017621.	0.3	1
13411	Increased Virulence of Outer Membrane Porin Mutants of <i>Mycobacterium abscessus</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 706207.	1.5	3
13412	Phylogeographic reconstructions can be biased by ancestral shared alleles: The case of the polymorphic lichen <i>Bryoria fuscescens</i> in Europe and North Africa. <i>Molecular Ecology</i> , 2021, 30, 4845-4865.	2.0	2
13413	New genetic markers for Sapotaceae phylogenomics: More than 600 nuclear genes applicable from family to population levels. <i>Molecular Phylogenetics and Evolution</i> , 2021, 160, 107123.	1.2	17
13414	A conserved role for arrow in posterior axis patterning across Arthropoda. <i>Developmental Biology</i> , 2021, 475, 91-105.	0.9	14

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13415	Rhodococcus spelaei sp. nov., isolated from a cave, and proposals that Rhodococcus biphenylivorans is a later synonym of Rhodococcus pyridinivorans, Rhodococcus qingshengii and Rhodococcus baikunurensis are later synonyms of Rhodococcus erythropolis, and Rhodococcus percolatus and Rhodococcus imtechensis are later synonyms of Rhodococcus opacus. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	22
13416	Analysis of Bacterial Communities on North Sea Macroalgae and Characterization of the Isolated Planctomycetes Adhaeretur mobilis gen. nov., sp. nov., Roseimaritima multifibrata sp. nov., Rosistilla ulvae sp. nov. and Rubripirellula lacrimiformis sp. nov.. Microorganisms, 2021, 9, 1494.	1.6	34
13417	Transmission dynamics and forecasts of the COVID-19 pandemic in Mexico, March-December 2020. PLoS ONE, 2021, 16, e0254826.	1.1	11
13418	The methylome of the model arbuscular mycorrhizal fungus, Rhizophagus irregularis, shares characteristics with early diverging fungi and Dikarya. Communications Biology, 2021, 4, 901.	2.0	17
13419	Gene tree and species tree reconciliation with endosymbiotic gene transfer. Bioinformatics, 2021, 37, i120-i132.	1.8	5
13420	Filling the gaps: The mitogenomes of Afrotropical egg-guarding frogs based on historical type material and a re-assessment of the nomenclatural status of Alexteroon Perret, 1988 (Hyperoliidae). Zoologischer Anzeiger, 2021, 293, 215-224.	0.4	4
13421	Functional diversity of microbial communities in inactive seafloor sulfide deposits. FEMS Microbiology Ecology, 2021, 97, .	1.3	16
13422	Whole-Genome SNP Analysis Identifies Putative Mycobacterium bovis Transmission Clusters in Livestock and Wildlife in Catalonia, Spain. Microorganisms, 2021, 9, 1629.	1.6	6
13424	A new species of <i>Aspicilia</i> (<i>Megasporaceae</i>), with a new lichenicolous <i>Sagediopsis</i> (<i>Adelococcaceae</i>), from the Falkland Islands. Lichenologist, 2021, 53, 307-315.	0.5	1
13425	Direct Molecular Evidence for an Ancient, Conserved Developmental Toolkit Controlling Posttranscriptional Gene Regulation in Land Plants. Molecular Biology and Evolution, 2021, 38, 4765-4777.	3.5	1
13426	Plastid RNA editing reduction accompanied with genetic variations in Cymbidium, a genus with diverse lifestyle modes. Plant Diversity, 2022, 44, 316-321.	1.8	5
13430	Molecular-Based Reappraisal of a Historical Record of Dothistroma Needle Blight in the Centre of the Mediterranean Region. Forests, 2021, 12, 983.	0.9	5
13431	Sandaracinobacteroides hominis gen. nov., sp. nov., isolated from human skin. Archives of Microbiology, 2021, 203, 5067-5074.	1.0	12
13432	A new subfamily classification of the <i>Citrus</i> family (Rutaceae) based on six nuclear and plastid markers. Taxon, 2021, 70, 1035-1061.	0.4	35
13433	Andean uplift, drainage basin formation, and the evolution of plants living in fast-flowing aquatic ecosystems in northern South America. New Phytologist, 2021, 232, 2175-2190.	3.5	6
13434	The complete mitochondrial genome of a non-biting midge <i>Polypedilum unifascium</i> (Tokunaga), Tj ETQq1 1 0.784314 rgBT / Over	0.2	19
13435	Delineation of a novel environmental phylogroup of the genus Acinetobacter encompassing Acinetobacter terrae sp. nov., Acinetobacter terrestris sp. nov. and three other tentative species. Systematic and Applied Microbiology, 2021, 44, 126217.	1.2	40
13436	Evolutionary transition to XY sex chromosomes associated with Y-linked duplication of a male hormone gene in a terrestrial isopod. Heredity, 2021, 127, 266-277.	1.2	5

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13437	Taxonomic Revision of the Genus <i>Lactifluus</i> (Russulales, Basidiomycota) of South Korea. <i>Mycobiology</i> , 2021, 49, 308-345.	0.6	1
13438	Comparative genomics of <i>Edwardsiella ictaluri</i> revealed four distinct host-specific genotypes and thirteen potential vaccine candidates. <i>Genomics</i> , 2021, 113, 1976-1987.	1.3	10
13439	The complete chloroplast genome of <i>Agropyron pectinatum</i> (M. Bieb.) P. Beauv.. Mitochondrial DNA Part B: Resources, 2021, 6, 2512-2513.	0.2	0
13440	Révision du genre <i>Ammodaucus</i> (Apiaceae) en Afrique du Nord. <i>Candollea</i> , 2021, 76, .	0.1	1
13441	Evidence for the existence of a new genus <i>Chlamydiifrater</i> gen. nov. inside the family Chlamydiaceae with two new species isolated from flamingo (<i>Phoenicopterus roseus</i>): <i>Chlamydiifrater phoenicopteri</i> sp. nov. and <i>Chlamydiifrater volucris</i> sp. nov.. <i>Systematic and Applied Microbiology</i> , 2021, 44, 126200.	1.2	24
13442	Non-adaptive evolutionary processes governed the diversification of a temperate conifer lineage after its migration into the tropics. <i>Molecular Phylogenetics and Evolution</i> , 2021, 160, 107125.	1.2	9
13443	Gene duplications and phylogenomic conflict underlie major pulses of phenotypic evolution in gymnosperms. <i>Nature Plants</i> , 2021, 7, 1015-1025.	4.7	68
13444	Novel hyperthermophilic crenarchaeon <i>Infirmifilum lucidum</i> gen. nov. sp. nov., reclassification of <i>Thermofilum uzonense</i> as <i>Infirmifilum uzonense</i> comb. nov. and assignment of the family Thermofilaceae to the order Thermofilales ord. nov.. <i>Systematic and Applied Microbiology</i> , 2021, 44, 126200.	1.2	15
13445	<i>Apilactobacillus nanyangensis</i> sp. nov., <i>Secundilactobacillus hailunensis</i> sp. nov., <i>Secundilactobacillus yichangensis</i> sp. nov., <i>Levilactobacillus andaensis</i> sp. nov., <i>Levilactobacillus wangkuiensis</i> sp. nov., <i>Levilactobacillus lanxiensis</i> sp. nov., <i>Lactacaseibacillus mingshuiensis</i> sp. nov. and <i>Lactacaseibacillus suilingensis</i> sp. nov., isolated from traditional Chinese pickle and the gut of honeybee (<i>Apis mellifera</i>). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	39
13446	<i>Rahnella laticis</i> sp. nov. and <i>Rahnella contaminans</i> sp. nov., and emended description of the genus <i>Rahnella</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	17
13447	<i>Gulosibacter sediminis</i> sp. nov., isolated from Indian Ocean marine sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	4
13448	Microzooplankton diversity and potential role in carbon cycling of contrasting Southern Ocean productivity regimes. <i>Journal of Marine Systems</i> , 2021, 219, 103531.	0.9	9
13449	Genomic data reveal the biogeographical and demographic history of <i>Ammospiza</i> sparrows in northeast tidal marshes. <i>Journal of Biogeography</i> , 2021, 48, 2360-2374.	1.4	4
13451	Genomic signatures of admixture and selection are shared among populations of <i>Zaprionus indianus</i> across the western hemisphere. <i>Molecular Ecology</i> , 2021, 30, 6193-6210.	2.0	4
13452	Insight into the Phylogenetic Relationships among Three Subfamilies within Heptageniidae (Insecta: Tj ETQqO O O rgBT /Overlock 10 Tf 5 2021, 12, 656.	1.0	10
13453	Towards the Well-Tempered Chloroplast DNA Sequences. <i>Plants</i> , 2021, 10, 1360.	1.6	7
13454	Contrasting genetic signal of recolonization after rainforest fragmentation in African trees with different dispersal abilities. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	4
13455	Recent population differentiation in the habitat specialist Glossy Antshrike (Aves: Thamnophilidae) across Amazonian seasonally flooded forests. <i>Ecology and Evolution</i> , 2021, 11, 11826-11838.	0.8	2

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13456	Arnebia euchroma, a Plant Species of Cold Desert in the Himalayas, Harbors Beneficial Cultivable Endophytes in Roots and Leaves. <i>Frontiers in Microbiology</i> , 2021, 12, 696667.	1.5	35
13457	Phylogeny based on ultra-conserved elements clarifies the evolution of rails and allies (Ralloidea) and is the basis for a revised classification. <i>Auk</i> , 2021, 138, .	0.7	14
13458	Molecular phylogeny of European Runcinida (Gastropoda, Heterobranchia): the discover of an unexpected pool of complex species, with special reference to the case of <i>Runcina coronata</i> . <i>Zoological Journal of the Linnean Society</i> , 2022, 194, 761-788.	1.0	7
13459	A phylogenomic examination of Palmyra Atoll's corallimorpharian invader. <i>Coral Reefs</i> , 2022, 41, 673-685.	0.9	5
13461	Human Papillomavirus Detection by Whole-Genome Next-Generation Sequencing: Importance of Validation and Quality Assurance Procedures. <i>Viruses</i> , 2021, 13, 1323.	1.5	11
13462	Parallel evolution of trehalose production machinery in anhydrobiotic animals via recurrent gene loss and horizontal transfer. <i>Open Biology</i> , 2021, 11, 200413.	1.5	17
13463	A novel characteristic of a phytoplankton as a potential source of straight-chain alkanes. <i>Scientific Reports</i> , 2021, 11, 14190.	1.6	7
13464	Phylogenomic systematics of the spotted skunks (Carnivora, Mephitidae, Spilogale): Additional species diversity and Pleistocene climate change as a major driver of diversification. <i>Molecular Phylogenetics and Evolution</i> , 2022, 167, 107266.	1.2	9
13465	Evolution of a neuromuscular sexual dimorphism in the <i>Drosophila montium</i> species group. <i>Scientific Reports</i> , 2021, 11, 15272.	1.6	3
13466	Crystal structure of a key enzyme for anaerobic ethane activation. <i>Science</i> , 2021, 373, 118-121.	6.0	27
13467	Phylogenomic Assessment of Biodiversity Using a Reference-Based Taxonomy: An Example With Horned Lizards (<i>Phrynosoma</i>). <i>Frontiers in Ecology and Evolution</i> , 2021, 9, .	1.1	13
13468	The microbiome of the habitat-forming brown alga <i>Fucus vesiculosus</i> (Phaeophyceae) has similar cross-Atlantic structure that reflects past and present drivers. <i>Journal of Phycology</i> , 2021, 57, 1681-1698.	1.0	17
13469	Assembly of the complete mitochondrial genome of an endemic plant, <i>Scutellaria tsinyunensis</i> , revealed the existence of two conformations generated by a repeat-mediated recombination. <i>Planta</i> , 2021, 254, 36.	1.6	46
13470	The chromosome-level reference genome assembly for <i>Dendrobium officinale</i> and its utility of functional genomics research and molecular breeding study. <i>Acta Pharmaceutica Sinica B</i> , 2021, 11, 2080-2092.	5.7	54
13472	Evaluation of Potential Transfer of the Pathogen <i>Saprolegnia parasitica</i> between Farmed Salmonids and Wild Fish. <i>Pathogens</i> , 2021, 10, 926.	1.2	7
13473	Molecular and morphological phylogeny of host-specific <i>Dactylogyrus</i> parasites (Monogenea) sheds new light on the puzzling Middle Eastern origin of European and African lineages. <i>Parasites and Vectors</i> , 2021, 14, 372.	1.0	10
13474	The Conservation of Chloroplast Genome Structure and Improved Resolution of Intrafamilial Relationships of Crassulaceae. <i>Frontiers in Plant Science</i> , 2021, 12, 631884.	1.7	16
13475	Sequence data from isolated lichen-associated melanized fungi enhance delimitation of two new lineages within Chaetothyriomycetidae. <i>Mycological Progress</i> , 2021, 20, 911-927.	0.5	11

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13476	Genomics and transcriptomics yields a system-level view of the biology of the pathogen <i>Naegleria fowleri</i> . <i>BMC Biology</i> , 2021, 19, 142.	1.7	18
13477	A molecular re-evaluation of <i>Parmelia encryptata</i> with notes on its distribution. <i>Lichenologist</i> , 2021, 53, 341-345.	0.5	1
13478	Taxonomy and Molecular Phylogeny of Two New Urostyleid Ciliates (Protozoa: Ciliophora) From Chinese Wetlands and Establishment of a New Genus. <i>Frontiers in Microbiology</i> , 2021, 12, 707954.	1.5	6
13479	A preliminary study of <i>Badimia Vězda</i> (Ramalinaceae) in East Asia. <i>Lichenologist</i> , 2021, 53, 327-334.	0.5	0
13480	Comparisons within the Rice GA 2-Oxidase Gene Family Revealed Three Dominant Paralogs and a Functional Attenuated Gene that Led to the Identification of Four Amino Acid Variants Associated with GA Deactivation Capability. <i>Rice</i> , 2021, 14, 70.	1.7	5
13482	Evolution of hes gene family in vertebrates: the hes5 cluster genes have specifically increased in frogs. <i>Bmc Ecology and Evolution</i> , 2021, 21, 147.	0.7	3
13483	Interstrain Variability of Human Vaginal <i>Lactobacillus crispatus</i> for Metabolism of Biogenic Amines and Antimicrobial Activity against Urogenital Pathogens. <i>Molecules</i> , 2021, 26, 4538.	1.7	8
13484	Complete mitochondrial genome of the highly fecund <i>Bombyx mori</i> Linnaeus, 1758 (Lepidoptera: Tj ETQq1 1.0.784314 rgBT /Ov	0.2	0
13485	The whole-genome sequence of the novel yeast species <i>Metschnikowia persimmonesis</i> isolated from medicinal plant <i>Diospyros kaki</i> Thunb. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	4
13486	First record of the genus <i>Hildenbrandia</i> (Florideophyceae: Hildenbrandiales) from French Polynesia and description of <i>H. Tahitiensis</i> sp. nov.. <i>Journal of Asia-Pacific Biodiversity</i> , 2021, 14, 607-612.	0.2	3
13487	Build a better bootstrap and the RAWR shall beat a random path to your door: phylogenetic support estimation revisited. <i>Bioinformatics</i> , 2021, 37, i111-i119.	1.8	1
13488	The role of interspecies recombination in the evolution of antibiotic-resistant pneumococci. <i>ELife</i> , 2021, 10, .	2.8	21
13489	Genomic Elucidation of a COVID-19 Resurgence and Local Transmission of SARS-CoV-2 in Guangzhou, China. <i>Journal of Clinical Microbiology</i> , 2021, 59, e0007921.	1.8	5
13490	Nationwide genomic atlas of soil-dwelling <i>Listeria</i> reveals effects of selection and population ecology on pangenome evolution. <i>Nature Microbiology</i> , 2021, 6, 1021-1030.	5.9	54
13491	Parallel functional reduction in the mitochondria of apicomplexan parasites. <i>Current Biology</i> , 2021, 31, 2920-2928.e4.	1.8	26
13492	Hundreds of nuclear and plastid loci yield novel insights into orchid relationships. <i>American Journal of Botany</i> , 2021, 108, 1166-1180.	0.8	35
13493	Shaping the biology of citrus: I. Genomic determinants of evolution. <i>Plant Genome</i> , 2021, 14, e20104.	1.6	4
13494	The British chalk specialist <i>Lecidea lichenicola</i> auct. revealed as a new genus of Lichinomycetes. <i>Fungal Biology</i> , 2021, 125, 495-504.	1.1	1

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13495	The utilisation of CytB and COI barcodes for the identification of bloodmeals and Culicoides species (Diptera: Ceratopogonidae) reveals a variety of novel wildlife hosts in South Africa.. Acta Tropica, 2021, 219, 105913.	0.9	7
13496	Genomic Evidence for Speciation with Gene Flow in Broadcast Spawning Marine Invertebrates. Molecular Biology and Evolution, 2021, 38, 4683-4699.	3.5	17
13497	The complete chloroplast genome sequence of Paris polyphylla var. alba H.Li & R.J.Mitchell and its phylogenetic analysis. Mitochondrial DNA Part B: Resources, 2021, 6, 2503-2504.	0.2	1
13498	The complete chloroplast genome sequence of medicinal plant: <i>Peganum nigellastrum</i> (Zygophyllaceae). Mitochondrial DNA Part B: Resources, 2021, 6, 2387-2388.	0.2	0
13499	Evolution of Superoxide Dismutases and Catalases in Cyanobacteria: Occurrence of the Antioxidant Enzyme Genes before the Rise of Atmospheric Oxygen. Journal of Molecular Evolution, 2021, 89, 527-543.	0.8	8
13500	Concordance-Based Approaches for the Inference of Relationships and Molecular Rates with Phylogenomic Data Sets. Systematic Biology, 2022, 71, 943-958.	2.7	11
13501	Phylogenetic relationships among subclades within the Trinity bristle snail species complex, riverine barriers, and re-classification. California Fish and Wildlife Journal, 2021, , 107-145.	0.2	4
13502	Accelerating Phylogenetics Using FPGAs in the Cloud. IEEE Micro, 2021, 41, 24-30.	1.8	2
13504	tinselRâ€”an R Shiny Application for Annotating Phylogenetic Trees. Microbiology Resource Announcements, 2021, 10, e0022721.	0.3	0
13505	Characterization, Pathogenicity, Phylogeny, and Comparative Genomic Analysis of <i>Pseudomonas tolaasii</i> Strains Isolated from Various Mushrooms in China. Phytopathology, 2022, 112, 521-534.	1.1	2
13506	Multigene phylogenetic data place monoraphid diatoms Schizostauron and Astartiella along with other fistulaâ€”bearing genera in the Stauroneidaceae 1. Journal of Phycology, 2021, 57, 1472-1491.	1.0	5
13507	Multi-omics approach highlights differences between RLP classes in Arabidopsis thaliana. BMC Genomics, 2021, 22, 557.	1.2	13
13508	Draft Genome Sequences of the Three <i>Massilia</i> Strains AB1, ST3, and ZL223. Microbiology Resource Announcements, 2021, 10, e0045121.	0.3	1
13509	First historical genome of a crop bacterial pathogen from herbarium specimen: Insights into citrus canker emergence. PLoS Pathogens, 2021, 17, e1009714.	2.1	8
13510	Phylogenomics of the bumblebee catfishes (Siluriformes: Pseudopimelodidae) using ultraconserved elements. Journal of Zoological Systematics and Evolutionary Research, 0, , .	0.6	7
13512	Different rates of pollen and seed gene flow cause branchâ€”length and geographic cytonuclear discordance within Asian butternuts. New Phytologist, 2021, 232, 388-403.	3.5	21
13513	Integrative phylogenomics reveals a Permian origin of Adephaga beetles. Systematic Entomology, 2021, 46, 968-990.	1.7	15
13514	Phylogenetic analyses and species delimitation of Nephrotettix Matsumura (Hemiptera: Cicadellidae:) Tj ETQq1 1 0.784314 rgBT /Over 202-214.	0.4	4

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13516	Molecular Biology and Pathological Process of an Infectious Bronchitis Virus with Enteric Tropism in Commercial Broilers. <i>Viruses</i> , 2021, 13, 1477.	1.5	5
13517	Deep-Sea Carbonates Are a Reservoir of Fossil Microbes Previously Inhabiting Cold Seeps. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	1
13518	Phylogenetic Position of Shiraia-Like Endophytes on Bamboos and the Diverse Biosynthesis of Hypocrellin and Hypocrellin Derivatives. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 563.	1.5	3
13520	Evolution of a c-di-GMP anti- β switch. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	11
13521	Evidence of Adaptive Evolution in Wolbachia-Regulated Gene DNMT2 and Its Role in the Dipteran Immune Response and Pathogen Blocking. <i>Viruses</i> , 2021, 13, 1464.	1.5	8
13522	The Chloroplast Phylogenomics and Systematics of <i>Zoysia</i> (Poaceae). <i>Plants</i> , 2021, 10, 1517.	1.6	6
13523	A new lineage of mazaediate fungi in the Eurotiomycetes: Cryptocaliciomycetidae subclass. nov., based on the new species <i>Cryptocalicium blascoi</i> and the revision of the ascoma evolution. <i>Mycological Progress</i> , 2021, 20, 889-904.	0.5	6
13524	Evolutionary Insights Into Two Widespread Ectomycorrhizal Fungi (<i>Pisolithus</i>) From Comparative Analysis of Mitochondrial Genomes. <i>Frontiers in Microbiology</i> , 2021, 12, 583129.	1.5	2
13527	Stemphylium Leaf Blight of Welsh Onion (<i>Allium fistulosum</i>): An Emerging Disease in Sanxing, Taiwan. <i>Plant Disease</i> , 2021, 105, 4121-4131.	0.7	5
13528	Draft Genome Sequence of the Ectomycorrhizal Fungus <i>Astraeus odoratus</i> from Northern Thailand. <i>Microbiology Resource Announcements</i> , 2021, 10, e0004421.	0.3	0
13529	Improved inference of tandem domain duplications. <i>Bioinformatics</i> , 2021, 37, i133-i141.	1.8	0
13530	Relict groups of spiny frogs indicate Late Paleogene-Early Neogene trans-Tibet dispersal of thermophile faunal elements. <i>PeerJ</i> , 2021, 9, e11793.	0.9	7
13531	Global biogeography of chemosynthetic symbionts reveals both localized and globally distributed symbiont groups. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	15
13532	Species diversity of freshwater shrimp in Henan Province, China, based on morphological characters and <i>COI</i> mitochondrial gene. <i>Ecology and Evolution</i> , 2021, 11, 10502-10514.	0.8	5
13533	The long-time orphan protist <i>Meringosphaera mediterranea</i> Lohmann, 1902 [1903] is a centrohelid heliozoan. <i>Journal of Eukaryotic Microbiology</i> , 2021, 68, e12860.	0.8	4
13534	Chromosome-level genome assembly of <i>Scapharca kagoshimensis</i> reveals the expanded molecular basis of heme biosynthesis in ark shells. <i>Molecular Ecology Resources</i> , 2022, 22, 295-306.	2.2	5
13535	Diversity and Pathogenicity of Pectobacterium Species Responsible for Causing Soft Rot and Blackleg of Potato in the Columbia Basin. <i>American Journal of Potato Research</i> , 2021, 98, 267.	0.5	2
13536	Preinvasion Assessment of Exotic Bark Beetle-Vectored Fungi to Detect Tree-Killing Pathogens. <i>Phytopathology</i> , 2022, 112, 261-270.	1.1	12

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13537	Revealing the full biosphere structure and versatile metabolic functions in the deepest ocean sediment of the Challenger Deep. <i>Genome Biology</i> , 2021, 22, 207.	3.8	27
13538	Salmonella Paratyphi B; Public Health and Parental Choice. <i>Pediatric Infectious Disease Journal</i> , 2021, 40, e374-e378.	1.1	3
13540	Genomic evidence for the parallel regression of melatonin synthesis and signaling pathways in placental mammals. <i>Open Research Europe</i> , 0, 1, 75.	2.0	3
13541	Diverse Profile of Fermentation Byproducts From Thin Stillage. <i>Frontiers in Bioengineering and Biotechnology</i> , 2021, 9, 695306.	2.0	16
13543	Ecology, Morphology, Phylogeny and Taxonomic Revision of Giant Radiolarians, <i>Orodaria</i> ord. nov. (Radiolaria; Rhizaria; SAR). <i>Protist</i> , 2021, 172, 125808.	0.6	6
13544	Dynamics of Baltic Sea phages driven by environmental changes. <i>Environmental Microbiology</i> , 2021, 23, 4576-4594.	1.8	5
13545	Diversity and biogeography of Mediterranean freshwater blennies (Blenniidae, Salaria). <i>Diversity and Distributions</i> , 2021, 27, 1832-1847.	1.9	6
13546	Two NLR immune receptors acquired high-affinity binding to a fungal effector through convergent evolution of their integrated domain. <i>ELife</i> , 2021, 10, .	2.8	38
13548	Haplotype-resolved genome assembly provides insights into evolutionary history of the tea plant <i>Camellia sinensis</i> . <i>Nature Genetics</i> , 2021, 53, 1250-1259.	9.4	157
13549	Remotely sensed between-individual functional trait variation in a temperate forest. <i>Ecology and Evolution</i> , 2021, 11, 10834-10867.	0.8	13
13550	“Jumping Jack” Genomic Microsatellites Underscore the Distinctiveness of Closely Related <i>Pseudoperonospora cubensis</i> and <i>Pseudoperonospora humuli</i> and Provide New Insights Into Their Evolutionary Past. <i>Frontiers in Microbiology</i> , 2021, 12, 686759.	1.5	3
13551	Non-invasive surveys of mammalian viruses using environmental DNA. <i>Methods in Ecology and Evolution</i> , 2021, 12, 1941-1952.	2.2	10
13552	RNase-based self-incompatibility in cacti. <i>New Phytologist</i> , 2021, 231, 2039-2049.	3.5	12
13553	Increasing Frequency and Transmission of HIV-1 Non-B Subtypes Among Men Who Have Sex With Men in the Swiss HIV Cohort Study. <i>Journal of Infectious Diseases</i> , 2022, 225, 306-316.	1.9	5
13554	<i>Canoparmelia amazonica</i> , <i>Myelochroa lindmanii</i> and <i>Parmelinella salacinifera</i> belong to <i>Parmelinella</i> (Parmeliaceae). <i>Bryologist</i> , 2021, 124, .	0.1	1
13555	A new species of the <i>Dendropsophus decipiens</i> Group (Anura: Hylidae) from Northeastern Brazil. <i>PLoS ONE</i> , 2021, 16, e0248112.	1.1	3
13556	Unraveling Genetic Diversity Amongst European Hazelnut (<i>Corylus avellana</i> L.) Varieties in Turkey. <i>Frontiers in Plant Science</i> , 2021, 12, 661274.	1.7	8
13557	<i>Ethelia hawaiiensis</i> (Etheliaceae, Rhodophyta), a New Mesophotic Marine Alga from Manawai (Pearl and) Tj ETQq1 1,0,784314 rgBT /Ov	0.2	6

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13558	Evolution of the MLO gene families in octoploid strawberry (<i>Fragaria</i> – <i>Ananassa</i>) and progenitor diploid species identified potential genes for strawberry powdery mildew resistance. Horticulture Research, 2021, 8, 153.	2.9	11
13559	Molecular Characterization of the Common Snook, <i>Centropomus undecimalis</i> (Bloch, 1792) in the Usumacinta Basin. Diversity, 2021, 13, 347.	0.7	3
13560	Molecular Phylogeny of Unicellular Marine Coccoid Green Algae Revealed New Insights into the Systematics of the Ulvophyceae (Chlorophyta). Microorganisms, 2021, 9, 1586.	1.6	5
13561	Genomic Diversity of <i>Haemophilus influenzae</i> Serotype a in an Outbreak Community—Alaska, 2018. Journal of Infectious Diseases, 2021, , .	1.9	0
13562	Comparative Phylogeography of Floreana's Lizards Supports Galápagos Pleistocene Paleogeographical Model and Informs Conservation Management Decisions. Journal of Herpetology, 2021, 55, .	0.2	2
13563	Reconstruction of ancestral karyotype illuminates chromosome evolution in the genus <i>Cucumis</i> . Plant Journal, 2021, 107, 1243-1259.	2.8	23
13564	<i>Arenibaculum pallidiluteum</i> gen. nov., sp. nov., a novel bacterium in the family Azospirillaceae, isolated from desert soil, and reclassification of <i>Skermanella xinjiangensis</i> to a new genus <i>Deserticella</i> as <i>Deserticella xinjiangensis</i> comb. nov., and transfer of the genera <i>Indioceanicola</i> and <i>Oleisolibacter</i> from the family Rhodospirillaceae to the family Azospirillaceae. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	22
13565	New species of Lirata Cameron (Hymenoptera: Eucharitidae) with an identification key and phylogenetic analysis. Zoologischer Anzeiger, 2021, 293, 263-272.	0.4	0
13566	Culture Media Based on Leaf Strips/Root Segments Create Compatible Host/Organ Setup for in vitro Cultivation of Plant Microbiota. Frontiers in Sustainable Food Systems, 2021, 5, .	1.8	3
13567	An integrated morpho–molecular study of <i>Salicornia</i> (Amaranthaceae–Chenopodiaceae) in Iran proves Irano–Turanian region the major center of diversity of annual glasswort species. Taxon, 0, , .	0.4	5
13569	Discovery of a deeply divergent and highly endemic frog lineage from Borneo: A taxonomic revision of <i>Kalophrynus nubicola</i> Dring, 1983 with descriptions of two new species (Amphibia: Anura: Tj ETQq0 0 0 rgBT /Overlook 10 Tf150 337 Td		
13570	Diversity, host specificity and biogeography in the Cladocorynidae (Hydrozoa, Capitata), with description of a new genus. Cladistics, 2022, 38, 13-37.	1.5	7
13571	Plastome–based phylogeny improves community phylogenetics of subtropical forests in China. Molecular Ecology Resources, 2022, 22, 319-333.	2.2	6
13572	Description of the marine predator <i>Sericomyxa perlucida</i> gen. et sp. nov., a cultivated representative of the deepest branching lineage of vampyrellid amoebae (Vampyrellida, Rhizaria). Journal of Eukaryotic Microbiology, 2021, 68, e12864.	0.8	6
13573	Characterisation of <i>Listeria monocytogenes</i> food-associated isolates to assess environmental fitness and virulence potential. International Journal of Food Microbiology, 2021, 350, 109247.	2.1	18
13574	Next-generation sequencing of the mitochondrial genome of <i>Thamnaconus septentrionalis</i> Gunther, 1877 (Aluteridae: Thamnaconus) specimen collected in China. Mitochondrial DNA Part B: Resources, 2021, 6, 2198-2199.	0.2	3
13575	The complete mitochondrial genome of <i>Coriandrum sativum</i> . Mitochondrial DNA Part B: Resources, 2021, 6, 2391-2392.	0.2	2
13576	Comparing Ultraconserved Elements and Exons for Phylogenomic Analyses of Middle American Cichlids: When Data Agree to Disagree. Genome Biology and Evolution, 2021, 13, .	1.1	18

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13577	Complete mitochondrial genome of Asian longhorned tick, <i>Haemaphysalis longicornis</i> , Neumann, 1901 (Acari: Ixodida: Ixodidae) identified in the United States. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2402-2405.	0.2	1
13578	Improving Phylogenies Based on Average Nucleotide Identity, Incorporating Saturation Correction and Nonparametric Bootstrap Support. <i>Systematic Biology</i> , 2022, 71, 396-409.	2.7	14
13580	Corn diseases in Algeria: first report of three <i>Bipolaris</i> and two <i>Exserohilum</i> species causing leaf spot and leaf blight diseases. <i>Cereal Research Communications</i> , 0, , 1.	0.8	3
13581	Description of three species of ophioplithacids, including a new species, from a deep seamount in the Northwest Pacific Ocean. <i>PeerJ</i> , 2021, 9, e11566.	0.9	3
13583	Genomic analysis of Shiga toxin-producing <i>Escherichia coli</i> O157:H7 from cattle and pork-production related environments. <i>Npj Science of Food</i> , 2021, 5, 15.	2.5	6
13584	In vivo evolution of an emerging zoonotic bacterial pathogen in an immunocompromised human host. <i>Nature Communications</i> , 2021, 12, 4495.	5.8	6
13585	A new desert-dwelling oomycete, <i>Pustula persica</i> sp. nov., on <i>Gymnarrhena micrantha</i> (<i>Asteraceae</i>) from Iran. <i>Mycoscience</i> , 2021, 62, 239-243.	0.3	1
13586	Diversification of mandarin citrus by hybrid speciation and apomixis. <i>Nature Communications</i> , 2021, 12, 4377.	5.8	31
13587	DNA Barcodes Combined with Multilocus Data of Representative Taxa Can Generate Reliable Higher-Level Phylogenies. <i>Systematic Biology</i> , 2022, 71, 382-395.	2.7	35
13588	Biocontrol Activity of <i>Bacillus</i> spp. and <i>Pseudomonas</i> spp. Against <i>Botrytis cinerea</i> and Other Cannabis Fungal Pathogens. <i>Phytopathology</i> , 2022, 112, 549-560.	1.1	24
13589	An Update on Trichoderma Mitogenomes: Complete De Novo Mitochondrial Genome of the Fungal Biocontrol Agent <i>Trichoderma harzianum</i> (Hypocreales, Sordariomycetes), an Ex-Neotype Strain CBS 226.95, and Tracing the Evolutionary Divergences of Mitogenomes in <i>Trichoderma</i> . <i>Microorganisms</i> , 2021, 9, 1564.	1.6	8
13590	Impact of Landscape on Host-Parasite Genetic Diversity and Distribution Using the Puumala orthohantavirus Bank Vole System. <i>Microorganisms</i> , 2021, 9, 1516.	1.6	1
13591	Comparative chloroplast genome analysis of <i>Impatiens</i> species (Balsaminaceae) in the karst area of China: insights into genome evolution and phylogenomic implications. <i>BMC Genomics</i> , 2021, 22, 571.	1.2	27
13592	A Morpho-molecular Perspective on the Diversity and Evolution of <i>Spumellaria</i> (Radiolaria). <i>Protist</i> , 2021, 172, 125806.	0.6	10
13594	A phylogenomic approach resolves the backbone of <i>Prunus</i> (Rosaceae) and identifies signals of hybridization and allopolyploidy. <i>Molecular Phylogenetics and Evolution</i> , 2021, 160, 107118.	1.2	30
13595	Molecular phylogeny and classification of <i>Nudariina</i> (Lepidoptera: Erebiidae) with emphasis on the genera <i>Barsine</i> Walker, <i>Ammatho</i> Walker and <i>Ovipennis</i> Hampson. <i>Systematic Entomology</i> , 2021, 46, 1045-1059.	1.7	5
13596	Chromosome organization and gene expansion in the highly fragmented genome of the ciliate <i>Strombidium stylifer</i> . <i>Journal of Genetics and Genomics</i> , 2021, 48, 908-916.	1.7	13
13597	Human-to-Cattle <i>Mycobacterium tuberculosis</i> Complex Transmission in the United States. <i>Frontiers in Veterinary Science</i> , 2021, 8, 691192.	0.9	17

#	ARTICLE	IF	CITATIONS
13599	A phylogenomic perspective on gene tree conflict and character evolution in Caprifoliaceae using target enrichment data, with Zabelioideae recognized as a new subfamily. <i>Journal of Systematics and Evolution</i> , 2021, 59, 897-914.	1.6	41
13600	The roles of aridification and sea level changes in the diversification and persistence of freshwater fish lineages. <i>Molecular Ecology</i> , 2021, 30, 4866-4883.	2.0	10
13601	TRAPID 2.0: a web application for taxonomic and functional analysis of <i>de novo</i> transcriptomes. <i>Nucleic Acids Research</i> , 2021, 49, e101-e101.	6.5	21
13602	Molecular Evolutionary Dynamics of Energy Limited Microorganisms. <i>Molecular Biology and Evolution</i> , 2021, 38, 4532-4545.	3.5	3
13603	Large-scale protein level comparison of Deltaproteobacteria reveals cohesive metabolic groups. <i>ISME Journal</i> , 2022, 16, 307-320.	4.4	71
13604	Morphological and molecular data on tadpoles of the westernmost Himalayan spiny frog <i>Allopaia hazarensis</i> (Dubois & Khan, 1979). <i>ZooKeys</i> , 2021, 1049, 67-77.	0.5	6
13605	A shift to shorter cuticular hydrocarbons accompanies sexual isolation among <i>Drosophila americana</i> group populations. <i>Evolution Letters</i> , 2021, 5, 521-540.	1.6	4
13606	Molecular phylogeny and morphology of <i>Carinadinium</i> gen. nov. (Dinophyceae, Gonyaulacales), including marine sand-dwelling dinoflagellate species formerly classified within <i>Thecadinium</i> . <i>European Journal of Protistology</i> , 2021, 81, 125835.	0.5	3
13607	Characterization of the complete mitochondrial genome of the swine kidney worm <i>Stephanurus dentatus</i> (Nematoda: Syngamidae) and phylogenetic implications. <i>Veterinary Parasitology</i> , 2021, 295, 109475.	0.7	4
13610	Repeated parallel losses of inflexed stamens in Moraceae: Phylogenomics and generic revision of the tribe Moreae and the reinstatement of the tribe Olmedieae (Moraceae). <i>Taxon</i> , 2021, 70, 946-988.	0.4	12
13611	MYCOBACTERIA IN SKIN LESIONS AND THE HABITAT OF THE ENDANGERED HOUSTON TOAD (ANAXYRUS) Tj ETQq0.0 0 rgBT ₃ /Overlock	0.3	3
13612	Description of the Fifth New Species of <i>Russula</i> subsect. <i>Maculatinae</i> from Pakistan Indicates Local Diversity Hotspot of Ectomycorrhizal Fungi in Southwestern Himalayas. <i>Life</i> , 2021, 11, 662.	1.1	2
13613	A new species of <i>Procambarus</i> (Decapoda, Cambaridae) from the State of Quer�taro, Mexico. <i>ZooKeys</i> , 2021, 1048, 1-21.	0.5	1
13614	Phylogeny and sex chromosome evolution of Palaeognathae. <i>Journal of Genetics and Genomics</i> , 2022, 49, 109-119.	1.7	10
13615	Phylogenomics of <i>Palythoa</i> (Hexacorallia: Scleractinia): probing species boundaries in a globally distributed genus. <i>Coral Reefs</i> , 0, , 1.	0.9	2
13616	<i>Hanseniaspora smithiae</i> sp. nov., a Novel Apiculate Yeast Species From Patagonian Forests That Lacks the Typical Genomic Domestication Signatures for Fermentative Environments. <i>Frontiers in Microbiology</i> , 2021, 12, 679894.	1.5	10
13617	Release LTP_12_2020, featuring a new ARB alignment and improved 16S rRNA tree for prokaryotic type strains. <i>Systematic and Applied Microbiology</i> , 2021, 44, 126218.	1.2	44
13618	Comparative Genomics Provide Insights Into Function and Evolution of Odorant Binding Proteins in <i>Cydia pomonella</i> . <i>Frontiers in Physiology</i> , 2021, 12, 690185.	1.3	4

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13619	New morphological data on the rare sigmodontine <i>Mindomys hammondi</i> (Rodentia, Cricetidae), an arboreal oryzomyine from north-western Andean montane forests. <i>Neotropical Biology and Conservation</i> , 2021, 16, 397-410.	0.4	1
13620	Defensive hypervariable regions confer superinfection exclusion in microviruses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	13
13621	Molecular systematics, higher rank classification and Gondwanan origins of <i>Cryptocephalinae</i> leaf beetles. <i>Zoologica Scripta</i> , 2021, 50, 592-615.	0.7	5
13622	The complete chloroplast genome of <i>Platynerium wallichii</i> (Polypodiaceae), an endangered and ornamental fern species. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2313-2315.	0.2	0
13623	Evolution of genome space occupation in ferns: linking genome diversity and species richness. <i>Annals of Botany</i> , 2023, 131, 59-70.	1.4	14
13624	Museum genomics reveals the Xerces blue butterfly (<i>Glaucopsyche xerces</i>) was a distinct species driven to extinction. <i>Biology Letters</i> , 2021, 17, 20210123.	1.0	15
13625	Phylogenetics of mud snakes (Squamata: Serpentes: Homalopsidae): A paradox of both undescribed diversity and taxonomic inflation. <i>Molecular Phylogenetics and Evolution</i> , 2021, 160, 107109.	1.2	17
13626	Complete chloroplast genomes of <i>Camellia pubipetala</i> Y. Wan et S. Z. Huang and <i>Camellia debaoensis</i> R. C. Hu et Y. Q. Liufu. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2381-2382.	0.2	0
13627	The complete chloroplast genome of <i>Artocarpus altilis</i> (Moraceae) and phylogenetic relationships. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2291-2293.	0.2	1
13628	Phylogenomics With Hyb-Seq Unravels Korean <i>Hosta</i> Evolution. <i>Frontiers in Plant Science</i> , 2021, 12, 645735.	1.7	3
13629	The E3-ligase AoUBR1 in N-end rule pathway is involved in the vegetative growth, secretome, and trap formation in <i>Arthrobotrys oligospora</i> . <i>Fungal Biology</i> , 2021, 125, 532-540.	1.1	6
13632	Spatial Genetic Structure of the Insect-Vectored Conifer Pathogen <i>Leptographium wageneri</i> Suggests Long Distance Gene Flow Among Douglas-fir Plantations in Western Oregon. <i>Frontiers in Forests and Global Change</i> , 2021, 4, .	1.0	1
13633	Plastid Phylogenomic Data Offers Novel Insights Into the Taxonomic Status of the <i>Trichosanthes kirilowii</i> Complex (Cucurbitaceae) in South Korea. <i>Frontiers in Plant Science</i> , 2021, 12, 559511.	1.7	3
13634	Reconstructing Dipsacales phylogeny using Angiosperms353: issues and insights. <i>American Journal of Botany</i> , 2021, 108, 1122-1142.	0.8	13
13635	Large-scale whole-genome resequencing unravels the domestication history of <i>Cannabis sativa</i> . <i>Science Advances</i> , 2021, 7, .	4.7	79
13636	Genome Characterization, Comparison and Phylogenetic Analysis of Complete Mitochondrial Genome of <i>Evolvulus alsinoides</i> Reveals Highly Rearranged Gene Order in Solanales. <i>Life</i> , 2021, 11, 769.	1.1	10
13637	The complete chloroplast genome sequence of China <i>Lindera praecox</i> (Lauraceae) and intra-species diversity. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2162-2163.	0.2	1
13638	The complete chloroplast genome sequence of <i>Bambusa stenoaurita</i> (Bambusoideae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2184-2185.	0.2	2

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13639	New gregarine species (Apicomplexa) from tunicates show an evolutionary history of host switching and suggest a problem with the systematics of Lankesteria and Lecudina. <i>Journal of Invertebrate Pathology</i> , 2021, 183, 107622.	1.5	2
13641	Genomic diversity and ecology of human-associated <i>Akkermansia</i> species in the gut microbiome revealed by extensive metagenomic assembly. <i>Genome Biology</i> , 2021, 22, 209.	3.8	65
13642	<i>Leptosphaerulina</i> species isolated from golf turfgrass in China, with description of <i>L. macrospora</i> , sp. nov.. <i>Mycologia</i> , 2021, 113, 1-12.	0.8	3
13643	Characterization of the complete mitochondrial genome of <i>Abscondita cerata</i> (Olivier, 1911) (Coleoptera: Lampyridae) and its phylogenetic implications. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2528-2530.	0.2	3
13644	Using host genetics to infer the global spread and evolutionary history of HCV subtype 3a. <i>Virus Evolution</i> , 2021, 7, veab065.	2.2	0
13645	<i>Pseudomonas lactucae</i> sp. nov., a pathogen causing bacterial rot of lettuce in Japan. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	6
13646	<i>Lactobacillus corticis</i> sp. nov., isolated from hardwood bark. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	9
13647	A thermodynamic model of protein structure evolution explains empirical amino acid substitution matrices. <i>Protein Science</i> , 2021, 30, 2057-2068.	3.1	13
13648	A New Pipeline for Removing Paralogs in Target Enrichment Data. <i>Systematic Biology</i> , 2022, 71, 410-425.	2.7	28
13649	Extensive human-mediated jump dispersal within and across the native and introduced ranges of the invasive termite <i>Reticulitermes flavipes</i> . <i>Molecular Ecology</i> , 2021, 30, 3948-3964.	2.0	19
13650	SARS-CoV-2 RBD antibodies that maximize breadth and resistance to escape. <i>Nature</i> , 2021, 597, 97-102.	13.7	385
13651	Variation of virulence of five <i>Aspergillus fumigatus</i> isolates in four different infection models. <i>PLoS ONE</i> , 2021, 16, e0252948.	1.1	9
13652	Alone on an island: The reassessment of an enigmatic species of Handmaiden Moth (Lepidoptera, Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	0.7	2
13653	New taxa in Glomeromycota: Polonosporaceae fam. nov., Polonospora gen. nov., and <i>P. polonica</i> comb. nov.. <i>Mycological Progress</i> , 2021, 20, 941-951.	0.5	6
13654	Distinct lineages and population genomic structure of the coral <i>Pachyseris speciosa</i> in the small equatorial reef system of Singapore. <i>Coral Reefs</i> , 2022, 41, 575-585.	0.9	7
13655	Fungi inhabiting attine ant colonies: reassessment of the genus <i>Escovopsis</i> and description of <i>Luteomyces</i> and <i>Sympodiorosea</i> gens. nov.. <i>IMA Fungus</i> , 2021, 12, 23.	1.7	8
13656	The Morphology, Taxonomy, and Phylogenetic Analyses of Five Freshwater Colonial Peritrich Ciliates (Alveolata, Ciliophora), Including the Descriptions of Two New Species. <i>Frontiers in Microbiology</i> , 2021, 12, 718821.	1.5	7
13661	Identification and Full Characterisation of Two Novel Crustacean Infecting Members of the Family Nudiviridae Provides Support for Two Subfamilies. <i>Viruses</i> , 2021, 13, 1694.	1.5	9

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13662	Comprehensive Strain-Level Analysis of the Gut Microbe <i>Faecalibacterium prausnitzii</i> in Patients with Liver Cirrhosis. <i>MSystems</i> , 2021, 6, e0077521.	1.7	6
13663	Global genome analysis reveals a vast and dynamic anellovirus landscape within the human virome. <i>Cell Host and Microbe</i> , 2021, 29, 1305-1315.e6.	5.1	59
13665	Decisive Effects of Life Stage on the Gut Microbiota Discrepancy Between Two Wild Populations of Hibernating Asiatic Toads (<i>Bufo gargarizans</i>). <i>Frontiers in Microbiology</i> , 2021, 12, 665849.	1.5	6
13666	Phylogenetic reappraisal and epitypification of <i>Laccaria macrocystidiata</i> (Hydnangiaceae, Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 0,1	0.1	2
13668	Horizontal Transfer of Microbial Toxin Genes to Gall Midge Genomes. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	7
13669	Comparative genomics and in silico gene evaluation involved in the probiotic potential of <i>Bifidobacterium longum</i> 51A. <i>Gene</i> , 2021, 795, 145781.	1.0	7
13670	Pyrethroid metabolism by eleven <i>Helicoverpa armigera</i> P450s from the CYP6B and CYP9A subfamilies. <i>Insect Biochemistry and Molecular Biology</i> , 2021, 135, 103597.	1.2	27
13671	Population Analysis of <i>Vibrio cholerae</i> in Aquatic Reservoirs Reveals a Novel Sister Species (<i>Vibrio</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 15 1,4	1.4	15
13673	<i>Stagonosporopsis pogostemonis</i> : A Novel Ascomycete Fungus Causing Leaf Spot and Stem Blight on <i>Pogostemon cablin</i> (Lamiaceae) in South China. <i>Pathogens</i> , 2021, 10, 1093.	1.2	9
13674	Investigation of two cases of <i>Mycobacterium chelonae</i> infection in haemato-oncology patients using whole-genome sequencing and a potential link to the hospital water supply. <i>Journal of Hospital Infection</i> , 2021, 114, 111-116.	1.4	6
13675	Evolution of reproductive structures for in-flight mating in thynnine wasps (Hymenoptera: Thynnidae:) Tj ETQq0 0,0 rgBT /Overlock 1 0,8	0.8	1
13676	Purple sulfur bacteria fix N ₂ via molybdenum-nitrogenase in a low molybdenum Proterozoic ocean analogue. <i>Nature Communications</i> , 2021, 12, 4774.	5.8	24
13677	Shaping the biology of citrus: II. Genomic determinants of domestication. <i>Plant Genome</i> , 2021, 14, e20133.	1.6	2
13678	A novel reference dated phylogeny for the genus <i>Spodoptera</i> Guenée (Lepidoptera: Noctuidae:) Tj ETQq1 1 0.784314 rgBT /Overlock 30 1,2	1.2	30
13679	Assessing topological congruence among concatenation-based phylogenomic approaches in empirical datasets. <i>Molecular Phylogenetics and Evolution</i> , 2021, 161, 107086.	1.2	5
13680	Identification of a pathway for electron uptake in <i>Shewanella oneidensis</i> . <i>Communications Biology</i> , 2021, 4, 957.	2.0	39
13681	Plant-bacteria associations are phylogenetically structured in the phyllosphere. <i>Molecular Ecology</i> , 2021, 30, 5572-5587.	2.0	15
13682	Application of shotgun metagenomics sequencing and targeted sequence capture to detect circulating porcine viruses in the Dutch-German border region. <i>Transboundary and Emerging Diseases</i> , 2022, 69, 2306-2319.	1.3	5

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13683	Phylogenetic Signal, Congruence, and Uncertainty across Bacteria and Archaea. <i>Molecular Biology and Evolution</i> , 2021, 38, 5514-5527.	3.5	42
13684	Systematics of the Giant Sedges of <i>Carex</i> Sect. <i>Rhynchocystis</i> (Cyperaceae) in Macaronesia with Description of Two New Species. <i>Systematic Botany</i> , 2021, 46, 304-320.	0.2	1
13685	Evolution of the Insect PPK Gene Family. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	15
13686	Type specimen sequencing, multilocus analyses, and species delimitation methods recognize the cosmopolitan <i>Corallina berteroi</i> and establish the northern Japanese <i>C. yendoi</i> sp. nov. (Corallinaceae, Rhodophyta). <i>Journal of Phycology</i> , 2021, 57, 1659-1672.	1.0	15
13687	Integrated Whole-Genome Sequencing Infrastructure for Outbreak Detection and Source Tracing of <i>Salmonella enterica</i> Serotype Enteritidis. <i>Foodborne Pathogens and Disease</i> , 2021, 18, 582-589.	0.8	8
13688	Multiresistance to Nonazole Fungicides in <i>Aspergillus fumigatus</i> TR ₃₄ /L98H Azole-Resistant Isolates. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, e0064221.	1.4	13
13689	Molecular evidence for a single origin of ultrafiltration-based excretory organs. <i>Current Biology</i> , 2021, 31, 3629-3638.e2.	1.8	28
13690	Complete chloroplast genome of the green alga <i>Chaetophora lobata</i> (Chlorophyceae, Chlorophyta): morphological features and phylogenetic and comparative analysis. <i>European Journal of Phycology</i> , 0, 1-12.	0.9	0
13692	DNA barcode sheds light on species boundaries in the common morphologically variable rove beetle <i>Quedius umbrinus</i> -complex that puzzled taxonomists for more than a century (Coleoptera). <i>Tj ETQq0 0 0 rg8.5/Overlæk 10 Tf 50</i>	1.5	15
13693	Maximum antigen diversification in a lyme bacterial population and evolutionary strategies to overcome pathogen diversity. <i>ISME Journal</i> , 2022, 16, 447-464.	4.4	8
13695	Glutamate 73 Promotes Anti-arrhythmic Effects of Voltage-Dependent Anion Channel Through Regulation of Mitochondrial Ca ²⁺ Uptake. <i>Frontiers in Physiology</i> , 2021, 12, 724828.	1.3	4
13698	Recombination Facilitates Adaptive Evolution in Rhizobial Soil Bacteria. <i>Molecular Biology and Evolution</i> , 2021, 38, 5480-5490.	3.5	7
13700	Species and genera in <i>Aleurodiscus</i> sensu lato as viewed from the Southern Hemisphere. <i>Mycologia</i> , 2021, 113, 1-14.	0.8	5
13701	Characterization of the complete plastid genome of <i>Abies forrestii</i> (Pinaceae) from southwest China. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2772-2774.	0.2	2
13702	The complete chloroplast genome sequence of <i>Callitriche palustris</i> (Plantaginaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2777-2778.	0.2	1
13703	The complete chloroplast genome of an endemic plant to Korea, <i>Cardamine amaraeformis</i> Nakai.: genome structure and phylogenetic analysis. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2725-2726.	0.2	3
13704	<i>Jinshanibacter allomyrinae</i> sp. nov., isolated from larvae of <i>Allomyrina dichotoma</i> , proposal of <i>Insectihabitans xujianqingii</i> gen. nov., comb. nov. and emended descriptions of the genera <i>Jinshanibacter</i> , <i>Limnobaculum</i> and <i>Pragia</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	20
13705	A new nomenclature for the livestock-associated <i>Mycobacterium tuberculosis</i> complex based on phylogenomics. <i>Open Research Europe</i> , 0, 1, 100.	2.0	2

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13706	A fossil-calibrated time-tree of all Australian freshwater fishes. <i>Molecular Phylogenetics and Evolution</i> , 2021, 161, 107180.	1.2	2
13707	Coleofasciculaceae, a Monophyletic Home for the <i>Microcoleus steenstrupii</i> Complex and Other Desiccation-tolerant Filamentous Cyanobacteria. <i>Journal of Phycology</i> , 2021, 57, 1563-1579.	1.0	23
13708	Statistical analysis of GC-biased gene conversion and recombination hotspots in eukaryotic genomes. , 2021, , .		0
13709	Influence of elevation on bioregionalisation: A case study of the Sino-Himalayan flora. <i>Journal of Biogeography</i> , 2021, 48, 2578-2587.	1.4	4
13710	Seadragon genome analysis provides insights into its phenotype and sex determination locus. <i>Science Advances</i> , 2021, 7, .	4.7	32
13711	Characterization of the chloroplast genome sequence of <i>Bonia amplexicaulis</i> (L.C.Chia, H.L.Fung & Tj ETQq1 1 0.784314 rgBT /Overl	0.2	1
13712	Phylogenomics of <i>Porites</i> from the Arabian Peninsula. <i>Molecular Phylogenetics and Evolution</i> , 2021, 161, 107173.	1.2	9
13713	Molecular phylogenetics of sub-Saharan African natricine snakes, and the biogeographic origins of the Seychelles endemic <i>Lycognathophis seychellensis</i> . <i>Molecular Phylogenetics and Evolution</i> , 2021, 161, 107152.	1.2	8
13714	The Resistome and Mobilome of Multidrug-Resistant <i>Staphylococcus sciuri</i> C2865 Unveil a Transferable Trimethoprim Resistance Gene, Designated <i>dfrE</i> , Spread Unnoticed. <i>MSystems</i> , 2021, 6, e0051121.	1.7	7
13715	Population Genomics of <i>emm4</i> Group A <i>Streptococcus</i> Reveals Progressive Replacement with a Hypervirulent Clone in North America. <i>MSystems</i> , 2021, 6, e0049521.	1.7	5
13716	Derived woodiness and annual habit evolved in African umbellifers as alternative solutions for coping with drought. <i>BMC Plant Biology</i> , 2021, 21, 383.	1.6	2
13717	Two new species of <i>Neopestalotiopsis</i> from southern China. <i>Biodiversity Data Journal</i> , 2021, 9, e70446.	0.4	7
13718	Phylogeny, species delimitation and biogeography of the endemic Palearctic tribe Tomarini (Lepidoptera: Lycaenidae). <i>Zoological Journal of the Linnean Society</i> , 2022, 196, 630-646.	1.0	5
13719	The genome of the thin-necked bladder worm <i>Taenia hydatigena</i> reveals evolutionary strategies for helminth survival. <i>Communications Biology</i> , 2021, 4, 1004.	2.0	2
13720	<i>Cryptococcus depauperatus</i> , a close relative of the human-pathogen <i>C. neoformans</i> , associated with coffee leaf rust (<i>Hemileia vastatrix</i>) in Cameroon. <i>Brazilian Journal of Microbiology</i> , 2021, 52, 2205-2214.	0.8	4
13721	Phylogenomics and evolutionary history of <i>Oreobates</i> (Anura: Craugastoridae) Neotropical frogs along elevational gradients. <i>Molecular Phylogenetics and Evolution</i> , 2021, 161, 107167.	1.2	1
13722	Species Delimitation and Conservation in Taxonomically Challenging Lineages: The Case of Two Clades of <i>Capurodendron</i> (Sapotaceae) in Madagascar. <i>Plants</i> , 2021, 10, 1702.	1.6	6
13723	Pan-Genome of Novel <i>Pantoea stewartii</i> subsp. <i>indologenes</i> Reveals Genes Involved in Onion Pathogenicity and Evidence of Lateral Gene Transfer. <i>Microorganisms</i> , 2021, 9, 1761.	1.6	5

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13725	A genome epidemiological study of mycobacterium tuberculosis in subpopulations with high and low incidence rate in Guangxi, South China. <i>BMC Infectious Diseases</i> , 2021, 21, 840.	1.3	3
13726	Genomic comparison of non-photosynthetic plants from the family Balanophoraceae with their photosynthetic relatives. <i>PeerJ</i> , 2021, 9, e12106.	0.9	7
13727	A Widespread Bacterial Secretion System with Diverse Substrates. <i>MBio</i> , 2021, 12, e0195621.	1.8	30
13729	KPC-2-Producing Carbapenem-Resistant <i>Klebsiella pneumoniae</i> of the Uncommon ST29 Type Carrying OXA-926, a Novel Narrow-Spectrum OXA β -Lactamase. <i>Frontiers in Microbiology</i> , 2021, 12, 701513.	1.5	8
13730	Characterization of Mariner transposons in seven species of <i>Rhus</i> gall aphids. <i>Scientific Reports</i> , 2021, 11, 16349.	1.6	4
13731	A widely diverged locus involved in locomotor adaptation in <i>Heliconius</i> butterflies. <i>Science Advances</i> , 2021, 7, .	4.7	9
13732	Identification of novel aphid-killing bacteria to protect plants. <i>Microbial Biotechnology</i> , 2022, 15, 1203-1220.	2.0	6
13733	Phylogeography and molecular species delimitation reveal cryptic diversity in <i>Potamolithus</i> (Caenogastropoda: Tateidae) of the southwest basin of the Andes. <i>Scientific Reports</i> , 2021, 11, 15735.	1.6	3
13734	Phylogenomic resolution of the <i>Ceratitis</i> FARQ complex (Diptera: Tephritidae). <i>Molecular Phylogenetics and Evolution</i> , 2021, 161, 107160.	1.2	6
13735	Distinct patterns of within-host virus populations between two subgroups of human respiratory syncytial virus. <i>Nature Communications</i> , 2021, 12, 5125.	5.8	16
13736	Taxonomy and Phylogeny of Three Species of <i>Dysteria</i> (Ciliophora, Phyllopharyngea) Including the Description of <i>Dysteria ozakii</i> nom. nov.. <i>Protist</i> , 2021, 172, 125831.	0.6	8
13737	pplacerDC. , 2021, , .		1
13739	Characterization and Comparative Analysis of Complete Chloroplast Genomes of Three Species From the Genus <i>Astragalus</i> (Leguminosae). <i>Frontiers in Genetics</i> , 2021, 12, 705482.	1.1	10
13740	A New Distinctive Species of <i>Schizanthus</i> (Solanaceae) and the Reinstatement of <i>Schizanthus fallax</i> . <i>Systematic Botany</i> , 2021, 46, 456-469.	0.2	1
13741	Co-Occurrence of Viruses, Plant Pathogens, and Symbionts in an Underexplored Hemipteran Clade. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 715998.	1.8	1
13742	Proposal of <i>Lactococcus garvieae</i> subsp. <i>bovis</i> Varsha and Nampoothiri 2016 as a later heterotypic synonym of <i>Lactococcus formosensis</i> Chen et al. 2014 and <i>Lactococcus formosensis</i> subsp. <i>bovis</i> comb. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	11
13743	<i>Aborjinia corallicola</i> sp. n., a new nematode species (Nematoda: Marimermithidae) associated with the bamboo coral <i>Acanella arbuscula</i> (Johnson). <i>Systematic Parasitology</i> , 2021, 98, 559-579.	0.5	7
13744	<i>Basidiobolus omanensis</i> sp. nov. Causing Angioinvasive Abdominal Basidiobolomycosis. <i>Journal of Fungi</i> (Basel, Switzerland), 2021, 7, 653.	1.5	7

#	ARTICLE	IF	CITATIONS
13745	Deorphanization of novel biogenic amine-gated ion channels identifies a new serotonin receptor for learning. <i>Current Biology</i> , 2021, 31, 4282-4292.e6.	1.8	13
13750	Iron Oxidation by a Fused Cytochrome-Porin Common to Diverse Iron-Oxidizing Bacteria. <i>MBio</i> , 2021, 12, e0107421.	1.8	34
13751	Drosophyla: Resources for Drosophilid Phylogeny and Systematics. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	45
13752	Tailed Lytic Bacteriophages of Soft Rot Pectobacteriaceae. <i>Microorganisms</i> , 2021, 9, 1819.	1.6	7
13753	Cross-species analysis between the maize smut fungi <i>Ustilago maydis</i> and <i>Sporisorium reilianum</i> highlights the role of transcriptional change of effector orthologs for virulence and disease. <i>New Phytologist</i> , 2021, 232, 719-733.	3.5	13
13754	A remarkable legion of guests: Diversity and host specificity of army ant symbionts. <i>Molecular Ecology</i> , 2021, 30, 5229-5246.	2.0	11
13755	Lycophyte transcriptomes reveal two whole-genome duplications in Lycopodiaceae: Insights into the polyploidization of Phlegmariurus. <i>Plant Diversity</i> , 2022, 44, 262-270.	1.8	6
13756	Identification of novel bat coronaviruses sheds light on the evolutionary origins of SARS-CoV-2 and related viruses. <i>Cell</i> , 2021, 184, 4380-4391.e14.	13.5	261
13757	Hb adaptation to hypoxia in high-altitude fishes: Fresh evidence from schizothoracinae fishes in the Qinghai-Tibetan Plateau. <i>International Journal of Biological Macromolecules</i> , 2021, 185, 471-484.	3.6	8
13758	The complete chloroplast genome sequence of <i>Bromus catharticus</i> Vahl. (Poaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2825-2827.	0.2	1
13759	Population structure, genomic diversity and demographic history of Komodo dragons inferred from whole-genome sequencing. <i>Molecular Ecology</i> , 2021, 30, 6309-6324.	2.0	11
13761	The genomic epidemiology of multi-drug resistant invasive non-typhoidal <i>Salmonella</i> in selected sub-Saharan African countries. <i>BMJ Global Health</i> , 2021, 6, e005659.	2.0	16
13762	New types of <i>scp</i> -ATP-grasp ligase are associated with the novel pathway for complicated mycosporine-like amino acid production in desiccation-tolerant cyanobacteria. <i>Environmental Microbiology</i> , 2021, 23, 6420-6432.	1.8	9
13763	<i>Campylobacter jejuni</i> genotypes are associated with post-infection irritable bowel syndrome in humans. <i>Communications Biology</i> , 2021, 4, 1015.	2.0	24
13764	Origin and evolution of the Haustoriidae (Amphipoda): a eulogy for the Haustoriidira. <i>Zoological Journal of the Linnean Society</i> , 2022, 194, 1252-1267.	1.0	1
13765	Complete Genomic Characterization and Identification of <i>Saccharomycopsis phalluae</i> sp. nov., a Novel Pathogen Causes Yellow Rot Disease on <i>Phallus rubrovolvatus</i> . <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 707.	1.5	8
13766	The complete chloroplast genome sequence of <i>Camellia zhaiana</i> (Theaceae), a critically endangered species from China. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2425-2426.	0.2	0
13767	Phylogeny of <i>Phyllachora</i> species on bamboo and <i>P. cephalostachyi</i> sp. nov. from China. <i>Phytotaxa</i> , 2021, 514, 158-166.	0.1	0

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13768	Aurantimicrobium photophilum sp. nov., a non-photosynthetic bacterium adjusting its metabolism to the diurnal light cycle and reclassification of Cryobacterium mesophilum as Terrimesophilobacter mesophilus gen. nov., comb. nov.. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	16
13769	Complete chloroplast genome of the mixotrophic chrysophyte <i>Poterioochromonas malhamensis</i> (Ochromonadales, Synurophyceae) from Van Lake in Eastern Anatolia. Mitochondrial DNA Part B: Resources, 2021, 6, 2719-2721.	0.2	1
13770	Complete plastid genome sequence of <i>Neolitsea aciculata</i> (Laurales: Lauraceae), an evergreen broad-leaved tree endemic to East Asia. Mitochondrial DNA Part B: Resources, 2021, 6, 2553-2555.	0.2	1
13771	Complete chloroplast genome features and phylogenetic implications of <i>Cardamine fallax</i> (O. E.) Tj ETQq1 1,0,784314,rgBT/O	0.2	2
13772	Comparative analysis of the complete chloroplast genome between tetraploidy and diploidy of <i>Cyclocarya paliurus</i> (Batal.) Iljinskaja. Mitochondrial DNA Part B: Resources, 2021, 6, 2669-2671.	0.2	1
13773	Sponges of Western Mediterranean seamounts: new genera, new species and new records. PeerJ, 2021, 9, e11879.	0.9	8
13774	DNA barcoding reveals different cestode helminth species in northern European marine and freshwater ringed seals. International Journal for Parasitology: Parasites and Wildlife, 2021, 15, 255-261.	0.6	5
13776	Molecular data and phylogenetic analysis of <i>Myxobolus pseudonobilis</i> n. sp. infecting the gill filaments of silver carp, <i>Hypophthalmichthys molitrix</i> Valenciennes, 1844. Parasitology International, 2021, 83, 102314.	0.6	2
13777	Evidence for Middle Miocene origin and morphological evolutionary stasis in a <i>Barbacenia</i> Inselberg clade (Velloziaceae). Molecular Phylogenetics and Evolution, 2021, 161, 107163.	1.2	3
13778	Plastome-based phylogenomics elucidate relationships in rare Isoetes species groups from the Neotropics. Molecular Phylogenetics and Evolution, 2021, 161, 107177.	1.2	15
13779	New contributions to the taxonomy of urostyleid ciliates (Ciliophora, Hypotrichia), with establishment of a new genus and new species. European Journal of Protistology, 2021, 80, 125810.	0.5	14
13780	Genomic Analysis of Family UBA6911 (Group 18 <i>Acidobacteria</i>) Expands the Metabolic Capacities of the Phylum and Highlights Adaptations to Terrestrial Habitats. Applied and Environmental Microbiology, 2021, 87, e0094721.	1.4	7
13781	Butyryl/Caproyl-CoA:Acetate CoA-transferase: cloning, expression and characterization of the key enzyme involved in medium-chain fatty acid biosynthesis. Bioscience Reports, 2021, 41, .	1.1	9
13782	Diversity of Deep-Sea Scale-Worms (Annelida, Polynoidae) in the Clarion-Clipperton Fracture Zone. Frontiers in Marine Science, 2021, 8, .	1.2	5
13783	Genetic Background and Antibiotic Resistance Profiles of <i>K. pneumoniae</i> NDM-1 Strains Isolated from UTI, ABU, and the GI Tract, from One Hospital in Poland, in Relation to Strains Nationally and Worldwide. Genes, 2021, 12, 1285.	1.0	4
13784	Genomic Variation Influences <i>Methanothermococcus</i> Fitness in Marine Hydrothermal Systems. Frontiers in Microbiology, 2021, 12, 714920.	1.5	3
13785	First reports of the sexual morphs of <i>Diaporthe forlicesenica</i> nom. nov. and <i>Diaporthe goulteri</i> (Diaporthaceae, Diaporthales) revealed by molecular phylogenetics. Phytotaxa, 2021, 516, 1-27.	0.1	0
13786	Phylogeography, colouration, and cryptic speciation across the Indo-Pacific in the sea urchin genus <i>Echinothrix</i> . Scientific Reports, 2021, 11, 16568.	1.6	3

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13787	Fowl adenovirus strains 1/A and 11/D isolated from birds with reovirus infection. PLoS ONE, 2021, 16, e0256137.	1.1	8
13788	One year into the pandemic: Short-term evolution of SARS-CoV-2 and emergence of new lineages. Infection, Genetics and Evolution, 2021, 92, 104869.	1.0	49
13789	Review of the Merodon natans group with description of a new species, a key to the adults of known species of the natans lineage and first descriptions of some preimaginal stages. Arthropod Systematics and Phylogeny, 0, 79, 343-378.	5.5	8
13790	Phylogeography of the Poecilimon ampliatus species group (Orthoptera: Tettigoniidae) in the context of the Pleistocene glacial cycles and the origin of the only thelytokous parthenogenetic phaneropterine bush-cricket. Arthropod Systematics and Phylogeny, 0, 79, 401-418.	5.5	5
13791	Tight Adherence (Tad) Pilus Genes Indicate Putative Niche Differentiation in Phytoplankton Bloom Associated Rhodobacterales. Frontiers in Microbiology, 2021, 12, 718297.	1.5	16
13792	Novel PhoH-encoding vibriophages with lytic activity against environmental Vibrio strains. Archives of Microbiology, 2021, 203, 5321-5331.	1.0	7
13795	Novel saprobic Hermatomyces species (Hermatomycetaceae, Pleosporales) from China (Yunnan) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50 5	0.8	8
13796	Accessory Genomic Epidemiology of Cocirculating Acinetobacter baumannii Clones. MSystems, 2021, 6, e0062621.	1.7	15
13797	Intimate genetic relationships and fungicide resistance in multiple strains of <i>Aspergillus fumigatus</i> isolated from a plant bulb. Environmental Microbiology, 2021, 23, 5621-5638.	1.8	7
13798	Plastome and Nuclear Phylogenies of Dwarf Mistletoes (<i>Arceuthobium</i> : Viscaceae). Systematic Botany, 2021, 46, 389-402.	0.2	1
13799	Maxicircle architecture and evolutionary insights into Trypanosoma cruzi complex. PLoS Neglected Tropical Diseases, 2021, 15, e0009719.	1.3	9
13800	A Reassessment of the Little-Known Amazonian Fern Diplazium praestans Based on Molecular and Morphological Evidence. Systematic Botany, 2021, 46, 260-272.	0.2	0
13801	A tree of leaves: Phylogeny and historical biogeography of the leaf insects (Phasmatodea: Phylliidae). Communications Biology, 2021, 4, 932.	2.0	28
13802	A new species of Long-eared Brown Bat of the genus <i>Histiotus</i> (Chiroptera) and the revalidation of <i>Histiotus colombiae</i> . Caldasia, 2021, 43, 221-234.	0.1	11
13803	Resource diversity relationships in bacterial communities reflect the network structure of microbial metabolism. Nature Ecology and Evolution, 2021, 5, 1424-1434.	3.4	65
13804	Characterization of chloroplast genome of Eleusine coracana, a highly adaptable cereal crop with high nutritional reputation. Mitochondrial DNA Part B: Resources, 2021, 6, 2816-2818.	0.2	0
13805	Forest and Plantation Soil Microbiomes Differ in Their Capacity to Suppress Feedback Between Geosmithia morbida and Rhizosphere Pathogens of J. nigra Seedlings. Phytobiomes Journal, 0, , .	1.4	1
13806	The complete mitochondrial genome of the Variable Platyfish Xiphophorus variatus. Mitochondrial DNA Part B: Resources, 2021, 6, 2640-2642.	0.2	1

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13807	The complete chloroplast genome sequence of <i>Bambusa albolineata</i> (bambusodae). Mitochondrial DNA Part B: Resources, 2021, 6, 2748-2749.	0.2	0
13808	The complete chloroplast genome sequence of medicinal plant: <i>Cynanchum thesioides</i> (Asclepiadaceae). Mitochondrial DNA Part B: Resources, 2021, 6, 2592-2593.	0.2	2
13809	Genetic Diversity of Multidrug-Resistant <i>Pseudomonas aeruginosa</i> Isolates Carrying blaVIM-2 and blaKPC-2 Genes That Spread on Different Genetic Environment in Colombia. Frontiers in Microbiology, 2021, 12, 663020.	1.5	12
13812	Molecular Phylogenetics of the Chub Suckers (Teleostei: Catostomidae: Erimyzon) Inferred from Nuclear and Mitochondrial Loci. Ichthyology and Herpetology, 2021, 109, .	0.3	3
13814	Genomic insights into the diversity, virulence and resistance of <i>Klebsiella pneumoniae</i> extensively drug resistant clinical isolates. Microbial Genomics, 2021, 7, .	1.0	5
13815	Newly identified proviruses in Thermotogota suggest that viruses are the vehicles on the highways of interphylum gene sharing. Environmental Microbiology, 2021, 23, 7105-7120.	1.8	4
13816	Genome of <i>Serratia plymuthica</i> UBCF_13, Insight into diverse unique traits. F1000Research, 0, 10, 826.	0.8	0
13817	Incongruences between nuclear and plastid phylogenies challenge the identification of correlates of diversification in <i>Gentiana</i> in the European Alpine System. Alpine Botany, 2022, 132, 29-50.	1.1	9
13818	Plastome variation and phylogeny of <i>Taxillus</i> (Loranthaceae). PLoS ONE, 2021, 16, e0256345.	1.1	10
13819	North Sea spring bloom-associated Gammaproteobacteria fill diverse heterotrophic niches. Environmental Microbiomes, 2021, 16, 15.	2.2	32
13820	Pan-Genome-Wide Analysis of <i>Pantoea ananatis</i> Identified Genes Linked to Pathogenicity in Onion. Frontiers in Microbiology, 2021, 12, 684756.	1.5	11
13821	Genomic and Experimental Investigations of <i>Auriscalpium</i> and <i>Strobilurus</i> Fungi Reveal New Insights into Pinecone Decomposition. Journal of Fungi (Basel, Switzerland), 2021, 7, 679.	1.5	1
13822	Taxonomic revision of the Peyssonneliales (Rhodophyta): Circumscribing the authentic <i>Peyssonnelia</i> clade and proposing four new genera and seven new species. Journal of Phycology, 2021, 57, 1749-1767.	1.0	9
13823	Novel species of <i>Alternaria</i> section <i>Nimbya</i> from Iran as revealed by morphological and molecular data. Mycologia, 2021, 113, 1-16.	0.8	4
13824	Comparative Genomic and Transcriptomic Analysis of <i>Naegleria fowleri</i> Clinical and Environmental Isolates. MSphere, 2021, 6, e0063721.	1.3	8
13825	Phylogenetic position and morphology of <i>Raphidiophrys elongata</i> sp. nov. (Haptista: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 147 Protistology, 2021, 81, 125836.	0.5	5
13826	Unexpected organellar locations of ESCRT machinery in <i>Giardia intestinalis</i> and complex evolutionary dynamics spanning the transition to parasitism in the lineage Fornicata. BMC Biology, 2021, 19, 167.	1.7	8
13828	Characterization of Emerging Pathogens Carrying blaKPC-2 Gene in IncP-6 Plasmids Isolated From Urban Sewage in Argentina. Frontiers in Cellular and Infection Microbiology, 2021, 11, 722536.	1.8	10

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13829	Molecular cloning and immune characterization of CIITA in artificially challenged Chinese tongue sole (<i>Cynoglossus semilaevis</i>) with <i>Vibrio harveyi</i> . <i>Developmental and Comparative Immunology</i> , 2021, 121, 104091.	1.0	2
13830	Host specificity of Hepatocystis infection in short-nosed fruit bats (<i>Cynopterus brachyotis</i>) in Singapore. <i>International Journal for Parasitology: Parasites and Wildlife</i> , 2021, 15, 35-42.	0.6	0
13831	New Contributions to the Diversity of Hypotrichous Ciliates: Description of a New Genus and Two New Species (Protozoa, Ciliophora). <i>Frontiers in Microbiology</i> , 2021, 12, 712269.	1.5	4
13832	Global co-occurrence of methanogenic archaea and methanotrophic bacteria in <i>Microcystis</i> aggregates. <i>Environmental Microbiology</i> , 2021, 23, 6503-6519.	1.8	13
13834	Small pigmented eukaryote assemblages of the western tropical North Atlantic around the Amazon River plume during spring discharge. <i>Scientific Reports</i> , 2021, 11, 16200.	1.6	4
13836	Divergence and hybridization in sea turtles: Inferences from genome data show evidence of ancient gene flow between species. <i>Molecular Ecology</i> , 2021, 30, 6178-6192.	2.0	24
13840	Phylogenomic and Macroevolutionary Evidence for an Explosive Radiation of a Plant Genus in the Miocene. <i>Systematic Biology</i> , 2022, 71, 589-609.	2.7	26
13841	De novo assembly, annotation, and comparative analysis of 26 diverse maize genomes. <i>Science</i> , 2021, 373, 655-662.	6.0	282
13842	Genomic introgression from a distant congener in the Levant fritillary butterfly, <i>Melitaea acentria</i> . <i>Molecular Ecology</i> , 2021, 30, 4819-4832.	2.0	7
13843	Antimicrobial Activities of Endophytic Fungal Crude Extracts Isolated from Cashew Tree (<i>Anacardium</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	0.2	2
13844	Macrofungi of urban Tilia avenues and gardens in Hungary. <i>Global Ecology and Conservation</i> , 2021, 28, e01672.	1.0	3
13845	A phylogeny of <i>Antirrhinum</i> reveals parallel evolution of alpine morphology. <i>New Phytologist</i> , 2021, , .	3.5	9
13846	An integrative analysis uncovers a new, pseudo-cryptic species of Amazonian marmoset (Primates): Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.6	17
13847	TAPER: Pinpointing errors in multiple sequence alignments despite varying rates of evolution. <i>Methods in Ecology and Evolution</i> , 2021, 12, 2145-2158.	2.2	13
13848	The coral symbiont <i>Candidatus Aquarickettsia</i> is variably abundant in threatened Caribbean acroporids and transmitted horizontally. <i>ISME Journal</i> , 2022, 16, 400-411.	4.4	21
13849	Phylosymbiotic Structures of the Microbiota in <i>Mollitrichosiphum tenuicorpus</i> (Hemiptera: Aphididae): Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	1.4	3
13850	Comparative Chloroplast Genomics in Phyllanthaceae Species. <i>Diversity</i> , 2021, 13, 403.	0.7	6
13851	A Genomic Catalog of Stress Response Genes in Anaerobic Fungi for Applications in Bioproduction. <i>Frontiers in Fungal Biology</i> , 2021, 2, .	0.9	1

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13854	Molecular systematics and biogeographic history of the African climbing-mouse complex (<i>Dendromus</i>). <i>Molecular Phylogenetics and Evolution</i> , 2021, 161, 107166.	1.2	16
13855	Phylogeny and biogeography of the pantropical whip spider family Charinidae (Arachnida: Amblypygi). <i>Zoological Journal of the Linnean Society</i> , 2022, 194, 136-180.	1.0	10
13856	Mitochondrial Genomes of <i>Hestina persimilis</i> and <i>Hestinalis nama</i> (Lepidoptera, Nymphalidae): Genome Description and Phylogenetic Implications. <i>Insects</i> , 2021, 12, 754.	1.0	2
13857	Gene-Metabolite Network Analysis Revealed Tissue-Specific Accumulation of Therapeutic Metabolites in <i>Mallotus japonicus</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 8835.	1.8	3
13858	Formation of Macro- and Microrefugia Explains Morphological Divergence of the Eurasian Jay <i>Garrulus glandarius</i> in the Japanese Archipelago. <i>Acta Ornithologica</i> , 2021, 56, .	0.1	2
13859	Genome-wide identification and comparative analysis of Cry toxin receptor families in 7 insect species with a focus on <i>Spodoptera litura</i> . <i>Insect Science</i> , 2022, 29, 783-800.	1.5	6
13860	The metabolic footprint of <i>Clostridia</i> and <i>Erysipelotrichia</i> reveals their role in depleting sugar alcohols in the cecum. <i>Microbiome</i> , 2021, 9, 174.	4.9	17
13862	Multispecies Coalescent: Theory and Applications in Phylogenetics. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2021, 52, 247-268.	3.8	28
13864	<i>Euphrasia ultima</i> , a new locally endemic diploid species from the Ortler/Ortles range (Italy), is a close relative of widespread allotetraploid <i>E. minima</i> . <i>Plant Biosystems</i> , 0, , 1-15.	0.8	0
13866	Evolution of <i>Acinetobacter baumannii</i> in Clinical Bacteremia Patients. <i>Infection and Drug Resistance</i> , 2021, Volume 14, 3553-3562.	1.1	3
13867	Species in lichen-forming fungi: balancing between conceptual and practical considerations, and between phenotype and phylogenomics. <i>Fungal Diversity</i> , 2021, 109, 99-154.	4.7	55
13868	Whole Genome Sequencing Links <i>Mycobacterium bovis</i> From Cattle, Cheese and Humans in Baja California, Mexico. <i>Frontiers in Veterinary Science</i> , 2021, 8, 674307.	0.9	6
13869	PhyloFisher: A phylogenomic package for resolving eukaryotic relationships. <i>PLoS Biology</i> , 2021, 19, e3001365.	2.6	51
13870	Sequencing and de Novo Assembly of Abaca (<i>Musa textilis</i> (L.) var. Abuab Genome. <i>Genes</i> , 2021, 12, 1202.	1.0	9
13871	<i>Amanita submelleialba</i> sp. nov. in section <i>Amanita</i> from northern Thailand. <i>Phytotaxa</i> , 2021, 513, 129-140.	0.1	2
13872	Life cycle truncation in <i>Digenea</i> , a case study of <i>Neophasis</i> spp. (Acanthocolpidae). <i>International Journal for Parasitology: Parasites and Wildlife</i> , 2021, 15, 158-172.	0.6	3
13874	Comparative genomics of two inbred lines of the potato cyst nematode <i>Globodera rostochiensis</i> reveals disparate effector family-specific diversification patterns. <i>BMC Genomics</i> , 2021, 22, 611.	1.2	6
13875	The Easter Egg Weevil (<i>Pachyrhynchus</i>) genome reveals syntenic patterns in Coleoptera across 200 million years of evolution. <i>PLoS Genetics</i> , 2021, 17, e1009745.	1.5	14

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13876	Multiple Losses of MSH1, Gain of mtMutS, and Other Changes in the MutS Family of DNA Repair Proteins in Animals. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	7
13877	Population genomics of transposable element activation in the highly repressive genome of an agricultural pathogen. <i>Microbial Genomics</i> , 2021, 7, .	1.0	8
13878	High-quality evergreen azalea genome reveals tandem duplication-facilitated low-altitude adaptability and floral scent evolution. <i>Plant Biotechnology Journal</i> , 2021, 19, 2544-2560.	4.1	35
13879	Analysis of the complete chloroplast genomes of <i>Scutellaria tsinyunensis</i> and <i>Scutellaria tubrifera</i> (Lamiaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2672-2680.	0.2	4
13880	Characterization and phylogenetic analysis of the complete chloroplast genome of <i>Amaranthus viridis</i> (Amaranthaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2610-2612.	0.2	0
13881	The complete chloroplast genome of <i>Rhododendron molle</i> and its phylogenetic position within Ericaceae. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2587-2588.	0.2	6
13882	The complete chloroplast genome of <i>Lessertia frutescens</i> (L.) Goldblatt & J. C. Manning (Leguminosae), an important medicinal plant species from Southern Africa. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2767-2769.	0.2	0
13883	The complete chloroplast genome of <i>Petunia exserta</i> (Solanaceae: Petunioideae), an endangered ornamental species. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2619-2621.	0.2	0
13884	Multiple Gene Segments Are Associated with Enhanced Virulence of Clade 2.3.4.4 H5N8 Highly Pathogenic Avian Influenza Virus in Mallards. <i>Journal of Virology</i> , 2021, 95, e0095521.	1.5	16
13885	Unraveling the plant diversity of the Amazonian <i>canga</i> through DNA barcoding. <i>Ecology and Evolution</i> , 2021, 11, 13348-13362.	0.8	6
13886	Discovery of the <i>Pseudomonas</i> Polyene Protegencin by a Phylogeny-Guided Study of Polyene Biosynthetic Gene Cluster Diversity. <i>MBio</i> , 2021, 12, e0071521.	1.8	16
13887	Just keep it simple? Benchmarking the accuracy of taxonomy assignment software in metabarcoding studies. <i>Molecular Ecology Resources</i> , 2021, 21, 2187-2189.	2.2	8
13888	Increased abundance of secreted hydrolytic enzymes and secondary metabolite gene clusters define the genomes of latent plant pathogens in the Botryosphaeriaceae. <i>BMC Genomics</i> , 2021, 22, 589.	1.2	22
13889	DISCO: Species Tree Inference using Multicopy Gene Family Tree Decomposition. <i>Systematic Biology</i> , 2022, 71, 610-629.	2.7	20
13890	Temporal and palaeoclimatic context of the evolution of insular woodiness in the Canary Islands. <i>Ecology and Evolution</i> , 2021, 11, 12220-12231.	0.8	18
13891	Delimitation despite discordance: Evaluating the species limits of a confounding species complex in the face of mitonuclear discordance. <i>Ecology and Evolution</i> , 2021, 11, 12739-12753.	0.8	11
13892	Morpho-molecular description of a new HAB species, <i>Pseudocochlodinium profundisulcus</i> gen. et sp. nov., and its LSU rRNA gene based genetic diversity and geographical distribution. <i>Harmful Algae</i> , 2021, 108, 102098.	2.2	13
13893	Three Draft Genome Sequences of White Spot Syndrome Virus from India. <i>Microbiology Resource Announcements</i> , 2021, 10, e0057921.	0.3	2

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13894	Comparative Genomic Analysis Reveals Genetic Variation and Adaptive Evolution in the Pathogenicity-Related Genes of <i>Phytophthora capsici</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 694136.	1.5	4
13896	HPV DeepSeq: An Ultra-Fast Method of NGS Data Analysis and Visualization Using Automated Workflows and a Customized Papillomavirus Database in CLC Genomics Workbench. <i>Pathogens</i> , 2021, 10, 1026.	1.2	4
13897	Taxonomic and phylogenetic insights into novel Ascomycota from contaminated soils in Yunnan, China. <i>Phytotaxa</i> , 2021, 513, 203-225.	0.1	0
13898	Phylogenomic relationships and species identification of the olive genus <i>Olea</i> (Oleaceae). <i>Journal of Systematics and Evolution</i> , 2022, 60, 1263-1280.	1.6	36
13899	Congruence between oceanic dispersal modelling and phylogeography explains recent evolutionary history of <i>Cycas</i> species with buoyant seeds. <i>New Phytologist</i> , 2021, 232, 1863-1875.	3.5	15
13900	Novel <i>Acinetobacter baumannii</i> Bacteriophage Aristophanes Encoding Structural Polysaccharide Deacetylase. <i>Viruses</i> , 2021, 13, 1688.	1.5	9
13902	Mixed Acid Fermentation of Carbohydrate-Rich Dairy Manure Hydrolysate. <i>Frontiers in Bioengineering and Biotechnology</i> , 2021, 9, 724304.	2.0	11
13904	Variational inference using approximate likelihood under the coalescent with recombination. <i>Genome Research</i> , 2021, 31, 2107-2119.	2.4	4
13907	Genetic composition and evolution of the prevalent <i>Mycobacterium tuberculosis</i> lineages 2 and 4 in the Chinese and Zhejiang Province populations. <i>Cell and Bioscience</i> , 2021, 11, 162.	2.1	3
13908	Ionotropic receptor 8a is involved in the attraction of <i>Helicoverpa armigera</i> to acetic acid. <i>Insect Science</i> , 2022, 29, 657-668.	1.5	10
13909	Additions to the microfungi in Taiwan: introducing <i>Pseudorobillarda camelliae-sinensis</i> sp. nov., (Pseudorobillardaceae) and new host records of pleosporalean taxa in mountainous habitats. <i>Phytotaxa</i> , 2021, 516, .	0.1	0
13910	A molecular phylogeny of <i>Thuridilla</i> Bergh, 1872 sea slugs (Gastropoda, Sacoglossa) reveals a case of flamboyant and cryptic radiation in the marine realm. <i>Cladistics</i> , 2021, 37, 647-676.	1.5	11
13911	Virus-associated organosulfur metabolism in human and environmental systems. <i>Cell Reports</i> , 2021, 36, 109471.	2.9	38
13912	Novel tRNA gene rearrangements in the mitochondrial genomes of praying mantises (Mantodea: Tj ETQq1 1 0.784314 rgBT /Overlock). <i>Macromolecules</i> , 2021, 185, 403-411.	3.6	14
13913	<i>Castela</i> (Simaroubaceae), an impressive New World radiation of thorny shrubs destined for edaphically dry habitats. <i>Revista Brasileira De Botanica</i> , 2022, 45, 237-249.	0.5	8
13915	Pre-meiotic 21-nucleotide reproductive phasiRNAs emerged in seed plants and diversified in flowering plants. <i>Nature Communications</i> , 2021, 12, 4941.	5.8	21
13916	Survey of Ticks and Tick-Borne Rickettsial and Protozoan Pathogens in Eswatini. <i>Pathogens</i> , 2021, 10, 1043.	1.2	10
13918	The Physiology and Biogeochemistry of SUP05. <i>Annual Review of Marine Science</i> , 2022, 14, 261-275.	5.1	15

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13919	Ciliate SSU-rDNA reference alignments and trees for phylogenetic placements of metabarcoding data. <i>Metabarcoding and Metagenomics</i> , 0, 5, .	0.0	6
13920	Risk of transfusion-transmitted hepatitis E virus infection from pool-tested platelets and plasma. <i>Journal of Hepatology</i> , 2022, 76, 46-52.	1.8	17
13921	Backbone phylogeny and evolution of Apioideae (Apiaceae): New insights from phylogenomic analyses of plastome data. <i>Molecular Phylogenetics and Evolution</i> , 2021, 161, 107183.	1.2	47
13922	Three new species of <i>Smithiomyces</i> from tropical Asia support an amphi-Pacific disjunct distribution in the genus. <i>Mycologia</i> , 2021, 113, 1-13.	0.8	1
13923	Ancient viral genomes reveal introduction of human pathogenic viruses into Mexico during the transatlantic slave trade. <i>ELife</i> , 2021, 10, .	2.8	23
13924	Complete plastome phylogeny and an update on <i>cox1</i> intron evolution of Hyoscyameae (Solanaceae). <i>Organisms Diversity and Evolution</i> , 2021, 21, 521-532.	0.7	0
13925	The Interspecific Fungal Hybrid <i>Verticillium longisporum</i> Displays Subgenome-Specific Gene Expression. <i>MBio</i> , 2021, 12, e0149621.	1.8	8
13926	Alternative Transmission Patterns in Independently Acquired Nutritional Cosymbionts of Dictyopharidae Planthoppers. <i>MBio</i> , 2021, 12, e0122821.	1.8	22
13927	Pan-genome of <i>Raphanus</i> highlights genetic variation and introgression among domesticated, wild, and weedy radishes. <i>Molecular Plant</i> , 2021, 14, 2032-2055.	3.9	56
13928	The genome of <i>Cymbidium sinense</i> revealed the evolution of orchid traits. <i>Plant Biotechnology Journal</i> , 2021, 19, 2501-2516.	4.1	46
13929	Characterization and phylogenetic analysis of the complete plastome of <i>Veronica undulata</i> (Plantaginaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2706-2707.	0.2	1
13930	Colistin and Carbapenem-Resistant <i>Acinetobacter baumannii</i> Aci46 in Thailand: Genome Analysis and Antibiotic Resistance Profiling. <i>Antibiotics</i> , 2021, 10, 1054.	1.5	8
13931	Single-Strand Conformation Polymorphism Fingerprint Method for Dictyostelids. <i>Frontiers in Microbiology</i> , 2021, 12, 708685.	1.5	2
13932	The complete chloroplast genome sequence of <i>Arundo formosana</i> Hack. (Poaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2819-2821.	0.2	0
13933	Assessing the origins of the European Plagues following the Black Death: A synthesis of genomic, historical, and ecological information. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	16
13934	Massive gene rearrangement in mitogenomes of phytoseiid mites. <i>International Journal of Biological Macromolecules</i> , 2021, 186, 33-39.	3.6	10
13935	Revisiting the phylogeny of microsporidia. <i>International Journal for Parasitology</i> , 2021, 51, 855-864.	1.3	27
13936	Afro-alpine flagships revisited II: elucidating the evolutionary relationships and species boundaries in the giant senecios (<i>Dendrosenecio</i> , Asteraceae). <i>Alpine Botany</i> , 2022, 132, 89-105.	1.1	6

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13937	Systematic revision of <i>Gatesona</i> (Crassiclitellata, Lumbricidae), an endemic earthworm genus from the Massif Central (France). <i>PLoS ONE</i> , 2021, 16, e0255978.	1.1	5
13938	Evolution of host use in fungivorous ciid beetles (Coleoptera: Ciidae): Molecular phylogeny focusing on Japanese taxa. <i>Molecular Phylogenetics and Evolution</i> , 2021, 162, 107197.	1.2	9
13939	Genome-Based Taxonomy of <i>Brevundimonas</i> with Reporting <i>Brevundimonas huaxiensis</i> sp. nov.. <i>Microbiology Spectrum</i> , 2021, 9, e0011121.	1.2	15
13940	BASE: A novel workflow to integrate nonubiquitous genes in comparative genomics analyses for selection. <i>Ecology and Evolution</i> , 2021, 11, 13029-13035.	0.8	5
13941	Ohashia , a new genus of Derris -like Millettoid legumes (Leguminosae, Papilionoideae) as revealed by molecular phylogenetic evidence. <i>Taxon</i> , 0, , .	0.4	0
13942	Highly Diverse Shrub Willows (<i>Salix</i> L.) Share Highly Similar Plastomes. <i>Frontiers in Plant Science</i> , 2021, 12, 662715.	1.7	12
13943	The Conserved <i>Colletotrichum</i> spp. Effector Candidate CEC3 Induces Nuclear Expansion and Cell Death in Plants. <i>Frontiers in Microbiology</i> , 2021, 12, 682155.	1.5	12
13944	Evidence of hybridization between Yaqui catfish <i>Ictalurus pricei</i> (Rutter, 1896) and channel catfish <i>Ictalurus punctatus</i> (Rafinesque, 1818) in north-west Mexico revealed by analysis of mitochondrial and nuclear genes. <i>Aquatic Conservation: Marine and Freshwater Ecosystems</i> , 2021, 31, 3334-3341.	0.9	3
13945	The dark side of pseudoscorpion diversity: The German Barcode of Life campaign reveals high levels of undocumented diversity in European false scorpions. <i>Ecology and Evolution</i> , 2021, 11, 13815-13829.	0.8	14
13946	Systematic revision of the limestone karst-restricted land snail genus <i>Aenigmatoconcha</i> (Eupulmonata: Helicarionidae), with description of a new species. <i>European Journal of Taxonomy</i> , 0, 767, 55-82.	0.6	6
13947	Phylogeography of the wide-host range panglobal plant pathogen <i>Phytophthora cinnamomi</i> . <i>Molecular Ecology</i> , 2021, 30, 5164-5178.	2.0	19
13948	Genomic portrait of community-associated methicillin-resistant <i>Staphylococcus aureus</i> ST772-SCCmec V lineage from India. <i>Gene Reports</i> , 2021, 24, 101235.	0.4	3
13949	Detection and molecular characteristics of <i>Pyelosomum cochlear</i> (Digenea: Pronocephalidae) in the urinary bladder of the green sea turtle (<i>Chelonia mydas</i>) in the Northwest Pacific Ocean. <i>Infection, Genetics and Evolution</i> , 2021, 93, 104962.	1.0	0
13950	Comparative Mitogenomes of Two <i>Coreamachilis</i> Species (Microcoryphia: Machilidae) along with Phylogenetic Analyses of Microcoryphia. <i>Insects</i> , 2021, 12, 795.	1.0	4
13951	Cophylogenetic analyses of <i>Trachymyrmex</i> ant-fungal specificity: One to one with some exceptions. <i>Molecular Ecology</i> , 2021, 30, 5605-5620.	2.0	6
13952	Phylogeography of the endemic red-tailed cicadas of New Zealand (Hemiptera: Cicadidae): <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50</i> of Hudson's <i>Rhodopsalta microdora</i> . <i>Zoological Journal of the Linnean Society</i> , 2022, 195, 1219-1244.	1.0	8
13953	Chromosome-scale genome assembly and population genomics provide insights into the adaptation, domestication, and flavonoid metabolism of Chinese plum. <i>Plant Journal</i> , 2021, 108, 1174-1192.	2.8	16
13954	Phylogenomic and comparative genomic analyses of species of the family Pseudomonadaceae: Proposals for the genera <i>Halopseudomonas</i> gen. nov. and <i>Atopomonas</i> gen. nov., merger of the genus <i>Oblitimonas</i> with the genus <i>Thiopseudomonas</i> , and transfer of some misclassified species of the genus <i>Pseudomonas</i> into other genera. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	101

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13955	Molecular phylogenetic and morphological evidence reveal a rare limacoid snail genus, <i>Khmerquantula</i> gen. nov. (Eupulmonata: Dyakiidae) from Cambodia. <i>Systematics and Biodiversity</i> , 2021, 19, 1049-1061.	0.5	3
13956	Transcriptome and Resequencing Analyses Provide Insight into Differences in Organic Acid Accumulation in Two Pear Varieties. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9622.	1.8	5
13957	Transitional genomes and nutritional role reversals identified for dual symbionts of adelgids (Aphidoidea: Adelgidae). <i>ISME Journal</i> , 2022, 16, 642-654.	4.4	11
13958	Revisiting Linnaean and Wallacean Shortfalls in Mindanao Fanged Frogs: The <i>Limnonectes magnus</i> Complex Consists of Only Two Species. <i>Herpetological Monographs</i> , 2021, 35, .	1.1	3
13959	Whole-genome sequencing reveals forgotten lineages and recurrent hybridizations within the kelp genus <i>Alaria</i> (Phaeophyceae). <i>Journal of Phycology</i> , 2021, 57, 1721-1738.	1.0	10
13960	Complete genome sequence and identification of polyunsaturated fatty acid biosynthesis genes of the myxobacterium <i>Minicycstis rosea</i> DSM 24000T. <i>BMC Genomics</i> , 2021, 22, 655.	1.2	6
13961	Genomic and functional evidence reveals convergent evolution in fishes on the Tibetan Plateau. <i>Molecular Ecology</i> , 2021, 30, 5752-5764.	2.0	10
13962	Gene Analysis, Cloning, and Heterologous Expression of Protease from a Micromycete <i>Aspergillus ochraceus</i> Capable of Activating Protein C of Blood Plasma. <i>Microorganisms</i> , 2021, 9, 1936.	1.6	2
13963	<i>Methylomonas albis</i> sp. nov. and <i>Methylomonas fluvii</i> sp. nov.: Two cold-adapted methanotrophs from the river Elbe and emended description of the species <i>Methylovulum psychrotolerans</i> . <i>Systematic and Applied Microbiology</i> , 2021, 44, 126248.	1.2	18
13964	Chromosome-scale assembly and whole-genome sequencing of 266 giant panda roundworms provide insights into their evolution, adaptation and potential drug targets. <i>Molecular Ecology Resources</i> , 2022, 22, 768-785.	2.2	6
13965	Activation of EGFR signaling by Tc-Vein and Tc-Spitz regulates the metamorphic transition in the red flour beetle <i>Tribolium castaneum</i> . <i>Scientific Reports</i> , 2021, 11, 18807.	1.6	3
13966	New record of the wood-associated sea star <i>Caymanostella</i> , with notes on the phylogenetic position of the family Caymanostellidae (Asteroidea). <i>Zoological Journal of the Linnean Society</i> , 2022, 194, 14-35.	1.0	3
13967	Complete Mitochondrial Genome Sequence of the Gulf Coast Tick (<i>Amblyomma maculatum</i>). <i>Microbiology Resource Announcements</i> , 2021, 10, e0043121.	0.3	0
13968	Performance and competitiveness of red vs. green phenotypes of a cyanobacterium grown under artificial lake browning. <i>Algae</i> , 2021, 36, 195-206.	0.9	7
13969	Systematics of the Arboreal Neotropical "thorelli" Clade of Centruroides Bark Scorpions (Buthidae) and the Efficacy of Mini-Barcodes for Museum Specimens. <i>Diversity</i> , 2021, 13, 441.	0.7	1
13970	<i>Neopestalotiopsis</i> Species Associated with Flower Diseases of <i>Macadamia integrifolia</i> in Australia. <i>Journal of Fungi</i> (Basel, Switzerland), 2021, 7, 771.	1.5	11
13971	Population dynamics linked to glacial cycles in <i>Cercis chuniana</i> F. P. Metcalf (Fabaceae) endemic to the montane regions of subtropical China. <i>Evolutionary Applications</i> , 2021, 14, 2647-2663.	1.5	4
13972	DdaSTE12 is involved in trap formation, ring inflation, conidiation, and vegetative growth in the nematode-trapping fungus <i>Drechlerella dactyloides</i> . <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 7379-7393.	1.7	14

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13973	FunOrder: A robust and semi-automated method for the identification of essential biosynthetic genes through computational molecular co-evolution. <i>PLoS Computational Biology</i> , 2021, 17, e1009372.	1.5	9
13974	Phylogenomic relationships and historical biogeography in the South American vegetable ivory palms (Phytelephea). <i>Molecular Phylogenetics and Evolution</i> , 2022, 166, 107314.	1.2	3
13975	Geography-dependent symbiont communities in two oligophagous aphid species. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	6
13976	High Arsenic Levels Increase Activity Rather than Diversity or Abundance of Arsenic Metabolism Genes in Paddy Soils. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0138321.	1.4	9
13977	The genomic basis of army ant chemosensory adaptations. <i>Molecular Ecology</i> , 2021, 30, 6627-6641.	2.0	9
13978	<i>Simplicillium pech-merlensis</i> , a new fungal species isolated from the air of the Pech-Merle show cave. <i>Phytotaxa</i> , 2021, 521, 80-94.	0.1	3
13979	Transfer of the thecate amoebae <i>Lecythium spinosum</i> and <i>Pamphagus armatus</i> to <i>Rhizaspis</i> (Thecofilosea, Cercozoa, Rhizaria). <i>European Journal of Protistology</i> , 2021, , 125843.	0.5	0
13981	Re-Emergence and Spread of Haemorrhagic Septicaemia in Germany: The Wolf as a Vector?. <i>Microorganisms</i> , 2021, 9, 1999.	1.6	1
13982	Genetic differences between Japan and other countries in <i>cyp51A</i> polymorphisms of <i>Aspergillus fumigatus</i> . <i>Mycoses</i> , 2021, 64, 1354-1365.	1.8	10
13983	Uncovering Symbionts Across the Psyllid Tree of Life and the Discovery of a New <i>Liberibacter</i> Species, <i>Candidatus Liberibacter capsica</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 739763.	1.5	15
13984	Phylogeny-based conservation priorities for Australian freshwater fishes. <i>Conservation Biology</i> , 2022, 36, .	2.4	5
13985	The Archean origin of oxygenic photosynthesis and extant cyanobacterial lineages. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2021, 288, 20210675.	1.2	48
13986	In-depth Phylogenomic Analysis of Arbuscular Mycorrhizal Fungi Based on a Comprehensive Set of de novo Genome Assemblies. <i>Frontiers in Fungal Biology</i> , 2021, 2, .	0.9	15
13987	The mitochondrial genome of <i>Eurycantha calcarata</i> Lucas, 1869 (Phasmatodea: Lonchodinae) and its phylogeny. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 3109-3111.	0.2	2
13988	Characterization of the complete chloroplast genome sequence of <i>Rubus rufus</i> Focke (Rosaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 3093-3094.	0.2	2
13989	High-Quality Genome of the Medicinal Plant <i>Strobilanthes cusia</i> Provides Insights Into the Biosynthesis of Indole Alkaloids. <i>Frontiers in Plant Science</i> , 2021, 12, 742420.	1.7	10
13990	High quality haplotype-resolved genome assemblies of <i>Populus tomentosa</i> Carr., a stabilized interspecific hybrid species widespread in Asia. <i>Molecular Ecology Resources</i> , 2022, 22, 786-802.	2.2	19
13991	The complete chloroplast genome of a shrub species, <i>Smilax glabra</i> (Smilacaceae) from Guangdong, China. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 3064-3066.	0.2	1

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13992	MOSGA 2: Comparative genomics and validation tools. Computational and Structural Biotechnology Journal, 2021, 19, 5504-5509.	1.9	4
13993	Metagenomic analysis of ancient dental calculus reveals unexplored diversity of oral archaeal Methanobrevibacter. Microbiome, 2021, 9, 197.	4.9	18
13994	The complete chloroplast genome of <i>Cycas bifida</i> , an extremely small population protected species. Mitochondrial DNA Part B: Resources, 2021, 6, 2960-2961.	0.2	2
13995	Horizontal transfer and subsequent explosive expansion of a DNA transposon in sea kraits (<i>Callisophinae</i>) (<i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 150 13</i>)		
13996	Haploid Genome Analysis Reveals a Tandem Cluster of Four HSP20 Genes Involved in the High-Temperature Adaptation of <i>Corioliopsis trogii</i> . Microbiology Spectrum, 2021, 9, e0028721.	1.2	7
13997	<i>Colletotrichum acutatum</i> and <i>Colletotrichum nymphaeae</i> causing blossom blight and fruit anthracnose on olives in southern Brazil. European Journal of Plant Pathology, 2021, 161, 993.	0.8	1
13998	Comparative Genomic Analysis of Novel <i>Bifidobacterium longum</i> subsp. <i>longum</i> Strains Reveals Functional Divergence in the Human Gut Microbiota. Microorganisms, 2021, 9, 1906.	1.6	11
13999	The first mitochondrial 5-methylcytosine map in a non-model teleost (<i>Oreochromis niloticus</i>) reveals extensive strand-specific and non-CpG methylation. Genomics, 2021, 113, 3050-3057.	1.3	6
14000	Phylogeography of a widely distributed plant species reveals cryptic genetic lineages with parallel phenotypic responses to warming and drought conditions. Ecology and Evolution, 2021, 11, 13986-14002.	0.8	8
14001	First report of <i>Bursaphelenchus leoni</i> Baujard, 1980 (Nematoda: Parasitaphelenchidae) from Pine Forests of Turkey. Kahramanmaraş Sırtçın İktisadi ve Sosyal Üniversitesi Dergisi, 0, , .	0.2	0
14002	Chromosome-level genome assembly of the mirid predator <i>Cyrtorhinus lividipennis</i> Reuter (Hemiptera: Miridae), an important natural enemy in the rice ecosystem. Molecular Ecology Resources, 2022, 22, 1086-1099.	2.2	7
14003	Relaxed selection on male mitochondrial genes in DUI bivalves eases the need for mitonuclear coevolution. Journal of Evolutionary Biology, 2021, 34, 1722-1736.	0.8	10
14004	Evolution and Potential Function in Molluscs of Neuropeptide and Receptor Homologues of the Insect Allatostatins. Frontiers in Endocrinology, 2021, 12, 725022.	1.5	5
14006	Whole genome sequencing reveals great diversity of <i>Vibrio</i> spp in prawns at retail. Microbial Genomics, 2021, 7, .	1.0	7
14008	Eight species of <i>Lintonium</i> Stunkard & Nigrelli, 1930 (Digenea: Fellodistomidae) in Australian tetraodontiform fishes. Systematic Parasitology, 2021, 98, 595-624.	0.5	4
14009	Phylogenetic position of <i>Bupleurum sikangense</i> inferred from the complete chloroplast genome sequence. Gene, 2021, 798, 145801.	1.0	11
14010	The complete chloroplast genome of the national tree of Peru, quina (<i>Cinchona officinalis</i> L.) (<i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 102 0.2 5</i>)		
14011	Whole genome sequences reveal the <i>Xanthomonas perforans</i> population is shaped by the tomato production system. ISME Journal, 2022, 16, 591-601.	4.4	6

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14012	Human respiratory syncytial virus diversity and epidemiology among patients hospitalized with severe respiratory illness in South Africa, 2012–2015. <i>Influenza and Other Respiratory Viruses</i> , 2022, 16, 222-235.	1.5	9
14013	EVOLUTION OF THE CHOLLAS (CACTACEAE). <i>Madroño</i> , 2021, 68, .	0.3	0
14014	Phylogenetic relationships and biogeography of the <i>Hybomys</i> division (Muridae: Murinae: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 662 Td	0.4	1
14015	Extensive genomic rearrangements mediated by repetitive sequences in plastomes of <i>Medicago</i> and its relatives. <i>BMC Plant Biology</i> , 2021, 21, 421.	1.6	25
14016	A Combined Transcriptomics and Proteomics Approach Reveals the Differences in the Predatory and Defensive Venoms of the Molluscivorous Cone Snail <i>Cylinderochlamys ammiralis</i> (Caenogastropoda: Conidae). <i>Toxins</i> , 2021, 13, 642.	1.5	8
14019	Microdiversity characterizes prevalent phylogenetic clades in the glacier-fed stream microbiome. <i>ISME Journal</i> , 2022, 16, 666-675.	4.4	28
14020	Virulence of Enterovirus A71 Fluctuates Depending on the Phylogenetic Clade Formed in the Epidemic Year and Epidemic Region. <i>Journal of Virology</i> , 2021, 95, e0151521.	1.5	2
14021	Evolutionary history of two rare endemic conifer species from the eastern Qinghai–Tibet Plateau. <i>Annals of Botany</i> , 2021, 128, 903-918.	1.4	5
14022	Odorant-binding proteins in canine anal sac glands indicate an evolutionarily conserved role in mammalian chemical communication. <i>Bmc Ecology and Evolution</i> , 2021, 21, 182.	0.7	6
14023	Increased rates of secondary bacterial infections, including <i>Enterococcus</i> bacteremia, in patients hospitalized with coronavirus disease 2019 (COVID-19). <i>Infection Control and Hospital Epidemiology</i> , 2022, 43, 1416-1423.	1.0	40
14024	Ophiostomatoid fungi associated with pine bark beetles and infested pines in south-eastern Australia, including <i>Graphilbum ipis-grandicollis</i> sp. nov.. <i>IMA Fungus</i> , 2021, 12, 24.	1.7	12
14025	Insights into the Genetic Evolution of Duck Hepatitis A Virus in Egypt. <i>Animals</i> , 2021, 11, 2741.	1.0	3
14026	Direct Metatranscriptomic Survey of the Sunflower Microbiome and Virome. <i>Viruses</i> , 2021, 13, 1867.	1.5	6
14027	Phylogeny, character evolution and taxonomic revision of <i>Causonis</i> , a segregate genus from <i>Cayratia</i> (Vitaceae). <i>Taxon</i> , 0, , .	0.4	6
14028	Unraveling the Hidden Diversity of the Native White Claw Crayfish in the Iberian Peninsula. <i>Frontiers in Ecology and Evolution</i> , 2021, 9, .	1.1	2
14029	<i>Lasiodiplodia</i> species diversity associated with coconut leaf blight and stem-end rot in Northeastern Brazil. <i>European Journal of Plant Pathology</i> , 2022, 162, 45-61.	0.8	1
14030	<i>Pseudomonas</i> Phage MD8: Genetic Mosaicism and Challenges of Taxonomic Classification of Lambdoid Bacteriophages. <i>International Journal of Molecular Sciences</i> , 2021, 22, 10350.	1.8	10
14031	A New Species of Microtegu Lizard (Gymnophthalmidae: Cercosaurinae) from Amazonian Ecuador. <i>Journal of Herpetology</i> , 2021, 55, .	0.2	2

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14032	The emerging vertebrate model species for neurophysiological studies is <i>Danio rerio</i> , new species (Teleostei: Cyprinidae). <i>Scientific Reports</i> , 2021, 11, 18942.	1.6	14
14033	Patterns of Coevolutionary Adaptations across Time and Space in Mouse Gammaretroviruses and Three Restrictive Host Factors. <i>Viruses</i> , 2021, 13, 1864.	1.5	5
14034	The Hidden Genomic Diversity, Specialized Metabolite Capacity, and Revised Taxonomy of <i>Burkholderia</i> <i>Sensu Lato</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 726847.	1.5	16
14037	The complete chloroplast genome sequence of <i>Phalaenopsis wilsonii</i> Rolfe, a vulnerable wild moth orchid species (Orchidaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2903-2905.	0.2	3
14038	The complete mitochondrial genome of <i>Trichonephila clavipes</i> (Araneae: Araneidae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2986-2988.	0.2	0
14039	Transcriptome analysis and genetic diversity of <i>Allium victorialis</i> germplasms from the Changbai Mountains. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2915-2923.	0.2	1
14040	Pragmatic Assignment of Species Groups Based on Primary Species Hypotheses: The Case of a Dominant Component of the Southern Ocean Benthic Fauna. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	5
14041	The <i>Euscaphis japonica</i> genome and the evolution of malvids. <i>Plant Journal</i> , 2021, 108, 1382-1399.	2.8	6
14042	Multi-Gene Phylogeny and Taxonomy of <i>Hydnellum</i> (Bankeraceae, Basidiomycota) from China. <i>Journal of Fungi</i> (Basel, Switzerland), 2021, 7, 818.	1.5	6
14043	Using a supermatrix approach to explore phylogenetic relationships, divergence times, and historical biogeography of Saxifragales. <i>Turkish Journal of Botany</i> , 2021, 45, 440-456.	0.5	2
14044	Phylogeny and subcellular localization analyses reveal distinctions in monocot and eudicot class IV acyl-CoA-binding proteins. <i>Planta</i> , 2021, 254, 71.	1.6	4
14045	Complete chloroplast genome of <i>Isoetes hypsophila</i> (Isoetaceae), the Endangered quillwort in China. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2908-2909.	0.2	1
14046	The complete chloroplast genome and phylogenetic analysis of <i>Citrus clementina</i> (Rutaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2926-2927.	0.2	3
14047	Mycorrhizal status is a poor predictor of the distribution of herbaceous species along the gradient of soil nutrient availability in coastal and grassland habitats. <i>Mycorrhiza</i> , 2021, 31, 577-587.	1.3	2
14048	Stable-Isotope-Informed, Genome-Resolved Metagenomics Uncovers Potential Cross-Kingdom Interactions in Rhizosphere Soil. <i>MSphere</i> , 2021, 6, e0008521.	1.3	34
14049	Microbial methylglyoxal metabolism contributes towards growth promotion and stress tolerance in plants. <i>Environmental Microbiology</i> , 2022, 24, 2817-2836.	1.8	4
14050	Validation of <i>Hosta alata</i> (Asparagaceae) as a new species and its phylogenetic affinity. <i>PhytoKeys</i> , 2021, 181, 79-93.	0.4	6
14051	The genomic architecture of EBV and infected gastric tissue from precursor lesions to carcinoma. <i>Genome Medicine</i> , 2021, 13, 146.	3.6	9

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14052	Revision of the genus <i>Restingomyces</i> , including two new species from Mexico. <i>Mycologia</i> , 2021, 113, 1-11.	0.8	1
14053	OXA-900, a Novel OXA Sub-Family Carbapenemase Identified in <i>Citrobacter freundii</i> , Evades Detection by Commercial Molecular Diagnostics Tests. <i>Microorganisms</i> , 2021, 9, 1898.	1.6	4
14054	Cytonuclear discordance in the crowned-sparrows, <i>Zonotrichia atricapilla</i> and <i>Zonotrichia leucophrys</i> . <i>Molecular Phylogenetics and Evolution</i> , 2021, 162, 107216.	1.2	7
14056	Epidemiological Analysis of <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar Dublin in German Cattle Herds Using Whole-Genome Sequencing. <i>Microbiology Spectrum</i> , 2021, 9, e0033221.	1.2	10
14057	Testing the potential contribution of <i>Wolbachia</i> to speciation when cytoplasmic incompatibility becomes associated with host-related reproductive isolation. <i>Molecular Ecology</i> , 2022, 31, 2935-2950.	2.0	8
14058	The expansion and diversity of the <i>CYP75</i> gene family in Vitaceae. <i>PeerJ</i> , 2021, 9, e12174.	0.9	6
14059	A high-quality genome assembly of <i>Jasminum sambac</i> provides insight into floral trait formation and Oleaceae genome evolution. <i>Molecular Ecology Resources</i> , 2022, 22, 724-739.	2.2	18
14060	A conspectus of <i>Tephrosieris</i> (Asteraceae: Senecioneae) in Europe outside Russia and notes on the decline of the genus. <i>Willdenowia</i> , 2021, 51, .	0.5	3
14061	Authentication of medicinal herb <i>Wikstroemia indica</i> using novel DNA markers derived from the chloroplast genome sequences. <i>Journal of Applied Research on Medicinal and Aromatic Plants</i> , 2021, 24, 100315.	0.9	3
14064	Three novel sooty moulds species of <i>Trichomerium</i> from Yunnan, China. <i>Phytotaxa</i> , 2021, 518, 271-280.	0.1	0
14066	<i>Retiboletus</i> (<i>Boletaceae</i>) in northern Thailand: one novel species and two first records. <i>Mycoscience</i> , 2021, 62, 297-306.	0.3	2
14068	Rejection of the reclassification of <i>Leuconostoc gasicomitatum</i> as <i>Leuconostoc gelidum</i> subsp. <i>gasicomitatum</i> based on whole genome analysis. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	7
14069	Phylogeographic Clustering Suggests that Distinct Clades of <i>Salmonella enterica</i> Serovar Mississippi Are Endemic in Australia, the United Kingdom, and the United States. <i>MSphere</i> , 2021, 6, e0048521.	1.3	3
14070	Complex photobiont diversity in the marine lichen <i>Lichina pygmaea</i> . <i>Journal of the Marine Biological Association of the United Kingdom</i> , 2021, 101, 667-674.	0.4	9
14071	Within the roots of <i>Pleurothallidinae</i> (Orchidaceae): An evolutionary analysis. <i>Flora: Morphology, Distribution, Functional Ecology of Plants</i> , 2021, 282, 151883.	0.6	2
14072	Measuring Phylogenetic Information of Incomplete Sequence Data. <i>Systematic Biology</i> , 2021, .	2.7	1
14073	How many species does the <i>Psammobates tentorius</i> (tent tortoise) species complex (Reptilia,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 107 Zoological Systematics and Evolutionary Research, 0, .	0.6	2
14074	A <i>w</i> AlbB <i>Wolbachia</i> Transinfection Displays Stable Phenotypic Effects across Divergent <i>Aedes aegypti</i> Mosquito Backgrounds. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0126421.	1.4	20

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14075	Chromosome-level genome assembly of <i>Gynostemma pentaphyllum</i> provides insights into gypenoside biosynthesis. <i>DNA Research</i> , 2021, 28, .	1.5	14
14076	Clinical Molecular and Genomic Epidemiology of <i>Morganella morganii</i> in China. <i>Frontiers in Microbiology</i> , 2021, 12, 744291.	1.5	9
14077	The Molecular Epidemiology and Clinical Phylogenetics of Rhinoviruses Among Paediatric Cases in Sydney, Australia. <i>International Journal of Infectious Diseases</i> , 2021, 110, 69-74.	1.5	7
14078	Cultivation of particle-associated heterotrophic bacteria during a spring phytoplankton bloom in the North Sea. <i>Systematic and Applied Microbiology</i> , 2021, 44, 126232.	1.2	4
14079	In vivo Selection of Imipenem Resistance Among Ceftazidime-Avibactam-Resistant, Imipenem-Susceptible <i>Klebsiella pneumoniae</i> Isolate With KPC-33 Carbapenemase. <i>Frontiers in Microbiology</i> , 2021, 12, 727946.	1.5	6
14080	A biogeographical analysis of <i>Muhlenbergia</i> (Poaceae: Chloridoideae: Cynodonteae): Tj ETQq1 1 0.784314 rgBT /Overlçk 10 T 5	1.6	3
14081	Neofunctionalization of an ancient domain allows parasites to avoid intraspecific competition by manipulating host behaviour. <i>Nature Communications</i> , 2021, 12, 5489.	5.8	15
14082	High-Quality de novo Chromosome-Level Genome Assembly of a Single <i>Bombyx mori</i> With BmNPV Resistance by a Combination of PacBio Long-Read Sequencing, Illumina Short-Read Sequencing, and Hi-C Sequencing. <i>Frontiers in Genetics</i> , 2021, 12, 718266.	1.1	5
14083	Pandora: nucleotide-resolution bacterial pan-genomics with reference graphs. <i>Genome Biology</i> , 2021, 22, 267.	3.8	26
14085	Adaptation of Fig Wasps (Agaodinae) to Their Host Revealed by Large-Scale Transcriptomic Data. <i>Insects</i> , 2021, 12, 815.	1.0	5
14086	Isolation and endemism in subterranean aquatic snails: unexpected case of <i>Montenegrospeum bogici</i> (Pezomachus et Glaser, 2012) (Gastropoda: Truncatelloidea: Hydrobiidae). <i>Hydrobiologia</i> , 2021, 848, 4967-4990.	1.0	7
14087	<i>Flavobacterium ercyesense</i> sp. nov., a putative non-pathogenic fish symbiont. <i>Archives of Microbiology</i> , 2021, 203, 5783-5792.	1.0	10
14088	Mitochondrial Genomes, Phylogenetic Associations, and SNP Recovery for the Key Invasive Ponto-Caspian Amphipods in Europe. <i>International Journal of Molecular Sciences</i> , 2021, 22, 10300.	1.8	9
14089	Characterization of the β -tubulin gene family in <i>Ascaris lumbricoides</i> and <i>Ascaris suum</i> and its implication for the molecular detection of benzimidazole resistance. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009777.	1.3	13
14091	Little known <i>Curculigo brevipolia</i> deserves a species rank: evidences from morphological, cytological and molecular data. <i>Journal of Asia-Pacific Biodiversity</i> , 2021, 14, 613-621.	0.2	1
14092	Paraphyly and low levels of genetic divergence in morphologically distinct taxa: revision of the <i>Pseudoanthidium scapulare</i> complex of carder bees (Apoidea: Megachilidae: Anthidiini). <i>Zoological Journal of the Linnean Society</i> , 2022, 195, 1287-1337.	1.0	18
14093	The complete chloroplast genome sequence of rare and endangered <i>Camellia pubipetala</i> Y. Wan & S. Z. Huang (Theaceae) of South China. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2893-2895.	0.2	0
14094	Systematics of the Relictual Asian Scorpion Family Pseudochactidae Gromov, 1998, with a Review of Cavernicolous, Troglotic, and Troglomorphic Scorpions. <i>Bulletin of the American Museum of Natural History</i> , 2021, 453, .	1.2	5

#	ARTICLE	IF	CITATIONS
14096	Prospecting Endophytic Bacteria Endowed With Plant Growth Promoting Potential Isolated From <i>Camellia sinensis</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 738058.	1.5	15
14097	Geographical parthenogenesis in the brown alga <i>Scytosiphon lomentaria</i> (Scytosiphonaceae): Sexuals in warm waters and parthenogens in cold waters. <i>Molecular Ecology</i> , 2021, 30, 5814-5830.	2.0	9
14098	Association of <i>Lasiodiplodia theobromae</i> with die-back and decline of nutmeg as revealed through phenotypic, pathogenicity and phylogenetic analyses. <i>3 Biotech</i> , 2021, 11, 422.	1.1	2
14099	Molecular divergence among Yellow-spotted Barbet <i>Buccanodon duchaillui</i> populations suggests unrecognised diversity. <i>Bulletin of the British Ornithologists' Club</i> , 2021, 141, .	0.1	0
14100	Superficially described and ignored for 92 years, rediscovered and emended: <i>Apodera angatakere</i> (Amoebozoa: Arcellinida: Hyalospheniformes) is a new flagship testate amoeba taxon from Aotearoa (New Zealand). <i>Journal of Eukaryotic Microbiology</i> , 2021, 68, e12867.	0.8	4
14101	A database and checklist of geometrid moths (Lepidoptera) from Colombia. <i>Biodiversity Data Journal</i> , 2021, 9, e68693.	0.4	4
14102	A molecular phylogeny of <i>Tetrastemma</i> and its allies (Nemertea, Monostilifera). <i>Zoologica Scripta</i> , 2021, 50, 824-836.	0.7	10
14103	Microbes support enhanced nitrogen requirements of coral holobionts in a high CO ₂ environment. <i>Molecular Ecology</i> , 2021, 30, 5888-5899.	2.0	14
14104	Phylogenomic approach reveals strong signatures of introgression in the rapid diversification of neotropical true fruit flies (Anastrepha: Tephritidae). <i>Molecular Phylogenetics and Evolution</i> , 2021, 162, 107200.	1.2	8
14105	Genomic insights into the origin, domestication and diversification of <i>Brassica juncea</i> . <i>Nature Genetics</i> , 2021, 53, 1392-1402.	9.4	66
14106	Gene tree quality affects empirical coalescent branch length estimation. <i>Zoologica Scripta</i> , 0, , .	0.7	9
14107	Avian Neo-Sex Chromosomes Reveal Dynamics of Recombination Suppression and W Degeneration. <i>Molecular Biology and Evolution</i> , 2021, 38, 5275-5291.	3.5	25
14108	Antimicrobial resistance and genomic characterization of <i>Salmonella</i> Dublin isolates in cattle from the United States. <i>PLoS ONE</i> , 2021, 16, e0249617.	1.1	8
14109	Development and phylogenetic utilities of a new set of single-/low-copy nuclear genes in Senecioneae (Asteraceae), with new insights into the tribal position and the relationships within subtribe Tussilaginatae. <i>Molecular Phylogenetics and Evolution</i> , 2021, 162, 107202.	1.2	4
14110	Plastomes in the holoparasitic family Balanophoraceae: Extremely high AT content, severe gene content reduction, and two independent genetic code changes. <i>Molecular Phylogenetics and Evolution</i> , 2021, 162, 107208.	1.2	11
14111	Phylogenomic Insights into the Independent Origins of Sterile Marginal Flowers in <i>Viburnum</i> . <i>International Journal of Plant Sciences</i> , 2021, 182, 591-608.	0.6	0
14113	Rapid Macrosatellite Evolution Promotes X-Linked Hybrid Male Sterility in a Feline Interspecies Cross. <i>Molecular Biology and Evolution</i> , 2021, 38, 5588-5609.	3.5	8
14114	Genome Evolution of Filamentous Cyanobacterium <i>Nostoc</i> Species: From Facultative Symbiosis to Free Living. <i>Microorganisms</i> , 2021, 9, 2015.	1.6	4

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14115	Multiple lines of evidence supports the two varieties of <i>Halenia elliptica</i> (Gentianaceae) as two species. <i>Plant Diversity</i> , 2022, 44, 290-299.	1.8	5
14116	Extracting "legacy loci"™ from an invertebrate sequence capture data set. <i>Zoologica Scripta</i> , 2022, 51, 14-31.	0.7	9
14118	Evolutionary Signatures Governing the Codon Usage Bias in Coronaviruses and Their Implications for Viruses Infecting Various Bat Species. <i>Viruses</i> , 2021, 13, 1847.	1.5	15
14119	Capturing single-copy nuclear genes, organellar genomes, and nuclear ribosomal DNA from deep genome skimming data for plant phylogenetics: A case study in Vitaceae. <i>Journal of Systematics and Evolution</i> , 2021, 59, 1124-1138.	1.6	43
14120	A new species of <i>Gymnopus</i> sect. <i>Androsacei</i> (Omphalotaceae, Agaricales) from China. <i>Phytotaxa</i> , 2021, 521, 1-14.	0.1	4
14121	Phylogenetic significance of the characteristics of simple sequence repeats at the genus level based on the complete chloroplast genome sequences of Cyatheaceae. <i>Ecology and Evolution</i> , 2021, 11, 14327-14340.	0.8	13
14122	<i>Salmonella enterica</i> from a soldier from the 1652 siege of Barcelona (Spain) supports historical transatlantic epidemic contacts. <i>IScience</i> , 2021, 24, 103021.	1.9	2
14123	"Ancient DNA" reveals that the scientific name for an extinct tortoise from Cape Verde refers to an extant South American species. <i>Scientific Reports</i> , 2021, 11, 17537.	1.6	4
14124	Evolutionary origin of a tetraploid <i>Allium</i> species on the Qinghai-Tibet Plateau. <i>Molecular Ecology</i> , 2021, 30, 5780-5795.	2.0	11
14125	Admixture may be extensive among hyperdominant Amazon rainforest tree species. <i>New Phytologist</i> , 2021, 232, 2520-2534.	3.5	13
14126	Clarifying confusion " <i>Prorocentrum triestinum</i> J.Schiller and <i>Prorocentrum redfieldii</i> Bursa (Prorocentrales, Dinophyceae) are two different species. <i>European Journal of Phycology</i> , 2022, 57, 207-226.	0.9	3
14128	Systematic review of the genus <i>Ostracodinium</i> (Ciliophora, Entodiniomorphida, Ophryoscolecidae) and notes on the taxonomy of <i>Ostracodinium rugoloricatum</i> Kofoid & MacLennan, 1932. <i>Zootaxa</i> , 2021, 5039, 252-262.	0.2	1
14129	Decomposing the sources of SARS-CoV-2 fitness variation in the United States. <i>Virus Evolution</i> , 2021, 7, veab073.	2.2	14
14130	Whole-genome sequencing of brown-marbled grouper (<i>Epinephelus fuscoguttatus</i>) provides insights into adaptive evolution and growth differences. <i>Molecular Ecology Resources</i> , 2022, 22, 711-723.	2.2	16
14131	Heterogeneous Genetic Diversity Estimation of a Promising Domestication Medicinal Motherwort <i>Leonurus Cardiaca</i> Based on Chloroplast Genome Resources. <i>Frontiers in Genetics</i> , 2021, 12, 721022.	1.1	7
14132	First draft genome assemblies of <i>Pleochaeta shiraiana</i> and <i>Phyllactinia moricola</i> , two tree-parasitic powdery mildew fungi with hemiendophytic mycelia. <i>Phytopathology</i> , 2021, , .	1.1	3
14133	Population dynamics of caribou shaped by glacial cycles before the last glacial maximum. <i>Molecular Ecology</i> , 2021, 30, 6121-6143.	2.0	19
14134	Interactome and evolutionary conservation of Dictyostelid small GTPases and their direct regulators. <i>Small GTPases</i> , 2022, 13, 239-254.	0.7	3

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14135	Acylsugars protect <i>Nicotiana benthamiana</i> against insect herbivory and desiccation. <i>Plant Molecular Biology</i> , 2022, 109, 505-522.	2.0	20
14136	The complete chloroplast genome of <i>Lonicera pampaninii</i> Levl. and its phylogenetic analysis. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 3025-3027.	0.2	3
14137	<i>Ganoderma</i> (Ganodermataceae, Basidiomycota) Species from the Greater Mekong Subregion. <i>Journal of Fungi</i> (Basel, Switzerland), 2021, 7, 819.	1.5	18
14139	The complete chloroplast genome of the ephemeral plant <i>Isatis minima</i> (brassicaceae) of northwest China. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 3018-3020.	0.2	0
14140	Characterization and phylogenetic analysis of the complete plastome of <i>Amaranthus retroflexus</i> L. (Amaranthaceae), an annual weeds. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2847-2848.	0.2	0
14141	The complete mitochondrial genome of <i>Schizoneuraphis gallarum</i> van der Goot, 1917 (Hemiptera: Tj ETQq1 1 0.784314 rgBT /Overlock 1	0.2	1
14142	Isolation, Identification, and Antibacterial Mechanisms of <i>Bacillus amyloliquefaciens</i> QSB-6 and Its Effect on Plant Roots. <i>Frontiers in Microbiology</i> , 2021, 12, 746799.	1.5	32
14143	The biogeographic differentiation of algal microbiomes in the upper ocean from pole to pole. <i>Nature Communications</i> , 2021, 12, 5483.	5.8	29
14144	Insights into angiosperm evolution, floral development and chemical biosynthesis from the <i>Aristolochia fimbriata</i> genome. <i>Nature Plants</i> , 2021, 7, 1239-1253.	4.7	51
14145	Exploring the Genomic Diversity and Antimicrobial Susceptibility of <i>Bifidobacterium pseudocatenulatum</i> in a Vietnamese Population. <i>Microbiology Spectrum</i> , 2021, 9, e0052621.	1.2	6
14146	The genome sequence provides insights into salt tolerance of <i>Achnatherum splendens</i> (Gramineae), a constructive species of alkaline grassland. <i>Plant Biotechnology Journal</i> , 2022, 20, 116-128.	4.1	18
14147	Systematic Revision of the Arboreal Neotropical <i>Thorellia</i> Clade of <i>Centruroides</i> Marx, 1890, Bark Scorpions (Buthidae C.L. Koch, 1837) with Descriptions of Six New Species. <i>Bulletin of the American Museum of Natural History</i> , 2021, 452, .	1.2	2
14148	Taxonomy and phylogenetic appraisal of <i>Leptosphaeria chatkalica</i> sp. nov. (Leptosphaeriaceae.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 26	0.1	1
14149	Genome of the Giant Panda Roundworm Illuminates Its Host Shift and Parasitic Adaptation. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 366-381.	3.0	13
14150	<i>Adlercreutzia rubneri</i> sp. nov., a resveratrol-metabolizing bacterium isolated from human faeces and emended description of the genus <i>Adlercreutzia</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	17
14152	Hydrolytic Enzymes Producing Bacterial Endophytes of Some Poaceae Plants. <i>Polish Journal of Microbiology</i> , 2021, 70, 297-304.	0.6	18
14153	The complete chloroplast genome and characteristics analysis of <i>Musa basjoo</i> Siebold. <i>Molecular Biology Reports</i> , 2021, 48, 7113-7125.	1.0	3
14154	Phylogenomics reveals the evolution of root nodulating alpha- and beta-Proteobacteria (rhizobia). <i>Microbiological Research</i> , 2021, 250, 126788.	2.5	18

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14155	Phylogenomic Variation at the Population-Species Interface and Assessment of Gigantism in a Model Wolf Spider Genus (<i>Lycosidae</i> , <i>Schizocosa</i>). <i>Insect Systematics and Diversity</i> , 2021, 5, .	0.7	3
14156	Multi-tissue transcriptome analysis of two <i>Begonia</i> species reveals dynamic patterns of evolution in the chalcone synthase gene family. <i>Scientific Reports</i> , 2021, 11, 17773.	1.6	6
14157	Is Phylogeographic Congruence Predicted by Historical Habitat Stability, or Ecological Co-associations?. <i>Insect Systematics and Diversity</i> , 2021, 5, .	0.7	3
14159	One Crop Disease, How Many Pathogens? <i>Podosphaera xanthii</i> and <i>Erysiphe vignae</i> sp. nov. Identified as the Two Species that Cause Powdery Mildew of Mungbean (<i>Vigna radiata</i>) and Black Gram (<i>V. mungo</i>) in Australia. <i>Phytopathology</i> , 2021, 111, 1193-1206.	1.1	11
14160	Genetic features of <i>Salmonella enterica</i> subspecies <i>diarizonae</i> serovar 61:k:1,5 isolated from abortion cases in sheep, United States, 2020. <i>Research in Veterinary Science</i> , 2021, 138, 125-136.	0.9	2
14161	Insights into 6S RNA in lactic acid bacteria (LAB). <i>BMC Genomic Data</i> , 2021, 22, 29.	0.7	1
14162	Highly diverse flavobacterial phages isolated from North Sea spring blooms. <i>ISME Journal</i> , 2022, 16, 555-568.	4.4	32
14164	<i>Alternaria guilanica</i> sp. nov., a new fungal pathogen causing leaf spot and blight on eggplant in Iran. <i>Phytotaxa</i> , 2021, 520, 184-194.	0.1	3
14166	On the continuum of evolution: a putative new hybrid speciation event in <i>Opuntia</i> (Cactaceae) between a native and an introduced species in southern South America. <i>Systematics and Biodiversity</i> , 2021, 19, 1026-1039.	0.5	5
14168	Evolutionary Trajectories toward Ceftazidime-Avibactam Resistance in <i>Klebsiella pneumoniae</i> Clinical Isolates. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, e0057421.	1.4	41
14170	Investigating Sources of Conflict in Deep Phylogenomics of Vetigastropod Snails. <i>Systematic Biology</i> , 2022, 71, 1009-1022.	2.7	10
14171	The reduced ARF regulatory system in <i>Giardia intestinalis</i> pre-dates the transition to parasitism in the lineage Fornicata. <i>International Journal for Parasitology</i> , 2021, 51, 825-839.	1.3	5
14172	A <i>Phelipanche ramosa</i> KAI2 protein perceives strigolactones and isothiocyanates enzymatically. <i>Plant Communications</i> , 2021, 2, 100166.	3.6	31
14173	Colistin Resistance Mechanisms in Clinical <i>Escherichia coli</i> and <i>Klebsiella</i> spp. Isolates from the Western Cape of South Africa. <i>Microbial Drug Resistance</i> , 2021, 27, 1249-1258.	0.9	9
14174	Early-Life Microbial Restitution Reduces Colitis Risk Promoted by Antibiotic-Induced Gut Dysbiosis in Interleukin 10 ^{-/-} Mice. <i>Gastroenterology</i> , 2021, 161, 940-952.e15.	0.6	20
14175	Evolution of viral variants in remdesivir-treated and untreated SARS-CoV-2-infected pediatric patients. <i>Journal of Medical Virology</i> , 2022, 94, 161-172.	2.5	13
14176	Seasonal abundance and host-plant affinities of <i>Longitarsus basutoensis</i> and related flea beetles associated with the invasive <i>Senecio madagascariensis</i> in their native range in KwaZulu-Natal, South Africa. <i>Biological Control</i> , 2021, 160, 104681.	1.4	5
14177	Lessons for preparedness and reasons for concern from the early COVID-19 epidemic in Iran. <i>Epidemics</i> , 2021, 36, 100472.	1.5	17

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14178	Adaptive radiation and speciation in Rhipicephalus ticks: A medley of novel hosts, nested predator-prey food webs, off-host periods and dispersal along temperature variation gradients. <i>Molecular Phylogenetics and Evolution</i> , 2021, 162, 107178.	1.2	13
14179	Morphology and Phylogeny of <i>Gnomoniopsis</i> (Gnomoniaceae, Diaporthales) from Fagaceae Leaves in China. <i>Journal of Fungi</i> (Basel, Switzerland), 2021, 7, 792.	1.5	23
14180	The influence of alfalfa-switchgrass intercropping on microbial community structure and function. <i>Environmental Microbiology</i> , 2021, 23, 6828-6843.	1.8	5
14182	A revision of <i>Dryopteris</i> sect. <i>Diclisodon</i> (Dryopteridaceae) based on morphological and molecular evidence with description of a new species. <i>Plant Diversity</i> , 2022, 44, 181-190.	1.8	2
14183	<i>Veronaea aquatica</i> sp. nov. (Herpotrichiellaceae, Chaetothyriales, Eurotiomycetes) from submerged bamboo in China. <i>Biodiversity Data Journal</i> , 2021, 9, e64505.	0.4	3
14184	Identification of Fish Species and Toxins Implicated in a Snapper Food Poisoning Event in Sabah, Malaysia, 2017. <i>Toxins</i> , 2021, 13, 657.	1.5	6
14185	Microbial bioindicators of Stony Coral Tissue Loss Disease identified in corals and overlying waters using a rapid field-based sequencing approach. <i>Environmental Microbiology</i> , 2022, 24, 1166-1182.	1.8	34
14186	Evolution of a Cytoplasmic Determinant: Evidence for the Biochemical Basis of Functional Evolution of the Novel Germ Line Regulator Oskar. <i>Molecular Biology and Evolution</i> , 2021, 38, 5491-5513.	3.5	5
14187	Parallel pathways for recruiting effector proteins determine centromere drive and suppression. <i>Cell</i> , 2021, 184, 4904-4918.e11.	13.5	40
14188	Revegetation in Japan overlooks geographical genetic structure of native <i>Artemisia indica</i> var. <i>maximowiczii</i> populations. <i>Restoration Ecology</i> , 2022, 30, e13567.	1.4	6
14189	Horizontal gene transfer-mediated bacterial strain variation affects host fitness in <i>Drosophila</i> . <i>BMC Biology</i> , 2021, 19, 187.	1.7	4
14190	Characterization and Transformation of reg Cluster Genes in <i>Volvox powersii</i> Enable Investigation of Convergent Evolution of Cellular Differentiation in <i>Volvox</i> . <i>Protist</i> , 2021, 172, 125834.	0.6	1
14191	Beneficial Cyanosphere Heterotrophs Accelerate Establishment of Cyanobacterial Biocrust. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0123621.	1.4	15
14192	<i>Yuxiensis granularis</i> gen. et sp. nov., a Novel Quercus-Bearing Fungal Taxon Added to Scortechiniaceae and Inclusion of Parasymphodiellaceae in Coronophorales Based on Phylogenetic Evidence. <i>Life</i> , 2021, 11, 1011.	1.1	1
14193	Diversity and Systematics of Limbless Skinks (<i>Anomalopus</i>) from Eastern Australia and the Skeletal Changes that Accompany the Substrate Swimming Body Form. <i>Journal of Herpetology</i> , 2021, 55, .	0.2	2
14194	Feeding the Microbes: A Strategy to Control Verticillium Wilt. <i>Agronomy</i> , 2021, 11, 1946.	1.3	3
14196	Rare and widespread: integrating Bayesian MCMC approaches, Sanger sequencing and Hyb-Seq phylogenomics to reconstruct the origin of the enigmatic Rand Flora genus <i>Camptoloma</i> . <i>American Journal of Botany</i> , 2021, 108, 1673-1691.	0.8	6
14197	<i>Aspergillus fumigatus</i> versus Genus <i>Aspergillus</i> : Conservation, Adaptive Evolution and Specific Virulence Genes. <i>Microorganisms</i> , 2021, 9, 2014.	1.6	4

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14198	A new species of cryptic cyanobacteria isolated from the epidermis of a bottlenose dolphin and as a bioaerosol. <i>Phycologia</i> , 2021, 60, 603-618.	0.6	2
14199	The complete chloroplast genome of <i>Prinsepia uniflora</i> (Rosaceae), a medicinal plant found in northwest China. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 3057-3058.	0.2	0
14200	Complete chloroplast genome sequence of <i>Solanum erianthum</i> : genome structure and genomic resources. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 3070-3072.	0.2	0
14201	Thermal stress induces tissue damage and a broad shift in regenerative signaling pathways in the honey bee digestive tract. <i>Journal of Experimental Biology</i> , 2021, 224, .	0.8	12
14202	Phylogeography of the East Asian grassland plant, <i>Viola orientalis</i> (Violaceae), inferred from plastid and nuclear restriction site-associated DNA sequencing data. <i>Journal of Plant Research</i> , 2021, 134, 1181-1198.	1.2	7
14203	Characterization of the complete chloroplast genome of the Taiwan alder <i>Alnus formosana</i> (Betulaceae) based on next-generation sequencing technology. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2841-2842.	0.2	0
14204	The complete chloroplast genome of <i>Narcissus</i> "Pink Charm"™. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 3089-3090.	0.2	0
14205	Molecular epidemiologic characteristics of hemagglutinin from five waves of avian influenza A (H7N9) virus infection, from 2013 to 2017, in Zhejiang Province, China. <i>Archives of Virology</i> , 2021, 166, 3323-3332.	0.9	0
14206	Multi-locus phylogeny with dense Guiana Shield sampling supports new suprageneric classification of the neotropical three-barbeled catfishes (Siluriformes: Heptapteridae). <i>Molecular Phylogenetics and Evolution</i> , 2021, 162, 107186.	1.2	8
14207	Phylogeny of Micronesian emperor fishes and evolution of trophic types. <i>Molecular Phylogenetics and Evolution</i> , 2021, 162, 107207.	1.2	1
14208	Plastomes from tribe Plantagineae (Plantaginaceae) reveal infrageneric structural synapomorphies and localized hypermutation for <i>Plantago</i> and functional loss of <i>ndh</i> genes from <i>Littorella</i> . <i>Molecular Phylogenetics and Evolution</i> , 2021, 162, 107217.	1.2	23
14209	Identification and functional characterization of sex pheromone receptors in mirid bugs (Heteroptera: Miridae). <i>Insect Biochemistry and Molecular Biology</i> , 2021, 136, 103621.	1.2	6
14210	The genome of the minute marine rotifer <i>Proales similis</i> : Genome-wide identification of 401 G protein-coupled receptor (GPCR) genes. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2021, 39, 100861.	0.4	6
14211	Phylogenetics and historical biogeography of <i>Solanum</i> section <i>Brevantherum</i> (Solanaceae). <i>Molecular Phylogenetics and Evolution</i> , 2021, 162, 107195.	1.2	5
14212	Whole-genome analysis uncovers loss of <i>bla_Z</i> associated with carriage isolates belonging to methicillin-resistant <i>Staphylococcus aureus</i> (MRSA) clone ST5-VI in Cape Verde. <i>Journal of Global Antimicrobial Resistance</i> , 2021, 26, 77-83.	0.9	2
14213	Arms race in a cell: genomic, transcriptomic, and proteomic insights into intracellular phage-bacteria interplay in deep-sea snail holobionts. <i>Microbiome</i> , 2021, 9, 182.	4.9	7
14214	Genomic and Phenotypic Analysis of Heat and Sanitizer Resistance in <i>Escherichia coli</i> from Beef in Relation to the Locus of Heat Resistance. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0157421.	1.4	8
14215	Genome-wide analysis provides a deeper understanding of the population structure of the <i>Salmonella enterica</i> serotype Paratyphi B complex in Bangladesh. <i>Microbial Genomics</i> , 2021, 7, .	1.0	2

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14216	Genetic Diversity of the <i>Fusarium oxysporum</i> Complex Isolated from the Grassland Biome of South Africa. <i>Phytopathology</i> , 2021, 111, 1459-1469.	1.1	2
14217	The wastewater protist <i>Rhogostoma minus</i> (Thecofilosea, Rhizaria) is abundant, widespread, and hosts Legionellales. <i>Water Research</i> , 2021, 203, 117566.	5.3	11
14218	<i>Desulfovibrio</i> feeding <i>Methanobacterium</i> with electrons in conductive methanogenic aggregates from coastal zones. <i>Water Research</i> , 2021, 202, 117490.	5.3	70
14219	Phylogeny and structural peculiarities of the EB proteins of diatoms. <i>Journal of Structural Biology</i> , 2021, 213, 107775.	1.3	1
14220	Dissemination of <i>Mycobacterium abscessus</i> via global transmission networks. <i>Nature Microbiology</i> , 2021, 6, 1279-1288.	5.9	47
14221	A reanalysis of the data in Sharkey et al.'s (2021) minimalist revision reveals that BINs do not deserve names, but BOLD Systems needs a stronger commitment to open science. <i>Cladistics</i> , 2022, 38, 264-275.	1.5	64
14222	Molecular systematics and taxonomic overview of the bird's nest fungi (Nidulariaceae). <i>Fungal Biology</i> , 2021, 125, 693-703.	1.1	10
14223	Conserved ancestral tropical niche but different continental histories explain the latitudinal diversity gradient in brush-footed butterflies. <i>Nature Communications</i> , 2021, 12, 5717.	5.8	33
14224	Diversification of <i>Cynoglossinae</i> genera (Cynoglosseae-Boraginaceae) in the western Irano-Turanian bioregion. <i>Botany</i> , 2021, 99, 541-553.	0.5	3
14225	<i>Cortinarius subsalor</i> and <i>C. tibeticisalor</i> spp. nov., two new species from the section <i>Delibuti</i> from China. <i>PeerJ</i> , 2021, 9, e11982.	0.9	3
14226	Whole Genome Sequence of <i>Alternaria alternata</i> , the Causal Agent of Black Spot of Kiwifruit. <i>Frontiers in Microbiology</i> , 2021, 12, 713462.	1.5	7
14227	Taxonomy and Phylogeny of the Dileptid Ciliate Genus <i>Paradileptus</i> (Protista: Ciliophora), With a Brief Review and Redescriptions of Two Species Isolated From a Wetland in Northern China. <i>Frontiers in Microbiology</i> , 2021, 12, 709566.	1.5	4
14228	Replacement of owl monkey centromere satellite by a newly evolved variant was a recent and rapid process. <i>Genes To Cells</i> , 2021, 26, 979-986.	0.5	2
14229	The diversity and community structure of symbiotic cyanobacteria in hornworts inferred from long-read amplicon sequencing. <i>American Journal of Botany</i> , 2021, 108, 1731-1744.	0.8	26
14230	Genetic and Ecogeographic Controls on Species Cohesion in Australia's Most Diverse Lizard Radiation. <i>American Naturalist</i> , 2022, 199, E57-E75.	1.0	6
14231	A molecular approach to the phylogeny of the moss genus <i>Pseudocrossidium</i> (Pottiaceae, Tj ETQq1 1 0.784314 rgBT 4/Overloc	1.6	4
14233	The genomic history of the Middle East. <i>Cell</i> , 2021, 184, 4612-4625.e14.	13.5	25
14234	MODB: a comprehensive mitochondrial genome database for Mollusca. <i>Database: the Journal of Biological Databases and Curation</i> , 2021, 2021, .	1.4	1

#	ARTICLE	IF	CITATIONS
14235	Habrosia (Caryophyllaceae) a monotypic genus endemic to Western Asia. Acta Botanica Croatica, 2021, 80, .	0.3	1
14237	Stropharia populicola (Strophariaceae, Agaricales), a new species from China. Phytotaxa, 2021, 518, 251-260.	0.1	0
14238	StAR-Related Lipid Transfer (START) Domains Across the Rice Pangenome Reveal How Ontogeny Recapitulated Selection Pressures During Rice Domestication. Frontiers in Genetics, 2021, 12, 737194.	1.1	2
14239	Two new species of Dugesia (Platyhelminthes, Tricladida, Dugesiidae) from the tropical monsoon forest in southern China. ZooKeys, 2021, 1059, 89-116.	0.5	5
14240	Phylogeny of African Long-Fingered Frogs (Arthroleptidae: Cardioglossa) Reveals Recent Allopatric Divergences in Coloration. Ichthyology and Herpetology, 2021, 109, .	0.3	1
14241	Disentangling the complex alpha taxonomy of Andean populations of <i>Ctenomys</i> (Rodentia: Tj ETQq1 1 0.784314 rgBT /Overl... Journal of Mammalogy, 2021, 102, 1405-1425.	0.6	8
14243	<i>Verrucomicrobiota</i> are specialist consumers of sulfated methyl pentoses during diatom blooms. ISME Journal, 2022, 16, 630-641.	4.4	62
14244	Widespread retention of ohnologs in key developmental gene families following whole-genome duplication in arachnospulmonates. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	21
14245	Discovery of Novel Viruses Associated With the Invasive Cane Toad (<i>Rhinella marina</i>) in Its Native and Introduced Ranges. Frontiers in Microbiology, 2021, 12, 733631.	1.5	7
14246	Comparative Genomic Analysis Provides Insights into the Evolution and Genetic Diversity of Community-Genotype Sequence Type 72 <i>Staphylococcus aureus</i> Isolates. MSystems, 2021, 6, e0098621.	1.7	10
14247	Evolution of Anisogamy in Organisms with Parthenogenetic Gametes. American Naturalist, 2021, 198, 360-378.	1.0	7
14248	Development and evaluation of a custom bait design based on 469 single-copy protein-coding genes for exon capture of isopods (Philosciidae: Haloniscus). PLoS ONE, 2021, 16, e0256861.	1.1	2
14249	Five new species of the land snail genus Landouria Godwin-Austen, 1918 (Gastropoda, Camaenidae) from northeastern Thailand, with note on genitalia and radula morphology of Landouria diplogamma (Möllendorff, 1902). European Journal of Taxonomy, 0, 767, .	0.6	3
14251	Inter-glacial isolation caused divergence of cold-adapted species: the case of the snow partridge. Environmental Epigenetics, 2022, 68, 489-498.	0.9	4
14252	Comparative Chloroplast Genomics and Phylogenetic Analysis of Zygophyllum (Zygophyllaceae) of China. Frontiers in Plant Science, 2021, 12, 723622.	1.7	12
14253	Cohnella cholangitidis sp. nov., a novel species of the genus Cohnella isolated from a clinical specimen in Korea. Archives of Microbiology, 2021, 203, 6053-6060.	1.0	2
14254	Ancient and modern genomes unravel the evolutionary history of the rhinoceros family. Cell, 2021, 184, 4874-4885.e16.	13.5	49
14255	High molecular diversity and divergent subpopulations of the begomovirus cnidoscolus mosaic leaf deformation virus associated with Cnidoscolus urens. Archives of Virology, 2021, 166, 3289-3299.	0.9	0

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14256	Modeling Ocean Color Niche Selection by <i>Synechococcus</i> Blue-Green Acclimators. Journal of Geophysical Research: Oceans, 2021, 126, e2021JC017434.	1.0	1
14257	Incursions of divergent genotypes, evolution of virulence and host jumps shape a continental clonal population of the stripe rust pathogen <i>Puccinia striiformis</i> . Molecular Ecology, 2021, 30, 6566-6584.	2.0	19
14259	Defensive nymphs and water repellency in previously unknown galls of the social aphid <i>Colophina monstifera</i> (Hemiptera: Acanthosomatidae: Eriosomatinae). Entomological Science, 2021, 24, 391-398.	0.3	3
14260	The first case of <i>Planococcus glaciei</i> found in blood, a report from the Czech Republic. Folia Microbiologica, 2022, 67, 121-127.	1.1	2
14261	Listeriosis associated with pre-prepared sandwich consumption in hospital in England, 2017.. Epidemiology and Infection, 2021, 149, 1-31.	1.0	3
14262	Multiple introductions of multidrug-resistant typhoid associated with acute infection and asymptomatic carriage, Kenya. ELife, 2021, 10, .	2.8	29
14263	Oligotyping and metagenomics reveal distinct <i>Candidatus Accumulibacter</i> communities in side-stream versus conventional full-scale enhanced biological phosphorus removal (EBPR) systems. Water Research, 2021, 206, 117725.	5.3	23
14264	<i>Melanogaster coccolobae</i> sp. nov. (Paxillaceae, Boletales), a tropical hypogeous fungus from the urban areas of Quintana Roo, Mexico. Acta Botanica Mexicana, 2021, , e1896.	0.1	2
14265	<i>Aggregata polibraxiona</i> n. sp. (Apicomplexa: Aggregatidae) from <i>Octopus bimaculatus</i> Verrill, 1883 (Mollusca: Cephalopoda) from the Gulf of California, Mexico. European Journal of Protistology, 2021, 81, 125825.	0.5	5
14266	Molecular characterisation of a new tenuivirus from <i>Festuca</i> sp.. Virus Research, 2021, 304, 198509.	1.1	3
14267	Species composition and conservation status of shark from fishery landings and fish markets in Sri Lanka revealed by DNA barcoding. Fisheries Research, 2021, 242, 106045.	0.9	4
14268	Genomic and biochemical characterization of antifungal compounds produced by <i>Bacillus subtilis</i> PMB102 against <i>Alternaria brassicicola</i> . Microbiological Research, 2021, 251, 126815.	2.5	18
14269	Foodborne illness caused by muscarine-containing mushrooms and identification of mushroom remnants using phylogenetics and LC-MS/MS. Food Control, 2021, 128, 108182.	2.8	12
14270	Complex evolutionary history of felid anelloviruses. Virology, 2021, 562, 176-189.	1.1	13
14271	A taxonomist's nightmare – Cryptic diversity in Caribbean intertidal arthropods (Arachnida, Acari.) Tj ETQq0 0 0 rgBT /Overlock 10 T	1.2	19
14272	Essential oil of Noni, <i>Morinda citrifolia</i> L., fruits controls the rice stem-rot disease without detrimentally affect beneficial fungi and ladybeetles. Industrial Crops and Products, 2021, 170, 113728.	2.5	8
14273	The grass root endophytic fungus <i>Flavomyces fulophazii</i> : An abundant source of tetramic acid and chlorinated azaphilone derivatives. Phytochemistry, 2021, 190, 112851.	1.4	5
14274	SARS-CoV-2 Delta Variant among Asiatic Lions, India. Emerging Infectious Diseases, 2021, 27, 2723-2725.	2.0	66

#	ARTICLE	IF	CITATIONS
14275	Arundinella tengchongensis (Poaceae), a name at new rank and newly combined based on morphological and molecular data. Nordic Journal of Botany, 2021, 39, .	0.2	0
14276	Phylogeographic analysis of Saxifraga fortunei complex (Saxifragaceae) reveals multiple origins of morphological and ecological variations in the Japanese Archipelago. Molecular Phylogenetics and Evolution, 2021, 163, 107230.	1.2	5
14277	Plastid phylogenomic analyses of Fagales reveal signatures of conflict and ancient chloroplast capture. Molecular Phylogenetics and Evolution, 2021, 163, 107232.	1.2	37
14278	Arbidol targeting influenza virus A Hemagglutinin; A comparative study. Biophysical Chemistry, 2021, 277, 106663.	1.5	9
14279	Metagenomic insights into the effect of thermal hydrolysis pre-treatment on microbial community of an anaerobic digestion system. Science of the Total Environment, 2021, 791, 148096.	3.9	31
14280	Thecamoeba astrologa n. sp. " A new species of the genus Thecamoeba (Amoebozoa, Discosea,) Tj ETQq1 1 0.784314 rgBT /Overlock 2021, 81, 125837.	0.5	2
14281	Discordance in a South African <i>Memecylon</i> Clade (Melastomataceae): Evidence for Reticulate Evolution. International Journal of Plant Sciences, 2021, 182, 682-694.	0.6	5
14282	Comparative fruit morphology and its systematic significance in <i>Ferula</i> (Apiaceae) species from different growth habitats. Flora: Morphology, Distribution, Functional Ecology of Plants, 2021, 283, 151899.	0.6	1
14283	Genome-Wide Identification and Low-Temperature Expression Analysis of bHLH Genes in <i>Prunus mume</i> . Frontiers in Genetics, 2021, 12, 762135.	1.1	15
14284	The genome of the zoonotic malaria parasite <i>Plasmodium simium</i> reveals adaptations to host switching. BMC Biology, 2021, 19, 219.	1.7	21
14285	Acceleration of polychlorinated biphenyls remediation in soil via sewage sludge amendment. Journal of Hazardous Materials, 2021, 420, 126630.	6.5	32
14286	Global patterns in culturable soil yeast diversity. IScience, 2021, 24, 103098.	1.9	8
14287	Shifts from <i>cis</i> -to <i>trans</i> -splicing of five mitochondrial introns in <i>Tolypanthus maclurei</i> . PeerJ, 2021, 9, e12260.	0.9	11
14288	Snails riding mantis shrimps: Ectoparasites evolved from ancestors living as commensals on the host's burrow wall. Molecular Phylogenetics and Evolution, 2021, 163, 107122.	1.2	4
14289	Biogeography of the monocotyledon astelioid clade (Asparagales): A history of long-distance dispersal and diversification with emerging habitats. Molecular Phylogenetics and Evolution, 2021, 163, 107203.	1.2	2
14290	In and out: Evolution of viral sequences in the mitochondrial genomes of legumes (Fabaceae). Molecular Phylogenetics and Evolution, 2021, 163, 107236.	1.2	9
14291	The complete mitochondrial genome of <i>Choroterpes</i> (<i>Euthralus</i>) <i>yixingensis</i> (Ephemeroptera:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 107 Gene, 2021, 800, 145833.	1.0	7
14292	Genomic analysis of the carboxylesterase family in the salmon louse (<i>Lepeophtheirus salmonis</i>). Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology, 2021, 248, 109095.	1.3	1

#	ARTICLE	IF	CITATIONS
14293	Genotyping-By-Sequencing diversity analysis of international Vanilla collections uncovers hidden diversity and enables plant improvement. <i>Plant Science</i> , 2021, 311, 111019.	1.7	17
14294	When good mitochondria go bad: Cyto-nuclear discordance in landfowl (Aves: Galliformes). <i>Gene</i> , 2021, 801, 145841.	1.0	17
14295	Gene flow in phylogenomics: Sequence capture resolves species limits and biogeography of Afromontane forest endemic frogs from the Cameroon Highlands. <i>Molecular Phylogenetics and Evolution</i> , 2021, 163, 107258.	1.2	8
14296	Macroevolutionary analyses of ciliates associated with hosts support high diversification rates. <i>International Journal for Parasitology</i> , 2021, 51, 967-976.	1.3	1
14297	The widespread IS200/IS605 transposon family encodes diverse programmable RNA-guided endonucleases. <i>Science</i> , 2021, 374, 57-65.	6.0	152
14298	Reduced sialidase activity of influenza A(H3N2) neuraminidase associated with positively charged amino acid substitutions. <i>Journal of General Virology</i> , 2021, 102, .	1.3	4
14299	Photoautotrophic poly(3-hydroxybutyrate) production by a wild-type <i>Synechococcus elongatus</i> isolated from an extreme environment. <i>Bioresource Technology</i> , 2021, 337, 125508.	4.8	9
14300	Morphology and molecular phylogeny of the anaerobic freshwater ciliate <i>Urostomides spinosus</i> nov. spec. (Ciliophora, Armophorea, Metopida) from China. <i>European Journal of Protistology</i> , 2021, 81, 125823.	0.5	13
14301	Introgression is widespread in the radiation of carnivorous <i>Nepenthes</i> pitcher plants. <i>Molecular Phylogenetics and Evolution</i> , 2021, 163, 107214.	1.2	8
14302	UCE Phylogenomics, detection of a putative hybrid population, and one older mitogenomic node age of <i>Batrachuperus</i> salamanders. <i>Molecular Phylogenetics and Evolution</i> , 2021, 163, 107239.	1.2	0
14303	Description of four <i>Millepora</i> spp. transcriptomes and their potential to delimit the Caribbean fire coral species. <i>Marine Genomics</i> , 2021, 59, 100863.	0.4	0
14304	Genomic-based surveillance reveals high ongoing transmission of multi-drug-resistant <i>Mycobacterium tuberculosis</i> in Southern Brazil. <i>International Journal of Antimicrobial Agents</i> , 2021, 58, 106401.	1.1	12
14305	A phylogeny of white-eyes based on ultraconserved elements. <i>Molecular Phylogenetics and Evolution</i> , 2021, 164, 107273.	1.2	5
14306	Molecular phylogenetic analysis of the problematic genus <i>Cardicola</i> (Digenea: Aporocotylidae) indicates massive polyphyly, dramatic morphological radiation and host-switching. <i>Molecular Phylogenetics and Evolution</i> , 2021, 164, 107290.	1.2	7
14307	Genomic phylogeography of the White-crowned Manakin <i>Pseudopipra pipra</i> (Aves: Pipridae) illuminates a continental-scale radiation out of the Andes. <i>Molecular Phylogenetics and Evolution</i> , 2021, 164, 107205.	1.2	12
14308	Reconstruction of the evolutionary biogeography reveal the origins and diversification of oysters (<i>Bivalvia</i> : <i>Ostreidae</i>). <i>Molecular Phylogenetics and Evolution</i> , 2021, 164, 107268.	1.2	15
14309	<i>Borrelia duttonii</i> -like spirochetes parasitize <i>Meriones persicus</i> in East Azerbaijan Province of Iran. <i>Ticks and Tick-borne Diseases</i> , 2021, 12, 101825.	1.1	1
14310	Phylogenomics and molecular signatures support division of the order Neisseriales into emended families Neisseriaceae and Chromobacteriaceae and three new families Aquaspirillaceae fam. nov., Chitinibacteraceae fam. nov., and Leeiaceae fam. nov.. <i>Systematic and Applied Microbiology</i> , 2021, 44, 126251.	1.2	46

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14311	The evolutionary history of vines in a neotropical biodiversity hotspot: Phylogenomics and biogeography of a large passion flower clade (<i>Passiflora</i> section <i>Decaloba</i>). <i>Molecular Phylogenetics and Evolution</i> , 2021, 164, 107260.	1.2	8
14312	The draft genome of the Asian corn borer yields insights into ecological adaptation of a devastating maize pest. <i>Insect Biochemistry and Molecular Biology</i> , 2021, 138, 103638.	1.2	8
14313	Adaptive selection signatures in river buffalo with emphasis on immune and major histocompatibility complex genes. <i>Genomics</i> , 2021, 113, 3599-3609.	1.3	5
14314	Genome-wide analysis reveals widespread roles for RcREM genes in floral organ development in <i>Rosa chinensis</i> . <i>Genomics</i> , 2021, 113, 3881-3894.	1.3	7
14315	The <i>Clausena lansium</i> (Wampee) genome reveal new insights into the carbazole alkaloids biosynthesis pathway. <i>Genomics</i> , 2021, 113, 3696-3704.	1.3	11
14316	Biogeography, reproductive biology and phylogenetic divergence within the <i>Fungiidae</i> (mushroom) <i>Tj ETQq1 1 0.784314 rgBJ /Overlo</i>	1.2	7
14317	An updated phylogenetic and biogeographic analysis based on genome skimming data reveals convergent evolution of shrubby habit in <i>Clematis</i> in the Pliocene and Pleistocene. <i>Molecular Phylogenetics and Evolution</i> , 2021, 164, 107259.	1.2	5
14318	Plastid phylogenomics improves resolution of phylogenetic relationship in the <i>Cheirostylis</i> and <i>Goodyera</i> clades of <i>Goodyerinae</i> (<i>Orchidoideae</i> , <i>Orchidaceae</i>). <i>Molecular Phylogenetics and Evolution</i> , 2021, 164, 107269.	1.2	14
14319	Dated phylogeny and ancestral range estimation of sand scorpions (<i>Buthidae</i> : <i>Buthacus</i>) reveal Early Miocene divergence across land bridges connecting Africa and Asia. <i>Molecular Phylogenetics and Evolution</i> , 2021, 164, 107212.	1.2	5
14320	Speciation along the elevation gradient: Divergence of <i>Roscoea</i> species within the south slope of the Himalayas. <i>Molecular Phylogenetics and Evolution</i> , 2021, 164, 107292.	1.2	10
14321	Isolation, characterization, and comparative genomic analysis of vB_PlaP_SV21, new bacteriophage of <i>Paenibacillus</i> larvae. <i>Virus Research</i> , 2021, 305, 198571.	1.1	5
14322	Phylogenetic analysis and population structure of <i>Pseudomonas alloputida</i> . <i>Genomics</i> , 2021, 113, 3762-3773.	1.3	12
14323	Sequential colonization of oceanic archipelagos led to a species-level radiation in the common chaffinch complex (<i>Aves</i> : <i>Fringilla</i> <i>coelebs</i>). <i>Molecular Phylogenetics and Evolution</i> , 2021, 164, 107291.	1.2	19
14324	Molecular phylogeny of Neotropical Parrot Snakes (<i>Serpentes</i> : <i>Colubrinae</i> : <i>Leptophis</i>) supports underestimated species richness. <i>Molecular Phylogenetics and Evolution</i> , 2021, 164, 107267.	1.2	1
14325	MiDSytem: A comprehensive online system for de novo assembly and analysis of microbial genomes. <i>New Biotechnology</i> , 2021, 65, 42-52.	2.4	2
14326	Nonribosomal peptide synthetases and nonribosomal cyanopeptides synthesis in <i>Microcystis</i> : A comparative genomics study. <i>Algal Research</i> , 2021, 59, 102432.	2.4	3
14327	A wolf spider from South American grasslands: phylogenetic placement and redescription of <i>Paratrochosina amica</i> (Mello-Leitão 1941). <i>Zoologischer Anzeiger</i> , 2021, 295, 1-11.	0.4	4
14328	Emergence and adaptive evolution of influenza D virus. <i>Microbial Pathogenesis</i> , 2021, 160, 105193.	1.3	5

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14329	Metabolism of chiral sulfonate compound 2,3-dihydroxypropane-1-sulfonate (DHPS) by <i>Roseobacter</i> bacteria in marine environment. <i>Environment International</i> , 2021, 157, 106829.	4.8	8
14330	Phylogenomics, divergence time estimation and trait evolution provide a new look into the Gracilariales (Rhodophyta). <i>Molecular Phylogenetics and Evolution</i> , 2021, 165, 107294.	1.2	22
14331	Plant genotype and seasonality drive fine changes in olive root microbiota. <i>Current Plant Biology</i> , 2021, 28, 100219.	2.3	13
14332	<i>Tenebriella</i> gen. nov. “The dark twin of <i>Oscillatoria</i> . <i>Molecular Phylogenetics and Evolution</i> , 2021, 165, 107293.	1.2	11
14333	Rates and patterns of molecular evolution in bryophyte genomes, with focus on complex thalloid liverworts, Marchantiopsida. <i>Molecular Phylogenetics and Evolution</i> , 2021, 165, 107295.	1.2	12
14334	A comprehensive phylogeny of dwarf geckos of the genus <i>Lygodactylus</i> , with insights into their systematics and morphological variation. <i>Molecular Phylogenetics and Evolution</i> , 2021, 165, 107311.	1.2	5
14335	Furin cleavage sites in the spike proteins of bat and rodent coronaviruses: Implications for virus evolution and zoonotic transfer from rodent species. <i>One Health</i> , 2021, 13, 100282.	1.5	19
14336	The evolution and biogeographic history of epiphytic thalloid liverworts. <i>Molecular Phylogenetics and Evolution</i> , 2021, 165, 107298.	1.2	4
14337	Sympatric and independently evolving lineages in the <i>Thoropa miliaris</i> “ <i>T. taophora</i> species complex (Anura: Cycloramphidae). <i>Molecular Phylogenetics and Evolution</i> , 2022, 166, 107220.	1.2	1
14338	Integrated molecular and affiliation network analysis: Core-periphery social clustering is associated with HIV transmission patterns. <i>Social Networks</i> , 2022, 68, 107-117.	1.3	2
14339	Exploiting multi-level parallel metaheuristics and heterogeneous computing to boost phylogenetics. <i>Future Generation Computer Systems</i> , 2022, 127, 208-224.	4.9	2
14340	Ultraconserved elements-based systematics reveals evolutionary patterns of host-plant family shifts and phytophagy within the predominantly parasitoid braconid wasp subfamily Doryctinae. <i>Molecular Phylogenetics and Evolution</i> , 2022, 166, 107319.	1.2	5
14341	Exon-capture data and locus screening provide new insights into the phylogeny of flatfishes (Pleuronectoidei). <i>Molecular Phylogenetics and Evolution</i> , 2022, 166, 107315.	1.2	5
14342	Phylogenomics, floral evolution, and biogeography of <i>Lithospermum</i> L. (Boraginaceae). <i>Molecular Phylogenetics and Evolution</i> , 2022, 166, 107317.	1.2	2
14343	Evolutionary history of CAM photosynthesis in Neotropical <i>Clusia</i> : insights from genomics, anatomy, physiology and climate. <i>Botanical Journal of the Linnean Society</i> , 2022, 199, 538-556.	0.8	16
14344	Genome-scale phylogenies reveal relationships among <i>Parastagonospora</i> species infecting domesticated and wild grasses. <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2021, .	1.6	3
14345	First records and three new species of the family Symphytognathidae (Arachnida, Araneae) from Thailand, and the circumscription of the genus <i>Crassinatha</i> Wunderlich, 1995. <i>ZooKeys</i> , 2021, 1012, 21-53.	0.5	4
14346	Characterization of the chloroplast genome and its inference on the phylogenetic position of <i>Incarvillea sinensis</i> Lam. (Bignoniaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 263-264.	0.2	2

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14347	Complete chloroplast genome of <i>Engelhardtia fenzlii</i> (Juglandaceae). Mitochondrial DNA Part B: Resources, 2021, 6, 288-289.	0.2	2
14348	The complete chloroplast genome sequence of <i>Lotus corniculatus</i> L.. Mitochondrial DNA Part B: Resources, 2021, 6, 189-190.	0.2	1
14350	The complete chloroplast genome of <i>Scutellaria scordifolia</i> (Labiatae). Mitochondrial DNA Part B: Resources, 2021, 6, 84-85.	0.2	1
14356	Phylogeography and systematics of <i>Algyroides</i> (Sauria: Lacertidae) of the Balkan Peninsula. <i>Zoologica Scripta</i> , 2021, 50, 282-299.	0.7	4
14357	The Draft Genome Sequence of a New Land-Hopper <i>Platorchestia hallaensis</i> . <i>Frontiers in Genetics</i> , 2020, 11, 621301.	1.1	1
14358	Elevated diversity in loci linked to facial morphology is consistent with the hypothesis that individual facial recognition is important across hominoids. <i>American Journal of Physical Anthropology</i> , 2021, 174, 785-791.	2.1	0
14359	Color morphs of the coral, <i>Acropora tenuis</i> , show different responses to environmental stress and different expression profiles of fluorescent-protein genes. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	11
14360	Phylogenomics reveals the basis of adaptation of <i>Pseudorhizobium</i> species to extreme environments and supports a taxonomic revision of the genus. <i>Systematic and Applied Microbiology</i> , 2021, 44, 126165.	1.2	33
14361	<i>Pseudomonas allii</i> sp. nov., a pathogen causing soft rot of onion in Japan. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	22
14362	Differential disease severity and whole-genome sequence analysis for human influenza A/H1N1pdm virus in 2015–2016 influenza season. <i>Virus Evolution</i> , 2021, 7, veab044.	2.2	7
14363	Phylogenetic Relationships Within <i>Chrysogorgia</i> (Alcyonacea: Octocorallia), a Morphologically Diverse Genus of Octocoral, Revealed Using a Target Enrichment Approach. <i>Frontiers in Marine Science</i> , 2021, 7, .	1.2	15
14364	Mitochondrial genome of <i>Bulinus truncatus</i> (Gastropoda: Lymnaeoidea): Implications for snail systematics and schistosome epidemiology. <i>Current Research in Parasitology and Vector-borne Diseases</i> , 2021, 1, 100017.	0.7	6
14365	Phylogenetics of <i>Leptocereus</i> (Cactaceae) on Hispaniola: clarifying species limits in the <i>L. weingartianus</i> complex and a new species from the Sierra de Bahoruco. <i>PhytoKeys</i> , 2021, 172, 17-37.	0.4	13
14366	Extensive hybridization between two Andean warbler species with shallow divergence in mtDNA. <i>Auk</i> , 2021, 138, .	0.7	8
14367	Felsenstein Phylogenetic Likelihood. <i>Journal of Molecular Evolution</i> , 2021, 89, 134-145.	0.8	9
14368	<i>Crittendenia</i> gen. nov., a new lichenicolous lineage in the Agaricostilbomyces (Pucciniomycotina), and a review of the biology, phylogeny and classification of lichenicolous heterobasidiomycetes. <i>Lichenologist</i> , 2021, 53, 103-116.	0.5	10
14369	<i>Amyntas corticis</i> genome reveals molecular mechanisms behind global distribution. <i>Communications Biology</i> , 2021, 4, 135.	2.0	6
14370	Plotting for change: an analytical framework to aid decisions on which lineages are candidate species in phylogenomic species discovery. <i>Biological Journal of the Linnean Society</i> , 2022, 135, 117-137.	0.7	11

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14371	A molecular perspective on the systematics of the spider crab genus <i>Libinia</i> Leach, 1815 (Majoidea:Epialtidae). <i>Invertebrate Systematics</i> , 2021, , .	0.5	1
14372	The history of foot-and-mouth disease virus serotype C: the first known extinct serotype?. <i>Virus Evolution</i> , 2021, 7, .	2.2	35
14374	Matrilineal evidence for genetic structure and Late Pleistocene demographic expansion of the Ornate goby <i>Istigobius ornatus</i> (Teleostei: Gobiidae) in the Persian Gulf and Oman Sea. <i>Marine Ecology</i> , 2021, 42, .	0.4	3
14375	A target enrichment probe set for resolving the flagellate land plant tree of life. <i>Applications in Plant Sciences</i> , 2021, 9, e11406.	0.8	42
14376	Signatures of Post-Glacial Genetic Isolation and Human-Driven Migration in the <i>Dothistroma</i> Needle Blight Pathogen in Western Canada. <i>Phytopathology</i> , 2021, 111, 116-127.	1.1	15
14377	Forecasting System of Computational Time of DFT/TDDFT Calculations under the Multiverse Ansatz via Machine Learning and Cheminformatics. <i>ACS Omega</i> , 2021, 6, 2001-2024.	1.6	6
14378	Uncovering the hidden taxonomic diversity of fungi in Oman. <i>Fungal Diversity</i> , 2021, 106, 229-268.	4.7	11
14379	Adaptive divergence in the neglected alpine moss <i>Lewinskya killiasii</i> (Orthotrichaceae), an example of vicariance on different rock types in bryophytes. <i>Botanical Journal of the Linnean Society</i> , 2022, 198, 456-481.	0.8	3
14380	Application of 5S Ribosomal DNA for Molecular Taxonomy of Subtribe Loliinae (Poaceae). <i>Cytology and Genetics</i> , 2021, 55, 10-18.	0.2	11
14381	Platypus and echidna genomes reveal mammalian biology and evolution. <i>Nature</i> , 2021, 592, 756-762.	13.7	85
14382	Reproductive phasiRNA loci and DICER-LIKE5, but not microRNA loci, diversified in monocotyledonous plants. <i>Plant Physiology</i> , 2021, 185, 1764-1782.	2.3	17
14383	Systematics and the Unexpected High Mitochondrial Genetic Divergence of <i>Nelsonia goldmani</i> (Rodentia: Cricetidae) from Mexican Highlands. <i>Journal of Mammalian Evolution</i> , 2021, 28, 939-951.	1.0	6
14384	The intestinal microbiota and metabolites in patients with anorexia nervosa. <i>Gut Microbes</i> , 2021, 13, 1-25.	4.3	58
14385	Recreated Ancestral Opsin Associated with Marine to Freshwater Croaker Invasion Reveals Kinetic and Spectral Adaptation. <i>Molecular Biology and Evolution</i> , 2021, 38, 2076-2087.	3.5	15
14386	Dinoflagellates alter their carbon and nutrient metabolic strategies across environmental gradients in the central Pacific Ocean. <i>Nature Microbiology</i> , 2021, 6, 173-186.	5.9	45
14387	A new Late Cretaceous leaf mine <i>Leucopteroptera spirala</i> gen. et sp. nov. (Lepidoptera: Tj ETQq1 1 0.784314 rgBT /Overlock 10T Systematic Palaeontology, 2021, 19, 131-144.	0.6	15
14389	The diversity and function of sourdough starter microbiomes. <i>ELife</i> , 2021, 10, .	2.8	77
14390	Analysis of bacterial communities in a municipal duck pond during a phytoplankton bloom and isolation of <i>Anatolimnocola aggregata</i> gen. nov., sp. nov., <i>Lacipirellula limnantheis</i> sp. nov. and <i>Urbifossella limnaea</i> gen. nov., sp. nov. belonging to the phylum <i>Planctomycetes</i> . <i>Environmental Microbiology</i> , 2021, 23, 1379-1396.	1.8	35

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14391	Complete chloroplast genome sequences of <i>Corydalis edulis</i> and <i>Corydalis shensiana</i> (Papaveraceae). Mitochondrial DNA Part B: Resources, 2021, 6, 257-258.	0.2	6
14392	Seeing the true colours: three new species of Obama (Platyhelminthes:Continenticola) from remnants of Atlantic forest in southern Brazil based on an integrative approach. Invertebrate Systematics, 2021, , .	0.5	1
14393	Genetic and morphological analyses uncover a new record and a cryptic species in Allonais (Clitellata: Naididae). Biologia (Poland), 2021, 76, 1705.	0.8	1
14394	Inferring Core Genome Phylogenies for Bacteria. Methods in Molecular Biology, 2021, 2242, 59-68.	0.4	2
14395	Gnotobiotic rainbow trout (<i>Oncorhynchus mykiss</i>) model reveals endogenous bacteria that protect against <i>Flavobacterium columnare</i> infection. PLoS Pathogens, 2021, 17, e1009302.	2.1	34
14396	Laboulbeniomyces, Enigmatic Fungi With a Turbulent Taxonomic History. , 2021, , 263-283.		8
14397	Repeated colonization of caves leads to phenotypic convergence in catfishes (Siluriformes: <i>Trichomycterus</i>) at a small geographical scale. Zoological Journal of the Linnean Society, 2021, 193, 772-788.	1.0	1
14398	Rediscovery of <i>Mazus lanceifolius</i> reveals a new genus and a new species in Mazaceae. PhytoKeys, 2021, 171, 1-24.	0.4	6
14400	An atlas of CNV maps in cattle, goat and sheep. Science China Life Sciences, 2021, 64, 1747-1764.	2.3	27
14401	Three new species of subterranean amphipods (Pseudocrangonyctidae: <i>Pseudocrangonyx</i>) from limestone caves in South Korea. PeerJ, 2021, 9, e10786.	0.9	4
14402	The complete chloroplast genome sequence of <i>Sargentodoxa cuneata</i> : genome structure and genomic resources. Mitochondrial DNA Part B: Resources, 2021, 6, 245-246.	0.2	1
14403	Characterization of the complete plastid genome of <i>Lysimachia christinae</i> Hance (Primulaceae). Mitochondrial DNA Part B: Resources, 2021, 6, 268-270.	0.2	0
14404	Settling the identity and phylogenetic position of the psychrotolerant green algal genus <i>Coleochlamys</i> (Trebouxiophyceae). Phycologia, 2021, 60, 135-147.	0.6	5
14405	Domain Unknown Function DUF1668-Containing Genes in Multiple Lineages Are Responsible for F1 Pollen Sterility in Rice. Frontiers in Plant Science, 2020, 11, 632420.	1.7	6
14406	Increase in HIV-1-transmitted drug resistance among ART-naïve youths at the China-Myanmar border during 2009 ~ 2017. BMC Infectious Diseases, 2021, 21, 93.	1.3	6
14408	Pleistocene climatic fluctuations promoted alternative evolutionary histories in <i>Phytelephas aequatorialis</i> , an endemic palm from western Ecuador. Journal of Biogeography, 2021, 48, 1023-1037.	1.4	8
14409	The starlet sea anemone, <i>Nematostella vectensis</i> , possesses body region-specific bacterial associations with spirochetes dominating the capitulum. FEMS Microbiology Letters, 2021, 368, .	0.7	7
14410	<i>DMSP</i> synthesis genes distinguish two types of <i>DMSP</i> producer phenotypes. Environmental Microbiology, 2021, 23, 1656-1669.	1.8	6

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14411	Two pleosporalean root-colonizing fungi, <i>Fuscosphaeria hungarica</i> gen. et sp. nov. and <i>Delitschia chaetomioides</i> , from a semiarid grassland in Hungary. <i>Mycological Progress</i> , 2021, 20, 39-50.	0.5	3
14412	Genomic Evidence for Sequestration of Influenza A Virus Lineages in Sea Duck Host Species. <i>Viruses</i> , 2021, 13, 172.	1.5	1
14413	Utility of whole-genome sequencing during an investigation of multiple foodborne outbreaks of <i>Shigella sonnei</i> . <i>Epidemiology and Infection</i> , 2021, 149, e71.	1.0	6
14414	Detection of <i>Pratylenchus zeae</i> and <i>P. brachyurus</i> parasitizing plants from the caatinga biome, Ceará, Brazil. <i>Journal of Nematology</i> , 2021, 53, 1-5.	0.4	2
14415	An outbreak of human listeriosis associated with frozen sweet corn consumption: Investigations in the UK. <i>International Journal of Food Microbiology</i> , 2021, 338, 108994.	2.1	19
14416	Differentiation in the eastern Asian <i>Periphyllus koelreuteriae</i> (Hemiptera: Aphididae) species complex driven by climate and host plant. <i>Biological Journal of the Linnean Society</i> , 2021, 132, 509-520.	0.7	2
14417	Four new <i>Micarea</i> species from the montane cloud forests of Taita Hills, Kenya. <i>Lichenologist</i> , 2021, 53, 81-94.	0.5	5
14419	Evolutionary relationships of <i>Metchnikovella dogieli</i> Paskerova et al., 2016 (Microsporidia). <i>Trends in Microbiology</i> , 2021, 29, 525-534.	0.6	6
14420	Pearl Sac Gene Expression Profiles Associated With Pearl Attributes in the Silver-Lip Pearl Oyster, <i>Pinctada maxima</i> . <i>Frontiers in Genetics</i> , 2020, 11, 597459.	1.1	11
14422	Gut lactate-producing bacteria promote CD4 T cell recovery on Anti-retroviral therapy in HIV-infected patients. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 2928-2937.	1.9	3
14423	Genomic diversity of <i>Escherichia coli</i> isolates from backyard chickens and guinea fowl in the Gambia. <i>Microbial Genomics</i> , 2021, 7, .	1.0	13
14424	<i>Thelopsis</i> challenges the generic circumscription in the <i>Gyalectaceae</i> and brings new insights to the taxonomy of <i>Ramonia</i> . <i>Lichenologist</i> , 2021, 53, 45-61.	0.5	3
14425	The complete chloroplast genome of <i>Melicope pteleifolia</i> (Rutaceae), a traditional medicinal plant in Southeast China. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 60-61.	0.2	1
14426	Species diversity and biogeography of an ancient frog clade from the Guiana Shield (Anura): phenotypic diversification. <i>Biological Journal of the Linnean Society</i> , 2021, 132, 233-256.	0.7	23
14427	Heightened resistance to host type 1 interferons characterizes HIV-1 at transmission and after antiretroviral therapy interruption. <i>Science Translational Medicine</i> , 2021, 13, .	5.8	54
14428	Comparative transcriptomics highlights convergent evolution of energy metabolic pathways in group-living spiders. <i>Zoological Research</i> , 2021, 42, 195-206.	0.9	4
14429	Mitochondrial DNA suggests Hybridization in Freshwater Stingrays <i>Potamotrygon</i> (POTAMOTRYGONIDAE: MYLIOBATIFORMES) from the Xingu river, Amazonia and reveals speciation in <i>Paratrygon aireba</i> . <i>Anais Da Academia Brasileira De Ciencias</i> , 2021, 93, .	0.3	3
14430	<i>Cortinarius</i> subgenus <i>Leproclybe</i> , unexpected diversity and significant differences in species compositions between western and eastern North America. <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2021, . .	1.6	6

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14431	Spatial patterns and conservation of genetic and phylogenetic diversity of wildlife in China. <i>Science Advances</i> , 2021, 7, .	4.7	47
14432	Genome Synteny Analysis and Phylogenetic Position of <i>S. indicum</i> . <i>Compendium of Plant Genomes</i> , 2021, , 267-273.	0.3	0
14433	Phylogenetics of the skyhoppers (<i>Kosciuscola</i>) of the Australian Alps: evolutionary and conservation implications. <i>Pacific Conservation Biology</i> , 2021, , .	0.5	3
14434	Taxonomic challenges posed by discordant evolutionary scenarios supported by molecular and morphological data in the Amazonian <i>Synallaxis rutilans</i> group (Aves: Furnariidae). <i>Zoological Journal of the Linnean Society</i> , 2022, 195, 65-87.	1.0	0
14435	The genera <i>Leucoagaricus</i> and <i>Leucocoprinus</i> in the Dominican Republic. <i>Mycologia</i> , 2021, 113, 348-389.	0.8	4
14436	The <i>Cymbidium goeringii</i> genome provides insight into organ development and adaptive evolution in orchids. <i>Ornamental Plant Research</i> , 2021, 1, 1-13.	0.2	7
14438	<i>Clostridium fessum</i> sp. nov., isolated from human faeces. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	10
14439	<i>Glycomyces terrestris</i> sp. nov., isolated from extremely arid soil from Yuanmou Earth Forest. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	4
14440	An integrative taxonomic approach resolves the <i>Prostanthera lasianthos</i> (Lamiaceae) species complex. <i>Australian Systematic Botany</i> , 2021, 34, 438.	0.3	5
14441	Phylogeny of <i>Dorstenia</i> (Moraceae) reveals the polyphyletic nature of its neotropical sections. <i>Rodriguesia</i> , 0, 72, .	0.9	1
14442	<i>Haloechothrix aidingensis</i> sp. nov., an actinomycete isolated from salt lake in Xinjiang province, north-west China. <i>Archives of Microbiology</i> , 2021, 203, 1801-1806.	1.0	7
14443	A roadmap for metagenomic enzyme discovery. <i>Natural Product Reports</i> , 2021, 38, 1994-2023.	5.2	76
14444	Evolutionary diversification in the hyper-diverse montane forests of the tropical Andes: radiation of <i>Macroparpaea</i> (<i>Gentianaceae</i>) and the possible role of range expansion. <i>Botanical Journal of the Linnean Society</i> , 2022, 199, 53-75.	0.8	5
14445	The integrative taxonomy of <i>Beauveria asiatica</i> and <i>B. bassiana</i> species complexes with whole-genome sequencing, morphometric and chemical analyses. <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2021, 47, 136-150.	1.6	7
14446	Sister species diverge in modality-specific courtship signal form and function. <i>Ecology and Evolution</i> , 2021, 11, 852-871.	0.8	7
14447	Evolutionary history drives aspects of stoichiometric niche variation and functional effects within a guild. <i>Ecology</i> , 2020, 101, e03100.	1.5	25
14448	Origin and evolution of a gibberellin-deactivating enzyme GAMT. <i>Plant Direct</i> , 2020, 4, e00287.	0.8	5
14449	PhyloGenes: An online phylogenetics and functional genomics resource for plant gene function inference. <i>Plant Direct</i> , 2020, 4, e00293.	0.8	23

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14450	Phylogenomics of the tropical plant family Ochnaceae using targeted enrichment of nuclear genes and 250+ taxa. <i>Taxon</i> , 2021, 70, 48-71.	0.4	14
14451	Molecular phylogenetics of <i>Phyllanthus</i> sensu lato (Phyllanthaceae): Towards coherent monophyletic taxa. <i>Taxon</i> , 2021, 70, 72-98.	0.4	15
14452	Neurospora from Natural Populations: Population Genomics Insights into the Life History of a Model Microbial Eukaryote. <i>Methods in Molecular Biology</i> , 2020, 2090, 313-336.	0.4	16
14453	Genotyping for Species Identification and Diversity Assessment Using Double-Digest Restriction Site-Associated DNA Sequencing (ddRAD-Seq). <i>Methods in Molecular Biology</i> , 2020, 2107, 159-187.	0.4	8
14454	Sequence Comparison Without Alignment: The SpaM Approaches. <i>Methods in Molecular Biology</i> , 2021, 2231, 121-134.	0.4	10
14455	Computational Methods for Predicting Effectors in Rust Pathogens. <i>Methods in Molecular Biology</i> , 2017, 1659, 73-83.	0.4	19
14456	Hepatitis C Virus Database and Bioinformatics Analysis Tools in the Virus Pathogen Resource (ViPR). <i>Methods in Molecular Biology</i> , 2019, 1911, 47-69.	0.4	4
14457	Multi-SpaM: A Maximum-Likelihood Approach to Phylogeny Reconstruction Using Multiple Spaced-Word Matches and Quartet Trees. <i>Lecture Notes in Computer Science</i> , 2018, , 227-241.	1.0	5
14458	Aerobic Hydrocarbon-Degrading Gammaproteobacteria: Oleiphilaceae and Relatives. , 2019, , 153-166.		1
14459	<i>Nicotiana attenuata</i> Genome Reveals Genes in the Molecular Machinery Behind Remarkable Adaptive Phenotypic Plasticity. <i>Compendium of Plant Genomes</i> , 2020, , 211-229.	0.3	5
14460	Diversification History of Neotropical Lecythidaceae, an Ecologically Dominant Tree Family of Amazon Rain Forest. <i>Fascinating Life Sciences</i> , 2020, , 791-809.	0.5	10
14461	Polynomial-Time Statistical Estimation of Species Trees Under Gene Duplication and Loss. <i>Lecture Notes in Computer Science</i> , 2020, , 120-135.	1.0	6
14462	The Evolution of the FLOWERING LOCUS T-Like (FTL) Genes in the Goosefoot Subfamily Chenopodioideae. , 2020, , 325-335.		5
14464	Accurate and Efficient Methods to Improve Multiple Circular Sequence Alignment. <i>Lecture Notes in Computer Science</i> , 2015, , 247-258.	1.0	10
14465	DNA Barcoding for Diagnosis and Monitoring of Fungal Plant Pathogens. <i>Fungal Biology</i> , 2017, , 87-122.	0.3	23
14466	Binary Particle Swarm Optimization Versus Hybrid Genetic Algorithm for Inferring Well Supported Phylogenetic Trees. <i>Lecture Notes in Computer Science</i> , 2016, , 165-179.	1.0	2
14467	Rare Genomic Changes. , 2017, , 195-211.		2
14468	Sources of Error and Incongruence in Phylogenomic Analyses. , 2017, , 173-193.		12

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14469	Overview of Phylogenetic Approaches to Mycorrhizal Biogeography, Diversity and Evolution. <i>Ecological Studies</i> , 2017, , 1-37.	0.4	7
14470	Taxonomy, Distribution, and Evolution of the Percidae. , 2015, , 3-60.		15
14471	<i>Shimazuella alba</i> sp. nov. isolated from desert soil and emended description of the genus <i>Shimazuella</i> Park et al. 2007. <i>Archives of Microbiology</i> , 2020, 202, 1831-1838.	1.0	8
14472	Molecular systematics of Rosoideae (Rosaceae). <i>Plant Systematics and Evolution</i> , 2020, 306, 1.	0.3	12
14473	Monitoring of Newcastle disease virus in environmental samples. <i>Archives of Virology</i> , 2017, 162, 2843-2846.	0.9	4
14474	<i>Roseomonas aeriglobus</i> sp. nov., isolated from an air-conditioning system. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 343-351.	0.7	10
14475	Guava decline: updating its etiology from <i>Fusarium solani</i> ™ to <i>Neocosmospora falciformis</i> . <i>European Journal of Plant Pathology</i> , 2021, 159, 455-460.	0.8	8
14476	A new morph of <i>Telmatochromis temporalis</i> (Cichlidae; Cichliformes) from Lake Tanganyika. <i>Hydrobiologia</i> , 2021, 848, 3655-3665.	1.0	2
14477	Intraspecific Diversity and Taxonomy of <i>Emmonsia crescens</i> . <i>Mycopathologia</i> , 2020, 185, 613-627.	1.3	15
14478	Multichromosomal structure and foreign tracts in the <i>Ombrophytum subterraneum</i> (Balanophoraceae) mitochondrial genome. <i>Plant Molecular Biology</i> , 2020, 103, 623-638.	2.0	23
14479	Description of <i>Vagococcus coleopterorum</i> sp. nov., isolated from the intestine of the diving beetle, <i>Cybister lewisianus</i> , and <i>Vagococcus hydrophili</i> sp. nov., isolated from the intestine of the dark diving beetle, <i>Hydrophilus acuminatus</i> , and emended description of the genus <i>Vagococcus</i> . <i>Journal of Microbiology</i> , 2021, 59, 132-141.	1.3	15
14480	The complete chloroplast genome sequence of an endangered mangrove tree <i>Lumnitzera littorea</i> (Combretaceae). <i>Conservation Genetics Resources</i> , 2018, 10, 911-913.	0.4	18
14481	A polyphasic approach to delineate species in <i>Bipolaris</i> . <i>Fungal Diversity</i> , 2020, 102, 225-256.	4.7	31
14482	The <i>Penium margaritaceum</i> Genome: Hallmarks of the Origins of Land Plants. <i>Cell</i> , 2020, 181, 1097-1111.e12.	13.5	153
14483	Paleolithic to Bronze Age Siberians Reveal Connections with First Americans and across Eurasia. <i>Cell</i> , 2020, 181, 1232-1245.e20.	13.5	71
14484	Prototypic SNARE Proteins Are Encoded in the Genomes of Heimdallarchaeota, Potentially Bridging the Gap between the Prokaryotes and Eukaryotes. <i>Current Biology</i> , 2020, 30, 2468-2480.e5.	1.8	24
14485	Molecular investigation of <i>Phryganella acropodia</i> Hertwig et Lesser, 1874 (Arcellinida, Amoebozoa). <i>European Journal of Protistology</i> , 2020, 75, 125707.	0.5	9
14486	Phylogeography and genetic lineages of <i>Aporrectodea rosea</i> (Lumbricidae, Annelida). <i>European Journal of Soil Biology</i> , 2020, 99, 103191.	1.4	3

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14487	Global Analysis of Gene Expression Profiles Provides Novel Insights into the Development and Evolution of the Large Crustacean <i>Eriocheir sinensis</i> . <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 443-454.	3.0	5
14488	Population genetics of two chromatic morphs of the Chagas disease vector <i>Rhodnius pallescens</i> Barber, 1932 in Panamá. <i>Infection, Genetics and Evolution</i> , 2020, 84, 104369.	1.0	2
14489	Phylogeny of the North-Central American clade of blood-sucking reduviid bugs of the tribe Triatomini (Hemiptera: Triatominae) based on the mitochondrial genome. <i>Infection, Genetics and Evolution</i> , 2020, 84, 104373.	1.0	14
14490	Beyond endemism, expanding conservation efforts: What can new distribution records reveal?. <i>Perspectives in Plant Ecology, Evolution and Systematics</i> , 2020, 45, 125543.	1.1	12
14491	Morphology, Ultrastructure, and Molecular Phylogeny of <i>Aphelidium collabens</i> sp. nov. (Aphelida), a Parasitoid of a Green Alga <i>Coccomyxa</i> sp.. <i>Protist</i> , 2020, 171, 125728.	0.6	12
14492	<i>Desulfamplus magnetovallimortis</i> gen. nov., sp. nov., a magnetotactic bacterium from a brackish desert spring able to biomineralize greigite and magnetite, that represents a novel lineage in the Desulfobacteraceae. <i>Systematic and Applied Microbiology</i> , 2017, 40, 280-289.	1.2	39
14493	<i>Candidatus Abditibacter</i> , a novel genus within the Cryomorphaeaceae, thriving in the North Sea. <i>Systematic and Applied Microbiology</i> , 2020, 43, 126088.	1.2	21
14494	Characterization of <i>Acinetobacter chengduensis</i> sp. nov., isolated from hospital sewage and capable of acquisition of carbapenem resistance genes. <i>Systematic and Applied Microbiology</i> , 2020, 43, 126092.	1.2	14
14495	Occurrence and molecular composition of methicillin-resistant <i>Staphylococcus aureus</i> isolated from ocular surfaces of horses presented with ophthalmologic disease. <i>Veterinary Microbiology</i> , 2018, 222, 1-6.	0.8	11
14496	BMP signaling plays a role in anterior-neural/head development, but not organizer activity, in the gastropod <i>Crepidula fornicata</i> . <i>Developmental Biology</i> , 2020, 463, 135-157.	0.9	20
14497	Whole-genome sequencing of the endemic Antarctic fungus <i>Antarctomyces pellizariae</i> reveals an ice-binding protein, a scarce set of secondary metabolites gene clusters and provides insights on Thelebolales phylogeny. <i>Genomics</i> , 2020, 112, 2915-2921.	1.3	19
14498	Mitochondrial genomes of three Bostrichiformia species and phylogenetic analysis of Polyphaga (Insecta, Coleoptera). <i>Genomics</i> , 2020, 112, 2970-2977.	1.3	5
14499	Pinpointing cryptic borders: Fine-scale phylogeography and genetic landscape analysis of the <i>Hormogaster elisae</i> complex (Oligochaeta, Hormogastridae). <i>Molecular Phylogenetics and Evolution</i> , 2017, 112, 185-193.	1.2	24
14500	Predatory colponemids are the sister group to all other alveolates. <i>Molecular Phylogenetics and Evolution</i> , 2020, 149, 106839.	1.2	16
14501	Unraveling the systematics and evolution of the <i>Geophagus</i> ™ <i>brasiliensis</i> (Cichliformes: Cichlidae) species complex. <i>Molecular Phylogenetics and Evolution</i> , 2020, 150, 106855.	1.2	18
14503	Prospective enzymes for omega-3 PUFA biosynthesis found in endoparasitic classes within the phylum Platyhelminthes. <i>Journal of Helminthology</i> , 2020, 94, e212.	0.4	6
14504	Poorly known sponges in the Mediterranean with the detection of some taxonomic inconsistencies. <i>Journal of the Marine Biological Association of the United Kingdom</i> , 2020, 100, 1247-1260.	0.4	5
14505	A chromosome-scale genome assembly of <i>Isatis indigotica</i> , an important medicinal plant used in traditional Chinese medicine. <i>Horticulture Research</i> , 2020, 7, 18.	2.9	58

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14506	The <i>C. difficile</i> toxin B membrane translocation machinery is an evolutionarily conserved protein delivery apparatus. <i>Nature Communications</i> , 2020, 11, 432.	5.8	20
14507	A proofreading-impaired herpesvirus generates populations with quasispecies-like structure. <i>Nature Microbiology</i> , 2019, 4, 2175-2183.	5.9	17
14508	CasX enzymes comprise a distinct family of RNA-guided genome editors. <i>Nature</i> , 2019, 566, 218-223.	13.7	346
14509	1,520 reference genomes from cultivated human gut bacteria enable functional microbiome analyses. <i>Nature Biotechnology</i> , 2019, 37, 179-185.	9.4	402
14510	A human gut bacterial genome and culture collection for improved metagenomic analyses. <i>Nature Biotechnology</i> , 2019, 37, 186-192.	9.4	420
14511	Combination anti-HIV-1 antibody therapy is associated with increased virus-specific T cell immunity. <i>Nature Medicine</i> , 2020, 26, 222-227.	15.2	108
14512	Evolutionary diversity in tropical tree communities peaks at intermediate precipitation. <i>Scientific Reports</i> , 2020, 10, 1188.	1.6	41
14513	Soil microbiomes mediate degradation of vinyl ester-based polymer composites. <i>Communications Materials</i> , 2020, 1, .	2.9	25
14514	Global-scale phylogenetic linguistic inference from lexical resources. <i>Scientific Data</i> , 2018, 5, 180189.	2.4	39
14515	Building an octaploid genome and transcriptome of the medicinal plant <i>Pogostemon cablin</i> from Lamiales. <i>Scientific Data</i> , 2018, 5, 180274.	2.4	17
14516	Pan-transcriptomic analysis identified common differentially expressed genes of <i>Acinetobacter baumannii</i> in response to polymyxin treatments. <i>Molecular Omics</i> , 2020, 16, 327-338.	1.4	7
14517	Uncovering the diversity of monogeneans (Platyhelminthes) on endemic cypriniform fishes of the Balkan Peninsula: new species of <i>Dactylogyrus</i> and comments on their phylogeny and host-parasite associations in a biogeographic context. <i>Parasite</i> , 2020, 27, 66.	0.8	10
14518	A new species, <i>Dactylosoma piperis</i> n. sp. (Apicomplexa, Dactylosomatidae), from the pepper frog <i>Leptodactylus labyrinthicus</i> (Anura, Leptodactylidae) from Mato Grosso State, Brazil.. <i>Parasite</i> , 2020, 27, 73.	0.8	6
14519	Phylogenetic relationships of the cuscuses (Diprotodontia : Phalangeridae) of island Southeast Asia and Melanesia based on the mitochondrial ND2 gene. <i>Australian Mammalogy</i> , 2020, 42, 266.	0.7	12
14520	New Australian Paronellidae (Collembola) reveal anomalies in existing tribal diagnoses. <i>Invertebrate Systematics</i> , 2017, 31, 375.	0.5	13
14521	Paleogenomics of echinoids reveals an ancient origin for the double-negative specification of micromeres in sea urchins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 5870-5877.	3.3	26
14522	Fruiting body form, not nutritional mode, is the major driver of diversification in mushroom-forming fungi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 32528-32534.	3.3	65
14523	Individualistic evolutionary responses of Central African rain forest plants to Pleistocene climatic fluctuations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 32509-32518.	3.3	26

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14524	Evolutionary determinism and convergence associated with water-column transitions in marine fishes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 33396-33403.	3.3	27
14525	A modern scleractinian coral with a two-component calcite- ¹⁸ O aragonite skeleton. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	22
14526	Complex subsurface hydrothermal fluid mixing at a submarine arc volcano supports distinct and highly diverse microbial communities. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 32627-32638.	3.3	36
14527	Evolution toward beta common chain receptor usage links the matrix proteins of HIV-1 and its ancestors to human erythropoietin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, e2021366118.	3.3	4
14528	An updated lineage-based tribal classification of Apiaceae subfamily Apioideae with special focus on Iranian genera. <i>Systematics and Biodiversity</i> , 2021, 19, 89-109.	0.5	11
14529	Predicting the spread-risk potential of chronic wasting disease to sympatric ungulate species. <i>Prion</i> , 2020, 14, 56-66.	0.9	18
14530	Signatures of cytoplasmic proteins in the exoproteome distinguish community- and hospital-associated methicillin-resistant <i>Staphylococcus aureus</i> USA300 lineages. <i>Virulence</i> , 2017, 8, 891-907.	1.8	19
14531	Antimicrobial resistance and gene regulation in Enteroaggregative <i>Escherichia coli</i> from Egyptian children with diarrhoea: Similarities and differences. <i>Virulence</i> , 2021, 12, 57-74.	1.8	13
14532	The complete mitochondrial genome of the critically endangered Atlantic humpback dolphin, <i>Sousa teuszii</i> (K ¹ 4kenthal, 1892). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 257-259.	0.2	1
14533	Next-generation sequencing yields the complete chloroplast genome of <i>Abies yuanbaoshanensis</i> , an endangered species from South China. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 3821-3822.	0.2	3
14534	Polynomial-Time Statistical Estimation of Species Trees Under Gene Duplication and Loss. <i>Journal of Computational Biology</i> , 2021, 28, 452-468.	0.8	23
14535	Extensive plastid-nuclear discordance in a recent radiation of <i>Nicotiana</i> section <i>Suaveolentes</i> (Solanaceae). <i>Botanical Journal of the Linnean Society</i> , 2020, 193, 546-559.	0.8	19
14536	Molecular data reveal hidden diversity in the central Andean species <i>Weberbaueria spathulifolia</i> (Thelypodieae: Brassicaceae). <i>Botanical Journal of the Linnean Society</i> , 2020, 193, 523-545.	0.8	1
14537	Outbreak of <i>Pseudomonas aeruginosa</i> Infections from a Contaminated Gastroscope Detected by Whole Genome Sequencing Surveillance. <i>Clinical Infectious Diseases</i> , 2021, 73, e638-e642.	2.9	26
14538	Phylogenetic Analysis Indicates a Longer Term Presence of the Globally Distributed H58 Haplotype of <i>Salmonella</i> Typhi in Southern India. <i>Clinical Infectious Diseases</i> , 2020, 71, 1856-1863.	2.9	21
14539	Exploring the abundance, metabolic potential and gene expression of subseafloor <i>Chloroflexi</i> in million-year-old oxic and anoxic abyssal clay. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	34
14540	A high-quality <i>de novo</i> genome assembly of one swamp eel (<i>Monopterus albus</i>) strain with PacBio and Hi-C sequencing data. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, 1-9.	0.8	15
14541	Golden orb-weaving spider (<i>Trichonephila clavipes</i>) silk genes with sex-biased expression and atypical architectures. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, 1-10.	0.8	11

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14542	Genome Assembly of the Ragweed Leaf Beetle: A Step Forward to Better Predict Rapid Evolution of a Weed Biocontrol Agent to Environmental Novelty. <i>Genome Biology and Evolution</i> , 2020, 12, 1167-1173.	1.1	10
14543	Symbiotic and Nonsymbiotic Members of the Genus <i>Ensifer</i> (syn. <i>Sinorhizobium</i>) Are Separated into Two Clades Based on Comparative Genomics and High-Throughput Phenotyping. <i>Genome Biology and Evolution</i> , 2020, 12, 2521-2534.	1.1	30
14544	Unbiased Subgenome Evolution in Allotetraploid Species of <i>Ephedra</i> and Its Implications for the Evolution of Large Genomes in Gymnosperms. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	19
14545	Nanopore Amplicon Sequencing Reveals Molecular Convergence and Local Adaptation of Rhodopsin in Great Lakes Salmonids. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	14
14546	Phylogenomics Identifies a New Major Subgroup of Apicomplexans, Marosporida <i>class nov.</i> , with Extreme Apicoplast Genome Reduction. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	23
14547	Comparative Genomics of Strictly Vertically Transmitted, Feminizing Microsporidia Endosymbionts of Amphipod Crustaceans. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	12
14548	Sequence of a <i>Coxiella</i> Endosymbiont of the Tick <i>Amblyomma nuttalli</i> Suggests a Pattern of Convergent Genome Reduction in the <i>Coxiella</i> Genus. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	14
14549	Extreme diversification driven by parallel events of massive loss of heterozygosity in the hybrid lineage of <i>Candida albicans</i> . <i>Genetics</i> , 2021, 217, .	1.2	16
14550	Repeated horizontal gene transfer of <i>GAL</i> actose metabolism genes violates Dollo's law of irreversible loss. <i>Genetics</i> , 2021, 217, .	1.2	18
14551	Chromosomal genome of <i>Triplophysa bleekeri</i> provides insights into its evolution and environmental adaptation. <i>GigaScience</i> , 2020, 9, .	3.3	19
14552	Integrative Taxonomy of Australian <i>Metopia</i> (Sarcophagidae: Miltogramminae) Reveals a New Species and Challenges Traditional Phylogeny. <i>Insect Systematics and Diversity</i> , 2020, 4, .	0.7	3
14553	The emergence of azithromycin-resistant <i>Salmonella</i> Typhi in Nepal. <i>JAC-Antimicrobial Resistance</i> , 2020, 2, dlaa109.	0.9	30
14554	Uncovering two phases of early intercontinental COVID-19 transmission dynamics. <i>Journal of Travel Medicine</i> , 2020, 27, .	1.4	28
14555	IQ-TREE 2: New Models and Efficient Methods for Phylogenetic Inference in the Genomic Era. <i>Molecular Biology and Evolution</i> , 2020, 37, 1530-1534.	3.5	5,960
14556	The <i>goddard</i> and <i>saturn</i> genes are essential for <i>Drosophila</i> male fertility and may have arisen <i>de novo</i> . <i>Molecular Biology and Evolution</i> , 2017, 34, msx057.	3.5	39
14557	LegumelP V3: from models to crops—an integrative gene discovery platform for translational genomics in legumes. <i>Nucleic Acids Research</i> , 2021, 49, D1472-D1479.	6.5	25
14558	Hormonal Diterpenoids Distinct to Gibberellins Regulate Protonema Differentiation in the Moss <i>Physcomitrium patens</i> . <i>Plant and Cell Physiology</i> , 2020, 61, 1861-1868.	1.5	5
14559	The Multispecies Coalescent Model Outperforms Concatenation Across Diverse Phylogenomic Data Sets. <i>Systematic Biology</i> , 2020, 69, 795-812.	2.7	47

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14560	Gene Tree Estimation Error with Ultraconserved Elements: An Empirical Study on <i>Pseudapis</i> Bees. <i>Systematic Biology</i> , 2021, 70, 803-821.	2.7	25
14561	Phylogenomic Discordance in the Eared Seals is best explained by Incomplete Lineage Sorting following Explosive Radiation in the Southern Hemisphere. <i>Systematic Biology</i> , 2021, 70, 786-802.	2.7	25
14562	Papillomaviruses infecting cetaceans exhibit signs of genome adaptation following a recombination event. <i>Virus Evolution</i> , 2020, 6, veaa038.	2.2	8
14563	Three arenaviruses in three subspecific natal multimammate mouse taxa in Tanzania: same host specificity, but different spatial genetic structure?. <i>Virus Evolution</i> , 2020, 6, veaa039.	2.2	18
14564	RDP5: a computer program for analyzing recombination in, and removing signals of recombination from, nucleotide sequence datasets. <i>Virus Evolution</i> , 2021, 7, veaa087.	2.2	257
14565	Simulating within host human immunodeficiency virus 1 genome evolution in the persistent reservoir. <i>Virus Evolution</i> , 2020, 6, veaa089.	2.2	7
14566	Molecular phylogeny of the limacoid snail family Dyakiidae in Southeast Asia, with the description of a new genus and species. <i>Zoological Journal of the Linnean Society</i> , 2021, 193, 250-280.	1.0	9
14567	Integrative taxonomy of giant crested <i>Eusirus</i> in the Southern Ocean, including the description of a new species (Crustacea: Amphipoda: Eusiridae). <i>Zoological Journal of the Linnean Society</i> , 2021, 193, 31-77.	1.0	5
14568	Mitogenomic phylogeny and fossil-calibrated mutation rates for all F- and M-type mtDNA genes of the largest freshwater mussel family, the Unionidae (Bivalvia). <i>Zoological Journal of the Linnean Society</i> , 2021, 193, 1088-1107.	1.0	20
14569	Phylogenetic revision of the shrimp genera <i>Ephyrina</i> , <i>Meningodora</i> and <i>Notostomus</i> (Acanthephyridae: Caridea). <i>Zoological Journal of the Linnean Society</i> , 2021, 193, 1002-1019.	1.0	7
14570	Species Identification in Plant-Associated Prokaryotes and Fungi Using DNA. <i>Phytobiomes Journal</i> , 2020, 4, 103-114.	1.4	7
14571	Contrasted histories of organelle and nuclear genomes underlying physiological diversification in a grass species. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20201960.	1.2	18
14572	Fatty acid bioconversion in harpacticoid copepods in a changing environment: a transcriptomic approach. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190645.	1.8	26
14573	<i>Hydrobacter penzbergensis</i> gen. nov., sp. nov., isolated from purified water. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 920-926.	0.8	25
14574	<i>Abyssivirga alkaniphila</i> gen. nov., sp. nov., an alkane-degrading, anaerobic bacterium from a deep-sea hydrothermal vent system, and emended descriptions of <i>Natranaerovirga pectinivora</i> and <i>Natranaerovirga hydrolytica</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 1724-1734.	0.8	48
14575	<i>Aliterella atlantica</i> gen. nov., sp. nov., and <i>Aliterella antarctica</i> sp. nov., novel members of coccoid Cyanobacteria. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 2853-2861.	0.8	36
14576	<i>Ruthenibacterium lactatiformans</i> gen. nov., sp. nov., an anaerobic, lactate-producing member of the family Ruminococcaceae isolated from human faeces. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 3041-3049.	0.8	36
14577	<i>Campylobacter geochelonis</i> sp. nov. isolated from the western Hermann's tortoise (<i>Testudo hermanni</i>) Tj ETQq1 1 0.784314 49 BT / Over	0.8	49

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14578	Marinicrinis sediminis gen. nov., sp. nov., isolated from marine sediment. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 3725-3730.	0.8	12
14579	Characterization of clinical and environmental isolates of Vibrio cidicii sp. nov., a close relative of Vibrio navarrensis. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 4148-4155.	0.8	21
14580	Wenzhouxiangella sediminis sp. nov., isolated from coastal sediment. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 4575-4579.	0.8	16
14581	Genome-based phylogeny and taxonomy of the "Enterobacteriales" TM : proposal for Enterobacterales ord. nov. divided into the families Enterobacteriaceae, Erwiniaceae fam. nov., Pectobacteriaceae fam. nov., Yersiniaceae fam. nov., Hafniaceae fam. nov., Morganellaceae fam. nov., and Budviciaceae fam. nov.. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 5575-5599.	0.8	792
14582	Proposal of a type strain for Frankia alni (Woronin 1866) Von Tubeuf 1895, emended description of Frankia alni, and recognition of Frankia casuarinae sp. nov. and Frankia elaeagni sp. nov.. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 5201-5210.	0.8	68
14583	Roseitalea porphyridii gen. nov., sp. nov., isolated from a red alga, and reclassification of Hoeflea suaedae Chung et al. 2013 as Pseudohoeflea suaedae gen. nov., comb. nov.. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 362-368.	0.8	22
14584	Flexivirga oryzae sp. nov., isolated from soil of a rice paddy, and emended description of the genus Flexivirga Anzai et al. 2012. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 479-484.	0.8	8
14585	Niveitalea solisilvae gen. nov., sp. nov., isolated from forest soil and emended description of the genus Flaviumibacter Zhang et al. 2010. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 1374-1380.	0.8	15
14586	Frankia coriariae sp. nov., an infective and effective microsymbiont isolated from Coriaria japonica. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 1266-1270.	0.8	37
14587	Fournierella massiliensis gen. nov., sp. nov., a new human-associated member of the family Ruminococcaceae. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 1393-1399.	0.8	33
14588	Parahaliea aestuarii sp. nov., isolated from the Asan Bay estuary. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 1431-1435.	0.8	11
14589	Streptomyces jeddahensis sp. nov., an oleaginous bacterium isolated from desert soil. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 1676-1682.	0.8	25
14590	Cloacibacterium caeni sp. nov., isolated from activated sludge. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 1688-1692.	0.8	16
14591	A proposal of Leuconostoc mesenteroides subsp. joggajibkimchii subsp. nov. and reclassification of Leuconostoc mesenteroides subsp. suionicum (Gu et al., 2012) as Leuconostoc suionicum sp. nov. based on complete genome sequences. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 2225-2230.	0.8	40
14592	Mycobacterium eburneum sp. nov., a non-chromogenic, fast-growing strain isolated from sputum. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 3174-3181.	0.8	13
14593	Molecules illuminate morphology: phylogenomics confirms convergent evolution among "oligotrichous" TM ciliates. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 3676-3682.	0.8	26
14594	Novosphingobium humi sp. nov., isolated from soil of a military shooting range. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 3083-3088.	0.8	17
14595	Frankia asymbiotica sp. nov., a non-infective actinobacterium isolated from Morella californica root nodule. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 4897-4901.	0.8	34

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14596	<i>Pacificibacter aestuarii</i> sp. nov., isolated from a tidal flat. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 3627-3632.	0.8	7
14597	Draft genome and description of <i>Consotaella salsifontis</i> gen. nov. sp. nov., a halophilic, free-living, nitrogen-fixing alphaproteobacterium isolated from an ancient terrestrial saline spring. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 3744-3751.	0.8	10
14598	<i>Spathaspora boniae</i> sp. nov., a D-xylose-fermenting species in the <i>Candida albicans</i> /Lodderomyces clade. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 3798-3805.	0.8	20
14599	<i>Agarilytica rhodophyticola</i> gen. nov., sp. nov., isolated from <i>Gracilaria blodgettii</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 3778-3783.	0.8	17
14600	<i>Parasphingopyxis algicola</i> sp. nov., isolated from a marine red alga <i>Asparagopsis taxiformis</i> and emended description of the genus <i>Parasphingopyxis</i> Uchida et al. 2012. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 3877-3881.	0.8	14
14601	<i>Sphingomonas frigidaeris</i> sp. nov., isolated from an air conditioning system. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 3907-3912.	0.8	23
14602	<i>Lentibacillus sediminis</i> sp. nov., isolated from a marine saltern. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 3946-3950.	0.8	10
14603	<i>Roseomonas aerofrigidensis</i> sp. nov., isolated from an air conditioner. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 4039-4044.	0.8	15
14604	<i>Tuwongella immobilis</i> gen. nov., sp. nov., a novel non-motile bacterium within the phylum Planctomycetes. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 4923-4929.	0.8	25
14605	<i>Corynebacterium gottingense</i> sp. nov., isolated from a clinical patient. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 4494-4499.	0.8	11
14606	<i>Heitmania</i> gen. nov., a new yeast genus in Microbotryomycetes, and description of three novel species: <i>Heitmania litseae</i> sp. nov., <i>Heitmania castanopsis</i> sp. nov. and <i>Heitmania elacocarpi</i> sp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 4534-4540.	0.8	4
14607	<i>Sphingobacterium humi</i> sp. nov., isolated from soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 4632-4638.	0.8	10
14608	Two novel species of rapidly growing mycobacteria: <i>Mycobacterium lehmannii</i> sp. nov. and <i>Mycobacterium neumannii</i> sp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 4948-4955.	0.8	12
14609	<i>Cohnella algarum</i> sp. nov., isolated from a freshwater green alga <i>Paulinella chromatophora</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 4767-4772.	0.8	24
14610	<i>Rhodosalinus sediminis</i> gen. nov., sp. nov., isolated from marine saltern. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 5108-5113.	0.8	10
14611	<i>Sphingobium paulinellae</i> sp. nov. and <i>Sphingobium algicola</i> sp. nov., isolated from a freshwater green alga <i>Paulinella chromatophora</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 5165-5171.	0.8	22
14612	<i>Bacillus marinisedimentorum</i> sp. nov., isolated from marine sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 198-203.	0.8	6
14613	<i>Aestuariococcus marinus</i> gen. nov., sp. nov., isolated from sea-tidal flat sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 260-265.	0.8	15

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14614	<i>Albirhodobacter confluentis</i> sp. nov., isolated from an estuary. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 289-293.	0.8	7
14615	<i>Methylobacterium frigidaeris</i> sp. nov., isolated from an air conditioning system. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 299-304.	0.8	13
14616	<i>Mixta</i> gen. nov., a new genus in the Erwiniaceae. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 1396-1407.	0.8	53
14617	<i>Tritonibacter horizontis</i> gen. nov., sp. nov., a member of the Rhodobacteraceae, isolated from the Deepwater Horizon oil spill. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 736-744.	0.8	25
14618	<i>Frankia saprophytica</i> sp. nov., an atypical, non-infective (Nodâ€™) and non-nitrogen fixing (Fixâ€™) actinobacterium isolated from <i>Coriaria nepalensis</i> root nodules. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 1090-1095.	0.8	20
14619	<i>Paraburkholderia aromaticivorans</i> sp. nov., an aromatic hydrocarbon-degrading bacterium, isolated from gasoline-contaminated soil. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 1251-1257.	0.8	49
14620	<i>Thioclava electrotropha</i> sp. nov., a versatile electrode and sulfur-oxidizing bacterium from marine sediments. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 1652-1658.	0.8	23
14621	<i>Butyricoccus porcorum</i> sp. nov., a butyrate-producing bacterium from swine intestinal tract. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 1737-1742.	0.8	33
14622	<i>Flavobacterium alvei</i> sp. nov., isolated from a freshwater river. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 1919-1924.	0.8	17
14623	<i>Kandeliimicrobium roseum</i> gen. nov., sp. nov., a new member of the family Rhodobacteraceae isolated from mangrove rhizosphere soil. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 2158-2164.	0.8	10
14624	<i>Polynucleobacter meluiroseus</i> sp. nov., a bacterium isolated from a lake located in the mountains of the Mediterranean island of Corsica. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 1975-1985.	0.8	18
14625	<i>Roseovarius salinarum</i> sp. nov., isolated from a marine solar saltern. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 1986-1991.	0.8	18
14626	<i>Lawsonibacter asaccharolyticus</i> gen. nov., sp. nov., a butyrate-producing bacterium isolated from human faeces. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 2074-2081.	0.8	41
14627	<i>Scheffersomyces stambukii</i> f.a., sp. nov., a d-xylose-fermenting species isolated from rotting wood. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 2306-2312.	0.8	8
14628	<i>Glycomyces sediminimaris</i> sp. nov., a new species of actinobacteria isolated from marine sediment. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 2357-2363.	0.8	9
14629	<i>Solimonas fluminis</i> sp. nov., isolated from a freshwater river. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 2755-2759.	0.8	9
14630	<i>Polynucleobacter hirudinilacicola</i> sp. nov. and <i>Polynucleobacter campilacus</i> sp. nov., both isolated from freshwater systems. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 2593-2601.	0.8	37
14631	Morphologic and molecular characterization of <i>Brachonella pulchra</i> (Kahl, 1927) comb. nov. (Armophorea, Ciliophora) with comments on cyst structure and formation. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 3052-3065.	0.8	11

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14632	<i>Solitalea longa</i> sp. nov., isolated from freshwater and emended description of the genus <i>Solitalea</i> . International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 2826-2831.	0.8	11
14633	<i>Frankia irregularis</i> sp. nov., an actinobacterium unable to nodulate its original host, <i>Casuarina equisetifolia</i> , but effectively nodulates members of the actinorhizal Rhamnales. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 2883-2914.	0.8	28
14634	<i>Kaistia algarum</i> sp. nov., isolated from a freshwater green alga <i>Paulinella chromatophora</i> . International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 3028-3033.	0.8	16
14635	<i>Drechmeria panacis</i> sp. nov., an endophyte isolated from <i>Panax notoginseng</i> . International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 3255-3259.	0.8	10
14636	<i>Mycobacterium syngnathidarum</i> sp. nov., a rapidly growing mycobacterium identified in syngnathid fish. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 3696-3700.	0.8	14
14637	<i>Staphylococcus cornubiensis</i> sp. nov., a member of the <i>Staphylococcus intermedius</i> Group (SIG). International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 3404-3408.	0.8	31
14638	<i>Desertimonas flava</i> gen. nov., sp. nov. isolated from a desert soil, and proposal of <i>Ilumatobacteraceae</i> fam. nov.. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 3593-3599.	0.8	22
14639	Description of a novel species of fast growing mycobacterium: <i>Mycobacterium kyogaense</i> sp. nov., a scotochromogenic strain received as <i>Mycobacterium vaccae</i> . International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 3726-3734.	0.8	10
14640	Refining the taxonomic structure of the phylum Acidobacteria. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 3796-3806.	0.8	101
14641	<i>Prevotella rara</i> sp. nov., isolated from human faeces. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 3818-3825.	0.8	14
14642	<i>Lactococcus termiticola</i> sp. nov., isolated from the gut of the wood-feeding higher termite <i>Nasutitermes takasagoensis</i> . International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 3832-3836.	0.8	10
14643	<i>Acinetobacter sichuanensis</i> sp. nov., recovered from hospital sewage in China. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 3897-3901.	0.8	8
14644	<i>Aestuariivirga litoralis</i> gen. nov., sp. nov., a proteobacterium isolated from a water sample, and proposal of <i>Aestuariivirgaceae</i> fam. nov.. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 299-306.	0.8	13
14645	<i>Enterobacter sichuanensis</i> sp. nov., recovered from human urine. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 3922-3927.	0.8	31
14646	<i>Planctomonas deserti</i> gen. nov., sp. nov., a new member of the family <i>Microbacteriaceae</i> isolated from soil of the Taklamakan desert. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 616-624.	0.8	15
14647	<i>Polynucleobacter paneuropaeus</i> sp. nov., characterized by six strains isolated from freshwater lakes located along a 3000 km north-south cross-section across Europe. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 203-213.	0.8	36
14648	<i>Calidifontimicrobium sediminis</i> gen. nov., sp. nov., a new member of the family <i>Comamonadaceae</i> . International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 434-440.	0.8	13
14649	<i>Enterobacter huaxiensis</i> sp. nov. and <i>Enterobacter chuandaensis</i> sp. nov., recovered from human blood. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 708-714.	0.8	26

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14650	<i>Collinsella vaginalis</i> sp. nov. strain Marseille-P2666T, a new member of the <i>Collinsella</i> genus isolated from the genital tract of a patient suffering from bacterial vaginosis. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 949-956.	0.8	12
14651	<i>Botryobacter ruber</i> gen. nov., sp. nov., a novel member of the family Hymenobacteraceae. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 821-827.	0.8	9
14652	<i>Streptacidiphilus bronchialis</i> sp. nov., a ciprofloxacin-resistant bacterium from a human clinical specimen; reclassification of <i>Streptomyces griseoplanus</i> as <i>Streptacidiphilus griseoplanus</i> comb. nov. and emended description of the genus <i>Streptacidiphilus</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 1047-1056.	0.8	20
14653	<i>Aggregatilinea lenta</i> gen. nov., sp. nov., a slow-growing, facultatively anaerobic bacterium isolated from subseafloor sediment, and proposal of the new order <i>Aggregatilineales</i> ord. nov. within the class <i>Anaerolineae</i> of the phylum <i>Chloroflexi</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 1185-1194.	0.8	32
14654	<i>Methanofervidicoccus abyssi</i> gen. nov., sp. nov., a hydrogenotrophic methanogen, isolated from a hydrothermal vent chimney in the Mid-Cayman Spreading Center, the Caribbean Sea. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 1225-1230.	0.8	17
14655	<i>Pradoshia eiseniae</i> gen. nov., sp. nov., a spore-forming member of the family <i>Bacillaceae</i> capable of assimilating 3-nitropropionic acid, isolated from the anterior gut of the earthworm <i>Eisenia fetida</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 1265-1273.	0.8	16
14656	<i>Novosphingobium meiothermophilum</i> sp. nov., isolated from a hot spring. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 1737-1743.	0.8	15
14657	<i>Thalassorhabdomicrobium marinisediminis</i> gen. nov., sp. nov., a member of the family <i>Hyphomonadaceae</i> isolated from the Bohai Sea. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 1794-1799.	0.8	8
14658	<i>Faecalibacillus intestinalis</i> gen. nov., sp. nov. and <i>Faecalibacillus faecis</i> sp. nov., isolated from human faeces. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 2120-2128.	0.8	18
14659	<i>Vagococcus bubulae</i> sp. nov., isolated from ground beef, and <i>Vagococcus vulneris</i> sp. nov., isolated from a human foot wound. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 2268-2276.	0.8	26
14660	<i>Streptomyces huasconensis</i> sp. nov., an haloalkalitolerant actinobacterium isolated from a high altitude saline wetland at the Chilean Altiplano. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 2315-2322.	0.8	18
14661	<i>Leptospira yasudae</i> sp. nov. and <i>Leptospira stimsonii</i> sp. nov., two new species of the pathogenic group isolated from environmental sources. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 1450-1456.	0.8	43
14662	<i>Providencia huaxiensis</i> sp. nov., recovered from a human rectal swab. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 2638-2643.	0.8	18
14663	<i>Acidimangrovimonas sediminis</i> gen. nov., sp. nov., isolated from mangrove sediment and reclassification of <i>Defluviimonas indica</i> as <i>Acidimangrovimonas indica</i> comb. nov. and <i>Defluviimonas pyrenivorans</i> as <i>Acidimangrovimonas pyrenivorans</i> comb. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 2445-2451.	0.8	19
14664	<i>Pseudomonas nitritolerans</i> sp. nov., a nitrite-tolerant denitrifying bacterium isolated from a nitrification/denitrification bioreactor. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 2471-2476.	0.8	9
14665	<i>Bifidobacterium jacchi</i> sp. nov., isolated from the faeces of a baby common marmoset (<i>Callithrix</i>) Tj ETQq1 1 0.784314 rgBT (Overlock 23)	0.8	23
14666	<i>Croceibacterium</i> gen. nov., with description of <i>Croceibacterium ferulae</i> sp. nov., an endophytic bacterium isolated from <i>Ferula sinkiangensis</i> K. M. Shen and reclassification of <i>Porphyrobacter mercurialis</i> as <i>Croceibacterium mercuriale</i> comb. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 2547-2554.	0.8	18
14667	<i>Aquirufa antheringensis</i> gen. nov., sp. nov. and <i>Aquirufa nivalisilvae</i> sp. nov., representing a new genus of widespread freshwater bacteria. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 2739-2749.	0.8	35

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14668	<i>Kosakonia quasisacchari</i> sp. nov. recovered from human wound secretion in China. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 3155-3160.	0.8	11
14669	<i>Pseudomonas huaxiensis</i> sp. nov., isolated from hospital sewage. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 3281-3286.	0.8	9
14670	<i>Mycolicibacterium stelleriae</i> sp. nov., a rapidly growing scotochromogenic strain isolated from <i>Stellera chamaejasme</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 3465-3471.	0.8	14
14671	<i>Apibacter muscae</i> sp. nov., a novel bacterial species isolated from house flies. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 3586-3592.	0.8	7
14672	<i>Facilibium subflavum</i> gen. nov., sp. nov. and <i>Cysteiniphilum halobium</i> sp. nov., new members of the family <i>Fastidiosibacteraceae</i> isolated from coastal seawater. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 3757-3764.	0.8	14
14673	<i>Prevotella brunnea</i> sp. nov., isolated from a wound of a patient. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 3933-3938.	0.8	7
14674	<i>Rhodoluna limnophila</i> sp. nov., a bacterium with 1.4 Mbp genome size isolated from freshwater habitats located in Salzburg, Austria. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 3946-3954.	0.8	18
14675	Phylogenomic analysis of <i>Haemophilus parasuis</i> and proposed reclassification to <i>Glaesserella parasuis</i> , gen. nov., comb. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 180-186.	0.8	51
14676	<i>Mesorhizobium norvegicum</i> sp. nov., a rhizobium isolated from a <i>Lotus corniculatus</i> root nodule in Norway. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 388-396.	0.8	10
14677	A phylogenomic and comparative genomic framework for resolving the polyphyly of the genus <i>Bacillus</i> : Proposal for six new genera of <i>Bacillus</i> species, <i>Peribacillus</i> gen. nov., <i>Cytobacillus</i> gen. nov., <i>Mesobacillus</i> gen. nov., <i>Neobacillus</i> gen. nov., <i>Metabacillus</i> gen. nov. and <i>Alkalihalobacillus</i> gen. nov., <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 406-438.	0.8	458
14678	<i>Enterobacter wuhouensis</i> sp. nov. and <i>Enterobacter quasihormaechei</i> sp. nov. recovered from human sputum. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 874-881.	0.8	22
14679	<i>Seonamhaeicola maritimus</i> sp. nov., isolated from coastal sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 902-908.	0.8	13
14680	<i>Pseudorivibacter rhizosphaerae</i> gen. nov., sp. nov., isolated from rhizosphere soil of <i>Camellia sinensis</i> (L.) O. Ktze and emended description of the genus <i>Rivibacter</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 1071-1078.	0.8	12
14681	<i>Frankia soli</i> sp. nov., an actinobacterium isolated from soil beneath <i>Ceanothus jepsonii</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 1203-1209.	0.8	18
14682	<i>Tepidiforma bonchosmolovskayae</i> gen. nov., sp. nov., a moderately thermophilic Chloroflexi bacterium from a Chukotka hot spring (Arctic, Russia), representing a novel class, <i>Tepidiformia</i> , which includes the previously uncultivated lineage OLB14. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 1192-1202.	0.8	44
14683	Update on the classification of higher ranks in the phylum Actinobacteria. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 1331-1355.	0.8	255
14684	Division of the genus <i>Chryseobacterium</i> : Observation of discontinuities in amino acid identity values, a possible consequence of major extinction events, guides transfer of nine species to the genus <i>Epilithonimonas</i> , eleven species to the genus <i>Kaistella</i> , and three species to the genus <i>Halpernia</i> gen. nov., with description of <i>Kaistella daneshvariae</i> sp. nov. and <i>Epilithonimonas vandammei</i> sp. nov. derived from clinical specimens. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 4432-4450.	0.8	215
14685	<i>Fluviispira multicolorata</i> gen. nov., sp. nov. and <i>Silvanigrella paludirubra</i> sp. nov., isolated from freshwater habitats. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 1630-1638.	0.8	18

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14686	<i>Chitinophaga vietnamensis</i> sp. nov., a multi-drug resistant bacterium infecting humans. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 1758-1768.	0.8	16
14687	<i>Carideicomes alvinocaridis</i> gen. nov., sp. nov., a marine bacterium isolated from shrimp gill in a hydrothermal field of Okinawa Trough. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 1777-1784.	0.8	10
14688	<i>Saezia sanguinis</i> gen. nov., sp. nov., a Betaproteobacteria member of order Burkholderiales, isolated from human blood. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 2016-2025.	0.8	10
14689	Genome-based classification of three novel actinobacteria from the Karakum Desert: <i>Jiangella asiatica</i> sp. nov., <i>Jiangella aurantiaca</i> sp. nov. and <i>Jiangella ureilytica</i> sp. nov. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 1993-2002.	0.8	15
14690	Two new scuticociliates from southern China: <i>Uronema apomarinum</i> sp. nov. and <i>Homalogastra parasetosa</i> sp. nov., with improved diagnoses of the genus <i>Homalogastra</i> and its type species <i>Homalogastra setosa</i> (Ciliophora, Oligohymenophorea). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 2405-2419.	0.8	3
14691	<i>Helicobacter labacensis</i> sp. nov., <i>Helicobacter mehlei</i> sp. nov., and <i>Helicobacter vulpis</i> sp. nov., isolated from gastric mucosa of red foxes (<i>Vulpes vulpes</i>). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 2395-2404.	0.8	22
14692	Reclassification of <i>Clostridium diolis</i> Biebl and SprÅrter 2003 as a later heterotypic synonym of <i>Clostridium beijerinckii</i> Donker 1926 (Approved Lists 1980) emend. Keis et al. 2001. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 2463-2466.	0.8	12
14693	Morphological redescription and neotypification of two poorly known tintinnine ciliates (<i>Alveolata</i> , Ciliophora, Tintinnina), with a phylogenetic investigation based on SSU rRNA gene sequences. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 2515-2530.	0.8	12
14694	Phylogenomic revision of the family Streptosporangiaceae, reclassification of <i>Desertactinospora gelatinilytica</i> as <i>Spongiactinospora gelatinilytica</i> comb. nov. and a taxonomic home for the genus <i>Sinosporangium</i> in the family Streptosporangiaceae. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 2569-2579.	0.8	17
14695	<i>Haemophilus seminalis</i> sp. nov., isolated from human semen. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 2588-2595.	0.8	10
14696	Genomic and genetic sequence information of strains assigned to the genus <i>Rhodopseudomonas</i> reveal the great heterogeneity of the group and identify strain <i>Rhodopseudomonas palustris</i> DSM 123T as the authentic type strain of this species. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 3932-3938.	0.8	17
14697	<i>Vitreimonas flagellata</i> gen. nov., sp. nov., a novel member of the family Hyphomonadaceae isolated from an activated sludge sample. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 2632-2639.	0.8	10
14698	Description of <i>Citrobacter cronae</i> sp. nov., isolated from human rectal swabs and stool samples. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 2998-3003.	0.8	18
14699	A taxonomic note on the genus <i>Lactobacillus</i> : Description of 23 novel genera, emended description of the genus <i>Lactobacillus</i> Beijerinck 1901, and union of Lactobacillaceae and Leuconostocaceae. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 2782-2858.	0.8	2,775
14700	<i>Lactobacillus garii</i> sp. nov., isolated from a fermented cassava product. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 3012-3017.	0.8	14
14701	<i>Pseudomonas kitaguniensis</i> sp. nov., a pathogen causing bacterial rot of Welsh onion in Japan. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 3018-3026.	0.8	17
14702	<i>Lactobacillus buchneri</i> subsp. <i>silagei</i> subsp. nov., isolated from rice grain silage. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 3111-3116.	0.8	17
14703	<i>Nocardiopsis deserti</i> sp. nov., isolated from a high altitude Atacama Desert soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 3210-3218.	0.8	15

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14704	<i>Francisella salimarina</i> sp. nov., isolated from coastal seawater. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 3264-3272.	0.8	12
14705	<i>Klebsiella indica</i> sp. nov., isolated from the surface of a tomato. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 3278-3286.	0.8	10
14706	<i>Kluyveromyces osmophilus</i> is not a synonym of <i>Zygosaccharomyces mellis</i> ; reinstatement as <i>Zygosaccharomyces osmophilus</i> comb. nov.. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 3374-3378.	0.8	7
14707	Polyphasic studies of new species of <i>Diaporthe</i> from native forest in Chile, with descriptions of <i>Diaporthe araucanorum</i> sp. nov., <i>Diaporthe foikelawen</i> sp. nov. and <i>Diaporthe patagonica</i> sp. nov.. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 3379-3390.	0.8	16
14708	<i>Amycolatopsis anabasis</i> sp. nov., a novel endophytic actinobacterium isolated from roots of <i>Anabasis elatior</i> . International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 3391-3398.	0.8	10
14709	<i>Modestobacter altitudinis</i> sp. nov., a novel actinobacterium isolated from Atacama Desert soil. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 3513-3527.	0.8	11
14710	Proposal to reclassify the proteobacterial classes Deltaproteobacteria and Oligoflexia, and the phylum Thermodesulfobacteria into four phyla reflecting major functional capabilities. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 5972-6016.	0.8	830
14711	<i>Bacillus pasinlerensis</i> sp. nov., a thermophilic bacterium isolated from a hot spring in Turkey. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 3865-3871.	0.8	17
14712	<i>Ningiella ruwaisensis</i> gen. nov., sp. nov., a member of the family Alteromonadaceae isolated from marine water of the Arabian Gulf. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 4130-4138.	0.8	22
14713	<i>Pseudomonas izuensis</i> sp. nov., a novel species isolated from Izu Oshima, Japan. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 4212-4216.	0.8	5
14714	<i>Pseudomonas defluvii</i> sp. nov., isolated from hospital sewage. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 4199-4203.	0.8	10
14715	<i>Aquirufa ecclesiirivi</i> sp. nov. and <i>Aquirufa beregesia</i> sp. nov., isolated from a small creek and classification of <i>Allopsuedarcicella aquatilis</i> as a later heterotypic synonym of <i>Aquirufa nivalisilvae</i> . International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 4602-4609.	0.8	13
14716	Six novel species of the obligate marine actinobacterium <i>Salinispora</i> , <i>Salinispora cortesiana</i> sp. nov., <i>Salinispora fenicalii</i> sp. nov., <i>Salinispora goodfellowii</i> sp. nov., <i>Salinispora mooreana</i> sp. nov., <i>Salinispora oceanensis</i> sp. nov. and <i>Salinispora vitiensis</i> sp. nov., and emended description of the genus <i>Salinispora</i> . International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 4668-4682.	0.8	40
14717	<i>Streptomyces harenosi</i> sp. nov., a home for a gifted strain isolated from Indonesian sand dune soil. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 4874-4882.	0.8	11
14718	<i>Rhizobium dioscoreae</i> sp. nov., a plant growth-promoting bacterium isolated from yam (<i>Dioscorea</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.8	15
14719	<i>Gulosibacter macacae</i> sp. nov., a novel actinobacterium isolated from <i>Macaca mulatta</i> faeces. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 5115-5122.	0.8	12
14720	<i>Yersinia artesiana</i> sp. nov., <i>Yersinia proxima</i> sp. nov., <i>Yersinia alsatica</i> sp. nov., <i>Yersinia vastinensis</i> sp. nov., <i>Yersinia thracica</i> sp. nov. and <i>Yersinia occitanica</i> sp. nov., isolated from humans and animals. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 5363-5372.	0.8	36
14721	<i>Fluviibacter phosphoraccumulans</i> gen. nov., sp. nov., a polyphosphate-accumulating bacterium of <i>Fluviibacteraceae</i> fam. nov., isolated from surface river water. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 5551-5560.	0.8	15

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14722	Rubrobacter tropicus sp. nov. and Rubrobacter marinus sp. nov., isolated from deep-sea sediment of the South China Sea. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 5576-5585.	0.8	13
14723	Robust demarcation of 17 distinct Bacillus species clades, proposed as novel Bacillaceae genera, by phylogenomics and comparative genomic analyses: description of Robertmurraya kyonggiensis sp. nov. and proposal for an emended genus Bacillus limiting it only to the members of the Subtilis and Cereus clades of species. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 5753-5798.	0.8	659
14724	Gramella bathymodioli sp. nov., isolated from a mussel inhabiting a hydrothermal field in the Okinawa Trough. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 5854-5860.	0.8	9
14725	Bifidobacteria in two-toed sloths (Choloepus didactylus): phylogenetic characterization of the novel taxon Bifidobacterium choloepi sp. nov.. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 6115-6125.	0.8	13
14726	Aurantiacibacter rhizosphaerae sp. nov., isolated from a rhizosphere mudflat of a halophyte and proposal to reclassify Erythrobacter suaedae Lee et al. 2019. and Erythrobacter flavus Yoon et al. 2003 as Aurantiacibacter suaedae comb. nov. and Qipengyuania flava comb. nov., respectively. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 6257-6265.	0.8	24
14727	Bacillus argentoratensis and Lactobacillus buchneri subsp. silagei as Lactocaseibacillus zhaodongensis comb. nov., Lactocaseibacillus zeae comb. nov., Lactiplantibacillus argentoratensis comb. nov. and Lentilactobacillus buchneri subsp. silagei comb. nov., respectively and Apilactobacillus kosoi as a later heterotypic synonym of Apilactobacillus micheneri. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 6414-6417.	0.8	43
14728	Pseudopontixanthobacter vadosimaris gen. nov., sp. nov., isolated from shallow sea near Kueishan Island. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 6444-6449.	0.8	10
14729	Micromonospora fluminis sp. nov., isolated from mountain river sediment. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 6428-6436.	0.8	8
14730	Pseudodesulfovibrio mercurii sp. nov., a mercury-methylating bacterium isolated from sediment. International Journal of Systematic and Evolutionary Microbiology, 2019, 71, .	0.8	13
14731	Pseudomonas kielensis sp. nov. and Pseudomonas baltica sp. nov., isolated from raw milk in Germany. International Journal of Systematic and Evolutionary Microbiology, 2019, 71, .	0.8	11
14732	Pseudomonas cyclaminis sp. nov., a pathogen causing bacterial bud blight of cyclamen in Japan. International Journal of Systematic and Evolutionary Microbiology, 2019, 71, .	0.8	8
14733	Elevation of Lactococcus lactis subsp. cremoris to the species level as Lactococcus cremoris sp. nov. and transfer of Lactococcus lactis subsp. tructae to Lactococcus cremoris as Lactococcus cremoris subsp. tructae comb. nov.. International Journal of Systematic and Evolutionary Microbiology, 2019, 71, .	0.8	43
14734	Ovalopodium rosalinum sp. nov., Planopodium haveli gen. nov, sp. nov., Planopodium desertum comb. nov. and new insights into phylogeny of the deeply branching members of the order Himatismenida (Amoebozoa). International Journal of Systematic and Evolutionary Microbiology, 2019, 71, .	0.8	3
14735	Characterization of a second open reading frame in genome segment 10 of bluetongue virus. Journal of General Virology, 2015, 96, 3280-3293.	1.3	93
14736	Molecular characterization of novel mucosotropic papillomaviruses from a Florida manatee (Trichechus manatus latirostris). Journal of General Virology, 2015, 96, 3545-3553.	1.3	3
14737	Genetic diversity of species Fowl aviadenovirus D and Fowl aviadenovirus E. Journal of General Virology, 2016, 97, 2323-2332.	1.3	31
14738	A highly pathogenic avian-derived influenza virus H5N1 with 2009 pandemic H1N1 internal genes demonstrates increased replication and transmission in pigs. Journal of General Virology, 2017, 98, 18-30.	1.3	13
14739	Deep sequencing analysis of tick-borne encephalitis virus from questing ticks at natural foci reveals similarities between quasispecies pools of the virus. Journal of General Virology, 2017, 98, 413-421.	1.3	10

#	ARTICLE	IF	CITATIONS
14740	A porcine enterovirus G associated with enteric disease contains a novel papain-like cysteine protease. <i>Journal of General Virology</i> , 2017, 98, 1305-1310.	1.3	43
14741	The genomic evolution of H1 influenza A viruses from swine detected in the United States between 2009 and 2016. <i>Journal of General Virology</i> , 2017, 98, 2001-2010.	1.3	54
14742	The impact of virus population diversity on the dynamics of cytomegalovirus DNAemia in allogeneic stem cell transplant recipients. <i>Journal of General Virology</i> , 2017, 98, 2530-2542.	1.3	10
14743	Identification of the same polyomavirus species in different African horseshoe bat species is indicative of short-range host-switching events. <i>Journal of General Virology</i> , 2017, 98, 2771-2785.	1.3	11
14744	Fish polyomaviruses belong to two distinct evolutionary lineages. <i>Journal of General Virology</i> , 2018, 99, 567-573.	1.3	19
14745	Baculovirus Kimura two-parameter species demarcation criterion is confirmed by the distances of 38 core gene nucleotide sequences. <i>Journal of General Virology</i> , 2018, 99, 1307-1320.	1.3	40
14746	Characterization of Trinit virus supports its reclassification in the family Peribunyaviridae. <i>Journal of General Virology</i> , 2019, 100, 137-144.	1.3	6
14747	Prediction of the molecular boundary and functionality of novel viral AlkB domains using homology modelling and principal component analysis. <i>Journal of General Virology</i> , 2019, 100, 691-703.	1.3	5
14748	The virome of an endangered stingless bee suffering from annual mortality in southern Brazil. <i>Journal of General Virology</i> , 2019, 100, 1153-1164.	1.3	23
14749	Detection and characterization of a novel bat-borne coronavirus in Singapore using multiple molecular approaches. <i>Journal of General Virology</i> , 2019, 100, 1363-1374.	1.3	27
14750	Analysis of genomic-length HBV sequences to determine genotype and subgenotype reference sequences. <i>Journal of General Virology</i> , 2020, 101, 271-283.	1.3	38
14751	Predicting the recombination potential of severe acute respiratory syndrome coronavirus 2 and Middle East respiratory syndrome coronavirus. <i>Journal of General Virology</i> , 2020, 101, 1251-1260.	1.3	12
14752	Use of whole-genome sequencing for the public health surveillance of <i>Shigella sonnei</i> in England and Wales, 2015. <i>Journal of Medical Microbiology</i> , 2016, 65, 882-884.	0.7	45
14753	Isolation and molecular characterization of group B <i>Streptococcus</i> from laboratory Long-Evans rats (<i>Rattus norvegicus</i>) with and without invasive group B streptococcal disease. <i>Journal of Medical Microbiology</i> , 2018, 67, 97-109.	0.7	3
14754	The nursing home elder microbiome stability and associations with age, frailty, nutrition and physical location. <i>Journal of Medical Microbiology</i> , 2018, 67, 40-51.	0.7	69
14755	In vivo acquisition and risk of inter-species spread of bla KPC-3-plasmid from <i>Klebsiella pneumoniae</i> to <i>Serratia marcescens</i> in the lower respiratory tract. <i>Journal of Medical Microbiology</i> , 2020, 69, 82-86.	0.7	5
14756	Matrix-assisted laser desorption/ionization time-of-flight MS for the accurate identification of <i>Burkholderia cepacia</i> complex and <i>Burkholderia gladioli</i> in the clinical microbiology laboratory. <i>Journal of Medical Microbiology</i> , 2020, 69, 1105-1113.	0.7	8
14757	Redefining the differences in gene content between <i>Yersinia pestis</i> and <i>Yersinia pseudotuberculosis</i> using large-scale comparative genomics. <i>Microbial Genomics</i> , 2015, 1, e000028.	1.0	9

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14758	Applying phylogenomics to understand the emergence of Shiga-toxin-producing <i>Escherichia coli</i> O157:H7 strains causing severe human disease in the UK. <i>Microbial Genomics</i> , 2015, 1, e000029.	1.0	105
14759	Repeated local emergence of carbapenem-resistant <i>Acinetobacter baumannii</i> in a single hospital ward. <i>Microbial Genomics</i> , 2016, 2, e000050.	1.0	65
14760	Pan-genomic perspective on the evolution of the <i>Staphylococcus aureus</i> USA300 epidemic. <i>Microbial Genomics</i> , 2016, 2, e000058.	1.0	34
14761	NASP: an accurate, rapid method for the identification of SNPs in WGS datasets that supports flexible input and output formats. <i>Microbial Genomics</i> , 2016, 2, e000074.	1.0	237
14762	Short-term evolution of Shiga toxin-producing <i>Escherichia coli</i> O157:H7 between two food-borne outbreaks. <i>Microbial Genomics</i> , 2016, 2, e000084.	1.0	45
14763	Monomorphic genotypes within a generalist lineage of <i>Campylobacter jejuni</i> show signs of global dispersion. <i>Microbial Genomics</i> , 2016, 2, e000088.	1.0	31
14764	Whole genome analysis of <i>Yersinia ruckeri</i> isolated over 27 years in Australia and New Zealand reveals geographical endemism over multiple lineages and recent evolution under host selection. <i>Microbial Genomics</i> , 2016, 2, e000095.	1.0	21
14765	Evolution of a zoonotic pathogen: investigating prophage diversity in enterohaemorrhagic <i>Escherichia coli</i> O157 by long-read sequencing. <i>Microbial Genomics</i> , 2016, 2, e000096.	1.0	46
14766	Genomic epidemiology of a national outbreak of post-surgical <i>Mycobacterium abscessus</i> wound infections in Brazil. <i>Microbial Genomics</i> , 2017, 3, e000111.	1.0	22
14767	Population genetic structuring of methicillin-resistant <i>Staphylococcus aureus</i> clone EMRSA-15 within UK reflects patient referral patterns. <i>Microbial Genomics</i> , 2017, 3, e000113.	1.0	19
14768	Phylogenomics and comparative genomics of <i>Lactobacillus salivarius</i> , a mammalian gut commensal. <i>Microbial Genomics</i> , 2017, 3, e000115.	1.0	86
14769	Whole-genome sequencing to investigate a non-clonal melioidosis cluster on a remote Australian island. <i>Microbial Genomics</i> , 2017, 3, e000117.	1.0	10
14770	Patchy promiscuity: machine learning applied to predict the host specificity of <i>Salmonella enterica</i> and <i>Escherichia coli</i> . <i>Microbial Genomics</i> , 2017, 3, e000135.	1.0	46
14771	Suspected cases of intracontinental <i>Burkholderia pseudomallei</i> sequence type homoplasy resolved using whole-genome sequencing. <i>Microbial Genomics</i> , 2017, 3, .	1.0	30
14772	A novel prophage identified in strains from <i>Salmonella enterica</i> serovar Enteritidis is a phylogenetic signature of the lineage ST-1974. <i>Microbial Genomics</i> , 2018, 4, .	1.0	9
14773	Whole-genome sequencing revealed concurrent outbreaks of shigellosis in the English Orthodox Jewish Community caused by multiple importations of <i>Shigella sonnei</i> from Israel. <i>Microbial Genomics</i> , 2018, 4, .	1.0	14
14774	Use of genomics to design a diagnostic assay to discriminate between <i>Streptococcus pneumoniae</i> and <i>Streptococcus pseudopneumoniae</i> . <i>Microbial Genomics</i> , 2018, 4, .	1.0	19
14775	Massive over-representation of solute-binding proteins (SBPs) from the tripartite tricarboxylate transporter (TTT) family in the genome of the β -proteobacterium <i>Rhodoplanes</i> sp. Z2-YC6860. <i>Microbial Genomics</i> , 2018, 4, .	1.0	5

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14776	Using glycolysis enzyme sequences to inform <i>Lactobacillus</i> phylogeny. <i>Microbial Genomics</i> , 2018, 4, .	1.0	9
14777	Pneumococcal vaccine impacts on the population genomics of non-typeable <i>Haemophilus influenzae</i> . <i>Microbial Genomics</i> , 2018, 4, .	1.0	12
14778	Metagenomic assembly of new (sub)polar Cyanobacteria and their associated microbiome from non-axenic cultures. <i>Microbial Genomics</i> , 2018, 4, .	1.0	23
14779	Multi-step genomic dissection of a suspected intra-hospital <i>Helicobacter cinaedi</i> outbreak. <i>Microbial Genomics</i> , 2019, 5, .	1.0	8
14780	HomoplasmyFinder: a simple tool to identify homoplasies on a phylogeny. <i>Microbial Genomics</i> , 2019, 5, .	1.0	57
14781	Genomic approaches used to investigate an atypical outbreak of <i>Salmonella</i> Adjame. <i>Microbial Genomics</i> , 2019, 5, .	1.0	11
14782	Whole-genome analysis of extraintestinal <i>Escherichia coli</i> sequence type 73 from a single hospital over a 2 year period identified different circulating clonal groups. <i>Microbial Genomics</i> , 2020, 6, .	1.0	14
14783	rPinecone: Define sub-lineages of a clonal expansion via a phylogenetic tree. <i>Microbial Genomics</i> , 2019, 5, .	1.0	10
14784	Global phylogenomics of multidrug-resistant <i>Salmonella enterica</i> serotype Kentucky ST198. <i>Microbial Genomics</i> , 2019, 5, .	1.0	69
14785	Assessing the impact, genomics and evolution of type II secretion across a large, medically important genus: the <i>Legionella</i> type II secretion paradigm. <i>Microbial Genomics</i> , 2019, 5, .	1.0	26
14786	Enterohaemorrhagic <i>Escherichia coli</i> O121:H19 acquired an extended-spectrum β -lactamase gene during the development of an outbreak in two nurseries. <i>Microbial Genomics</i> , 2019, 5, .	1.0	3
14787	Comparative genome analysis of <i>Lactobacillus mudanjiangensis</i> , an understudied member of the <i>Lactobacillus plantarum</i> group. <i>Microbial Genomics</i> , 2019, 5, .	1.0	9
14788	Comparative genomic analysis identifies X-factor (haemin)-independent <i>Haemophilus haemolyticus</i> : a formal re-classification of ' <i>Haemophilus intermedius</i> '. <i>Microbial Genomics</i> , 2020, 6, .	1.0	6
14789	Pangenome of <i>Acinetobacter baumannii</i> uncovers two groups of genomes, one of them with genes involved in CRISPR/Cas defence systems associated with the absence of plasmids and exclusive genes for biofilm formation. <i>Microbial Genomics</i> , 2019, 5, .	1.0	42
14790	Use of whole-genome sequencing to identify clusters of <i>Shigella flexneri</i> associated with sexual transmission in men who have sex with men in England: a validation study using linked behavioural data. <i>Microbial Genomics</i> , 2019, 5, .	1.0	16
14791	O-antigen biosynthesis gene clusters of <i>Escherichia albertii</i> : their diversity and similarity to <i>Escherichia coli</i> gene clusters and the development of an O-genotyping method. <i>Microbial Genomics</i> , 2019, 5, .	1.0	27
14792	The characterization of mobile colistin resistance (<i>mcr</i>) genes among 33â€000 <i>Salmonella enterica</i> genomes from routine public health surveillance in England. <i>Microbial Genomics</i> , 2020, 6, .	1.0	16
14793	Genome structure reveals the diversity of mating mechanisms in <i>Saccharomyces cerevisiae</i> x <i>Saccharomyces kudriavzevii</i> hybrids, and the genomic instability that promotes phenotypic diversity. <i>Microbial Genomics</i> , 2020, 6, .	1.0	22

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14794	Comparison of Shiga toxin-encoding bacteriophages in highly pathogenic strains of Shiga toxin-producing <i>Escherichia coli</i> O157:H7 in the UK. <i>Microbial Genomics</i> , 2020, 6, .	1.0	25
14795	Using genomics to understand inter- and intra- outbreak diversity of <i>Pasteurella multocida</i> isolates associated with fowl cholera in meat chickens. <i>Microbial Genomics</i> , 2020, 6, .	1.0	6
14796	Comparison of core-genome MLST, coreSNP and PFGE methods for <i>Klebsiella pneumoniae</i> cluster analysis. <i>Microbial Genomics</i> , 2020, 6, .	1.0	34
14797	Genomic surveillance of <i>Escherichia coli</i> ST131 identifies local expansion and serial replacement of subclones. <i>Microbial Genomics</i> , 2020, 6, .	1.0	33
14798	Genomic epidemiology and population structure of <i>Neisseria gonorrhoeae</i> in Norway, 2016–2017. <i>Microbial Genomics</i> , 2020, 6, .	1.0	20
14799	Bayesian reconstruction of <i>Mycobacterium tuberculosis</i> transmission networks in a high incidence area over two decades in Malawi reveals associated risk factors and genomic variants. <i>Microbial Genomics</i> , 2020, 6, .	1.0	18
14800	Analysis of the biodegradative and adaptive potential of the novel polychlorinated biphenyl degrader <i>Rhodococcus</i> sp. WAY2 revealed by its complete genome sequence. <i>Microbial Genomics</i> , 2020, 6, .	1.0	20
14801	<i>Mycobacterium bovis</i> genomics reveals transmission of infection between cattle and deer in Ireland. <i>Microbial Genomics</i> , 2020, 6, .	1.0	39
14802	Genomic sequence analysis of <i>Dissulfurirhabdus thermomarina</i> SH388 and proposed reassignment to <i>Dissulfurirhabdaceae</i> fam. nov.. <i>Microbial Genomics</i> , 2020, 6, .	1.0	2
14803	Phylogenetic distribution and evolutionary dynamics of <i>nod</i> and <i>T3SS</i> genes in the genus <i>Bradyrhizobium</i> . <i>Microbial Genomics</i> , 2020, 6, .	1.0	9
14804	A publicly accessible database for <i>Clostridioides difficile</i> genome sequences supports tracing of transmission chains and epidemics. <i>Microbial Genomics</i> , 2020, 6, .	1.0	22
14805	Diversification in immunogenicity genes caused by selective pressures in invasive meningococci. <i>Microbial Genomics</i> , 2020, 6, .	1.0	6
14806	Comparing serotyping with whole-genome sequencing for subtyping of non-typhoidal <i>Salmonella</i> enterica: a large-scale analysis of 37 serotypes with a public health impact in the USA. <i>Microbial Genomics</i> , 2020, 6, .	1.0	11
14807	Genomic diversity of <i>Escherichia coli</i> isolates from non-human primates in the Gambia. <i>Microbial Genomics</i> , 2020, 6, .	1.0	12
14808	Forensic genomics of a novel <i>Klebsiella quasipneumoniae</i> type from a neonatal intensive care unit in China reveals patterns of colonization, evolution and epidemiology. <i>Microbial Genomics</i> , 2020, 6, .	1.0	12
14809	Whole-genome epidemiology links phage-mediated acquisition of a virulence gene to the clonal expansion of a pandemic <i>Salmonella enterica</i> serovar Typhimurium clone. <i>Microbial Genomics</i> , 2020, 6, .	1.0	15
14810	Genomic epidemiology of nontoxigenic <i>Corynebacterium diphtheriae</i> from King County, Washington State, USA between July 2018 and May 2019. <i>Microbial Genomics</i> , 2020, 6, .	1.0	9
14811	Subtelomeres are fast-evolving regions of the <i>Streptomyces</i> linear chromosome. <i>Microbial Genomics</i> , 2019, 7, .	1.0	9

#	ARTICLE	IF	CITATIONS
14812	Phylogenetic context of Shiga toxin-producing <i>Escherichia coli</i> serotype O26:H11 in England. <i>Microbial Genomics</i> , 2021, 7, .	1.0	5
14813	Antibiotic resistance due to an unusual ColE1-type replicon plasmid in <i>Aeromonas salmonicida</i> . <i>Microbiology (United Kingdom)</i> , 2016, 162, 942-953.	0.7	22
14814	Genomic and physiological characterization of a laboratory-isolated <i>Acinetobacter schindleri</i> ACE strain that quickly and efficiently catabolizes acetate. <i>Microbiology (United Kingdom)</i> , 2017, 163, 1052-1064.	0.7	8
15441	Codon-based analysis of selection pressure and genetic structure in the <i>Psammobates tentorius</i> (Bell, 1828) species complex, and phylogeny inferred from both codons and amino acid sequences. <i>African Journal of Ecology</i> , 2021, 59, 497-509.	0.4	5
15442	Burrowing into the forest: Phylogeny of the Asian forest scorpions (Scorpionidae: Heterometrinae) and the evolution of ecomorphotypes. <i>Cladistics</i> , 2021, 37, 109-161.	1.5	4
15443	Phylogeography and host range of <i>Armillaria gallica</i> in riparian forests of the northern Great Plains, USA. <i>Forest Pathology</i> , 2021, 51, .	0.5	4
15444	The gammaproteobacterium <i>Achromatium</i> forms intracellular amorphous calcium carbonate and not (crystalline) calcite. <i>Geobiology</i> , 2021, 19, 199-213.	1.1	20
15445	<i>Parvularia atlantis</i> gen. et sp. nov., a Nucleariid Filose Amoeba (Holomycota, Opisthokonta). <i>Journal of Eukaryotic Microbiology</i> , 2018, 65, 170-179.	0.8	21
15446	Taxonomic phylogeny and taxonomy of the genus <i>Phacus</i> (Euglenida) based on morphological and molecular data. <i>Journal of Phycology</i> , 2020, 56, 1135-1156.	1.0	7
15447	Comparative genomics of figworts (<i>Scrophularia</i> , Scrophulariaceae), with implications for the evolution of <i>Scrophularia</i> and Lamiales. <i>Journal of Systematics and Evolution</i> , 2019, 57, 55-65.	1.6	37
15448	Shotgun mitogenomics across body size classes in a local assemblage of tropical Diptera: Phylogeny, species diversity and mitochondrial abundance spectrum. <i>Molecular Ecology</i> , 2017, 26, 5086-5098.	2.0	17
15449	Integrative species delimitation reveals cryptic diversity in the southern Appalachian <i>Antrodiaetus unicolor</i> (Araneae: Antrodiaetidae) species complex. <i>Molecular Ecology</i> , 2020, 29, 2269-2287.	2.0	40
15450	Comparative plastome genomics and phylogenomics of <i>Brachypodium</i> : flowering time signatures, introgression and recombination in recently diverged ecotypes. <i>New Phytologist</i> , 2018, 218, 1631-1644.	3.5	89
15451	Diversification of true water bugs revealed by transcriptome-based phylogenomics. <i>Systematic Entomology</i> , 2021, 46, 339-356.	1.7	16
15452	The role of African buffalo in the epidemiology of foot-and-mouth disease in sympatric cattle and buffalo populations in Kenya. <i>Transboundary and Emerging Diseases</i> , 2020, 67, 2206.	1.3	14
15454	Divergence time estimation of an ancient relict genus <i>Mankyua</i> (Ophioglossaceae) on the young volcanic Jejudo Island in Korea. <i>Korean Journal of Plant Taxonomy</i> , 2018, 48, 1-8.	0.3	1
15455	Rapid Identification of Different <i>Escherichia coli</i> Sequence Type 131 Clades. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	94
15456	Evolution of Diverse Effective N ² -Fixing Microsymbionts of <i>Cicer arietinum</i> following Horizontal Transfer of the <i>Mesorhizobium ciceri</i> CC1192 Symbiosis Integrative and Conjugative Element. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	16

#	ARTICLE	IF	CITATIONS
15457	Primer Design for an Accurate View of Picocyanobacterial Community Structure by Using High-Throughput Sequencing. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	9
15458	Transient Silencing of Antibiotic Resistance by Mutation Represents a Significant Potential Source of Unanticipated Therapeutic Failure. <i>MBio</i> , 2019, 10, .	1.8	39
15459	Genome Sequence of the Alphaproteobacterium <i>Blastochloris sulfovirdis</i> DSM 729, Which Requires Reduced Sulfur as a Growth Supplement and Contains Bacteriochlorophyll <i>a</i> . <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	3
15460	Draft Genome Sequence of Novel <i>Metschnikowia</i> sp. Strain JCM 33374, a Nectar Yeast Isolated from a Bumblebee. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	1
15461	Genomes of the <i>Candidatus</i> Actinomarinales ^o Order: Highly Streamlined Marine Epipelagic Actinobacteria. <i>MSystems</i> , 2020, 5, .	1.7	24
15462	Picophytoplankton in Blagopoluchia Bay (Novaya Zemlya Archipelago) and Adjacent Part of the Kara Sea. <i>Oceanology</i> , 2020, 60, 473-482.	0.3	6
15463	Ruiyupotamon, a new genus and four new species of freshwater crabs from northwestern Yunnan, China (Decapoda, Brachyura, Potamidae). <i>Crustaceana</i> , 2020, 93, 1315-1341.	0.1	7
15464	Reassessment and systematic position of the sinistral snails of genus <i>Hemiplecta</i> from Thailand (Eupulmonata: Ariophantidae), with description of two new species. <i>Contributions To Zoology</i> , 2020, 90, 183-215.	0.2	8
15465	Spec-seq unveils transcriptional subpopulations of antibody-secreting cells following influenza vaccination. <i>Journal of Clinical Investigation</i> , 2018, 129, 93-105.	3.9	40
15466	Towards a synthesis of the Caribbean biogeography of terrestrial arthropods. <i>BMC Evolutionary Biology</i> , 2020, 20, 12.	3.2	35
15467	Genomic mechanisms for cold tolerance and production of exopolysaccharides in the Arctic cyanobacterium <i>Phormidesmis priestleyi</i> BC1401. <i>BMC Genomics</i> , 2016, 17, 533.	1.2	81
15468	Genomic determination of minimum multi-locus sequence typing schemas to represent the genomic phylogeny of <i>Mycoplasma hominis</i> . <i>BMC Genomics</i> , 2016, 17, 964.	1.2	10
15469	Impacts of local population history and ecology on the evolution of a globally dispersed pathogen. <i>BMC Genomics</i> , 2020, 21, 369.	1.2	19
15470	Role of diversity-generating retroelements for regulatory pathway tuning in cyanobacteria. <i>BMC Genomics</i> , 2020, 21, 664.	1.2	13
15471	Genomic and phenotypic characterisation of invasive neonatal and colonising group B <i>Streptococcus</i> isolates from Slovenia, 2001–2018. <i>BMC Infectious Diseases</i> , 2020, 20, 958.	1.3	9
15473	Reclassification of <i>Chromobacterium violaceum</i> ATCC 31532 and its quorum biosensor mutant CV026 to <i>Chromobacterium subtsugae</i> . <i>AMB Express</i> , 2020, 10, 202.	1.4	29
15474	Ophiostomatoid fungi associated with <i>Ips subelongatus</i> , including eight new species from northeastern China. <i>IMA Fungus</i> , 2020, 11, 3.	1.7	17
15475	Mammalian Diversity and Matses Ethnomammalogy in Amazonian Peru Part 3: Marsupials (Didelphimorphia). <i>Bulletin of the American Museum of Natural History</i> , 2019, 2019, 1.	1.2	43

#	ARTICLE	IF	CITATIONS
15476	Systematics of the Short-Tailed Whipscorpion Genus <i>Stenochrus</i> Chamberlin, 1922 (Schizomida: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 Museum of Natural History, 2019, 2019, 1.	1.2	8
15477	Taxonomy and Phylogenetics of Nanometinae and Other Australasian Orb-Weaving Spiders (Araneae: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	1.2	8
15478	Systematic Revision of the Asian Forest Scorpions (Heterometrinae Simon, 1879), Revised Suprageneric Classification of Scorpionidae Latreille, 1802, and Revalidation of Rugodentidae Bastawade et al., 2005. Bulletin of the American Museum of Natural History, 2020, 442, .	1.2	9
15479	A Species-Level Phylogeny of Old World Fruit Bats with a New Higher-Level Classification of the Family Pteropodidae. American Museum Novitates, 2020, 2020, 1.	0.2	19
15480	Expansion segments in bacterial and archaeal 5S ribosomal RNAs. Rna, 2021, 27, 133-150.	1.6	9
15481	Tanousia zрманjae (Brusina, 1866) (Caenogastropoda: Truncatelloidea: Hydrobiidae): a living fossil. Folia Malacologica, 2015, 23, 263-271.	0.1	17
15482	Islamia zermanica (Radoman, 1973) (Caenogastropoda: Hydrobiidae): morphological and molecular distinctness. Folia Malacologica, 2016, 24, 25-30.	0.1	21
15483	Agrafia Szarowska et Falniowski, 2011 (Caenogastropoda: Hydrobiidae) in the Caucasus. Folia Malacologica, 2017, 25, 237-247.	0.1	17
15484	A new Montenegrospeum species from south Croatia (Mollusca: Gastropoda: Hydrobiidae). Folia Malacologica, 2018, 26, 25-34.	0.1	13
15485	Viviparus mamillatus (KÅ¼ster, 1852), and partial congruence between the morphology-, allozyme- and DNA-based phylogeny in European Viviparidae (Caenogastropoda: Architaenioglossa). Folia Malacologica, 2019, 27, 43-51.	0.1	6
15486	Monophyly of the Moitessieriidae Bourguignat, 1863 (Caenogastropoda: Truncatelloidea). Folia Malacologica, 2019, 27, 61-70.	0.1	9
15487	Species distinctness of Bithynia cettinensis Clessin, 1887 and B. zeta GlÅ¼ter et PeÅ¼iÅ¼t, 2007 (Caenogastropoda: Truncatelloidea). Folia Malacologica, 2019, 27, 111-118.	0.1	4
15488	Lanzaiopsis Bole, 1989 (Caenogastropoda: Truncatelloidea): its phylogenetic and zoogeographic relationships. Folia Malacologica, 2019, 27, 193-201.	0.1	1
15489	Measuring evolutionary rates of proteins in a structural context. F1000Research, 2017, 6, 1845.	0.8	14
15490	Measuring evolutionary rates of proteins in a structural context. F1000Research, 2017, 6, 1845.	0.8	10
15491	A TALE of shrimps: Genome-wide survey of homeobox genes in 120 species from diverse crustacean taxa. F1000Research, 2018, 7, 71.	0.8	2
15492	Comparative genomic analysis of crustacean hyperglycemic hormone (CHH) neuropeptide genes across diverse crustacean species. F1000Research, 2018, 7, 100.	0.8	7
15493	Isolation and initial propagation of guinea pig adenovirus (GPAdV) in Cavia porcellus cell lines. F1000Research, 2019, 8, 1597.	0.8	2

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15494	Independent accretion of TIM22 complex subunits in the animal and fungal lineages. <i>F1000Research</i> , 2020, 9, 1060.	0.8	7
15495	Complete genome of <i>Pieris rapae</i> , a resilient alien, a cabbage pest, and a source of anti-cancer proteins. <i>F1000Research</i> , 2016, 5, 2631.	0.8	47
15496	An improved <i>Plasmodium cynomolgi</i> genome assembly reveals an unexpected methyltransferase gene expansion. <i>Wellcome Open Research</i> , 2017, 2, 42.	0.9	43
15497	Evaluation of phylogenetic reconstruction methods using bacterial whole genomes: a simulation based study. <i>Wellcome Open Research</i> , 0, 3, 33.	0.9	18
15498	Complete assembly of a dengue virus type 3 genome from a recent genotype III clade by metagenomic sequencing of serum. <i>Wellcome Open Research</i> , 2018, 3, 44.	0.9	4
15499	Complete assembly of a dengue virus type 3 genome from a recent genotype III clade by metagenomic sequencing of serum. <i>Wellcome Open Research</i> , 2018, 3, 44.	0.9	6
15500	Long read assemblies of geographically dispersed <i>Plasmodium falciparum</i> isolates reveal highly structured subtelomeres. <i>Wellcome Open Research</i> , 2018, 3, 52.	0.9	114
15501	Rapid in-country sequencing of whole virus genomes to inform rabies elimination programmes. <i>Wellcome Open Research</i> , 2020, 5, 3.	0.9	30
15502	New insights into the phylogeny and biogeography of the <i>Gerbera</i> -Complex (Asteraceae: Mutisieae). <i>Taxon</i> , 2016, 65, 547-562.	0.4	13
15503	A New Quadrannulate Species of <i>Orobdella</i> (Hirudinida: Arhynchobdellida) Tj ETQq1 1 0.784314 Open Access / Overlock 10		
15504	Histology-free Descriptions for Seven Species of Interstitial Ribbon Worms in the Genus <i>Ototyphlonemertes</i> (Nemertea: Monostilifera) from Vietnam. <i>Species Diversity</i> , 2018, 23, 13-37.	0.1	10
15505	A New Quadrannulate Species of <i>Orobdella</i> (Hirudinida: Arhynchobdellida) Tj ETQq1 1 0.784314 Open Access / Overlock 10		
15506	Fungal Systematics and Evolution: FUSE 3. <i>Sydowia</i> , 2017, 69, 229-264.	3.7	15
15507	Fungal Systematics and Evolution: FUSE 5. <i>Sydowia</i> , 2019, 71, 141-245.	3.7	24
15508	Phylogenetic analysis of avian paramyxoviruses 1 isolated in Taiwan from 2010 to 2018 and evidence for their intercontinental dispersal by migratory birds. <i>Journal of Veterinary Medical Science</i> , 2020, 82, 1366-1375.	0.3	6
15509	Genomic Characterization Helps Dissecting an Outbreak of Listeriosis in Northern Italy. <i>PLOS Currents</i> , 2017, 9, .	1.4	7
15510	Best Practices for Data Sharing in Phylogenetic Research. <i>PLOS Currents</i> , 2014, 6, .	1.4	17
15511	Beyond the Whole-Genome Duplication: Phylogenetic Evidence for an Ancient Interspecies Hybridization in the Baker's Yeast Lineage. <i>PLoS Biology</i> , 2015, 13, e1002220.	2.6	321

#	ARTICLE	IF	CITATIONS
15512	Phylogenomics Reveals Three Sources of Adaptive Variation during a Rapid Radiation. <i>PLoS Biology</i> , 2016, 14, e1002379.	2.6	364
15513	MamO Is a Repurposed Serine Protease that Promotes Magnetite Biomineralization through Direct Transition Metal Binding in Magnetotactic Bacteria. <i>PLoS Biology</i> , 2016, 14, e1002402.	2.6	43
15514	Characterization of Greenbeard Genes Involved in Long-Distance Kind Discrimination in a Microbial Eukaryote. <i>PLoS Biology</i> , 2016, 14, e1002431.	2.6	49
15515	Evolution of High Cellulolytic Activity in Symbiotic <i>Streptomyces</i> through Selection of Expanded Gene Content and Coordinated Gene Expression. <i>PLoS Biology</i> , 2016, 14, e1002475.	2.6	68
15516	Phylosymbiosis: Relationships and Functional Effects of Microbial Communities across Host Evolutionary History. <i>PLoS Biology</i> , 2016, 14, e2000225.	2.6	475
15517	Transient Duplication-Dependent Divergence and Horizontal Transfer Underlie the Evolutionary Dynamics of Bacterial Cell-Cell Signaling. <i>PLoS Biology</i> , 2016, 14, e2000330.	2.6	34
15518	Frequency-dependent selection can forecast evolution in <i>Streptococcus pneumoniae</i> . <i>PLoS Biology</i> , 2020, 18, e3000878.	2.6	24
15519	Evolution and lineage dynamics of a transmissible cancer in Tasmanian devils. <i>PLoS Biology</i> , 2020, 18, e3000926.	2.6	23
15520	Daptomycin treatment impacts resistance in off-target populations of vancomycin-resistant <i>Enterococcus faecium</i> . <i>PLoS Biology</i> , 2020, 18, e3000987.	2.6	13
15521	ClipKIT: A multiple sequence alignment trimming software for accurate phylogenomic inference. <i>PLoS Biology</i> , 2020, 18, e3001007.	2.6	237
15522	Convergent evolution of diverse <i>Bacillus anthracis</i> outbreak strains toward altered surface oligosaccharides that modulate anthrax pathogenesis. <i>PLoS Biology</i> , 2020, 18, e3001052.	2.6	6
15523	ReproPhylo: An Environment for Reproducible Phylogenomics. <i>PLoS Computational Biology</i> , 2015, 11, e1004447.	1.5	16
15524	Phylogeny Reconstruction with Alignment-Free Method That Corrects for Horizontal Gene Transfer. <i>PLoS Computational Biology</i> , 2016, 12, e1004985.	1.5	27
15525	Improving Phylogeny Reconstruction at the Strain Level Using Peptidome Datasets. <i>PLoS Computational Biology</i> , 2016, 12, e1005271.	1.5	4
15526	Insect Resistance to <i>Bacillus thuringiensis</i> Toxin Cry2Ab Is Conferred by Mutations in an ABC Transporter Subfamily A Protein. <i>PLoS Genetics</i> , 2015, 11, e1005534.	1.5	155
15527	Interacting networks of resistance, virulence and core machinery genes identified by genome-wide epistasis analysis. <i>PLoS Genetics</i> , 2017, 13, e1006508.	1.5	85
15528	Adaptive introgression from distant Caribbean islands contributed to the diversification of a microendemic adaptive radiation of trophic specialist pupfishes. <i>PLoS Genetics</i> , 2017, 13, e1006919.	1.5	81
15529	A spectrum of verticality across genes. <i>PLoS Genetics</i> , 2020, 16, e1009200.	1.5	19

#	ARTICLE	IF	CITATIONS
15530	Recombination events are concentrated in the spike protein region of Betacoronaviruses. <i>PLoS Genetics</i> , 2020, 16, e1009272.	1.5	52
15531	A Phylogenetic and Phenotypic Analysis of <i>Salmonella enterica</i> Serovar Weltevreden, an Emerging Agent of Diarrheal Disease in Tropical Regions. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004446.	1.3	59
15532	Independent Origin and Global Distribution of Distinct <i>Plasmodium vivax</i> Duffy Binding Protein Gene Duplications. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0005091.	1.3	48
15533	Prevalence, diversity, and host associations of <i>Bartonella</i> strains in bats from Georgia (Caucasus). <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005428.	1.3	52
15534	Comparative genomics of <i>Cryptococcus neoformans</i> var. <i>grubii</i> associated with meningitis in HIV infected and uninfected patients in Vietnam. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005628.	1.3	45
15535	Using affinity propagation clustering for identifying bacterial clades and subclades with whole-genome sequences of <i>Francisella tularensis</i> . <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008018.	1.3	6
15536	SARS-CoV-2 lineage B.6 was the major contributor to early pandemic transmission in Malaysia. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008744.	1.3	29
15537	Epidemiology of tsutsugamushi disease and its relationship with meteorological factors in Xiamen city, China. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008772.	1.3	11
15538	<i>Salmonella</i> identified in pigs in Kenya and Malawi reveals the potential for zoonotic transmission in emerging pork markets. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008796.	1.3	17
15539	Molecular signatures of sexual communication in the phlebotomine sand flies. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008967.	1.3	8
15540	A Good Compromise: Rapid and Robust Species Proxies for Inventorying Biodiversity Hotspots Using the Terebridae (Gastropoda: Conoidea). <i>PLoS ONE</i> , 2014, 9, e102160.	1.1	31
15541	Integrative Taxonomy and Species Delimitation in Harvestmen: A Revision of the Western North American Genus <i>Sclerobunus</i> (Opiliones: Laniatores: Travunioidea). <i>PLoS ONE</i> , 2014, 9, e104982.	1.1	40
15542	First Molecular Data and the Phylogenetic Position of the Millipede-Like Centipede <i>Edentistoma octosulcatum</i> Tj ETQmÄřsvÄřry, 1882 (Chilopoda: Scolopendromorpha: Scolopendridae). <i>PLoS ONE</i> , 2014, 9, e112461.	1.1	6
15543	Evidence for Frozen-Niche Variation in a Cosmopolitan Parthenogenetic Soil Mite Species (<i>Acari</i>). Tj ETQq1 1 0.784314 rgBT /Overlock 15	1.1	15
15544	Morphological Examination and Phylogenetic Analyses of <i>Phycopeltis</i> spp. (Trentepohliales), Tj ETQq0 0 0 rgBT /Overlock 10 Tj 50 182 T	1.1	10
15545	Whole Genome Sequencing Based Characterization of Extensively Drug-Resistant <i>Mycobacterium tuberculosis</i> Isolates from Pakistan. <i>PLoS ONE</i> , 2015, 10, e0117771.	1.1	59
15546	Application of the Phylogenetic Species Concept to <i>Wallemia sebi</i> from House Dust and Indoor Air Revealed by Multi-Locus Genealogical Concordance. <i>PLoS ONE</i> , 2015, 10, e0120894.	1.1	23
15547	Genomic Characterization of <i>Burkholderia pseudomallei</i> Isolates Selected for Medical Countermeasures Testing: Comparative Genomics Associated with Differential Virulence. <i>PLoS ONE</i> , 2015, 10, e0121052.	1.1	25

#	ARTICLE	IF	CITATIONS
15548	Glutathione S-Transferase (GST) Gene Diversity in the Crustacean <i>Calanus finmarchicus</i> – Contributors to Cellular Detoxification. PLoS ONE, 2015, 10, e0123322.	1.1	53
15549	Distinctive Patterns of Evolution of the γ -Globin Gene (HBD) in Primates. PLoS ONE, 2015, 10, e0123365.	1.1	7
15550	Molecular Phylogeny of Grassland Caterpillars (Lepidoptera: Lymantriinae: Gynaephora) Endemic to the Qinghai-Tibetan Plateau. PLoS ONE, 2015, 10, e0127257.	1.1	13
15551	Two Tickets to Paradise: Multiple Dispersal Events in the Founding of Hoary Bat Populations in Hawai'i. PLoS ONE, 2015, 10, e0127912.	1.1	17
15552	MLgsc: A Maximum-Likelihood General Sequence Classifier. PLoS ONE, 2015, 10, e0129384.	1.1	4
15553	Species Delimitation in the Genus <i>Moschus</i> (Ruminantia: Moschidae) and Its High-Plateau Origin. PLoS ONE, 2015, 10, e0134183.	1.1	24
15554	A Survey of the ATP-Binding Cassette (ABC) Gene Superfamily in the Salmon Louse (<i>Lepeophtheirus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.1	19
15555	Cytogenetic and Molecular Data Demonstrate that the Bryconinae (Ostariophysi, Bryconidae) Species from Southeastern Brazil Form a Phylogenetic and Phylogeographic Unit. PLoS ONE, 2015, 10, e0137843.	1.1	11
15556	New Insights into Plagiogrammaeaceae (Bacillariophyta) Based on Multigene Phylogenies and Morphological Characteristics with the Description of a New Genus and Three New Species. PLoS ONE, 2015, 10, e0139300.	1.1	29
15557	Nuclear Markers Reveal Predominantly North to South Gene Flow in <i>Ixodes scapularis</i> , the Tick Vector of the Lyme Disease Spirochete. PLoS ONE, 2015, 10, e0139630.	1.1	26
15558	Bats, Trypanosomes, and Triatomines in Ecuador: New Insights into the Diversity, Transmission, and Origins of <i>Trypanosoma cruzi</i> and Chagas Disease. PLoS ONE, 2015, 10, e0139999.	1.1	59
15559	Phylogenetic Exploration of Nosocomial Transmission Chains of 2009 Influenza A/H1N1 among Children Admitted at Red Cross War Memorial Children's Hospital, Cape Town, South Africa in 2011. PLoS ONE, 2015, 10, e0141744.	1.1	12
15560	Complete Plastid Genome Sequencing of Four <i>Tilia</i> Species (Malvaceae): A Comparative Analysis and Phylogenetic Implications. PLoS ONE, 2015, 10, e0142705.	1.1	69
15561	Fidelity and Promiscuity in an Ant-Plant Mutualism: A Case Study of <i>Triplaris</i> and <i>Pseudomyrmex</i> . PLoS ONE, 2015, 10, e0143535.	1.1	18
15562	Heterogeneous Evolution of HIV-1 CRF01_AE in Men Who Have Sex with Men (MSM) and Other Populations in China. PLoS ONE, 2015, 10, e0143699.	1.1	10
15563	Successful Recovery of Nuclear Protein-Coding Genes from Small Insects in Museums Using Illumina Sequencing. PLoS ONE, 2015, 10, e0143929.	1.1	55
15564	Complete mitochondrial genome of the Verticillium-wilt causing plant pathogen <i>Verticillium nonalfalae</i> . PLoS ONE, 2016, 11, e0148525.	1.1	19
15565	Distinctive Architecture of the Chloroplast Genome in the Chlorodendrophycean Green Algae <i>Scheffelia dubia</i> and <i>Tetraselmis</i> sp. CCMP 881. PLoS ONE, 2016, 11, e0148934.	1.1	33

#	ARTICLE	IF	CITATIONS
15566	Expression Atlas of the Deubiquitinating Enzymes in the Adult Mouse Retina, Their Evolutionary Diversification and Phenotypic Roles. PLoS ONE, 2016, 11, e0150364.	1.1	10
15567	Enhancement of DNaseI Salt Tolerance by Mimicking the Domain Structure of DNase from an Extremely Halotolerant Bacterium <i>Thioalkalivibrio</i> sp. K90mix. PLoS ONE, 2016, 11, e0150404.	1.1	5
15568	Evolutionary Relationships and Biogeography of the Ant-Epiphytic Genus <i>Squamellaria</i> (Rubiaceae: <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50</i>	1.1	28
15569	<i>Senecio changii</i> (Asteraceae: Senecioneae), a New Species from Sichuan, China. PLoS ONE, 2016, 11, e0151423.	1.1	1
15570	Cellulose-Enriched Microbial Communities from Leaf-Cutter Ant (<i>Atta colombica</i>) Refuse Dumps Vary in Taxonomic Composition and Degradation Ability. PLoS ONE, 2016, 11, e0151840.	1.1	29
15571	Historical and Current Perspectives on the Systematics of the "Enigmatic" Diatom Genus <i>Rhoicosphenia</i> (Bacillariophyta), with Single and Multi-Molecular Marker and Morphological Analyses and Discussion on the Monophyly of "Monoraphid" Diatoms. PLoS ONE, 2016, 11, e0152797.	1.1	41
15572	Patterns of Phylogenetic Diversity of Subtropical Rainforest of the Great Sandy Region, Australia Indicate Long Term Climatic Refugia. PLoS ONE, 2016, 11, e0153565.	1.1	11
15573	The Complete Female- and Male-Transmitted Mitochondrial Genome of <i>Meretrix lamarckii</i> . PLoS ONE, 2016, 11, e0153631.	1.1	37
15574	Stepwise Evolution of Coral Biomineralization Revealed with Genome-Wide Proteomics and Transcriptomics. PLoS ONE, 2016, 11, e0156424.	1.1	61
15575	Short-Term Dynamic and Local Epidemiological Trends in the South American HIV-1B Epidemic. PLoS ONE, 2016, 11, e0156712.	1.1	19
15576	Complete Genomes of <i>Bacillus coagulans</i> S-lac and <i>Bacillus subtilis</i> TO-A JPC, Two Phylogenetically Distinct Probiotics. PLoS ONE, 2016, 11, e0156745.	1.1	40
15577	Next-Generation Mitogenomics: A Comparison of Approaches Applied to Caecilian Amphibian Phylogeny. PLoS ONE, 2016, 11, e0156757.	1.1	13
15578	Clarification of the Phylogenetic Framework of the Tribe Baorini (Lepidoptera: Hesperidae: <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 262 To</i>	1.1	17
15579	The Putative SLC Transporters <i>Mfsd5</i> and <i>Mfsd11</i> Are Abundantly Expressed in the Mouse Brain and Have a Potential Role in Energy Homeostasis. PLoS ONE, 2016, 11, e0156912.	1.1	35
15580	Investigation of Amphibian Mortality Events in Wildlife Reveals an On-Going Ranavirus Epidemic in the North of the Netherlands. PLoS ONE, 2016, 11, e0157473.	1.1	28
15581	Unraveling the Physiological Roles of the Cyanobacterium <i>Geitlerinema</i> sp. BBD and Other Black Band Disease Community Members through Genomic Analysis of a Mixed Culture. PLoS ONE, 2016, 11, e0157953.	1.1	13
15582	RuBisCO in Non-Photosynthetic Alga <i>Euglena longa</i> : Divergent Features, Transcriptomic Analysis and Regulation of Complex Formation. PLoS ONE, 2016, 11, e0158790.	1.1	31
15583	Sequential CCR5-Tropic HIV-1 Reactivation from Distinct Cellular Reservoirs following Perturbation of Elite Control. PLoS ONE, 2016, 11, e0158854.	1.1	4

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15584	Phylogeography of the Subgenus <i>Drosophila</i> (Diptera: Drosophilidae): Evolutionary History of Faunal Divergence between the Old and the New Worlds. <i>PLoS ONE</i> , 2016, 11, e0160051.	1.1	46
15585	Genome Sequence of the Edible Cultivated Mushroom <i>Lentinula edodes</i> (Shiitake) Reveals Insights into Lignocellulose Degradation. <i>PLoS ONE</i> , 2016, 11, e0160336.	1.1	110
15586	Patterns of Transcript Abundance of Eukaryotic Biogeochemically-Relevant Genes in the Amazon River Plume. <i>PLoS ONE</i> , 2016, 11, e0160929.	1.1	17
15587	A Cost-Effective Approach to Sequence Hundreds of Complete Mitochondrial Genomes. <i>PLoS ONE</i> , 2016, 11, e0160958.	1.1	9
15588	A Species-Level Phylogeny of Extant Snakes with Description of a New Colubrid Subfamily and Genus. <i>PLoS ONE</i> , 2016, 11, e0161070.	1.1	206
15589	Characterization of Toxin Complex Gene Clusters and Insect Toxicity of Bacteria Representing Four Subgroups of <i>Pseudomonas fluorescens</i> . <i>PLoS ONE</i> , 2016, 11, e0161120.	1.1	43
15590	Genomic Analysis Reveals Novel Diversity among the 1976 Philadelphia Legionnairesâ€™ Disease Outbreak Isolates and Additional ST36 Strains. <i>PLoS ONE</i> , 2016, 11, e0164074.	1.1	23
15591	More than 50% of <i>Clostridium difficile</i> Isolates from Pet Dogs in Flagstaff, USA, Carry Toxigenic Genotypes. <i>PLoS ONE</i> , 2016, 11, e0164504.	1.1	64
15592	Complex within a Complex: Integrative Taxonomy Reveals Hidden Diversity in <i>Cicadetta brevipennis</i> (Hemiptera: Cicadidae) and Unexpected Relationships with a Song Divergent Relative. <i>PLoS ONE</i> , 2016, 11, e0165562.	1.1	11
15593	Mitochondrial Genome Sequences and Structures Aid in the Resolution of Piroplasmida phylogeny. <i>PLoS ONE</i> , 2016, 11, e0165702.	1.1	92
15594	<i>Aspergillus sydowii</i> and Other Potential Fungal Pathogens in Gorgonian Octocorals of the Ecuadorian Pacific. <i>PLoS ONE</i> , 2016, 11, e0165992.	1.1	41
15595	Genomes of <i>Gardnerella</i> Strains Reveal an Abundance of Prophages within the Bladder Microbiome. <i>PLoS ONE</i> , 2016, 11, e0166757.	1.1	40
15596	Voltage-Gated Na ⁺ Channel Isoforms and Their mRNA Expression Levels and Protein Abundance in Three Electric Organs and the Skeletal Muscle of the Electric Eel <i>Electrophorus electricus</i> . <i>PLoS ONE</i> , 2016, 11, e0167589.	1.1	7
15597	Molecular Evidence of Transmission of Influenza A/H1N1 2009 on a University Campus. <i>PLoS ONE</i> , 2017, 12, e0168596.	1.1	7
15598	<i>Hedysarum</i> L. (Fabaceae: Hedysareae) Is Not Monophyletic â€” Evidence from Phylogenetic Analyses Based on Five Nuclear and Five Plastid Sequences. <i>PLoS ONE</i> , 2017, 12, e0170596.	1.1	32
15599	Genotyping-by-Sequencing in a Species Complex of Australian Hummock Grasses (<i>Triodia</i>): Methodological Insights and Phylogenetic Resolution. <i>PLoS ONE</i> , 2017, 12, e0171053.	1.1	28
15600	Integrative taxonomy of root-knot nematodes reveals multiple independent origins of mitotic parthenogenesis. <i>PLoS ONE</i> , 2017, 12, e0172190.	1.1	30
15601	Taming the late Quaternary phylogeography of the Eurasian wild ass through ancient and modern DNA. <i>PLoS ONE</i> , 2017, 12, e0174216.	1.1	40

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15602	Rapid forest clearing in a Myanmar proposed national park threatens two newly discovered species of geckos (Gekkonidae: <i>Cyrtodactylus</i>). PLoS ONE, 2017, 12, e0174432.	1.1	36
15603	Comparative genomics of <i>Burkholderia multivorans</i> , a ubiquitous pathogen with a highly conserved genomic structure. PLoS ONE, 2017, 12, e0176191.	1.1	17
15604	Evolution of microRNA in primates. PLoS ONE, 2017, 12, e0176596.	1.1	34
15605	Insights into intercontinental spread of Zika virus. PLoS ONE, 2017, 12, e0176710.	1.1	6
15606	DNA reference libraries of French Guianese mosquitoes for barcoding and metabarcoding. PLoS ONE, 2017, 12, e0176993.	1.1	28
15607	Dynamin-like proteins in <i>Trypanosoma brucei</i> : A division of labour between two paralogs?. PLoS ONE, 2017, 12, e0177200.	1.1	13
15608	More than one fungus in the pepper pot: Integrative taxonomy unmask hidden species within <i>Myriostoma coliforme</i> (Geastraceae, Basidiomycota). PLoS ONE, 2017, 12, e0177873.	1.1	23
15609	Transcriptome analysis of <i>Phytophthora litchii</i> reveals pathogenicity arsenals and confirms taxonomic status. PLoS ONE, 2017, 12, e0178245.	1.1	18
15610	Peripatric speciation in an endemic Macaronesian plant after recent divergence from a widespread relative. PLoS ONE, 2017, 12, e0178459.	1.1	8
15611	Across the Indian Ocean: A remarkable example of trans-oceanic dispersal in an austral mygalomorph spider. PLoS ONE, 2017, 12, e0180139.	1.1	28
15612	Circumscription of the genus <i>Lepra</i> , a recently resurrected genus to accommodate the "Variolaria" group of <i>Pertusaria</i> sensu lato (Pertusariales, Ascomycota). PLoS ONE, 2017, 12, e0180284.	1.1	12
15613	Phylogeography in <i>Nassarius</i> mud snails: Complex patterns in congeneric species. PLoS ONE, 2017, 12, e0180728.	1.1	7
15614	Species delimitation in frogs from South American temperate forests: The case of <i>Eupsophus</i> , a taxonomically complex genus with high phenotypic variation. PLoS ONE, 2017, 12, e0181026.	1.1	26
15615	Non-sister Sri Lankan white-eyes (genus <i>Zosterops</i>) are a result of independent colonizations. PLoS ONE, 2017, 12, e0181441.	1.1	15
15616	Transfer of the small diatoms <i>Thalassiosira proschkiniae</i> and <i>T. spinulata</i> to the genus <i>Minidiscus</i> and their taxonomic re-description. PLoS ONE, 2017, 12, e0181980.	1.1	11
15617	Patterns and rates of viral evolution in HIV-1 subtype B infected females and males. PLoS ONE, 2017, 12, e0182443.	1.1	16
15618	Multi-tissue RNA-seq and transcriptome characterisation of the spiny dogfish shark (<i>Squalus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 107 osmoregulation. PLoS ONE, 2017, 12, e0182756.	1.1	22
15619	Barcoding snakeheads (Teleostei, Channidae) revisited: Discovering greater species diversity and resolving perpetuated taxonomic confusions. PLoS ONE, 2017, 12, e0184017.	1.1	44

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15620	Rapid and recent diversification patterns in Anseriformes birds: Inferred from molecular phylogeny and diversification analyses. PLoS ONE, 2017, 12, e0184529.	1.1	48
15621	Screening of a long-term sample set reveals two Ranavirus lineages in British herpetofauna. PLoS ONE, 2017, 12, e0184768.	1.1	18
15622	Genetic diversity of Entamoeba: Novel ribosomal lineages from cockroaches. PLoS ONE, 2017, 12, e0185233.	1.1	12
15623	A single Danio rerio hars gene encodes both cytoplasmic and mitochondrial histidyl-tRNA synthetases. PLoS ONE, 2017, 12, e0185317.	1.1	10
15624	Decrypting the Polyporus dictyopus complex: Recovery of Atroporus Ryvarden and segregation of Neodictyopus gen. nov. (Polyporales, Basidiomycota). PLoS ONE, 2017, 12, e0186183.	1.1	15
15625	Testing efficacy of distance and tree-based methods for DNA barcoding of grasses (Poaceae tribe) Tj ETQq1 1 0.784314 rgBT/Overlo	1.1	18
15626	Highly divergent 16S rRNA sequences in ribosomal operons of Scytonema hyalinum (Cyanobacteria). PLoS ONE, 2017, 12, e0186393.	1.1	67
15627	Barcoding the butterflies of southern South America: Species delimitation efficacy, cryptic diversity and geographic patterns of divergence. PLoS ONE, 2017, 12, e0186845.	1.1	35
15628	How many species and under what names? Using DNA barcoding and GenBank data for west Central African amphibian conservation. PLoS ONE, 2017, 12, e0187283.	1.1	26
15629	Evolutionary history of callose synthases in terrestrial plants with emphasis on proteins involved in male gametophyte development. PLoS ONE, 2017, 12, e0187331.	1.1	31
15630	Phylogenetic inference using alignment-free methods for applications in microbial community surveys using 16s rRNA gene. PLoS ONE, 2017, 12, e0187940.	1.1	5
15631	Diversification rates, host plant shifts and an updated molecular phylogeny of Andean Eois moths (Lepidoptera: Geometridae). PLoS ONE, 2017, 12, e0188430.	1.1	16
15632	Convergent evolution and topologically disruptive polymorphisms among multidrug-resistant tuberculosis in Peru. PLoS ONE, 2017, 12, e0189838.	1.1	19
15633	Topological congruence between phylogenies of Anacanthorus spp. (Monogenea: Dactylogyridae) and their Characiformes (Actinopterygii) hosts: A case of host-parasite cospeciation. PLoS ONE, 2018, 13, e0193408.	1.1	11
15634	Genomic surveillance detects Salmonella enterica serovar Paratyphi A harbouring blaCTX-M-15 from a traveller returning from Bangladesh. PLoS ONE, 2020, 15, e0228250.	1.1	15
15635	The membrane receptors that appeared before their ligand: The different proposed scenarios. PLoS ONE, 2020, 15, e0231813.	1.1	3
15636	The ITS region provides a reliable DNA barcode for identifying reishi/lingzhi (Ganoderma) from herbal supplements. PLoS ONE, 2020, 15, e0236774.	1.1	8
15637	Phylogenetic analysis and ontogenetic changes in the cone opsins of the western mosquitofish (Gambusia affinis). PLoS ONE, 2020, 15, e0240313.	1.1	11

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15638	Comparative genome analysis of test algal strain NIVA-CHL1 (<i>Raphidocelis subcapitata</i>) maintained in microalgal culture collections worldwide. <i>PLoS ONE</i> , 2020, 15, e0241889.	1.1	4
15639	An integrative approach reveals five new species of highland papayas (<i>Caricaceae</i> , <i>Vasconcellea</i>) from northern Peru. <i>PLoS ONE</i> , 2020, 15, e0242469.	1.1	10
15640	Genetic diversity of SARS-CoV-2 and clinical, epidemiological characteristics of COVID-19 patients in Hanoi, Vietnam. <i>PLoS ONE</i> , 2020, 15, e0242537.	1.1	17
15641	The Two-Phase Emergence of Non Pandemic HIV-1 Group O in Cameroon. <i>PLoS Pathogens</i> , 2015, 11, e1005029.	2.1	22
15642	Diversity of <i>Mycobacterium tuberculosis</i> across Evolutionary Scales. <i>PLoS Pathogens</i> , 2015, 11, e1005257.	2.1	70
15643	Experimental Estimation of the Effects of All Amino-Acid Mutations to HIV-1's Envelope Protein on Viral Replication in Cell Culture. <i>PLoS Pathogens</i> , 2016, 12, e1006114.	2.1	96
15644	Vaccination has minimal impact on the intrahost diversity of H3N2 influenza viruses. <i>PLoS Pathogens</i> , 2017, 13, e1006194.	2.1	90
15645	A leucine aminopeptidase is involved in kinetoplast DNA segregation in <i>Trypanosoma brucei</i> . <i>PLoS Pathogens</i> , 2017, 13, e1006310.	2.1	21
15646	Fitness cost of reassortment in human influenza. <i>PLoS Pathogens</i> , 2017, 13, e1006685.	2.1	48
15647	Characterising the epidemic spread of influenza A/H3N2 within a city through phylogenetics. <i>PLoS Pathogens</i> , 2020, 16, e1008984.	2.1	17
15648	Mutations in <i>dnaA</i> and a cryptic interaction site increase drug resistance in <i>Mycobacterium tuberculosis</i> . <i>PLoS Pathogens</i> , 2020, 16, e1009063.	2.1	23
15649	Genomic analysis reveals an exogenous viral symbiont with dual functionality in parasitoid wasps and their hosts. <i>PLoS Pathogens</i> , 2020, 16, e1009069.	2.1	10
15650	Phylogenomics of 8,839 <i>Clostridioides difficile</i> genomes reveals recombination-driven evolution and diversification of toxin A and B. <i>PLoS Pathogens</i> , 2020, 16, e1009181.	2.1	35
15651	Tandem duplication of two tRNA genes in the mitochondrial genome of <i>Tagiades vajuna</i> (Lepidoptera: Tj ETQq1 1 0.784314, rgBT /Over 1.2, 28		
15652	First North American record of an unnamed West Palaearctic <i>Agrilus</i> (Coleoptera: Buprestidae) infesting European beech (<i>Fagus sylvatica</i>) in New York City, USA. <i>European Journal of Entomology</i> , 0, 116, 244-252.	1.2	7
15653	How many species of whipworms do we share? Whipworms from man and other primates form two phylogenetic lineages. <i>Folia Parasitologica</i> , 2015, 62, .	0.7	17
15654	Correlation between host specificity and genetic diversity for the muscle-dwelling fish parasite <i>Myxobolus pseudodispar</i> : examples of myxozoan host-shift?. <i>Folia Parasitologica</i> , 2016, 63, .	0.7	21
15655	Genetic diversity of <i>Echinococcus multilocularis</i> in red foxes in Poland: the first report of a haplotype of probable Asian origin. <i>Folia Parasitologica</i> , 2017, 64, .	0.7	22

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15656	Highly active rubiscos discovered by systematic interrogation of natural sequence diversity. <i>EMBO Journal</i> , 2020, 39, e104081.	3.5	72
15657	On the systematic position of the moss genus <i>Catocopium</i> , with a new approach to the peristome reduction study. <i>Arctoa</i> , 2015, 24, 389-415.	0.3	14
15658	The Unique Antimicrobial Recognition and Signaling Pathways in Tardigrades with a Comparison Across Ecdysozoa. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1137-1148.	0.8	14
15659	Genome Assembly and Analysis of the North American Mountain Goat (<i>Oreamnos americanus</i>) Reveals Species-Level Responses to Extreme Environments. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 437-442.	0.8	11
15660	Prokaryotic ancestry and gene fusion of a dual localized peroxiredoxin in malaria parasites. <i>Microbial Cell</i> , 2015, 2, 5-13.	1.4	9
15661	Brazilian tropical dry forest (Caatinga) in the spotlight: an overview of species of <i>Aspergillus</i> , <i>Penicillium</i> and <i>Talaromyces</i> (Eurotiales) and the description of <i>P. vascosobrinhou</i> sp. nov.. <i>Acta Botanica Brasilica</i> , 2020, 34, 409-429.	0.8	18
15662	<i>Fissuroma</i> (Aigialaceae: Pleosporales) appears to be hyperdiverse on <i>Arecaceae</i> : evidence from two new species from southern Thailand. <i>Acta Botanica Brasilica</i> , 2020, 34, 384-393.	0.8	4
15663	Survey for positively selected coding regions in the genome of the hematophagous tsetse fly <i>Glossina morsitans</i> identifies candidate genes associated with feeding habits and embryonic development. <i>Genetics and Molecular Biology</i> , 2020, 43, e20180311.	0.6	1
15664	Draft genome sequence of <i>Wickerhamomyces anomalus</i> LBCM1105, isolated from cachaça fermentation. <i>Genetics and Molecular Biology</i> , 2020, 43, e20190122.	0.6	7
15665	Phylogenetic relationships of the neon tetras <i>Paracheirodon</i> spp. (Characiformes: Characidae): Tj ETQq1 1 0.784314 rgBT /Overlock 100%. <i>Ichthyology</i> , 2020, 18, .	0.5	1
15666	Species delimitation reveals an underestimated diversity of Andean catfishes of the family <i>Astroblepidae</i> (Teleostei: Siluriformes). <i>Neotropical Ichthyology</i> , 2020, 18, .	0.5	6
15667	<i>Isodon hsiwenii</i> (Lamiaceae: Nepetoideae), A New Species From Yunnan, China. <i>Systematic Botany</i> , 2019, 44, 913-922.	0.2	11
15668	<i>Acer iranicum</i> (Sapindaceae), a New Species of Maple from Northern Iran. <i>Systematic Botany</i> , 2020, 45, 163-172.	0.2	3
15669	Mitochondrial DNA Sequence Phylogeny of <i>Daucus</i> . <i>Systematic Botany</i> , 2020, 45, 403-408.	0.2	3
15670	<i>Cichla cataractae</i> (Cichliformes: Cichlidae), new species of peacock bass from the Essequibo Basin, Guyana and Venezuela. <i>Proceedings of the Academy of Natural Sciences of Philadelphia</i> , 2020, 167, 69.	1.3	8
15671	<i>Lecanora markjohnstonii</i> (Lecanoraceae, lichenized Ascomycetes), a new sorediate crustose lichen from the southeastern United States. <i>Bryologist</i> , 2018, 121, 498-512.	0.1	10
15672	<i>Mohamedia</i> , a new genus of Lejeuneaceae (Marchantiophyta) from Oceania and tropical Asia. <i>Bryologist</i> , 2019, 122, 84.	0.1	8
15673	Advances in Calymperaceae (Dicranidae, Bryophyta): Phylogeny, divergence times and pantropical promiscuity. <i>Bryologist</i> , 2019, 122, 183.	0.1	5

#	ARTICLE	IF	CITATIONS
15674	High diversification in the Neoprotoparmelia multifera complex (Ascomycota, Parmeliaceae) in northeast Brazil revealed by DNA barcoding and phenotypical characters. <i>Bryologist</i> , 2019, 122, 539.	0.1	6
15675	Extremely low genetic diversity of <i>Stigonema</i> associated with <i>Stereocaulon</i> in eastern Canada. <i>Bryologist</i> , 2020, 123, 188.	0.1	12
15676	Hidden Diversity in the Mountain Chorus Frog (<i>Pseudacris brachyphona</i>) and the Diagnosis of a New Species of Chorus Frog in the Southeastern United States. <i>Copeia</i> , 2020, 108, .	1.4	4
15677	A New Species of Fairy Wrasse (Teleostei: Labridae: Cirrhitilabrus) from Mesophotic Coral Ecosystems of the Verde Island Passage, Philippines. <i>Copeia</i> , 2020, 108, 91.	1.4	5
15678	The Phylogeny of Carangiform Fishes: Morphological and Genomic Investigations of a New Fish Clade. <i>Copeia</i> , 2020, 108, 265.	1.4	23
15679	A New Species of <i>Hypomasticus</i> from Eastern Brazil Based on Morphological and Molecular Data (Characiformes, Anostomidae). <i>Copeia</i> , 2020, 108, 416.	1.4	5
15680	Molecular Phylogenetics of the Clingfishes (Teleostei: Gobiesocidae)â€™ Implications for Classification. <i>Copeia</i> , 2020, 108, .	1.4	14
15681	Phylogenetic Position and Description of a New Species of Medicinal Leech from the Eastern United States. <i>Journal of Parasitology</i> , 2019, 105, 587.	0.3	4
15682	Weak Genetic Differentiation among Populations of the Andean Ground Beetle <i>Pelmatellus columbianus</i> (Reiche, 1843) (Coleoptera: Carabidae). <i>The Coleopterists Bulletin</i> , 2019, 73, 411.	0.1	1
15683	Taxonomic Review of South American Butter Frogs: Phylogeny, Geographic Patterns, and Species Delimitation in the <i>Leptodactylus latrans</i> Species Group (Anura: Leptodactylidae). <i>Herpetological Monographs</i> , 2020, 34, .	1.1	15
15684	Integrative Systematic Revision of <i>Bolitoglossa celaque</i> (Caudata: Plethodontidae), with a new species from the Lenca Highlands of Honduras. <i>Herpetological Monographs</i> , 2020, 33, 48.	1.1	4
15685	Survey of Freshwater Red Algae from the Batrachospermales (Rhodophyta) in South Carolina. <i>Southeastern Naturalist</i> , 2019, 18, 451.	0.2	2
15686	A New, Morphologically Cryptic Species of <i>Adenomera</i> Closely Related to <i>Adenomera araucaria</i> from the Atlantic Forest of Southern Brazil (Anura, Leptodactylidae). <i>Journal of Herpetology</i> , 2019, 53, 131.	0.2	9
15687	The Phenology of the Symbiotic Association between <i>Ambystoma maculatum</i> and Unicellular Algae (Oophila) Using Molecular Techniques. <i>Journal of Herpetology</i> , 2020, 54, .	0.2	3
15689	Phylogenetic position of Neotropical <i>Bursera</i> -specialist mistletoes: the evolution of deciduousness and succulent leaves in <i>Psittacanthus</i> (Loranthaceae). <i>Botanical Sciences</i> , 2018, 96, 443-461.	0.3	5
15690	Genetic Basis of Hydrothermal Vent Adaptation in Bythograeidae Crabs: Insights from Adaptive Evolution of Mitochondrial Protein Coding Genes. <i>Pakistan Journal of Zoology</i> , 2019, 51, .	0.1	1
15691	Relation between Gene Content and Taxonomy in Chloroplasts. <i>International Journal of Bioscience, Biochemistry, Bioinformatics (IJBBB)</i> , 2017, 7, 41-50.	0.2	1
15694	Molecular-Genetic Characteristics of <i>Yersinia pestis</i> Strains Isolated in the Mongolian Territory of Transboundary Sailyugem Natural Plague Focus. <i>Problemy Osobo Opasnykh Infektsii</i> , 2019, , 34-42.	0.2	6

#	ARTICLE	IF	CITATIONS
15695	Tubulanus tamias sp. nov. (Nemertea: Palaeonemertea) with Two Different Types of Epidermal Eyes. Zoological Science, 2015, 32, 596.	0.3	6
15696	A New Epizoanthus Species (Cnidaria: Anthozoa: Epizoanthidae) Associated with the Gastropod Mollusk Guildfordia triumphans from Southern Japan. Zoological Science, 2019, 36, 259.	0.3	6
15697	Diurodrilus kunii sp. nov. (Annelida: Diurodrilidae) and a Molecular Phylogeny of the Genus. Zoological Science, 2019, 36, 250.	0.3	1
15698	Cephalodiscus planitectus sp. nov. (Hemichordata: Pterobranchia) from Sagami Bay, Japan. Zoological Science, 2020, 37, 79.	0.3	4
15699	Milnesium (Tardigrada: Apochela) in Japan: The First Confirmed Record of Milnesium tardigradum s.s. and Description of Milnesium pacificum sp. nov.. Zoological Science, 2020, 37, 1.	0.3	11
15700	Taxonomic Reappraisal of Lineus longifissus Auct. (Nemertea: Piliophora) from Japan for the First Time in 122 Years. Zoological Science, 2020, 37, 1.	0.3	4
15701	Two New Species of the Genus Eucorydia (Blattodea: Corydiidae) from the Nansei Islands in Southwest Japan. Zoological Science, 2020, 38, 90-102.	0.3	5
15702	SaffronTree: Fast, reference-free pseudo-phylogenomic trees from reads or contigs.. Journal of Open Source Software, 2017, 2, 243.	2.0	1
15703	Mitochondrial DNA Study Reveals the Cryptic Species Penaeus japonicus (form-II) in Indian Waters. Journal of Coastal Research, 2019, 86, 149.	0.1	1
15706	Samplings of Millipedes in Japan and Scarab Beetles in Hong Kong result in five new Species of Pristionchus (Nematoda: Diplogastridae). Journal of Nematology, 2018, 50, 587-610.	0.4	8
15707	Two new Species of <i>Pristionchus</i> (Nematoda: Diplogastridae) include the Gonochoristic Sister Species of <i>P. fissidentatus</i> . Journal of Nematology, 2019, 51, 1-14.	0.4	7
15708	Middle Pleistocene Cave Bear Genome Calibrates the Evolutionary History of Palaeartic Bears. SSRN Electronic Journal, 0, , .	0.4	6
15709	In silico analysis of the LRR receptor-like serine threonine kinases subfamily in Morus notabilis. Plant OMICS, 2016, 9, 319-326.	0.4	4
15710	MOLECULAR PHYLOGENY OF APHELIDIUM TRIBONEMAE REVEALS ITS SISTER RELATIONSHIP WITH A. AFF. MELOSIRAE (APHELIDA, OPISTHOSPORIDIA). Protistology, 2016, 10, .	0.0	9
15711	Complete Genome of Achalarus lyciades, The First Representative of the Eudaminae Subfamily of Skippers. Current Genomics, 2017, 18, 366-374.	0.7	22
15712	Brief Protocol for EDGE Bioinformatics: Analyzing Microbial and Metagenomic NGS Data. Bio-protocol, 2017, 7, e2622.	0.2	8
15713	High-resolution and Deep Phylogenetic Reconstruction of Ancestral States from Large Transcriptomic Data Sets. Bio-protocol, 2020, 10, e3566.	0.2	4
15714	A new species of the endemic Himalayan genus Liurana (Anura, Ceratobatrachidae) from southeastern Tibet, China, with comments on the distribution, reproductive biology, and conservation of the genus. Zoological Research, 2019, 40, 175-184.	0.9	4

#	ARTICLE	IF	CITATIONS
15715	Conserved sequences identify the closest living relatives of primates. <i>Zoological Research</i> , 2019, 40, 532-540.	0.9	8
15716	How little is known about "the little brown frogs": description of three new species of the genus <i>Leptobranchella</i> (Anura: Megophryidae) from Yunnan Province, China. <i>Zoological Research</i> , 2020, 41, 292-313.	0.9	17
15717	Taxonomic notes on Leptonetidae (Arachnida, Araneae) from China, with descriptions of one new genus and eight new species. <i>Zoological Research</i> , 2020, 41, 684-704.	0.9	14
15718	Recruitment of ubiquitin-activating enzyme UBA1 to DNA by poly(ADP-ribose) promotes ATR signalling. <i>Life Science Alliance</i> , 2018, 1, e201800096.	1.3	13
15719	Epidemiological and molecular investigation of a rubella outbreak, Romania, 2011 to 2012. <i>Eurosurveillance</i> , 2016, 21, .	3.9	10
15720	Recurrent seasonal outbreak of an emerging serotype of Shiga toxin-producing <i>Escherichia coli</i> (STEC) Tj ETQq1 1 O:784314 rgtBT /Over	3.9	21
15721	Multinational outbreak of travel-related <i>Salmonella</i> Chester infections in Europe, summers 2014 and 2015. <i>Eurosurveillance</i> , 2017, 22, .	3.9	31
15722	Genomic non-coding regions reveal hidden patterns of mumps virus circulation in Spain, 2005 to 2015. <i>Eurosurveillance</i> , 2018, 23, .	3.9	13
15723	Clonal expansion of community-associated methicillin-resistant <i>Staphylococcus aureus</i> (MRSA) in people who inject drugs (PWID): prevalence, risk factors and molecular epidemiology, Bristol, United Kingdom, 2012 to 2017. <i>Eurosurveillance</i> , 2019, 24, .	3.9	17
15724	Outbreak of Shiga toxin-producing <i>Escherichia coli</i> O157:H7 linked to raw drinking milk resolved by rapid application of advanced pathogen characterisation methods, England, August to October 2017. <i>Eurosurveillance</i> , 2019, 24, .	3.9	30
15725	Intense interseasonal influenza outbreaks, Australia, 2018/19. <i>Eurosurveillance</i> , 2019, 24, .	3.9	27
15726	Emergence of diversity in carbapenemase-producing <i>Escherichia coli</i> ST131, England, January 2014 to June 2016. <i>Eurosurveillance</i> , 2019, 24, .	3.9	24
15727	Impact of whole genome sequencing on the investigation of food-borne outbreaks of Shiga toxin-producing <i>Escherichia coli</i> serogroup O157:H7, England, 2013 to 2017. <i>Eurosurveillance</i> , 2019, 24, .	3.9	43
15728	SARS-CoV-2 infection in farmed minks, the Netherlands, April and May 2020. <i>Eurosurveillance</i> , 2020, 25, .	3.9	573
15729	Genesis of the novel human-infecting influenza A(H10N8) virus and potential genetic diversity of the virus in poultry, China. <i>Eurosurveillance</i> , 2014, 19, .	3.9	83
15730	A multi-country <i>Salmonella</i> Enteritidis phage type 14b outbreak associated with eggs from a German producer: "near real-time" application of whole genome sequencing and food chain investigations, United Kingdom, May to September 2014. <i>Eurosurveillance</i> , 2015, 20, .	3.9	77
15731	Notes on the <i>Delosperma</i> -Clade (Aizoaceae). <i>Haseltonia</i> , 2018, 2018, 100.	0.3	2
15732	Description and Phylogeny of a New Species of Andean Lizard (Gymnophthalmidae: Cercosaurinae) from the Huancabamba Depression. <i>South American Journal of Herpetology</i> , 2020, 18, 13.	0.5	5

#	ARTICLE	IF	CITATIONS
15733	Pathogenicity of <i>Ceratocystis fimbriata</i> from New Zealand kākara on kiwifruit cultivars. <i>New Zealand Plant Protection</i> , 2020, 73, 6-12.	0.3	2
15734	Molecular Organization of 5S Ribosomal DNA and Taxonomic Status of <i>Avenella flexuosa</i> (L.) Drejer (Poaceae). <i>Cytology and Genetics</i> , 2020, 54, 505-513.	0.2	8
15735	New species of <i>Inocybe</i> (Inocybaceae) from eastern North America1. <i>Journal of the Torrey Botanical Society</i> , 2019, 146, 213.	0.1	26
15736	Molecular Phylogeny and Systematics of the Sheath-Tailed Bats from the Middle East (Emballonuridae:). <i>Tj ETQq1 1 0,784314,rgBT /Ove</i>	0,2	4
15738	Introduction of Avian Influenza A(H6N5) Virus into Asia from North America by Wild Birds. <i>Emerging Infectious Diseases</i> , 2019, 25, 2138-2140.	2.0	18
15739	Zoonotic Alphaviruses in Fatal and Neurologic Infections in Wildlife and Nonequine Domestic Animals, South Africa. <i>Emerging Infectious Diseases</i> , 2020, 26, 1182-1191.	2.0	6
15740	Multihost Transmission of <i>Schistosoma mansoni</i> in Senegal, 2015â€“2018. <i>Emerging Infectious Diseases</i> , 2020, 26, 1234-1242.	2.0	29
15741	Whole-Genome Sequencing of Russian <i>Neisseria Gonorrhoeae</i> Isolates Related to ST 1407 Genogroup. <i>Acta Naturae</i> , 2018, 10, 68-76.	1.7	4
15742	Diversity and abundance of sulfate-reducing microorganisms in a Mediterranean lagoonal complex (Amvrakikos Gulf, Ionian Sea) derived from <i>dsrB</i> gene. <i>Aquatic Microbial Ecology</i> , 2017, 79, 209-219.	0.9	3
15743	Bacterial utilization of creatine in seawater. <i>Aquatic Microbial Ecology</i> , 2017, 80, 153-165.	0.9	4
15744	Dark N2 fixation: <i>nifH</i> expression in the redoxcline of the Black Sea. <i>Aquatic Microbial Ecology</i> , 2018, 82, 43-58.	0.9	17
15745	Chlorovirus and myovirus diversity in permafrost thaw ponds. <i>Aquatic Microbial Ecology</i> , 2018, 82, 209-224.	0.9	5
15746	Isolation of Tasmanian <i>Rickettsia</i> -like organism (RLO) from farmed salmonids: identification of multiple serotypes and confirmation of pathogenicity. <i>Diseases of Aquatic Organisms</i> , 2016, 122, 85-103.	0.5	8
15747	Detection and characterisation of haplosporidian parasites of the blue mussel <i>Mytilus edulis</i> , including description of the novel parasite <i>Minchinia mytili</i> n. sp.. <i>Diseases of Aquatic Organisms</i> , 2019, 133, 57-68.	0.5	8
15748	Investigating the natural resistance of blackfoot p-a%%KERN_ERR%%ua <i>Haliotis iris</i> to abalone viral ganglioneuritis using whole transcriptome analysis. <i>Diseases of Aquatic Organisms</i> , 2019, 135, 107-119.	0.5	7
15749	Pilchard orthomyxovirus (POMV). I. Characterisation of an emerging virus isolated from pilchards <i>Sardinops sagax</i> and Atlantic salmon <i>Salmo salar</i> . <i>Diseases of Aquatic Organisms</i> , 2020, 139, 35-50.	0.5	10
15750	First detection of infectious haematopoietic necrosis virus in farmed rainbow trout in North Macedonia. <i>Diseases of Aquatic Organisms</i> , 2020, 140, 219-225.	0.5	3
15751	<i>Ellipsomyxa ariusi</i> sp. nov. (Myxosporea: Ceratomyxidae), a new myxosporean infecting the gallbladder of threadfin sea catfish <i>Arius arius</i> in India. <i>Diseases of Aquatic Organisms</i> , 2020, 142, 83-97.	0.5	5

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15752	Identity and relationships of <i>Sempervivum tectorum</i> (Crassulaceae) in the Rhine Gorge area. <i>Willdenowia</i> , 2018, 48, 405.	0.5	4
15753	Molecular and morphological evidence reveals a new smut fungus, <i>Microbotryum arcticum</i> (Microbotryaceae), on <i>Silene uralensis</i> (Caryophyllaceae) from Greenland and Canada. <i>Willdenowia</i> , 2019, 49, 241.	0.5	8
15754	Phylogenetic studies in the Hoya group (Apocynaceae, Marsdenieae): the position of <i>Anatropanthus</i> and <i>Oreosparte</i> . <i>Willdenowia</i> , 2020, 50, 119.	0.5	11
15755	Genetic Diversity of <i>norA</i> , Coding for a Main Efflux Pump of <i>Staphylococcus aureus</i> . <i>Frontiers in Genetics</i> , 2018, 9, 710.	1.1	58
15756	Specific Evolution and Gene Family Expansion of Complement 3 and Regulatory Factor H in Fish. <i>Frontiers in Immunology</i> , 2020, 11, 568631.	2.2	21
15757	Robust Demarcation of the Family Caryophanaceae (Planococcaceae) and Its Different Genera Including Three Novel Genera Based on Phylogenomics and Highly Specific Molecular Signatures. <i>Frontiers in Microbiology</i> , 2019, 10, 2821.	1.5	160
15758	Morphologically Different <i>Pectobacterium brasiliense</i> Bacteriophages PP99 and PP101: Deacetylation of O-Polysaccharide by the Tail Spike Protein of Phage PP99 Accompanies the Infection. <i>Frontiers in Microbiology</i> , 2019, 10, 3147.	1.5	33
15759	Source Attribution Study of Sporadic <i>Salmonella</i> Derby Cases in France. <i>Frontiers in Microbiology</i> , 2020, 11, 889.	1.5	27
15760	Culturing of "Unculturable" Subsurface Microbes: Natural Organic Carbon Source Fuels the Growth of Diverse and Distinct Bacteria From Groundwater. <i>Frontiers in Microbiology</i> , 2020, 11, 610001.	1.5	26
15761	High-Zinc Supplementation of Weaned Piglets Affects Frequencies of Virulence and Bacteriocin Associated Genes Among Intestinal <i>Escherichia coli</i> Populations. <i>Frontiers in Veterinary Science</i> , 2020, 7, 614513.	0.9	6
15762	A Reference Genome of <i>Bursaphelenchus mucronatus</i> Provides New Resources for Revealing Its Displacement by Pinewood Nematode. <i>Genes</i> , 2020, 11, 570.	1.0	10
15763	Distribution of Phototrophic Purple Nonsulfur Bacteria in Massive Blooms in Coastal and Wastewater Ditch Environments. <i>Microorganisms</i> , 2020, 8, 150.	1.6	10
15764	Comparative Chloroplast Genomics of <i>Fritillaria</i> (Liliaceae), Inferences for Phylogenetic Relationships between <i>Fritillaria</i> and <i>Lilium</i> and Plastome Evolution. <i>Plants</i> , 2020, 9, 133.	1.6	31
15765	Diversity and Distribution Patterns of Endolichenic Fungi in Jeju Island, South Korea. <i>Sustainability</i> , 2020, 12, 3769.	1.6	17
15766	A Novel RNA Virus in the Parasitoid Wasp <i>Lysiphlebus fabarum</i> : Genomic Structure, Prevalence, and Transmission. <i>Viruses</i> , 2020, 12, 59.	1.5	7
15767	Computational Analysis of SARS-CoV-2 and SARS-Like Coronavirus Diversity in Human, Bat and Pangolin Populations. <i>Viruses</i> , 2021, 13, 49.	1.5	19
15768	Unique, Ancient Stygobiont Clade of Hydrobiidae (Truncatelloidea) in Bulgaria: the Origin of Cave Fauna. <i>Folia Biologica</i> , 2017, 65, 79-93.	0.1	12
15769	The <i>Decursivum</i> Group of <i>Elaphoglossum</i> sect. <i>Polytrichia</i> (Dryopteridaceae): Non-subulate Species Nested in an Otherwise Subulate-scaled Clade. <i>Annals of the Missouri Botanical Garden</i> , 2019, 104, 400-428.	1.3	3

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15770	An Elegy to Rangaeris, Including a Description of Two New Genera in the <i>Cyrtorchis</i> "Tridactyle Clade (Orchidaceae, Angraecinae). <i>Annals of the Missouri Botanical Garden</i> , 2020, 105, 300-322.	1.3	3
15771	Evolution of Angiosperm Pollen: 8. Lamiids. <i>Annals of the Missouri Botanical Garden</i> , 2020, 105, 323-376.	1.3	10
15772	Two new <i>Micarea</i> species (Pilocarpaceae) from Western Europe. <i>Plant and Fungal Systematics</i> , 2020, 65, 189-199.	0.7	5
15773	Novel colophorina-like genera and species from <i>Prunus</i> trees and vineyards in Germany. <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2020, 45, 46-67.	1.6	15
15774	Illuminating type collections of nectriaceous fungi in Saccardo's fungarium. <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2020, 45, 221-249.	1.6	13
15775	Fungal Planet description sheets: 1112-1181. <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2020, 45, 251-409.	1.6	63
15776	Adaptive response of <i>Pinus monticola</i> driven by positive selection upon resistance gene analogs (RGAs) of the TIR-NBS-LRR subfamily. <i>IForest</i> , 2017, 10, 237-241.	0.5	2
15777	Hidden diversity in European bees: <i>Andrena amieti</i> sp. n., a new Alpine bee species related to <i>Andrena bicolor</i> (Fabricius, 1775) (Hymenoptera, Apoidea, Andrenidae). <i>Alpine Entomology</i> , 0, 3, 11-38.	0.2	21
15778	Unveiling of a cryptic <i>Dicranomyia</i> (<i>Idiopyga</i>) from northern Finland using integrative approach (Diptera, Limoniidae). <i>Biodiversity Data Journal</i> , 2014, 2, e4238.	0.4	6
15779	Metabarcoding of marine nematodes - evaluation of reference datasets used in tree-based taxonomy assignment approach. <i>Biodiversity Data Journal</i> , 2016, 4, e10021.	0.4	10
15780	<i>Salix</i> transect of Europe: structured genetic variation and isolation-by-distance in the nettle psyllid, <i>Trioza urticae</i> (Psylloidea, Hemiptera), from Greece to Arctic Norway. <i>Biodiversity Data Journal</i> , 2017, 5, e10824.	0.4	7
15781	New evidence shows that <i>Pocillopora</i> "damicornis-like" corals in Singapore are actually <i>Pocillopora acuta</i> (Scleractinia: Pocilloporidae). <i>Biodiversity Data Journal</i> , 2017, 5, e11407.	0.4	42
15782	A new record of <i>Avrainvillea</i> cf. <i>erecta</i> (Berkeley) A. Gepp & E. S. Gepp (Bryopsidales). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 26 e21617</i> .	0.4	10
15783	New records of bats and terrestrial small mammals from the Seli River in Sierra Leone before the construction of a hydroelectric dam. <i>Biodiversity Data Journal</i> , 2019, 7, e34754.	0.4	4
15784	OLICH: A reference library of DNA barcodes for Nordic lichens. <i>Biodiversity Data Journal</i> , 2019, 7, e36252.	0.4	27
15785	Biodiversity between sand grains: Mei fauna composition across southern and western Sweden assessed by metabarcoding. <i>Biodiversity Data Journal</i> , 2020, 8, e51813.	0.4	4
15786	A new genus of <i>Bambusicolaceae</i> (Pleosporales) on <i>Corylus avellana</i> (Fagales) from Italy. <i>Biodiversity Data Journal</i> , 2020, 8, e55957.	0.4	6
15787	Karyotype and putative chromosomal inversion suggested by integration of cytogenetic and molecular data of the fungus-farming ant <i>Mycetomoellerius iheringi</i> Emery, 1888. <i>Comparative Cytogenetics</i> , 2020, 14, 197-210.	0.3	11

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15789	Phylogenetic relationships among the subfamilies of Dryinidae (Hymenoptera, Chrysidoidea) as reconstructed by molecular sequencing. <i>Journal of Hymenoptera Research</i> , 0, 45, 15-29.	0.8	21
15790	A new species of <i>Encarsia</i> (Hymenoptera, Aphelinidae) developing on ficus whitefly <i>Singhiella simplex</i> (Hemiptera, Aleyrodidae) in China and Taiwan. <i>Journal of Hymenoptera Research</i> , 0, 46, 85-90.	0.8	5
15791	North-Western Palaearctic species of <i>Pristiphora</i> (Hymenoptera, Tenthredinidae). <i>Journal of Hymenoptera Research</i> , 0, 59, 1-190.	0.8	3
15792	North-Western Palaearctic species of <i>Pristiphora</i> (Hymenoptera, Tenthredinidae). <i>Journal of Hymenoptera Research</i> , 0, 59, 1-190.	0.8	14
15793	DNA barcoding of rhopalosomatid larvae reveals a new host record and genetic evidence of a second species of <i>Rhopalosoma</i> Cresson (Hymenoptera, Rhopalosomatidae) in America north of Mexico. <i>Journal of Hymenoptera Research</i> , 0, 74, 35-46.	0.8	5
15794	Revisiting the host use and phylogeny of <i>Colastomion</i> Baker (Hymenoptera, Braconidae, Rogadinae), with a new host record from Japan. <i>Journal of Hymenoptera Research</i> , 0, 77, 175-186.	0.8	2
15795	Characterising planktonic dinoflagellate diversity in Singapore using DNA metabarcoding. <i>Metabarcoding and Metagenomics</i> , 0, 2, e25136.	0.0	23
15796	Metabarcoding of soil nematodes: the importance of taxonomic coverage and availability of reference sequences in choosing suitable marker(s). <i>Metabarcoding and Metagenomics</i> , 0, 3, .	0.0	37
15797	Exploring the potential of metabarcoding to disentangle macroinvertebrate community dynamics in intermittent streams. <i>Metabarcoding and Metagenomics</i> , 0, 4, .	0.0	12
15798	New reports, phylogenetic analysis, and a key to <i>Lactarius</i> Pers. in the Greater Yellowstone Ecosystem informed by molecular data. <i>MycKeys</i> , 0, 15, 1-58.	0.8	11
15799	Polypores and genus concepts in <i>Phanerochaetaceae</i> (Polyporales, Basidiomycota). <i>MycKeys</i> , 0, 17, 1-46.	0.8	54
15800	<i>Ganoderma sichuanense</i> (Ganodermataceae, Polyporales) new to Thailand. <i>MycKeys</i> , 0, 22, 27-43.	0.8	13
15801	<i>Monocillium gamsii</i> sp. nov. and <i>Monocillium bulbillosum</i> : two nematode-associated fungi parasitising the eggs of <i>Heterodera filipjevi</i> . <i>MycKeys</i> , 0, 27, 21-38.	0.8	16
15802	New nematicidal and antimicrobial secondary metabolites from a new species in the new genus, <i>Pseudobambusicola thailandica</i> . <i>MycKeys</i> , 2018, 33, 1-23.	0.8	25
15803	New <i>Fusarium</i> species from the Kruger National Park, South Africa. <i>MycKeys</i> , 2018, 34, 63-92.	0.8	30
15804	Short-spored <i>Subulicystidium</i> (Trechisporales, Basidiomycota): high morphological diversity and only partly clear species boundaries. <i>MycKeys</i> , 2018, 35, 41-99.	0.8	11
15805	Cryptic species diversity in polypores: the <i>Skeletocutis nivea</i> species complex. <i>MycKeys</i> , 2018, 36, 45-82.	0.8	19
15806	Additions to tribe Chromosereae (Basidiomycota, Hygrophoraceae) from China, including <i>Sinohygrocybe</i> gen. nov. and a first report of <i>Gloioxanthomyces nitidus</i> . <i>MycKeys</i> , 2018, 38, 59-76.	0.8	4

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15807	A discussion on the genus <i>Fomitiporella</i> (Hymenochaetaceae, Hymenochaetales) and first record of <i>F. americana</i> from southern South America. <i>MycKeys</i> , 2018, 38, 77-91.	0.8	8
15808	<i>Hydnophanerochaete</i> and <i>Odontoefibula</i> , two new genera of phanerochaetoid fungi (Polyporales). <i>Tj ETQq1 1 0.784314 rgBT /Overlock 19</i>	0.8	19
15809	Three new species of <i>Krogia</i> (Ramalinaceae, lichenised Ascomycota) from the Paleotropics. <i>MycKeys</i> , 2018, 40, 69-88.	0.8	6
15810	Beta-tubulin and Actin gene phylogeny supports <i>Phaeoacremonium ovale</i> as a new species from freshwater habitats in China. <i>MycKeys</i> , 2018, 41, 1-15.	0.8	12
15811	<i>Ravenelia piepenbringiae</i> and <i>Ravenelia hernandezii</i> , two new rust species on <i>Senegalia</i> (Fabaceae). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5</i>	0.8	5
15812	Description and distribution of <i>Tuber incognitum</i> sp. nov. and <i>Tuber anniae</i> in the Transmexican Volcanic Belt. <i>MycKeys</i> , 2018, 41, 17-27.	0.8	10
15813	Three new species of <i>Phanerochaete</i> (Polyporales, Basidiomycota). <i>MycKeys</i> , 2018, 41, 91-106.	0.8	9
15814	Six new species and reports of <i>Hydnum</i> (Cantharellales) from eastern North America. <i>MycKeys</i> , 2018, 42, 35-72.	0.8	15
15815	New host associations and a novel species for the gall-inducing acacia rust genus <i>Ravenelia</i> in South Africa. <i>MycKeys</i> , 2018, 43, 1-21.	0.8	7
15816	<i>Lecanicillium cauligalbarum</i> sp. nov. (Cordycipitaceae, Hypocreales), a novel fungus isolated from a stem-borer in the Yao Ren National Forest Mountain Park, Guizhou. <i>MycKeys</i> , 2018, 43, 59-74.	0.8	15
15817	<i>Lactifluus bicapillus</i> (Russulales, Russulaceae), a new species from the Guineo-Congolian rainforest. <i>MycKeys</i> , 2019, 45, 25-49.	0.8	4
15818	<i>Neostagonospora sichuanensis</i> gen. et sp. nov. (Phaeosphaeriaceae, Pleosporales) on <i>Phyllostachys heteroclada</i> (Poaceae) from Sichuan Province, China. <i>MycKeys</i> , 2019, 46, 119-150.	0.8	17
15819	The genus <i>Hebeloma</i> in the Rocky Mountain Alpine Zone. <i>MycKeys</i> , 2019, 46, 1-54.	0.8	19
15820	Four new species of <i>Tremella</i> (Tremellales, Basidiomycota) based on morphology and DNA sequence data. <i>MycKeys</i> , 2019, 47, 75-95.	0.8	10
15821	<i>Tuber pulchrosporum</i> sp. nov., a black truffle of the <i>Aestivum</i> clade (Tuberaceae, Pezizales) from the Balkan peninsula. <i>MycKeys</i> , 2019, 47, 35-51.	0.8	8
15822	<i>Rostania</i> revised: testing generic delimitations in Collemataceae (Peltigerales, Lecanoromycetes). <i>MycKeys</i> , 2019, 47, 17-33.	0.8	5
15823	Four new corticioid species in Trechisporales (Basidiomycota) from East Asia and notes on phylogeny of the order. <i>MycKeys</i> , 2019, 48, 97-113.	0.8	11
15824	Two new endophytic <i>Colletotrichum</i> species from <i>Nothapodytes pittosporoides</i> in China. <i>MycKeys</i> , 2019, 49, 1-14.	0.8	8

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15825	The genus <i>Castanediella</i> . MycoKeys, 2019, 51, 1-14.	0.8	3
15826	A new record of <i>Ganoderma tropicum</i> (Basidiomycota, Polyporales) for Thailand and first assessment of optimum conditions for mycelia production. MycoKeys, 2019, 51, 65-83.	0.8	13
15827	Four new East Asian species of <i>Aleurodiscus</i> with echinulate basidiospores. MycoKeys, 2019, 52, 71-87.	0.8	3
15828	A regional study of the genus <i>Phyllopsora</i> (Ramalinaceae) in Asia and Melanesia. MycoKeys, 2019, 53, 23-72.	0.8	5
15829	Phylogenetic placement of <i>Lepraria cryptovouauxii</i> sp. nov. (Lecanorales, Lecanoromycetes,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 582 T	0.8	5
15830	Updated taxonomy of <i>Lactifluus</i> section <i>Luteoli</i> : <i>L. russuliporus</i> from Australia and <i>L. caliendrifer</i> from Thailand. MycoKeys, 2019, 56, 13-32.	0.8	4
15831	Phylogenetic and morphological classification of <i>Ophiocordyceps</i> species on termites from Thailand. MycoKeys, 2019, 56, 101-129.	0.8	24
15832	Understanding the evolution of phenotypical characters in the <i>Micarea prasina</i> group (Pilocarpaceae) and descriptions of six new species within the group. MycoKeys, 2019, 57, 1-30.	0.8	14
15833	Phylogeny and species delimitations in the entomopathogenic genus <i>Beauveria</i> (Hypocreales,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 422	0.8	37
15834	Three novel insect-associated species of <i>Simplicillium</i> (Cordycipitaceae, Hypocreales) from Southwest China. MycoKeys, 2019, 58, 83-102.	0.8	21
15835	Additions to the knowledge of <i>Ganoderma</i> in Thailand: <i>Ganoderma casuarinicola</i> , a new record; and <i>Ganoderma thailandicum</i> sp. nov.. MycoKeys, 2019, 59, 47-65.	0.8	12
15836	Morphology and secondary chemistry in species recognition of <i>Parmelia omphalodes</i> group "evidence from molecular data with notes on the ecological niche modelling and genetic variability of photobionts. MycoKeys, 2019, 61, 39-74.	0.8	6
15837	Descriptions of five new species in <i>Entoloma</i> subgenus <i>Claudopus</i> from China, with molecular phylogeny of <i>Entoloma</i> s.l.. MycoKeys, 2019, 61, 1-26.	0.8	6
15838	Additions to Chaetothyriaceae (Chaetothyriales): <i>Longihyalospora</i> gen. nov. and <i>Ceramothyrium longivolcaniforme</i> , a new host record from decaying leaves of <i>Ficus ampelas</i> . MycoKeys, 2019, 61, 91-109.	0.8	6
15839	<i>Longistriata flava</i> (Boletaceae, Basidiomycota) "a new monotypic sequestrate genus and species from Brazilian Atlantic Forest. MycoKeys, 2020, 62, 53-73.	0.8	11
15840	Integrative taxonomy confirms three species of <i>Coniocarpon</i> (Arthoniaceae) in Norway. MycoKeys, 2020, 62, 27-51.	0.8	8
15841	<i>Arboricolonus simplex</i> gen. et sp. nov. and novelties in <i>Cadophora</i> , <i>Minutiella</i> and <i>Proliferodiscus</i> from <i>Prunus</i> wood in Germany. MycoKeys, 2020, 63, 119-161.	0.8	13
15842	Diversity of <i>Trametes</i> (Polyporales, Basidiomycota) in tropical Benin and description of new species <i>Trametes parvispora</i> . MycoKeys, 2020, 65, 25-47.	0.8	7

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15843	Hydnaceous fungi of China 8. Morphological and molecular identification of three new species of Sarcodon and a new record from southwest China. MycoKeys, 2020, 66, 83-103.	0.8	4
15844	Gnomoniopsis chinensis (Gnomoniaceae, Diaporthales), a new fungus causing canker of Chinese chestnut in Hebei Province, China. MycoKeys, 2020, 67, 19-32.	0.8	13
15845	Diversity and toxigenicity of fungi and description of Fusarium madaense sp. nov. from cereals, legumes and soils in north-central Nigeria. MycoKeys, 2020, 67, 95-124.	0.8	20
15846	Three new Curvularia species from clinical and environmental sources. MycoKeys, 2020, 68, 1-21.	0.8	4
15847	Three new species of Cortinarius subgenus Telamonia (Cortinariaceae, Agaricales) from China. MycoKeys, 2020, 69, 91-109.	0.8	6
15848	Taxonomy and phylogenetic appraisal of Spegazzinia musae sp. nov. and S. deightonii (Didymosphaeriaceae, Pleosporales) on Musaceae from Thailand. MycoKeys, 2020, 70, 19-37.	0.8	12
15849	Morpho-molecular diversity of Linocarpaceae (Chaetosphaeriales): Claviformispora gen. nov. from decaying branches of Phyllostachys heteroclada. MycoKeys, 2020, 70, 1-17.	0.8	6
15850	Diversity of Akanthomyces on moths (Lepidoptera) in Thailand. MycoKeys, 2020, 71, 1-22.	0.8	12
15851	Multi-gene phylogenetic evidence suggests Dictyoarthrinium belongs in Didymosphaeriaceae (Pleosporales, Dothideomycetes) and Dictyoarthrinium musae sp. nov. on Musa from Thailand. MycoKeys, 2020, 71, 101-118.	0.8	15
15852	Delimitation, new species and teleomorph-anamorph relationships in Codinaea, Dendrophoma, Paragaeumannomyces and Striatosphaeria (Chaetosphaeriaceae). MycoKeys, 2020, 74, 17-74.	0.8	14
15853	Taxonomic revision of Russula subsection Amoeniniae from South Korea. MycoKeys, 2020, 75, 1-29.	0.8	11
15854	A global meta-analysis of ITS rDNA sequences from material belonging to the genus Ganoderma (Basidiomycota, Polyporales) including new data from selected taxa. MycoKeys, 2020, 75, 71-143.	0.8	27
15855	The first genetic assessment of wild and farmed ball pythons (Reptilia, Serpentes, Pythonidae) in southern Togo. Nature Conservation, 0, 38, 37-59.	0.0	13
15856	Two European Cornus L. feeding leafmining moths, Antispila petryi Martini, 1899, sp. rev. and A. treitschkiella (Fischer von R��slerstamm, 1843) (Lepidoptera, Heliozelidae): an unjustified synonymy and overlooked range expansion. Nota Lepidopterologica, 2018, 41, 39-86.	0.6	11
15857	Selaginella dianzhongensis (Selaginellaceae), a new spikemoss from China. PhytoKeys, 2019, 118, 75-87.	0.4	11
15858	A new striking and critically endangered species of Nasa (Loasaceae, Cornales) from North Peru. PhytoKeys, 2019, 121, 13-28.	0.4	4
15859	The Callerya Group redefined and Tribe Wisterieae (Fabaceae) emended based on morphology and data from nuclear and chloroplast DNA sequences. PhytoKeys, 2019, 125, 1-112.	0.4	26
15860	New taxa of Rhododendron tschonoskii alliance (Ericaceae) from East Asia. PhytoKeys, 2019, 134, 97-114.	0.4	6

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15861	Systematics and relationships of Tryssophyton (Melastomataceae), with a second species from the Pakaraima Mountains of Guyana. <i>PhytoKeys</i> , 2019, 136, 1-21.	0.4	8
15862	<i>Scorzonera sensu lato</i> (Asteraceae, Cichorieae) – taxonomic reassessment in the light of new molecular phylogenetic and carpological analyses. <i>PhytoKeys</i> , 2020, 137, 1-85.	0.4	18
15863	<i>Cryptocarya kaengkrachanensis</i> , a new species of Lauraceae from Kaeng Krachan National Park, southwest Thailand. <i>PhytoKeys</i> , 2020, 140, 139-157.	0.4	7
15864	A dated phylogeny of the genus <i>Pennantia</i> (Pennantiaceae) based on whole chloroplast genome and nuclear ribosomal 18S–26S repeat region sequences. <i>PhytoKeys</i> , 2020, 155, 15-32.	0.4	5
15865	<i>Primula sunhangii</i> (Primulaceae): a new species from Hubei, Central China. <i>PhytoKeys</i> , 2020, 156, 103-112.	0.4	3
15866	An amazing new <i>Capsicum</i> (Solanaceae) species from the Andean-Amazonian Piedmont. <i>PhytoKeys</i> , 2020, 167, 13-29.	0.4	19
15867	<i>Monadelphina</i> (Euphorbiaceae, Plukenetieae), a new genus of Tragiinae from the Amazon rainforest of Venezuela and Brazil. <i>PhytoKeys</i> , 2020, 169, 119-135.	0.4	2
15868	A molecular phylogeny of Caraganeae (Leguminosae, Papilionoideae) reveals insights into new generic and infrageneric delimitations. <i>PhytoKeys</i> , 2016, 70, 111-137.	0.4	17
15869	Resurrection of the genus <i>Aphyllon</i> for New World broomrapes (Orobanchaceae). <i>PhytoKeys</i> , 2016, 75, 107-118.	0.4	8
15870	The identity of <i>Hypolepis robusta</i> , as a new synonym of <i>Hypolepis alpina</i> (Dennstaedtiaceae), based on morphology and DNA barcoding and the new distribution. <i>PhytoKeys</i> , 2018, 96, 35-45.	0.4	4
15871	<i>Carpinus tibetana</i> (Betulaceae), a new species from southeast Tibet, China. <i>PhytoKeys</i> , 2018, 98, 1-13.	0.4	9
15872	Mitochondrial sequence data indicate ‘Vicariance by Erosion’ as a mechanism of species diversification in North American Ptomaphagus (Coleoptera, Leiodidae, Cholevinae) cave beetles. <i>Subterranean Biology</i> , 0, 29, 35-57.	5.0	9
15873	Morphometrics and phylogeography of the cave-obligate land snail <i>Helicodiscus barri</i> (Gastropoda). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5</i>	5.0	10
15874	A phylogenetic and taxonomic review of baviine jumping spiders (Araneae, Salticidae, Baviini). <i>ZooKeys</i> , 2020, 1004, 27-97.	0.5	21
15875	Five million years in the darkness: A new troglomorphic species of <i>Cryptops</i> Leach, 1814 (Chilopoda). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5</i>	0.5	4
15877	Species limits and phylogeography of <i>Newportia</i> (Scolopendromorpha) and implications for widespread morphospecies. <i>ZooKeys</i> , 2015, 510, 65-77.	0.5	5
15878	Does the genetic structure of spring snail <i>Bythinella</i> (Caenogastropoda, Truncatelloidea) in Bulgaria reflect geological history?. <i>ZooKeys</i> , 2015, 518, 67-86.	0.5	10
15879	Two new phragmotic ant species from Africa: morphology and next-generation sequencing solve a caste association problem in the genus <i>Carebara</i> Westwood. <i>ZooKeys</i> , 2015, 525, 77-105.	0.5	20

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15880	Congruence between cytochrome oxidase I (COI) and morphological data in <i>Anuraphis</i> spp. (Hemiptera). <i>Tj ETQq0 0 0 rgBT /Overlock 10</i> 529, 123-144.	0.5	7
15881	Two new Truncatelloidea species from Melissotrypa Cave in Greece (Caenogastropoda). <i>ZooKeys</i> , 2015, 530, 1-14.	0.5	13
15882	New contributions to the molecular systematics and the evolution of host-plant associations in the genus <i>Chrysolina</i> (Coleoptera, Chrysomelidae, Chrysomelinae). <i>ZooKeys</i> , 2015, 547, 165-192.	0.5	7
15883	A new quadrannulate species of <i>Orobdella</i> (Hirudinida, Arhynchobdellida, Orobdellidae) from western Honshu, Japan. <i>ZooKeys</i> , 2016, 553, 33-51.	0.5	8
15884	<i>Cryptomyrus</i> : a new genus of Mormyridae (Teleostei, Osteoglossomorpha) with two new species from Gabon, West-Central Africa. <i>ZooKeys</i> , 2016, 561, 117-150.	0.5	14
15885	Revision of sinistral land snails of the genus <i>Camaena</i> (Stylommatophora, Camaenidae) from China based on morphological and molecular data, with description of a new species from Guangxi, China. <i>ZooKeys</i> , 2016, 584, 25-48.	0.5	10
15886	Eleven nominal species of <i>Burmoniscus</i> are junior synonyms of <i>B. kathmandius</i> (Schmalfuss, 1983) (Crustacea, Isopoda, Oniscidea). <i>ZooKeys</i> , 2016, 607, 1-24.	0.5	9
15887	Sumakuru, a deeply-diverging new genus of lyssomanine jumping spiders from Ecuador (Araneae: Tj ETQq1 1 0.784314 rgBT ₁ /Overlock 10)	0.5	1
15888	Phylogenetic placement of the Pacific Northwest subterranean endemic diving beetle <i>Stygoporus oregonensis</i> Larson & LaBonte (Dytiscidae, Hydroporinae). <i>ZooKeys</i> , 2016, 632, 75-91.	0.5	7
15889	A preliminary molecular phylogeny of the genus <i>Scobura</i> , with a synonym of <i>Scobura masutaroi</i> (Lepidoptera, Hesperiiidae). <i>ZooKeys</i> , 2016, 638, 33-44.	0.5	3
15890	Two new deep-reef basslets (Teleostei, Grammatidae, Lipogramma), with comments on the eco-evolutionary relationships of the genus. <i>ZooKeys</i> , 2016, 638, 45-82.	0.5	19
15891	Bees of the Azores: an annotated checklist (Apidae, Hymenoptera). <i>ZooKeys</i> , 2017, 642, 63-95.	0.5	14
15892	A new subterranean species of <i>Pseudocrangonyx</i> from China with an identification key to all species of the genus (Crustacea, Amphipoda, Pseudocrangonyctidae). <i>ZooKeys</i> , 2017, 647, 1-22.	0.5	10
15893	Making the most of your host: the <i>Metrosideros</i> -feeding psyllids (Hemiptera, Psylloidea) of the Hawaiian Islands. <i>ZooKeys</i> , 2017, 649, 1-163.	0.5	25
15894	Phylogenetic analysis of the genus <i>Laparocerus</i> , with comments on colonisation and diversification in Macaronesia (Coleoptera, Curculionidae, Entiminae). <i>ZooKeys</i> , 2017, 651, 1-77.	0.5	22
15895	An elusive Neotropical giant, <i>Hondurantemna chespiritoi</i> gen. n. & sp. n. (Antemniinae, Tj ETQq1 1 0.784314 rgBT /Overlock 10) 2017, 680, 73-104.	0.5	6
15896	Reinstatement of <i>Eschatoporiini</i> Blaisdell, 1906, a unique tribe of blind cavernicolous Tenebrionidae from California, with a new species from Napa County (Coleoptera, Tenebrionidae, Lagriinae). <i>ZooKeys</i> , 2017, 688, 135-149.	0.5	7
15897	A genome-wide phylogeny of jumping spiders (Araneae, Salticidae), using anchored hybrid enrichment. <i>ZooKeys</i> , 2017, 695, 89-101.	0.5	30

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15898	Three new species and the molecular phylogeny of Antipathozoanthus from the Indo-Pacific Ocean (Anthozoa, Hexacorallia, Zoantharia). ZooKeys, 2017, 725, 97-122.	0.5	12
15899	Distribution of endangered Italian gudgeon <i>Romanogobio benacensis</i> (Cypriniformes, Cyprinidae.) Tj ETQq1 1 0.784314 rgBT / Overlock 0.5	0.5	11
15900	A new species of the genus <i>Pseudocrangonyx</i> (Crustacea, Amphipoda, Pseudocrangonyctidae) from Korea. ZooKeys, 2018, 735, 27-44.	0.5	11
15901	Revision of the Hawaiian psyllid genus <i>Swezeyana</i> , with descriptions of seven new species (Hemiptera,) Tj ETQq1 1 0.784314 rgBT / Overlock 0.5	0.5	11
15902	A stable phylogenomic classification of Travunioidea (Arachnida, Opiliones, Laniatores) based on sequence capture of ultraconserved elements. ZooKeys, 2018, 760, 1-36.	0.5	34
15903	Sequence capture phylogenomics of eyeless <i>Cicurina</i> spiders from Texas caves, with emphasis on US federally-endangered species from Bexar County (Araneae, Hahniidae). ZooKeys, 2018, 769, 49-76.	0.5	23
15904	Hawaiian <i>Philodoria</i> (Lepidoptera, Gracillariidae, Ornixolinae) leaf mining moths on <i>Myrsine</i> (Primulaceae): two new species and biological data. ZooKeys, 2018, 773, 109-141.	0.5	4
15905	The complete mitochondrial genome of <i>Xizicus</i> (<i>Haploxizicus</i>) <i>maculatus</i> revealed by Next-Generation Sequencing and phylogenetic implication (Orthoptera, Meconematinae). ZooKeys, 2018, 773, 57-67.	0.5	6
15906	A molecular and conchological dissection of the <i>Georissa</i> of Malaysian Borneo (Gastropoda,) Tj ETQq0 0 0 rgBT / Overlock 0.5	0.5	6
15907	Systematics of Neotropical microteiid lizards (<i>Gymnophthalmidae</i> , <i>Cercosaurinae</i>), with the description of a new genus and species from the Andean montane forests. ZooKeys, 2018, 774, 105-139.	0.5	17
15908	New molecular sequences for two genera of marine planarians facilitate determination of their position in the phylogenetic tree, with new records for two species (<i>Platyhelminthes</i> , <i>Tricladida</i> .) Tj ETQq0 0 0 rgBT / Overlock 0.5	0.5	10
15909	Phylogeny of hydrothermal vent <i>Iphionidae</i> , with the description of a new species (<i>Aphroditiformia</i> .) Tj ETQq1 1 0.784314 rgBT / Overlock 0.5	0.5	10
15910	The phylogeny of pholcid spiders: a critical evaluation of relationships suggested by molecular data (<i>Araneae</i> , <i>Pholcidae</i>). ZooKeys, 2018, 789, 51-101.	0.5	33
15911	Stolonifera from shallow waters in the north-western Pacific: a description of a new genus and two new species within the <i>Arulidae</i> (<i>Anthozoa</i> , <i>Octocorallia</i>). ZooKeys, 2018, 790, 1-19.	0.5	9
15912	Review of Brazilian jawfishes of the genus <i>Opistognathus</i> with descriptions of two new species (<i>Teleostei</i> , <i>Opistognathidae</i>). ZooKeys, 2018, 794, 95-133.	0.5	5
15913	Analysis of mitochondrial genomes resolves the phylogenetic position of Chinese freshwater mussels (<i>Bivalvia</i> , <i>Unionidae</i>). ZooKeys, 2019, 812, 23-46.	0.5	21
15914	Cryptic diversity in <i>Lithobates warszewitschii</i> (<i>Amphibia</i> , <i>Anura</i> , <i>Ranidae</i>). ZooKeys, 2019, 838, 49-69.	0.5	6
15915	A new species of <i>Gracixalus</i> (<i>Anura</i> , <i>Rhacophoridae</i>) from Yunnan, China. ZooKeys, 2019, 851, 91-111.	0.5	7

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15916	Morphological and molecular study on <i>Yininemertes pratensis</i> (Nemertea, Pilidiophora,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 747 Td (H... family Lineidae. ZooKeys, 2019, 852, 31-51.	0.5	3
15917	Host plant associations in Western Palaearctic Longitarsus flea beetles (Chrysomelidae, Galerucinae,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 747 Td (H... 0.5	0.5	8
15918	A redescription of <i>Syncarpa composita</i> (Asciacea, Stolidobranchia) with an inference of its phylogenetic position within Styelidae. ZooKeys, 2019, 857, 1-15.	0.5	6
15919	Size variation and geographical distribution of the luminous earthworm <i>Pontodrilus litoralis</i> (Grube, 1855) (Clitellata, Megascolecidae) in Southeast Asia and Japan. ZooKeys, 2019, 862, 23-42.	0.5	6
15920	Taxonomic revision and phylogenetic position of the flying squirrel genus <i>Biswamoyopterus</i> (Mammalia, Rodentia, Sciuridae, Pteromyini) on the northern Indo-China peninsula. ZooKeys, 0, 872, 77-93.	0.5	1
15921	A first phylogenetic study on stoloniferous octocorals off the coast of Kota Kinabalu, Sabah, Malaysia, with the description of two new genera and five new species. ZooKeys, 2019, 872, 127-158.	0.5	8
15922	Revisited " the species of Tweeting vineyard snails, genus <i>Cantareus</i> Risso, 1826 (Stylommatophora,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 747 Td (H... 0.5	0.5	7
15923	DNA barcoding of aphid-associated ants (Hymenoptera, Formicidae) in a subtropical area of southern China. ZooKeys, 2019, 879, 117-136.	0.5	9
15924	Resolving species boundaries in the <i>Atlanta brunnea</i> species group (Gastropoda, Pterotracheoidea). ZooKeys, 2019, 899, 59-84.	0.5	5
15925	A new species of <i>Enteromius</i> (Actinopterygii, Cyprinidae, Smiliogastrinae) from the Awash River, Ethiopia, and the re-establishment of <i>E. akakianus</i> . ZooKeys, 2020, 902, 107-150.	0.5	10
15926	Host identification for the deep-sea snail genus <i>Haliella</i> with description of a new species (Caenogastropoda, Eulimidae). ZooKeys, 2020, 908, 19-30.	0.5	4
15927	Revision of the <i>Merodon serrulatus</i> group (Diptera, Syrphidae). ZooKeys, 2020, 909, 79-158.	0.5	13
15928	<i>Asianopis</i> gen. nov., a new genus of the spider family Deinopidae from Asia. ZooKeys, 2020, 911, 67-99.	0.5	3
15929	Systematics and Taxonomy of <i>Tonatia saurophila</i> Koopman & Williams, 1951 (Chiroptera,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 747 Td (H... 0.5	0.5	21
15930	Revision of the western Palaearctic species of <i>Aleiodes</i> Wesmäl (Hymenoptera, Braconidae,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 747 Td (H... 0.5	0.5	6
15931	Comparative genomics reveals bamboo feeding adaptability in the giant panda (Ailuropoda) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 747 Td (H... 0.5	0.5	4
15932	Sitticine jumping spiders: phylogeny, classification, and chromosomes (Araneae, Salticidae, Sitticini). ZooKeys, 2020, 925, 1-54.	0.5	12
15933	A remarkable new species of the millipede genus <i>Trachyjulus</i> Peters, 1864 (Diplopoda, Spirostreptida,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 747 Td (H... 0.5	0.5	9

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15934	Hungry scale worms: Phylogenetics of Peinaleopolynoe (Polynoidae, Annelida), with four new species. ZooKeys, 2020, 932, 27-74.	0.5	19
15935	A complete time-calibrated multi-gene phylogeny of the European butterflies. ZooKeys, 2020, 938, 97-124.	0.5	61
15936	Taxonomic revision and phylogenetic position of the flying squirrel genus <i>Biswamoyopterus</i> (Mammalia, Rodentia, Sciuridae, Pteromyini) on the northern Indo-China peninsula. ZooKeys, 2020, 939, 65-85.	0.5	3
15937	Systematics of <i>Pholidobolus</i> lizards (Squamata, Gymnophthalmidae) from southern Ecuador, with descriptions of four new species. ZooKeys, 2020, 954, 109-156.	0.5	10
15938	Revealing the stygobiotic and crenobiotic molluscan biodiversity hotspot in Caucasus: Part I. The phylogeny of stygobiotic Sadlerianinae Szarowska, 2006 (Mollusca, Gastropoda, Hydrobiidae) from Georgia with descriptions of five new genera and twenty-one new species. ZooKeys, 2020, 955, 1-77.	0.5	12
15939	A new cave amphipod, <i>Pseudocrangonyx wonkimi</i> sp. nov. (Crustacea, Amphipoda,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 542 T	0.5	2
15940	A new species of <i>Nephus</i> (<i>Nephus</i>) (Coleoptera, Coccinellidae) described from Reunion Island. ZooKeys, 2020, 962, 123-137.	0.5	2
15941	Uncovering the shell game with barcodes: diversity of meiofaunal Caecidae snails (Truncatelloidea,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 542 T	0.5	2
15942	A new species of <i>Kerkia</i> Radoman, 1978 (Caenogastropoda, Hydrobiidae) from Bosnia and Herzegovina. ZooKeys, 2020, 973, 17-33.	0.5	5
15943	Integrative taxonomic revision of the land snail genus <i>Sarika</i> Godwin-Austen, 1907 in Thailand, with descriptions of nine new species (Eupulmonata, Ariophantidae). ZooKeys, 2020, 976, 1-100.	0.5	10
15944	<i>Plectorhinchus makranensis</i> (Teleostei, Haemulidae), a new species of sweetlips from the Persian Gulf and the Gulf of Oman. ZooKeys, 2020, 980, 141-154.	0.5	3
15945	A reassessment of the genus <i>Oligoneuriopsis</i> Crass, 1947 (Ephemeroptera, Oligoneuriidae,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 542 T	0.5	5
15946	Hidden in plain sight: a new frog species of the genus <i>Blommersia</i> from the oceanic island of Mayotte, Comoros archipelago. ZooKeys, 2020, 994, 149-166.	0.5	4
15947	Four new species of the genus <i>Orobdella</i> from Shikoku and Awajishima island, Japan (Hirudinida,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 542 T	0.4	10
15948	A molecular phylogeny of <i>Pseudocrangonyx</i> from Japan, including a new subterranean species (Crustacea, Amphipoda, Pseudocrangonyctidae). Zoosystematics and Evolution, 2016, 92, 187-202.	0.4	23
15949	Diamond in the rough: a new species of fossorial diamond frog (<i>Rhombophryne</i>) from Ranomafana National Park, southeastern Madagascar. Zoosystematics and Evolution, 2017, 93, 143-155.	0.4	9
15950	Two new species of <i>Jesogammarus</i> from Japan (Crustacea, Amphipoda, Anisogammaridae), with comments on the validity of the subgenera <i>Jesogammarus</i> and <i>Annanogammarus</i> . Zoosystematics and Evolution, 2017, 93, 189-210.	0.4	8
15951	A new frog species of the subgenus <i>Asperomantis</i> (Anura, Mantellidae, Gephyromantis) from the Bealanana District of northern Madagascar. Zoosystematics and Evolution, 2017, 93, 451-466.	0.4	3

#	ARTICLE	IF	CITATIONS
15952	Molecular phylogenetic analysis of a taxonomically unstable ranid from Sumatra, Indonesia, reveals a new genus with gastromyzophorous tadpoles and two new species. <i>Zoosystematics and Evolution</i> , 2018, 94, 163-193.	0.4	14
15953	The evolutionary terrestrialization of planarian flatworms (Platyhelminthes, Tricladida,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 70	0.4	6
15954	Mitochondrial discordance in closely related Theridion spiders (Araneae, Theridiidae), with description of a new species of the <i>T. melanurum</i> group. <i>Zoosystematics and Evolution</i> , 2020, 96, 159-173.	0.4	11
15955	Dissemination of Carbapenem-Resistance among Multidrug Resistant <i>Pseudomonas aeruginosa</i> carrying Metallo-Beta-Lactamase Genes, including the Novel bla IMP - 65 Gene in Thailand. <i>Infection and Chemotherapy</i> , 2019, 51, 107.	1.0	18
15956	Following the Phoenician example: western Mediterranean colonization by <i>Spirobranchus</i> cf. <i>tetraceros</i> (Annelida: Serpulidae). <i>Scientia Marina</i> , 2020, 84, 83.	0.3	6
15957	<i>Megaselia scalaris</i> (Diptera: Phoridae), an Opportunist Parasitoid of Honey Bees in Cameroon. <i>African Entomology</i> , 2018, 26, 254-258.	0.6	8
15958	Comparative Analyses of the Complete Mitochondrial Genomes of Three Lamprotula (Bivalvia:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 50 Species Delimitation. <i>Malacologia</i> , 2020, 63, 51.	0.2	9
15959	Elucidation of the Biosynthetic Pathway of Vitamin B Groups and Potential Secondary Metabolite Gene Clusters Via Genome Analysis of a Marine Bacterium <i>Pseudoruegeria</i> sp. M32A2M. <i>Journal of Microbiology and Biotechnology</i> , 2020, 30, 505-514.	0.9	9
15960	Probing hidden diversity to enhance conservation of the endangered narrow-range endemic Eastern Cape rocky, <i>Sandelia bainsii</i> (Castelnau 1861). <i>Koedoe</i> , 2020, 62, .	0.3	5
15961	Origin of a High-Latitude Population of <i>Aedes aegypti</i> in Washington, DC. <i>American Journal of Tropical Medicine and Hygiene</i> , 2018, 98, 445-452.	0.6	36
15962	Global Outbreaks and Origins of a Chikungunya Virus Variant Carrying Mutations Which May Increase Fitness for <i>Aedes aegypti</i> : Revelations from the 2016 Mandera, Kenya Outbreak. <i>American Journal of Tropical Medicine and Hygiene</i> , 2019, 100, 1249-1257.	0.6	43
15963	Haiti Poliovirus Environmental Surveillance. <i>American Journal of Tropical Medicine and Hygiene</i> , 2019, 101, 1240-1248.	0.6	12
15964	Three Species of <i>Heteroperreya</i> (Hymenoptera: Pergidae) Feeding on Brazilian Peppertrees, <i>Schinus</i> spp. (Anacardiaceae), Including a New Species. <i>Proceedings of the Entomological Society of Washington</i> , 2019, 121, 704.	0.0	2
15965	Description of a new genus and species as the first gastropod species from caves in Iran. <i>Journal of Cave and Karst Studies</i> , 2019, , 233-243.	0.3	7
15966	<i>Listeria monocytogenes</i> in Cooked Chicken: Detection of an Outbreak in the United Kingdom (2016 to) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 50 <i>Food Protection</i> , 2020, 83, 2041-2052.	0.8	16
15968	Redescription of <i>Dexiotricha colpidiopsis</i> (Kahl, 1926) Jankowski, 1964 (Ciliophora,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 14 <i>Protozoologica</i> , 2018, 57, 95-106.	0.5	3
15969	Cellular growth and fatty acid content of Arctic chlamydomonadalean. <i>Algae</i> , 2016, 31, 61-71.	0.9	4
15970	Morphological and genetic diversity of <i>Euglena deses</i> group (Euglenophyceae) with emphasis on cryptic species. <i>Algae</i> , 2016, 31, 219-230.	0.9	11

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15971	Morphological, molecular, and chromosomal identification of dwarf haploid parthenosporophytes of <i>Tauya basicrassa</i> (Phaeophyceae, Laminariales) from the Sea of Okhotsk. <i>Algae</i> , 2017, 32, 15-28.	0.9	7
15972	Isolation and characterization of two phototropins in the freshwater green alga, <i>Spirogyra varians</i> (Streptophyta, Zygnematales). <i>Algae</i> , 2017, 32, 235-244.	0.9	2
15973	Morphological and molecular identification of <i>Alaria paradisea</i> (Phaeophyceae, Laminariales) from the Kurile Islands. <i>Algae</i> , 2018, 33, 37-48.	0.9	3
15974	A molecular investigation of <i>Saccharina sessilis</i> from the Aleutian Islands reveals a species complex, necessitating the new combination <i>Saccharina subsessilis</i> . <i>Algae</i> , 2018, 33, 157-166.	0.9	5
15975	Next-generation sequencing reveals the diversity of benthic diatoms in tidal flats. <i>Algae</i> , 2018, 33, 167-180.	0.9	16
15976	Genetic discontinuity of <i>Digenea</i> (Rhodomelaceae, Rhodophyta) from Mexico supports recognition of two new species, <i>D. mexicana</i> and <i>D. rafaелиi</i> . <i>Algae</i> , 2018, 33, 231-241.	0.9	15
15977	Intraspecific variations in macronutrient, amino acid, and fatty acid composition of mass-cultured <i>Teleaulax amphioxeia</i> (Cryptophyceae) strains. <i>Algae</i> , 2019, 34, 163-175.	0.9	15
15978	Species diversity and distribution of the genus <i>Colpomenia</i> (Scytosiphonaceae, Phaeophyceae) along the coast of China. <i>Algae</i> , 2019, 34, 217-228.	0.9	7
15979	Genetic diversity and distribution of edible scytosiphonacean algae from Ulleungdo Island, Korea. <i>Algae</i> , 2019, 34, 229-236.	0.9	2
15980	Taxonomic study of three new Antarctic <i>Asterochloris</i> (Trebouxiophyceae) based on morphological and molecular data. <i>Algae</i> , 2020, 35, 17-32.	0.9	9
15981	Occurrence and pathogenicity of <i>Pythium</i> (Oomycota) on <i>Ulva</i> species (Chlorophyta) at different salinities. <i>Algae</i> , 2020, 35, 79-89.	0.9	5
15982	A new species of marine algae from Korea based on morphology and molecular data: <i>Gelidium palmatum</i> sp. nov. (Gelidiales, Rhodophyta). <i>Algae</i> , 2020, 35, 33-43.	0.9	2
15983	Biodiversity of Hawaiian Peyssonneliales (Rhodophyta): <i>Sonderophycus copusii</i> sp. nov., a new species from the Northwestern Hawaiian Islands. <i>Algae</i> , 2020, 35, 145-155.	0.9	13
15984	Revealing hidden diversity in the <i>Sheathia arcuata</i> morphospecies (Batrachospermales, Rhodophyta) including four new species. <i>Algae</i> , 2020, 35, 213-224.	0.9	6
15985	Draft genome of the aquatic moss <i>Fontinalis antipyretica</i> (Fontinalaceae, Bryophyta). <i>GigaByte</i> , 0, 2020, 1-9.	0.0	12
15986	New molecular and morphological evidences favor a combination of <i>Blechnum bakeri</i> C.Chr. in <i>Cranfillia</i> Gasper & V.A.O.Dittrich (Blechnaceae, Polypodiopsida), thus extending the distribution of <i>Cranfillia</i> to Madagascar and East Africa. <i>Adansonia</i> , 2020, 42, .	0.1	3
15987	Molecular Assessment of the Tribes Strebloladiaceae and Polysiphonieae (Rhodomelaceae, Rhodophyta) in the British Isles Reveals New Records and Species that Require Taxonomic Revision. <i>Cryptogamie, Algologie</i> , 2020, 41, 55.	0.3	8
15988	Morphological and Molecular Evidence for Synonymy of <i>Cinclidotus confertus</i> 4th with <i>C. riparius</i> (Host ex Brid.) Arn.. <i>Cryptogamie, Bryologie</i> , 2019, 40, 259.	0.1	4

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15989	Integrative Taxonomic Revision of Marsupella (Gymnomitriaceae, Hepaticae) Reveals Neglected Diversity in Pacific Asia. <i>Cryptogamie, Bryologie</i> , 2019, 40, 59.	0.1	19
15990	Modern Taxonomic Approaches to Identifying Diatrypaceous Fungi from Marine Habitats, with a Novel Genus <i>Halocryptovalsa</i> Dayarathne & K.D.Hyde, Gen. Nov.. <i>Cryptogamie, Mycologie</i> , 2020, 41, 21.	0.2	21
15991	<i>Vittaliana mangrovei</i> Devadatha, Nikita, A.Baghela & V.V.Sarma, gen. nov, sp. nov. (Phaeosphaeriaceae), from Mangroves Near Pondicherry (India), Based on Morphology and Multigene Phylogeny. <i>Cryptogamie, Mycologie</i> , 2019, 40, 117.	0.2	11
15992	Revisiting Calohypsibiidae and Microhypsibiidae: <i>Fractonotus Pilato</i> , 1998 and its phylogenetic position within Isohypsibiidae (Eutardigrada: Parachela). <i>Zoosystema</i> , 2019, 41, 71.	0.2	10
15993	Phylogeny of the genus <i>Pinnixa</i> White, 1846 (Crustacea, Brachyura, Pinnotheridae) and allies inferred from mitochondrial and nuclear molecular markers, with generic reassignment of twenty-one species. <i>Zoosystema</i> , 2020, 42, 85.	0.2	6
15994	Mitogenomics of the Extinct Cave Lion, <i>Panthera spelaea</i> (Goldfuss, 1810), Resolve its Position within the Panthera Cats. <i>Open Quaternary</i> , 2016, 2, .	0.5	27
15995	A Genetic Study of a Newly Found Population of Siberian Salamander, <i>Salamandrella keyserlingii</i> (Amphibia, Caudata). <i>Current Herpetology</i> , 2019, 38, 122.	0.5	3
15996	Phylogenetic position of <i>Geitleribactron purpureum</i> (Synechococcales, Cyanobacteria / Cyanophyceae) and its implications for the taxonomy of Chamaesiphonaceae and Leptolyngbyaceae. <i>Fottea</i> , 2016, 16, 104-111.	0.4	3
15997	Genetic diversity in chrysophytes: Comparison of different gene markers. <i>Fottea</i> , 2017, 17, 209-221.	0.4	15
15998	<i>Myrmecia israeliensis</i> as the primary symbiotic microalga in squamulose lichens growing in European and Canary Island terricolous communities. <i>Fottea</i> , 2018, 18, 72-85.	0.4	24
15999	Difference without distinction? Gaps in cyanobacterial systematics; when more is just too much. <i>Fottea</i> , 2018, 18, 130-136.	0.4	13
16000	Molecular characterization of <i>Geitleria appalachiana</i> sp. nov. (Nostocales, Cyanobacteria) and formation of Geitleriaceae fam. nov.. <i>Fottea</i> , 2018, 18, 150-163.	0.4	11
16001	Evolutionary relationships between the varieties of green algae <i>Pediastrum boryanum</i> and <i>P. duplex</i> s.l. (Chlorophyceae, Hydrodictyaceae). <i>Fottea</i> , 2018, 18, 170-188.	0.4	8
16002	<i>Quadricoccopsis</i> gen. nov., a new genus of Quadricoccus-like algae in Oocystaceae from China (Trebouxiophyceae, Chlorophyta). <i>Fottea</i> , 2018, 18, 189-199.	0.4	7
16003	Polyphasic approach to a characteristic <i>Ulva</i> population from a limno-rheocrenic, mineral (chloride,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.4	3
16004	Taxonomic transfer of <i>Gongrosira fluminensis</i> Fritsch (Chaetophorales, Chlorophyceae) to <i>Lithotrichon Darienko et PrÄtschold</i> (Ulvales, Ulvophyceae) based on morphological observation and phylogenetic analyses. <i>Fottea</i> , 2019, 19, 25-32.	0.4	7
16005	<i>Nitzschia omanensis</i> sp. nov., a new diatom species from the marine coast of Oman, characterized by valve morphology and molecular data. <i>Fottea</i> , 2019, 19, 175-184.	0.4	3
16006	Phylogeny and taxonomy of Synechococcus-like cyanobacteria. <i>Fottea</i> , 2020, 20, 171-191.	0.4	59

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16007	Two new <i>Oculatella</i> (Oculatellaceae, Cyanobacteria) species in soil crusts from tropical semi-arid uplands of MÃ©xico. <i>Fottea</i> , 2020, 20, 160-170.	0.4	14
16008	Phylogeny of <i>Dyschoriste</i> (Acanthaceae). <i>Aliso</i> , 2015, 33, 77-89.	0.4	4
16009	<i>Eriocaulon karaavalense</i> (Eriocaulaceae), a New Species from India Based on Morphological and Molecular Evidence. <i>Annales Botanici Fennici</i> , 2019, 56, 305.	0.0	4
16010	Molecular phylogenies support taxonomic revision of three species of <i>Laurencia</i> (Rhodomelaceae,) Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.6	8
16011	Molecular study supports the position of the New Zealand endemic genus <i>Lamellomorpha</i> in the family Vulcanellidae (Porifera, Demospongiae, Tetractinellida), with the description of three new species. <i>European Journal of Taxonomy</i> , 2019, , .	0.6	5
16012	Reassessment of the taxonomic status of <i>Pseudopaludicola parnaiba</i> (Anura, Leptodactylidae,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 <i>Journal of Taxonomy</i> , 2020, , .	0.6	4
16013	High phenotypic plasticity of <i>Ganoderma sinense</i> (Ganodermataceae, Polyporales) in China. <i>Asian Journal of Mycology</i> , 2019, 2, 1-47.	1.8	15
16014	A family level rDNA based phylogeny of Cucurbitariaceae and Fenestellaceae with descriptions of new <i>Fenestella</i> species and <i>Neocucurbitaria</i> gen. nov.. <i>Mycosphere</i> , 2017, 8, 397-414.	1.9	22
16015	Taxonomy and phylogeny of <i>Sparticola muriformis</i> sp. nov. on decaying grass. <i>Mycosphere</i> , 2017, 8, 603-614.	1.9	5
16016	Phylogenetic investigations on freshwater fungi in Tubeufiaceae (Tubeufiales) reveals the new genus <i>Dictyospora</i> and new species <i>Chlamydotubeufia aquatica</i> and <i>Helicosporium flavum</i> . <i>Mycosphere</i> , 2017, 8, 917-933.	1.9	23
16017	Data enabled prediction analysis assigns folate/biopterin transporter (BT1) family to 36 hypothetical membrane proteins in <i>Leishmania donovani</i> . <i>Bioinformatics</i> , 2019, 15, 697-708.	0.2	2
16019	The Cryptic Complex (Hymenoptera: Apidae) in Austria: Phylogeny, Distribution, Habitat Usage and a Climatic Characterization Based on COI Sequence Data. <i>Zoological Studies</i> , 2016, 55, e13.	0.3	5
16020	Low Genetic Diversity in , an Endemic and Endangered Catfish from South Chile. <i>Zoological Studies</i> , 2016, 55, e16.	0.3	1
16021	A New Fissiparous Brittle Star, sp. nov. (Echinodermata, Ophiuroidea, Ophiacanthida), from Jeju Island, Korea. <i>Zoological Studies</i> , 2019, 58, e8.	0.3	8
16022	Evidence of Echolocation in the Common Shrew from Molecular Convergence with Other Echolocating Mammals. <i>Zoological Studies</i> , 2020, 59, e4.	0.3	3
16023	Magnetotactic bacteria as a new model for P sequestration in the ferruginous Lake Pavin. <i>Geochemical Perspectives Letters</i> , 0, , 35-41.	1.0	54
16025	De novo synthesis of a sunscreen compound in vertebrates. <i>ELife</i> , 2015, 4, .	2.8	71
16026	Complex transcriptional regulation and independent evolution of fungal-like traits in a relative of animals. <i>ELife</i> , 2015, 4, e08904.	2.8	59

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16027	Novel origin of lamin-derived cytoplasmic intermediate filaments in tardigrades. <i>ELife</i> , 2016, 5, e11117.	2.8	25
16028	Evolutionary genomics of epidemic visceral leishmaniasis in the Indian subcontinent. <i>ELife</i> , 2016, 5, .	2.8	147
16029	Comparative genomics explains the evolutionary success of reef-forming corals. <i>ELife</i> , 2016, 5, .	2.8	169
16030	The genome of the crustacean <i>Parhyale hawaiiensis</i> , a model for animal development, regeneration, immunity and lignocellulose digestion. <i>ELife</i> , 2016, 5, .	2.8	130
16031	Evolution of substrate specificity in a retained enzyme driven by gene loss. <i>ELife</i> , 2017, 6, .	2.8	23
16032	Chimeric origins of ochrophytes and haptophytes revealed through an ancient plastid proteome. <i>ELife</i> , 2017, 6, .	2.8	129
16033	Parallel evolution of influenza across multiple spatiotemporal scales. <i>ELife</i> , 2017, 6, .	2.8	112
16034	The genome of an intranuclear parasite, <i>Paramicrosporidium saccamoebae</i> , reveals alternative adaptations to obligate intracellular parasitism. <i>ELife</i> , 2017, 6, .	2.8	63
16035	A new genus of horse from Pleistocene North America. <i>ELife</i> , 2017, 6, .	2.8	61
16036	Evolutionary transitions between beneficial and phytopathogenic <i>Rhodococcus</i> challenge disease management. <i>ELife</i> , 2017, 6, .	2.8	81
16037	Gene flow mediates the role of sex chromosome meiotic drive during complex speciation. <i>ELife</i> , 2018, 7, .	2.8	68
16038	The <i>Aquilegia</i> genome provides insight into adaptive radiation and reveals an extraordinarily polymorphic chromosome with a unique history. <i>ELife</i> , 2018, 7, .	2.8	120
16039	Loss of <i>Fam60a</i> , a <i>Sin3a</i> subunit, results in embryonic lethality and is associated with aberrant methylation at a subset of gene promoters. <i>ELife</i> , 2018, 7, .	2.8	9
16040	Unravelling the history of hepatitis B virus genotypes A and D infection using a full-genome phylogenetic and phylogeographic approach. <i>ELife</i> , 2018, 7, .	2.8	28
16041	Privatisation rescues function following loss of cooperation. <i>ELife</i> , 2018, 7, .	2.8	24
16042	Molecular function limits divergent protein evolution on planetary timescales. <i>ELife</i> , 2019, 8, .	2.8	25
16043	Emergence of trait variability through the lens of nitrogen assimilation in <i>Prochlorococcus</i> . <i>ELife</i> , 2019, 8, .	2.8	57
16044	Immune genes are hotspots of shared positive selection across birds and mammals. <i>ELife</i> , 2019, 8, .	2.8	112

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16045	Interferon lambda 4 impacts the genetic diversity of hepatitis C virus. <i>ELife</i> , 2019, 8, .	2.8	28
16046	Pantonâ€“Valentine leucocidin is the key determinant of <i>Staphylococcus aureus</i> pyomyositis in a bacterial GWAS. <i>ELife</i> , 2019, 8, .	2.8	56
16047	Adaptation of hepatitis C virus to interferon lambda polymorphism across multiple viral genotypes. <i>ELife</i> , 2019, 8, .	2.8	15
16048	Independent amylase gene copy number bursts correlate with dietary preferences in mammals. <i>ELife</i> , 2019, 8, .	2.8	78
16049	Species specific differences in use of ANP32 proteins by influenza A virus. <i>ELife</i> , 2019, 8, .	2.8	68
16050	Extraocular, rod-like photoreceptors in a flatworm express xenopsin photopigment. <i>ELife</i> , 2019, 8, .	2.8	27
16051	Bacterial contribution to genesis of the novel germ line determinant oskar. <i>ELife</i> , 2020, 9, .	2.8	21
16052	Coupling adaptive molecular evolution to phylodynamics using fitness-dependent birth-death models. <i>ELife</i> , 2019, 8, .	2.8	18
16053	Combining genomics and epidemiology to analyse bi-directional transmission of <i>Mycobacterium bovis</i> in a multi-host system. <i>ELife</i> , 2019, 8, .	2.8	63
16054	Ancient origins of arthropod moulting pathway components. <i>ELife</i> , 2019, 8, .	2.8	26
16055	Hemimetabolous insects elucidate the origin of sexual development via alternative splicing. <i>ELife</i> , 2019, 8, .	2.8	61
16056	Demographic reconstruction from ancient DNA supports rapid extinction of the great auk. <i>ELife</i> , 2019, 8, .	2.8	15
16057	ASPEN, a methodology for reconstructing protein evolution with improved accuracy using ensemble models. <i>ELife</i> , 2019, 8, .	2.8	4
16058	Genetically diverse uropathogenic <i>Escherichia coli</i> adopt a common transcriptional program in patients with UTIs. <i>ELife</i> , 2019, 8, .	2.8	56
16059	Molecular basis of force-from-lipids gating in the mechanosensitive channel MscS. <i>ELife</i> , 2019, 8, .	2.8	84
16060	The MADS-box transcription factor PHERES1 controls imprinting in the endosperm by binding to domesticated transposons. <i>ELife</i> , 2019, 8, .	2.8	73
16061	RNA polymerase mutations cause cephalosporin resistance in clinical <i>Neisseria gonorrhoeae</i> isolates. <i>ELife</i> , 2020, 9, .	2.8	31
16062	Resurrection of a global, metagenomically defined gokushovirus. <i>ELife</i> , 2020, 9, .	2.8	29

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16063	Independent evolution of ancestral and novel defenses in a genus of toxic plants (Erysimum,) Tj ETQq0 0 0 rgBT /Oyerlock 10 Tf 50 742	2.8	52
16064	Symptom evolution following the emergence of maize streak virus. ELife, 2020, 9, .	2.8	13
16065	The DNA-binding protein HTa from Thermoplasma acidophilum is an archaeal histone analog. ELife, 2019, 8, .	2.8	18
16066	Indirect sexual selection drives rapid sperm protein evolution in abalone. ELife, 2019, 8, .	2.8	7
16067	Rarity is a more reliable indicator of land-use impacts on soil invertebrate communities than other diversity metrics. ELife, 2020, 9, .	2.8	20
16068	Systematic detection of horizontal gene transfer across genera among multidrug-resistant bacteria in a single hospital. ELife, 2020, 9, .	2.8	85
16069	The skin microbiome facilitates adaptive tetrodotoxin production in poisonous newts. ELife, 2020, 9, .	2.8	51
16070	HA stabilization promotes replication and transmission of swine H1N1 gamma influenza viruses in ferrets. ELife, 2020, 9, .	2.8	19
16071	Genome streamlining in a minute herbivore that manipulates its host plant. ELife, 2020, 9, .	2.8	33
16072	Evolution of a plant gene cluster in Solanaceae and emergence of metabolic diversity. ELife, 2020, 9, .	2.8	47
16073	Drivers and sites of diversity in the DNA adenine methylomes of 93 Mycobacterium tuberculosis complex clinical isolates. ELife, 2020, 9, .	2.8	24
16074	Molecular evidence of hybridization between pig and human Ascaris indicates an interbred species complex infecting humans. ELife, 2020, 9, .	2.8	42
16075	Asynchrony between virus diversity and antibody selection limits influenza virus evolution. ELife, 2020, 9, .	2.8	25
16076	Phylogenomics of white-eyes, a "great speciator"™, reveals Indonesian archipelago as the center of lineage diversity. ELife, 2020, 9, .	2.8	17
16077	Mixed cytomegalovirus genotypes in HIV-positive mothers show compartmentalization and distinct patterns of transmission to infants. ELife, 2020, 9, .	2.8	18
16078	Determining the probability of hemiplasy in the presence of incomplete lineage sorting and introgression. ELife, 2020, 9, .	2.8	25
16079	A gustatory receptor tuned to the steroid plant hormone brassinolide in Plutella xylostella (Lepidoptera: Plutellidae). ELife, 2020, 9, .	2.8	25
16080	Genetic identification and hybridization in the seagrass genus <i>Halophila</i> (Hydrocharitaceae) in Sri Lankan waters. PeerJ, 2020, 8, e10027.	0.9	12

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16081	Conflicting phylogenetic signals in plastomes of the tribe Laureae (Lauraceae). PeerJ, 2020, 8, e10155.	0.9	24
16082	DNA barcoding for identification of anuran species in the central region of South America. PeerJ, 2020, 8, e10189.	0.9	6
16083	Comparative analysis of tissue-specific transcriptomes in the funnel-web spider <i>Macrothele calpeiana</i> (Araneae, Hexathelidae). PeerJ, 2015, 3, e1064.	0.9	14
16084	Evolution of <i>Wolbachia</i> mutualism and reproductive parasitism: insight from two novel strains that co-infect cat fleas. PeerJ, 2020, 8, e10646.	0.9	43
16085	<i>Porphirobacter mercurialis</i> sp. nov., isolated from a stadium seat and emended description of the genus <i>Porphirobacter</i> . PeerJ, 2015, 3, e1400.	0.9	16
16086	Phylogenetic analysis of higher-level relationships within Hydroidolina (Cnidaria: Hydrozoa) using mitochondrial genome data and insight into their mitochondrial transcription. PeerJ, 2015, 3, e1403.	0.9	43
16087	The complete mitochondrial genome of <i>Lerema accius</i> and its phylogenetic implications. PeerJ, 2016, 4, e1546.	0.9	20
16088	Molecular phylogeny and taxonomy of the <i>Epictia goudotii</i> Species complex (Serpentes). Tj ETQq1 1 0.784314 rgBT /Overlock_10 Tf 504	0.9	12
16089	Revisiting the Zingiberales: using multiplexed exon capture to resolve ancient and recent phylogenetic splits in a charismatic plant lineage. PeerJ, 2016, 4, e1584.	0.9	72
16090	Phylogenetic and morphologic evidence confirm the presence of a new montane cloud forest associated bird species in Mexico, the Mountain Elaenia (<i>Elaenia frantzii</i> ; Aves: Passeriformes). Tj ETQq1 1 0.784314 rgBT /Overlock_10 Tf 504	0.9	12
16091	Analysis of five complete genome sequences for members of the class Peribacteria in the recently recognized Peregrinibacteria bacterial phylum. PeerJ, 2016, 4, e1607.	0.9	57
16092	First record of hybridization between green <i>Chelonia mydas</i> and hawksbill <i>Eretmochelys imbricata</i> sea turtles in the Southeast Pacific. PeerJ, 2016, 4, e1712.	0.9	7
16093	Genetic diversity and structure in the Endangered Allen Cays Rock Iguana, <i>Cyclura cyclura inornata</i> . PeerJ, 2016, 4, e1793.	0.9	12
16094	Breakdown of coevolution between symbiotic bacteria <i>Wolbachia</i> and their filarial hosts. PeerJ, 2016, 4, e1840.	0.9	86
16095	Gall-ID: tools for genotyping gall-causing phytopathogenic bacteria. PeerJ, 2016, 4, e2222.	0.9	37
16096	A multifunctional GH39 glycoside hydrolase from the anaerobic gut fungus <i>Orpinomyces</i> sp. strain C1A. PeerJ, 2016, 4, e2289.	0.9	26
16097	Ancient phylogenetic divergence of the enigmatic African rodent <i>Zenkerella</i> and the origin of anomalurid gliding. PeerJ, 2016, 4, e2320.	0.9	17
16098	Whole genome sequencing of <i>Streptococcus pneumoniae</i> : development, evaluation and verification of targets for serogroup and serotype prediction using an automated pipeline. PeerJ, 2016, 4, e2477.	0.9	129

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16099	A potential third Manta Ray species near the Yucatán Peninsula? Evidence for a recently diverged and novel genetic <i>Manta</i> group from the Gulf of Mexico. PeerJ, 2016, 4, e2586.	0.9	32
16100	Early evolution of polyisoprenol biosynthesis and the origin of cell walls. PeerJ, 2016, 4, e2626.	0.9	7
16101	Proliferation of group II introns in the chloroplast genome of the green alga <i>Oedocladium carolinianum</i> (Chlorophyceae). PeerJ, 2016, 4, e2627.	0.9	20
16102	Ten genes and two topologies: an exploration of higher relationships in skipper butterflies (Hesperiidae). PeerJ, 2016, 4, e2653.	0.9	44
16103	Proteogenomic analyses indicate bacterial methylotrophy and archaeal heterotrophy are prevalent below the grass root zone. PeerJ, 2016, 4, e2687.	0.9	124
16104	The first complete plastid genomes of Melastomataceae are highly structurally conserved. PeerJ, 2016, 4, e2715.	0.9	62
16105	<i>Legionella</i> shows a diverse secondary metabolism dependent on a broad spectrum Sfp-type phosphopantetheinyl transferase. PeerJ, 2016, 4, e2720.	0.9	5
16106	The complete chloroplast genome sequence of <i>Helwingia himalaica</i> (Helwingiaceae, Aquifoliales) and a chloroplast phylogenomic analysis of the Campanulidae. PeerJ, 2016, 4, e2734.	0.9	10
16107	The unique deep sea "land connection: interactive 3D visualization and molecular phylogeny of <i>Bathyhedyle bouchetin</i> . sp. (Bathyhedylidae n. fam.) – the first panpulmonate slug from bathyal zones. PeerJ, 2016, 4, e2738.	0.9	10
16108	Pursuing the quest for better understanding the taxonomic distribution of the system of doubly uniparental inheritance of mtDNA. PeerJ, 2016, 4, e2760.	0.9	81
16109	Next-generation sequencing of mixed genomic DNA allows efficient assembly of rearranged mitochondrial genomes in <i>Amolops chunganensis</i> and <i>Quasipaa boulengeri</i> . PeerJ, 2016, 4, e2786.	0.9	27
16110	Taxonomic revision and molecular phylogenetics of the <i>Idarnes incertus</i> species-group (Hymenoptera, Agaonidae, Sycophaginae). PeerJ, 2017, 5, e2842.	0.9	5
16111	The complete chloroplast genome sequence of an endemic monotypic genus <i>Hagenia</i> (Rosaceae): structural comparative analysis, gene content and microsatellite detection. PeerJ, 2017, 5, e2846.	0.9	33
16112	Genomic and transcriptomic resources for assassin flies including the complete genome sequence of <i>Proctacanthus coquilletti</i> (Insecta: Diptera: Asilidae) and 16 representative transcriptomes. PeerJ, 2017, 5, e2951.	0.9	23
16113	Evolutionary and functional implications of hypervariable loci within the skin virome. PeerJ, 2017, 5, e2959.	0.9	28
16114	Arrival and diversification of mabuyine skinks (Squamata: Scincidae) in the Neotropics based on a fossil-calibrated timetree. PeerJ, 2017, 5, e3194.	0.9	10
16115	The impacts of drift and selection on genomic evolution in insects. PeerJ, 2017, 5, e3241.	0.9	6
16116	Eocene Loranthaceae pollen pushes back divergence ages for major splits in the family. PeerJ, 2017, 5, e3373.	0.9	14

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16117	Calculating site-specific evolutionary rates at the amino-acid or codon level yields similar rate estimates. PeerJ, 2017, 5, e3391.	0.9	15
16118	The fossil Osmundales (Royal Ferns)â€™a phylogenetic network analysis, revised taxonomy, and evolutionary classification of anatomically preserved trunks and rhizomes. PeerJ, 2017, 5, e3433.	0.9	28
16119	A new parrot taxon from the YucatÃ¡n Peninsula, Mexicoâ€™its position within genus <i>Amazona</i> based on morphology and molecular phylogeny. PeerJ, 2017, 5, e3475.	0.9	5
16120	Early-branching euteleost relationships: areas of congruence between concatenation and coalescent model inferences. PeerJ, 2017, 5, e3548.	0.9	8
16121	Targeted NGS for species level phylogenomics: â€œmade to measureâ€•or â€œone size fits allâ€•? PeerJ, 2017, 5, e3569.	0.9	47
16122	Clinical streptococcal isolates, distinct from <i>Streptococcus pneumoniae</i> , but containing the Î²-glucosyltransferase gene and expressing serotype 37 capsular polysaccharide. PeerJ, 2017, 5, e3571.	0.9	11
16123	Evolutionary response to the Qinghai-Tibetan Plateau uplift: phylogeny and biogeography of <i>Ammopiptanthus</i> and tribe Thermopsidae (Fabaceae). PeerJ, 2017, 5, e3607.	0.9	22
16124	Symplectin evolved from multiple duplications in bioluminescent squid. PeerJ, 2017, 5, e3633.	0.9	7
16125	phydms: software for phylogenetic analyses informed by deep mutational scanning. PeerJ, 2017, 5, e3657.	0.9	21
16126	Comparative mitogenomic analysis of mirid bugs (Hemiptera: Miridae) and evaluation of potential DNA barcoding markers. PeerJ, 2017, 5, e3661.	0.9	49
16127	The complete mitochondrial genome of the grooved carpet shell, <i>Ruditapes decussatus</i> (Bivalvia). PeerJ, 2017, 5, e3670.	0.9	16
16128	Diversity, abundance, and host relationships of avian malaria and related haemosporidians in New Mexico pine forests. PeerJ, 2017, 5, e3700.	0.9	17
16129	PrePhyloPro: phylogenetic profile-based prediction of whole proteome linkages. PeerJ, 2017, 5, e3712.	0.9	15
16130	Ancient divergence time estimates in <i>Eutropis rugifera</i> support the existence of Pleistocene barriers on the exposed Sunda Shelf. PeerJ, 2017, 5, e3762.	0.9	17
16131	Genome-wide identification of the MADS-box transcription factor family in pear (<i>Pyrus</i>). PeerJ, 2017, 5, e3770.	0.9	38
16132	Cryptic biodiversity and phylogeographic patterns of Seychellois <i>Ligia</i> isopods. PeerJ, 2017, 5, e3894.	0.9	11
16133	Phylogenomic analysis of the Chilean clade of Liolaemus lizards (Squamata: Liolaemidae) based on sequence capture data. PeerJ, 2017, 5, e3941.	0.9	12
16134	The comparison of molecular and morphology-based phylogenies of trichaline net-winged beetles (Coleoptera: Lycidae: Metriorrhynchini) with description of a new subgenus. PeerJ, 2017, 5, e3963.	0.9	11

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16135	Molecular phylogeny and evolutionary history of <i>Moricandia</i> DC (Brassicaceae). PeerJ, 2017, 5, e3964.	0.9	10
16136	Land snails of <i>Leptopoma</i> Pfeiffer, 1847 in Sabah, Northern Borneo (Caenogastropoda: Tj ETQq1 1 0.784314 rgBT /Overlock 10 T	0.9	4
16137	The reanalysis of biogeography of the Asian tree frog, <i>Rhacophorus</i> (Anura: Rhacophoridae): geographic shifts and climatic change influenced the dispersal process and diversification. PeerJ, 2017, 5, e3995.	0.9	13
16138	Phylogeographic and population insights of the Asian common toad (<i>Bufo gargarizans</i>) in Korea and China: population isolation and expansions as response to the ice ages. PeerJ, 2017, 5, e4044.	0.9	29
16139	Substitutions into amino acids that are pathogenic in human mitochondrial proteins are more frequent in lineages closely related to human than in distant lineages. PeerJ, 2017, 5, e4143.	0.9	7
16140	A molecular phylogenetic appraisal of the acanthostomines <i>Acanthostomum</i> and <i>Timoniella</i> and their position within Cryptogonimidae (Trematoda: Opisthorchioidea). PeerJ, 2017, 5, e4158.	0.9	10
16141	Translating genomics into practice for real-time surveillance and response to carbapenemase-producing Enterobacteriaceae: evidence from a complex multi-institutional KPC outbreak. PeerJ, 2018, 6, e4210.	0.9	66
16142	A 250 plastome phylogeny of the grass family (Poaceae): topological support under different data partitions. PeerJ, 2018, 6, e4299.	0.9	138
16143	Molecular systematics of the subfamily Limenitidinae (Lepidoptera: Nymphalidae). PeerJ, 2018, 6, e4311.	0.9	13
16144	Inter-domain microbial diversity within the coral holobiont <i>Siderastrea siderea</i> from two depth habitats. PeerJ, 2018, 6, e4323.	0.9	28
16145	Out of Asia: mitochondrial evolutionary history of the globally introduced supralittoral isopod <i>Ligia exotica</i> . PeerJ, 2018, 6, e4337.	0.9	9
16146	Phylogenetic surveys on the newt genus <i>Tylostotriton sensu lato</i> (Salamandridae, Caudata) reveal cryptic diversity and novel diversification promoted by historical climatic shifts. PeerJ, 2018, 6, e4384.	0.9	17
16147	Genome rearrangements and phylogeny reconstruction in <i>Yersinia pestis</i> . PeerJ, 2018, 6, e4545.	0.9	11
16148	Accuracy of taxonomy prediction for 16S rRNA and fungal ITS sequences. PeerJ, 2018, 6, e4652.	0.9	223
16149	Molecular approaches uncover cryptic diversity in intertidal <i>Ligia</i> isopods (Crustacea, Isopoda.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	0.9	16
16150	Novel, non-symbiotic isolates of <i>Neorhizobium</i> from a dryland agricultural soil. PeerJ, 2018, 6, e4776.	0.9	6
16151	Tackling critical parameters in metazoan meta-barcoding experiments: a preliminary study based on <i>cox1</i> DNA barcode. PeerJ, 2018, 6, e4845.	0.9	6
16152	On the taxonomic status and distribution of African species of Otomops (Chiroptera: Molossidae). PeerJ, 2018, 6, e4864.	0.9	15

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16153	MIPhy: identify and quantify rapidly evolving members of large gene families. PeerJ, 2018, 6, e4873.	0.9	11
16154	Archaeal and bacterial diversity and community composition from 18 phylogenetically divergent sponge species in Vietnam. PeerJ, 2018, 6, e4970.	0.9	34
16155	Availability of Nanopore sequences in the genome taxonomy for <i>Vibrionaceae</i> systematics: Rumoiensis clade species as a test case. PeerJ, 2018, 6, e5018.	0.9	13
16156	Horizontally transferred genes in the ctenophore <i>Mnemiopsis leidyi</i> . PeerJ, 2018, 6, e5067.	0.9	7
16157	<i>AnnotationBustR</i> : an R package to extract subsequences from GenBank annotations. PeerJ, 2018, 6, e5179.	0.9	9
16158	Multiple transgressions and slow evolution shape the phylogeographic pattern of the blind cave-dwelling shrimp <i>Typhlocaris</i> . PeerJ, 2018, 6, e5268.	0.9	22
16159	Cytogenetic analyses in <i>Trinomys</i> (Echimyidae, Rodentia), with description of new karyotypes. PeerJ, 2018, 6, e5316.	0.9	2
16160	Patterns in evolutionary origins of heme, chlorophyll <i>a</i> and isopentenyl diphosphate biosynthetic pathways suggest non-photosynthetic periods prior to plastid replacements in dinoflagellates. PeerJ, 2018, 6, e5345.	0.9	19
16161	Multilocus molecular systematics of the circumtropical reef-fish genus <i>Abudefduf</i> (Pomacentridae): history, geography and ecology of speciation. PeerJ, 2018, 6, e5357.	0.9	6
16162	A bioinformatics approach to identifying <i>Wolbachia</i> infections in arthropods. PeerJ, 2018, 6, e5486.	0.9	41
16163	A simple method for data partitioning based on relative evolutionary rates. PeerJ, 2018, 6, e5498.	0.9	16
16164	Luciferin production and luciferase transcription in the bioluminescent copepod <i>Metridia lucens</i> . PeerJ, 2018, 6, e5506.	0.9	8
16165	A new species of <i>Leptobrachium</i> (Anura, Megophryidae) from western Thailand. PeerJ, 2018, 6, e5584.	0.9	9
16166	Identification of an aquaculture poriferan pest with Potential and its phylogenetic implications. PeerJ, 2018, 6, e5586.	0.9	13
16167	Geopolitical species revisited: genomic and morphological data indicate that the roundtail chub <i>Gila robusta</i> species complex (Teleostei, Cyprinidae) is a single species. PeerJ, 2018, 6, e5605.	0.9	8
16168	Metabolic marker gene mining provides insight in global <i>mcrA</i> diversity and, coupled with targeted genome reconstruction, sheds further light on metabolic potential of the <i>Methanomassiliicoccales</i> . PeerJ, 2018, 6, e5614.	0.9	34
16169	Characterization and comparative genomic analysis of virulent and temperate <i>Bacillus megaterium</i> bacteriophages. PeerJ, 2018, 6, e5687.	0.9	6
16170	Evolution of African barbs from the Lake Victoria drainage system, Kenya. PeerJ, 2018, 6, e5762.	0.9	2

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16171	Comparative systematics and phylogeography of <i>Quercus</i> Section <i>Cerris</i> in western Eurasia: inferences from plastid and nuclear DNA variation. PeerJ, 2018, 6, e5793.	0.9	43
16172	Proteorhodopsins dominate the expression of phototrophic mechanisms in seasonal and dynamic marine picoplankton communities. PeerJ, 2018, 6, e5798.	0.9	22
16173	Fast and accurate estimation of the covariance between pairwise maximum likelihood distances. PeerJ, 2014, 2, e583.	0.9	1
16174	Phylogenomics picks out the par excellence markers for species phylogeny in the genus <i>Staphylococcus</i> . PeerJ, 2018, 6, e5839.	0.9	9
16175	Culture-independent detection and characterisation of <i>Mycobacterium tuberculosis</i> and <i>M. africanum</i> in sputum samples using shotgun metagenomics on a benchtop sequencer. PeerJ, 2014, 2, e585.	0.9	113
16176	First steps towards assessing the evolutionary history and phylogeography of a widely distributed Neotropical grassland bird (Motacillidae: <i>Anthus correndera</i>). PeerJ, 2018, 6, e5886.	0.9	9
16177	Characteristics of the complete mitochondrial genome of <i>Suhpalacsa longialata</i> (Neuroptera). Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.9	15
16178	Genetic analysis reveals Finnish <i>Formica fennica</i> populations do not form a separate genetic entity from <i>F. exsecta</i> . PeerJ, 2018, 6, e6013.	0.9	5
16179	Combining ultraconserved elements and mtDNA data to uncover lineage diversity in a Mexican highland frog (<i>Sarcohyla</i> ; Hylidae). PeerJ, 2018, 6, e6045.	0.9	31
16180	Undocumented translocations spawn taxonomic inflation in Sri Lankan fire rasboras (Actinopterygii). Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 10	0.9	10
16181	Climatic niche evolution in the viviparous <i>Sceloporus torquatus</i> group (Squamata). Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 342 Td (f	0.9	10
16182	Genome organization and molecular characterization of the three <i>Formica exsecta</i> viruses FeV1, FeV2 and FeV4. PeerJ, 2019, 6, e6216.	0.9	13
16183	Extremely low levels of chloroplast genome sequence variability in <i>Astelia pumila</i> (Asteliaceae). Tj ETQq0 0 0 rgBT /Overlock 10 Tf 4	0.9	4
16184	Convergent origin of the narrowly lanceolate leaf in the genus <i>Aster</i> with special reference to an unexpected discovery of a new <i>Aster</i> species from East China. PeerJ, 2019, 7, e6288.	0.9	3
16185	Isolation of wheat bran-colonizing and metabolizing species from the human fecal microbiota. PeerJ, 2019, 7, e6293.	0.9	9
16186	Characterization of the complete chloroplast genomes of five <i>Populus</i> species from the western Sichuan plateau, southwest China: comparative and phylogenetic analyses. PeerJ, 2019, 7, e6386.	0.9	25
16187	Embracing heterogeneity: coalescing the Tree of Life and the future of phylogenomics. PeerJ, 2019, 7, e6399.	0.9	111
16188	A new ancient lineage of frog (Anura: Nyctibatrachidae: Astrobatrachinae subfam. nov.) endemic to the Western Ghats of Peninsular India. PeerJ, 2019, 7, e6457.	0.9	18

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16189	Environmental modulation of the proteomic profiles from closely phylogenetically related populations of the red seaweed <i>Plocamium brasiliense</i> . PeerJ, 2019, 7, e6469.	0.9	3
16190	Phylogeny and circumscription of <i>Dasyphyllum</i> (Asteraceae: Barnadesioideae) based on molecular data with the recognition of a new genus, <i>Archidasiphyllum</i> . PeerJ, 2019, 7, e6475.	0.9	11
16191	Revision of the Afro-Madagascan genus <i>Costularia</i> (Schoeneae, Cyperaceae): infrageneric relationships and species delimitation. PeerJ, 2019, 7, e6528.	0.9	4
16192	The synergistic effect of concatenation in phylogenomics: the case in <i>Pantoea</i> . PeerJ, 2019, 7, e6698.	0.9	11
16193	Non-host class II ribonucleotide reductase in <i>Thermus</i> viruses: sequence adaptation and host interaction. PeerJ, 2019, 7, e6700.	0.9	8
16194	Adaptive and degenerative evolution of the <i>S-Phase Kinase-Associated Protein 1-Like</i> family in <i>Arabidopsis thaliana</i> . PeerJ, 2019, 7, e6740.	0.9	7
16195	Phylogenomic analysis and revised classification of atypoid mygalomorph spiders (Araneae, Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 502 T	0.9	62
16196	Order, please! Uncertainty in the ordinal-level classification of Chlorophyceae. PeerJ, 2019, 7, e6899.	0.9	25
16197	Phylogeography of <i>Dictyota fasciola</i> and <i>Dictyota mediterranea</i> (Dictyotales, Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 427 Td implications. PeerJ, 2019, 7, e6916.	0.9	3
16198	The biogeography of <i>Elaphe sauromates</i> (Pallas, 1814), with a description of a new rat snake species. PeerJ, 2019, 7, e6944.	0.9	19
16199	Plastome phylogenomics and characterization of rare genomic changes as taxonomic markers in plastome groups 1 and 2 Poeae (Pooideae; Poaceae). PeerJ, 2019, 7, e6959.	0.9	16
16200	The role of dispersal for shaping phylogeographical structure of flightless beetles from the Andes. PeerJ, 2019, 7, e7226.	0.9	5
16201	First molecular approach to the octopus fauna from the southern Caribbean. PeerJ, 2019, 7, e7300.	0.9	7
16202	Integrating phylogeographic and ecological niche approaches to delimitating cryptic lineages in the blue-green damselfish (<i>Chromis viridis</i>). PeerJ, 2019, 7, e7384.	0.9	8
16203	A comprehensive molecular phylogeny of Geometridae (Lepidoptera) with a focus on enigmatic small subfamilies. PeerJ, 2019, 7, e7386.	0.9	49
16204	Plant host and drought shape the root associated fungal microbiota in rice. PeerJ, 2019, 7, e7463.	0.9	31
16205	Phylogenetic analysis of <i>Fritillaria cirrhosa</i> D. Don and its closely related species based on complete chloroplast genomes. PeerJ, 2019, 7, e7480.	0.9	30
16206	Phylogenomic analyses confirm a novel invasive North American <i>Corbicula</i> (Bivalvia: Cyrenidae) lineage. PeerJ, 2019, 7, e7484.	0.9	20

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16207	<i>Rhopalocnemis phalloides</i> has one of the most reduced and mutated plastid genomes known. PeerJ, 2019, 7, e7500.	0.9	25
16208	Molecular taxonomy of endemic coastal <i>Ligia</i> isopods from the Hawaiian Islands: re-description of <i>L. hawaiiensis</i> and description of seven novel cryptic species. PeerJ, 2019, 7, e7531.	0.9	9
16209	The rediscovery of the rare Vietnamese endemic <i>Eriophorum scabriculum</i> redefines generic limits in the Scirpo-Caricoid Clade (Cyperaceae). PeerJ, 2019, 7, e7538.	0.9	2
16210	The complete chloroplast genome of the Jerusalem artichoke (<i>Helianthus tuberosus</i> L.) and an adaptive evolutionary analysis of the <i>ycf2</i> gene. PeerJ, 2019, 7, e7596.	0.9	25
16211	A new record of kelp <i>Lessonia spicata</i> (Suhr) Santelices in the Sub-Antarctic Channels: implications for the conservation of the "huero negro" in the Chilean coast. PeerJ, 2019, 7, e7610.	0.9	6
16212	The complete mitochondrial genomes of five longicorn beetles (Coleoptera: Cerambycidae) and phylogenetic relationships within Cerambycidae. PeerJ, 2019, 7, e7633.	0.9	33
16213	Plastome sequences help to improve the systematic position of trinerved <i>Lindera</i> species in the family Lauraceae. PeerJ, 2019, 7, e7662.	0.9	21
16214	Comprehensive, structurally-informed alignment and phylogeny of vertebrate biogenic amine receptors. PeerJ, 2015, 3, e773.	0.9	20
16215	Phylogeny and biogeography of the African Bathyergidae: a review of patterns and processes. PeerJ, 2019, 7, e7730.	0.9	22
16216	Characterizing gene tree conflict in plastome-inferred phylogenies. PeerJ, 2019, 7, e7747.	0.9	91
16217	Automated, phylogeny-based genotype delimitation of the Hepatitis Viruses HBV and HCV. PeerJ, 2019, 7, e7754.	0.9	3
16218	Phylogenetic revision of the psammophilic <i>Trogloclerus</i> LeConte (Coleoptera: Tenebrionidae), with biogeographic implications for the Intermountain Region. PeerJ, 2019, 7, e8039.	0.9	6
16219	The systematics of the Cervidae: a total evidence approach. PeerJ, 2020, 8, e8114.	0.9	66
16220	Expression of extraocular <i>opsin</i> genes and light-dependent basal activity of blind cavefish. PeerJ, 2019, 7, e8148.	0.9	14
16221	The complete chloroplast genome of <i>Microcycas calocoma</i> (Miq.) A. DC. (Zamiaceae, Cycadales) and evolution in Cycadales. PeerJ, 2020, 8, e8305.	0.9	6
16222	Conserved novel ORFs in the mitochondrial genome of the ctenophore <i>Beroë forskalii</i> . PeerJ, 2020, 8, e8356.	0.9	16
16223	Comparative analysis of chloroplast genomes for five <i>Dicliptera</i> species (Acanthaceae): molecular structure, phylogenetic relationships, and adaptive evolution. PeerJ, 2020, 8, e8450.	0.9	29
16224	<i>Ooctonus vulgatus</i> (Hymenoptera, Mymaridae), a potential biocontrol agent to reduce populations of <i>Philaenus spumarius</i> (Hemiptera, Aphrophoridae) the main vector of <i>Xylella fastidiosa</i> in Europe. PeerJ, 2020, 8, e8591.	0.9	11

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16225	The complete mitogenome of <i>Arion vulgaris</i> Moquin-Tandon, 1855 (Gastropoda: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 747 Td (Stylommatophora). PeerJ, 2020, 8, e8603.	0.9	14
16226	Genomic analysis of variability in Delta-toxin levels between <i>Staphylococcus aureus</i> strains. PeerJ, 2020, 8, e8717.	0.9	12
16227	The complete mitochondrial genome of <i>Flavoperla biocellata</i> Chu, 1929 (Plecoptera: Perlidae) and the phylogenetic analyses of Plecoptera. PeerJ, 2020, 8, e8762.	0.9	4
16228	Co-expression clustering across flower development identifies modules for diverse floral forms in <i>Achimenes</i> (Gesneriaceae). PeerJ, 2020, 8, e8778.	0.9	8
16229	Very few sites can reshape the inferred phylogenetic tree. PeerJ, 2020, 8, e8865.	0.9	20
16230	Characterization of the mitochondrial genomes of two toads, <i>Anaxyrus americanus</i> (Anura: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 747 Td (Anura) analyses. PeerJ, 2020, 8, e8901.	0.9	4
16231	The mitochondrial phylogeny of land plants shows support for Setaphyta under composition-heterogeneous substitution models. PeerJ, 2020, 8, e8995.	0.9	18
16232	Phylogenetic relationships in the southern African genus <i>Drosanthemum</i> (Ruschioideae, Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 747 Td (Ruschioideae, Ruschiaceae). PeerJ, 2020, 8, e9001.	0.9	6
16233	Antifungal activity of 8-methoxynaphthalen-1-ol isolated from the endophytic fungus <i>Diatrype palmicola</i> MFLUCC 17-0313 against the plant pathogenic fungus <i>Athelia rolfsii</i> on tomatoes. PeerJ, 2020, 8, e9103.	0.9	10
16234	The mitochondrial genome of <i>Acroboloides varius</i> (Cephalobomorpha) confirms non-monophyly of Tylenchina (Nematoda). PeerJ, 2020, 8, e9108.	0.9	10
16235	Too packed to change: side-chain packing and site-specific substitution rates in protein evolution. PeerJ, 2015, 3, e911.	0.9	44
16236	Comparative analysis of four <i>Zantedeschia</i> chloroplast genomes: expansion and contraction of the IR region, phylogenetic analyses and SSR genetic diversity assessment. PeerJ, 2020, 8, e9132.	0.9	16
16237	Evaluating Eucalyptus leaf colonization by <i>Brasilonema octagenarum</i> (Cyanobacteria, Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 262 Td (Scytonema). PeerJ, 2020, 8, e9137.	0.9	2
16238	Here are the polyps: in situ observations of <i>jellyfish polyps and podocysts</i> on bivalve shells. PeerJ, 2020, 8, e9260.	0.9	9
16239	DiscoSnp-RAD: de novo detection of small variants for RAD-Seq population genomics. PeerJ, 2020, 8, e9291.	0.9	5
16240	Mitochondrial genome of the nonphotosynthetic mycoheterotrophic plant <i>Hypopitys monotropa</i> , its structure, gene expression and RNA editing. PeerJ, 2020, 8, e9309.	0.9	16
16241	Plastid genomes of the North American <i>Rhus integrifolia-ovata</i> complex and phylogenomic implications of inverted repeat structural evolution in <i>Rhus</i> L.. PeerJ, 2020, 8, e9315.	0.9	4
16242	Hiding in plain sight: DNA barcoding suggests cryptic species in all well-known Australian flower beetles (Scarabaeidae: Cetoniinae). PeerJ, 0, 8, e9348.	0.9	4

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16243	Addressing incomplete lineage sorting and paralogy in the inference of uncertain salmonid phylogenetic relationships. PeerJ, 2020, 8, e9389.	0.9	9
16244	Understanding genomic diversity, pan-genome, and evolution of SARS-CoV-2. PeerJ, 2020, 8, e9576.	0.9	19
16245	Six complete mitochondrial genomes of mayflies from three genera of Ephemerellidae (Insecta: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 66 relationships. PeerJ, 2020, 8, e9740.	0.9	20
16246	Plastid transit peptides“ where do they come from and where do they all belong? Multi-genome and pan-genomic assessment of chloroplast transit peptide evolution. PeerJ, 2020, 8, e9772.	0.9	13
16247	A taxonomic review of the genus <i>Astrocladus</i> (Echinodermata, Ophiuroidea, Euryalida,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 582	0.9	5
16248	The highly rearranged mitochondrial genomes of three economically important scale insects and the mitochondrial phylogeny of Coccoidea (Hemiptera: Sternorrhyncha). PeerJ, 2020, 8, e9932.	0.9	10
16249	One becomes two: second species of the <i>Euwallacea fornicatus</i> (Coleoptera: Curculionidae:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 15	0.9	15
16250	<i>Pterocladia feldmannii</i> sp. nov. and <i>P. hamelii</i> sp. nov. (Gelidiales, Rhodophyta), Two New Species Uncovered in Madagascar During the Atimo Vatae Expedition. Cryptogamie, Algologie, 2016, 37, 179-198.	0.3	8
16251	Insights into the Rare Mediterranean Endemic <i>Kallymenia spathulata</i> : DNA Phylogenies Resolve This Species as Halymeniaceae (Halymeniales) Rather than Kallymeniaceae (Gigartinales), with the Proposal of <i>Felicinia spathulata</i> comb. nov.. Cryptogamie, Algologie, 2018, 39, 339-347.	0.3	2
16252	Notes on the Marine Algae of the Bermudas. 16. Two New Epiphytic Species of <i>Champia</i> (Champiaceae,) Tj ETQq1 1 0,784314 rgBT /Ov	0.3	3
16253	Identity and Origin of the <i>Campylopus</i> (Leucobryaceae, Bryopsida) Species from Trindade Island (Brazil). Cryptogamie, Bryologie, 2016, 37, 241-250.	0.1	9
16254	Reinstatement of <i>Plagiochila</i> sect. <i>Abietinae</i> (Plagiochilaceae, Jungermanniopsida). Cryptogamie, Bryologie, 2016, 37, 351-360.	0.1	2
16255	Integrative Taxonomy Substantiates the Presence of Three <i>Radula</i> Species in Austria: <i>Radula complanata</i> , <i>R. lindenberghiana</i> , and <i>R. visianica</i> (Porellales, Jungermanniopsida). Cryptogamie, Bryologie, 2017, 38, 125-135.	0.1	2
16256	<i>Lepidolejeunea grandiocellata</i> sp. nov. (Lejeuneaceae, Porellales), a New Leafy Liverwort from the West Indies Based on Morphological and Molecular Evidence. Cryptogamie, Bryologie, 2017, 38, 253-263.	0.1	7
16257	The <i>Didymodon tophaceus</i> Complex (Pottiaceae, Bryophyta) Revisited: New Data Support the Subspecific Rank of Currently Recognized Species. Cryptogamie, Bryologie, 2018, 39, 241-257.	0.1	15
16258	The Wild Edible Mushroom <i>Pleurocollybia cibaria</i> from Peru is a Species of <i>Gerhardtia</i> in the Lyophyllaceae (Agaricales). Cryptogamie, Mycologie, 2017, 38, 205-212.	0.2	9
16259	Cylindrocarpon-Like (Ascomycota, Hypocreales) Species from the Amazonian Rain Forests in Ecuador: Additions to <i>Campylocarpon</i> and <i>Dactylonectria</i> . Cryptogamie, Mycologie, 2017, 38, 409-434.	0.2	3
16260	Novel Taxa within Nectriaceae: <i>Cosmosporella</i> gen. nov. and <i>Aquanectria</i> sp. nov. from Freshwater Habitats in China. Cryptogamie, Mycologie, 2018, 39, 169-192.	0.2	15

#	ARTICLE	IF	CITATIONS
16261	Additions to Taiwan Fungal Flora 1: Neomassariaceae fam. nov.. Cryptogamie, Mycologie, 2018, 39, 359-372.	0.2	8
16262	Lactarius Subg. Lactarius (Russulaceae) in Indian Himalaya: Two New Species with Morphology and Phylogenetic Inferences. Cryptogamie, Mycologie, 2018, 39, 467.	0.2	2
16263	Two New Setose Species of Marasmius from the Paran Riparian Forest in Argentina. Cryptogamie, Mycologie, 2018, 39, 483.	0.2	3
16264	Biogeography and ecological drivers of evolution in the Andes: resolving the phylogenetic backbone for <i>Calceolaria</i> (Calceolariaceae). Botanical Journal of the Linnean Society, 2022, 199, 76-92.	0.8	4
16265	Three new species of <i>Creptotrema</i> (Trematoda, Allocreadiidae) with an amended diagnosis of the genus and reassignment of <i>Auriculostoma</i> (Allocreadiidae), based on morphological and molecular evidence. Parasite, 2021, 28, 69.	0.8	5
16266	Multidrug-Resistant Methicillin-Resistant <i>Staphylococcus aureus</i> Associated with Bacteremia and Monocyte Evasion, Rio de Janeiro, Brazil. Emerging Infectious Diseases, 2021, 27, 2825-2835.	2.0	16
16267	Mitogenome and phylogenetic analyses support rapid diversification among species groups of small-eared shrews genus <i>Cryptotis</i> (Mammalia: Eulipotyphla: Soricidae). Zoological Research, 2021, 42, 739-745.	0.9	5
16268	Nuclear-plastid discordance indicates past introgression in <i>Epidendrum</i> species (Laeliinae: Tj ETQq1 1 0.784314 rgBT /Overl... 2022, 199, 357-371.	0.8	5
16269	OUP accepted manuscript. Journal of Mammalogy, 2022, 103, 255-274.	0.6	1
16270	Collection of Job Scheduling Prediction Methods. Lecture Notes in Computer Science, 2021, , 35-42.	1.0	0
16271	Ancient DNA of the pygmy marmoset type specimen <i>Cebuella pygmaea</i> (Spix, 1823) resolves a taxonomic conundrum. Zoological Research, 2021, 42, 761-771.	0.9	6
16272	Phylogeny, Biogeography, and Classification of the Elms (<i>Ulmus</i>). Systematic Botany, 2021, 46, 711-727.	0.2	3
16273	Elucidating the Evolutionary History of <i>Oenothera</i> Sect. <i>Pachylophus</i> (Onagraceae): A Phylogenomic Approach. Systematic Botany, 2021, 46, 799-811.	0.2	8
16274	Phylogenomics in the Hard Pines (<i>Pinus</i> subsection <i>Ponderosae</i> ; Pinaceae) Confirms Paraphyly in <i>Pinus ponderosa</i> and Places <i>Pinus jeffreyi</i> with the California Big Cone Pines. Systematic Botany, 2021, 46, 538-561.	0.2	6
16275	Molecular approaches reveal speciation between red- and blue-flowered plants in the Mediterranean <i>Lysimachia arvensis</i> and <i>L. monelli</i> (Primulaceae). Botanical Journal of the Linnean Society, 2022, 199, 557-577.	0.8	4
16276	A New Phylogenetic Hypothesis for Cereinae (Cactaceae) Points to a Monophyletic Subtribe. Systematic Botany, 2021, 46, 689-699.	0.2	4
16277	Phylogeny of a new ciliate family Clampidae fam. nov. (Protista: Ciliophora), with notes on morphology and morphogenesis. Zoological Journal of the Linnean Society, 2022, 196, 88-104.	1.0	4
16278	Complexity in Polyploid Species Origin and Establishment: <i>Arctostaphylos mewukka</i> (Ericaceae). Systematic Botany, 2021, 46, 666-677.	0.2	0

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16279	Phylogenomic analysis of <i>Tibouchina s.s.</i> (Melastomataceae) highlights the evolutionary complexity of Neotropical savannas. <i>Botanical Journal of the Linnean Society</i> , 2022, 199, 372-411.	0.8	4
16280	Analysis and Characteristics of Thermal Springs in Kazakhstan. <i>Microorganisms for Sustainability</i> , 2021, , 97-114.	0.4	1
16281	<i>Asperosporus subterraneus</i> , a new genus and species of sequestrate Agaricaceae found in Florida nursery production. <i>Fungal Systematics and Evolution</i> , 2021, 8, 91-100.	0.9	0
16282	The <i>Macrobiotus ariekammensis</i> species complex provides evidence for parallel evolution of claw elongation in macrobiotid tardigrades. <i>Zoological Journal of the Linnean Society</i> , 2022, 195, 1067-1099.	1.0	14
16283	species from south and south-eastern Australia (Ectocarpales, Phaeophyceae): a DNA barcoding approach. <i>Australian Systematic Botany</i> , 2021, 34, 587-594.	0.3	1
16284	Multilocus phylogeny, natural history traits and classification of natricine snakes (Serpentes: Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.6	16
16286	Fungi causing leaf spot diseases in <i>Lolium multiflorum</i> in Brazil. <i>Mycological Progress</i> , 2021, 20, 1175-1190.	0.5	8
16287	Complete Mitochondrial Genomes of <i>Metcalfa pruinosa</i> and <i>Salurnis marginella</i> (Hemiptera: Flatidae): Genomic Comparison and Phylogenetic Inference in Fulgoroidea. <i>Current Issues in Molecular Biology</i> , 2021, 43, 1391-1418.	1.0	4
16288	International High-Risk Clones Among Extended-Spectrum β -Lactamase-Producing <i>Escherichia coli</i> in Dhaka, Bangladesh. <i>Frontiers in Microbiology</i> , 2021, 12, 736464.	1.5	10
16289	The complete chloroplast genome sequence of <i>Elaeocarpus decipiens</i> (Elaeocarpaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 3130-3131.	0.2	2
16290	Bird nests as botanical time capsules: DNA barcoding identifies the contents of contemporary and historical nests. <i>PLoS ONE</i> , 2021, 16, e0257624.	1.1	4
16291	Complementary combination of multiplex high-throughput sc^2 DNA sequencing for molecular phylogeny. <i>Ecological Research</i> , 2022, 37, 171-181.	0.7	60
16292	Dead-End Hybridization in Walnut Trees Revealed by Large-Scale Genomic Sequence Data. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	21
16294	A chromosome-scale genome assembly and annotation of the spring orchid (<i>Cymbidium</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10	2.2	9
16295	High-quality genome assembly of an important biodiesel plant, <i>Euphorbia lathyris</i> L. <i>DNA Research</i> , 2021, 28, .	1.5	11
16297	The conformational cycle of prestin underlies outer-hair cell electromotility. <i>Nature</i> , 2021, 600, 553-558.	13.7	53
16298	Developing an efficient DNA barcoding system to differentiate between <i>Lilium</i> species. <i>BMC Plant Biology</i> , 2021, 21, 465.	1.6	5
16299	Taxonomic relationship between two small-sized <i>Chaetoceros</i> species (Bacillariophyta): <i>C. tenuissimus</i> and <i>C. salsugineus</i> , and comparison with <i>C. olympicus</i> sp. nov. from Catalan coastal waters (NW Mediterranean). <i>European Journal of Phycology</i> , 2022, 57, 277-296.	0.9	2

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16300	<i>Zeimonas arvi</i> gen. nov., sp. nov., of the family Burkholderiaceae, harboring biphenyl- and phenolic acid-metabolizing genes, isolated from a long-term ecological research field. Antonie Van Leeuwenhoek, 2021, 114, 2101-2111.	0.7	14
16302	The evolution of insect biodiversity. <i>Current Biology</i> , 2021, 31, R1299-R1311.	1.8	39
16303	Phylogenomic Analysis Substantiates the <i>gyrB</i> Gene as a Powerful Molecular Marker to Efficiently Differentiate the Most Closely Related Genera <i>Myxococcus</i> , <i>Corallocooccus</i> , and <i>Pyxidicooccus</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 763359.	1.5	8
16304	Cryptic diversity and phylogeography of the <i>Rhabdophis nuchalis</i> group (Squamata: Colubridae). <i>Molecular Phylogenetics and Evolution</i> , 2022, 166, 107325.	1.2	4
16305	Integrative Study of Genotypic and Phenotypic Diversity in the Eurasian Orchid Genus <i>Neotinea</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 734240.	1.7	2
16306	Use of plastid genome sequences in phylogeographic studies of tree species can be misleading without comprehensive sampling of co-occurring, related species. <i>Tree Genetics and Genomes</i> , 2021, 17, 1.	0.6	2
16307	Dynamic Subspecies Population Structure of <i>Vibrio cholerae</i> in Dhaka, Bangladesh. <i>Microbial Ecology</i> , 2022, 84, 730-745.	1.4	1
16309	Diversification along a benthic to pelagic gradient contributes to fish diversity in the world's largest lake (Lake Baikal, Russia). <i>Molecular Ecology</i> , 2022, 31, 238-251.	2.0	4
16310	<i>Aenigmanu</i> , a new genus of Picramniaceae from Western Amazonia. <i>Taxon</i> , 2021, 70, 1239.	0.4	1
16311	Peripheral structures in unlabelled trees and the accumulation of subgenomes in the evolution of polyploids. <i>Journal of Theoretical Biology</i> , 2022, 532, 110924.	0.8	4
16312	<i>Catenulispora pinistramenti</i> sp. nov., novel actinobacteria isolated from pine forest soil in Poland. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	6
16313	Global shifts in species richness have shaped carpet shark evolution. <i>Bmc Ecology and Evolution</i> , 2021, 21, 192.	0.7	2
16314	Phylogeny, classification, and character evolution of tribe Citharexyleae (Verbenaceae). <i>American Journal of Botany</i> , 2021, 108, 1982-2001.	0.8	3
16315	Emergence of 16S rRNA methyltransferases among carbapenemase-producing Enterobacterales in Spain studied by whole-genome sequencing. <i>International Journal of Antimicrobial Agents</i> , 2022, 59, 106456.	1.1	11
16316	Complete chloroplast genome sequences of five <i>Bruguiera</i> species (Rhizophoraceae): comparative analysis and phylogenetic relationships. <i>PeerJ</i> , 2021, 9, e12268.	0.9	13
16317	<i>Phytophthora heterospora</i> sp. nov., a New Pseudoconidia-Producing Sister Species of <i>P. palmivora</i> . <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 870.	1.5	13
16318	A new subfamily of ionotropic glutamate receptors unique to the echinoderms with putative sensory role. <i>Molecular Ecology</i> , 2021, 30, 6642-6658.	2.0	2
16319	The complete chloroplast genome of <i>Ixora chinensis</i> and phylogenetic relationships. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 3217-3221.	0.2	0

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16320	The Evolutionary History of New Zealand <i>Deschampsia</i> Is Marked by Long-Distance Dispersal, Endemism, and Hybridization. <i>Biology</i> , 2021, 10, 1001.	1.3	1
16321	Systematics of the rare Amazonian genus <i>Eutrachelophis</i> (Serpentes: Dipsadidae), with an emended diagnosis for <i>Eutrachelophis papilio</i> . <i>Zoologischer Anzeiger</i> , 2021, 295, 191-204.	0.4	2
16322	No hybrid snowcocks in the Altai—Hyper—variable markers can be problematic for phylogenetic inference. <i>Ecology and Evolution</i> , 2021, 11, 16354-16364.	0.8	1
16323	<i>Taxus yunnanensis</i> genome offers insights into gymnosperm phylogeny and taxol production. <i>Communications Biology</i> , 2021, 4, 1203.	2.0	15
16325	Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) in a Dog in Connecticut in February 2021. <i>Viruses</i> , 2021, 13, 2141.	1.5	5
16326	Insights into the functional expansion of the astacin peptidase family in parasitic helminths. <i>International Journal for Parasitology</i> , 2022, 52, 243-251.	1.3	5
16327	Pathogen—driven coevolution across the CBP60 plant immune regulator subfamilies confers resilience on the regulator module. <i>New Phytologist</i> , 2022, 233, 479-495.	3.5	14
16328	The complete mitochondrial genome of <i>Ophiocordyceps gracilis</i> and its comparison with related species. <i>IMA Fungus</i> , 2021, 12, 31.	1.7	7
16329	Cryptic diversity within the <i>Poecilochirus carabi</i> mite species complex phoretic on <i>Nicrophorus</i> burying beetles: Phylogeny, biogeography, and host specificity. <i>Molecular Ecology</i> , 2022, 31, 658-674.	2.0	4
16330	Hallstatt miners consumed blue cheese and beer during the Iron Age and retained a non-Westernized gut microbiome until the Baroque period. <i>Current Biology</i> , 2021, 31, 5149-5162.e6.	1.8	22
16332	The complete chloroplast genome of <i>Tripsacum laxum</i> (Gramineae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 3207-3208.	0.2	1
16334	Comparative Genomic Analysis and a Novel Set of Missense Mutation of the <i>Leptospira weillii</i> Serogroup Mini From the Urine of Asymptomatic Dogs in Thailand. <i>Frontiers in Microbiology</i> , 2021, 12, 731937.	1.5	1
16335	Comparative plastid genomics of Mazaceae: focusing on a new recognized genus, <i>Puchiumazus</i> . <i>Planta</i> , 2021, 254, 99.	1.6	2
16336	Novel <i>Botrytis</i> and <i>Cladosporium</i> Species Associated with Flower Diseases of Macadamia in Australia. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 898.	1.5	13
16337	Morphological and molecular variability of <i>Peridinium volzii</i> Lemmerm. (Peridiniaceae, Dinophyceae) and its relevance for infraspecific taxonomy. <i>Organisms Diversity and Evolution</i> , 2022, 22, 1-15.	0.7	2
16338	The complete mitochondrial genome of the file ramshorn snail <i>Planorbella pilsbryi</i> (Mollusca: Tj ETQq1 1 0.784314 rgBT /Over 0,2	0.2	7
16339	<i>Acinetobacter geminorum</i> sp. nov., isolated from human throat swabs. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	10
16340	Comparative analysis of integrative and conjugative mobile genetic elements in the genus <i>Mesorhizobium</i> . <i>Microbial Genomics</i> , 2021, 7, .	1.0	13

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16341	Characterization of the complete chloroplast genome of <i>Ammopiptanthus mongolicus</i> (Leguminosae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 3162-3163.	0.2	0
16342	A <i>Parachlorella kessleri</i> (Trebouxiophyceae, Chlorophyta) strain tolerant to high concentration of calcium chloride. <i>Journal of Eukaryotic Microbiology</i> , 2022, 69, e12872.	0.8	2
16343	The complete chloroplast genome and phylogenetic analysis of <i>Corydalis fangshanensis</i> W.T. Wang ex S.Y. He (Papaveraceae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 3171-3173.	0.2	5
16344	Genome sequencing of turmeric provides evolutionary insights into its medicinal properties. <i>Communications Biology</i> , 2021, 4, 1193.	2.0	23
16346	Characterization of the complete chloroplast genome of <i>Hedysarum polybotrys</i> var. <i>alaschanicum</i> (Fabaceae) and its phylogeny. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 3312-3313.	0.2	3
16347	Genome sequencing of the NIES Cyanobacteria collection with a focus on the heterocyst-forming clade. <i>DNA Research</i> , 2021, 28, .	1.5	12
16348	Phylogenomics and continental biogeographic disjunctions: insight from the Australian starflowers (<i>Calytrix</i>). <i>American Journal of Botany</i> , 2022, 109, 291-308.	0.8	7
16349	Sectional polyphyly and morphological homoplasy in Southeast Asian <i>Cyrtandra</i> (Gesneriaceae): consequences for the taxonomy of a mega-diverse genus. <i>Plant Systematics and Evolution</i> , 2021, 307, 1.	0.3	4
16350	The complete chloroplast genome of <i>Camellia osmantha</i> , an edible oil <i>Camellia</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 3169-3170.	0.2	2
16351	Genomic Characterisation of <i>Campylobacter jejuni</i> Isolates Recovered During Commercial Broiler Production. <i>Frontiers in Microbiology</i> , 2021, 12, 716182.	1.5	4
16352	On the Species Delimitation of the <i>Maddenia</i> Group of <i>Prunus</i> (Rosaceae): Evidence From Plastome and Nuclear Sequences and Morphology. <i>Frontiers in Plant Science</i> , 2021, 12, 743643.	1.7	13
16353	An Investigation of <i>Culicoides</i> (Diptera: Ceratopogonidae) as Potential Vectors of Medically and Veterinary Important Arboviruses in South Africa. <i>Viruses</i> , 2021, 13, 1978.	1.5	5
16355	Adaptation and genomic erosion in fragmented <i>Pseudomonas aeruginosa</i> populations in the sinuses of people with cystic fibrosis. <i>Cell Reports</i> , 2021, 37, 109829.	2.9	19
16356	A histology-free description of <i>Tetrastemma cupido</i> sp. nov. (Nemertea: Eumonostilfera) from Sagami Bay, Japan. <i>Marine Biology Research</i> , 2021, 17, 467-474.	0.3	7
16357	Stable climate corridors promote gene flow in the Cape sand snake species complex (Psammophiidae). <i>Zoologica Scripta</i> , 0, , .	0.7	3
16358	New Rainbow Sardine Species of <i>Dussumieria</i> (Teleostei: Clupeiformes: Dussumieriidae) from the East African Coast. <i>Ichthyology and Herpetology</i> , 2021, 109, .	0.3	2
16359	Molecular phylogeny reveals a new genus of freshwater mussels from the Mekong River Basin (Bivalvia: Unionidae). <i>European Journal of Taxonomy</i> , 0, 775, 119-142.	0.6	6
16360	Central and Northern European caterpillar assemblages show strong phylogenetic structure. <i>Functional Ecology</i> , 0, , .	1.7	0

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16361	A novel, divergent alkane monooxygenase (<sc><i>alkB</i></sc>) clade involved in crude oil biodegradation. Environmental Microbiology Reports, 2021, 13, 830-840.	1.0	9
16362	Genetic structure, diversity and distribution of a threatened lizard affected by widespread habitat fragmentation. Conservation Genetics, 2022, 23, 151-165.	0.8	4
16363	The complete chloroplast genome of <i>Onosma fuyunensis</i> Y. He & Q.R. Liu and its phylogenetic analysis. Mitochondrial DNA Part B: Resources, 2021, 6, 3142-3143.	0.2	4
16364	Distribution of bacteriocin genes in the lineages of Lactiplantibacillus plantarum. Scientific Reports, 2021, 11, 20063.	1.6	15
16365	Spatial and temporal coevolution of N2 neuraminidase and H1 and H3 hemagglutinin genes of influenza A virus in US swine. Virus Evolution, 2021, 7, veab090.	2.2	14
16366	Transmission Dynamics of Carbapenem-Resistant Klebsiella pneumoniae Sequence Type 11 Strains Carrying Capsular Loci KL64 and rmpA/rmpA2 Genes. Frontiers in Microbiology, 2021, 12, 736896.	1.5	11
16368	The biogeographical history of giant earthworms of the Metaphire formosae species group (Clitellata: Tj ETQq0 0 0 rgBT /Overlock 10 T Yonagunijima, Southern Ryukyus. Organisms Diversity and Evolution, 0, , 1.	0.7	5
16369	The complete chloroplast genome and phylogenetic analysis of <i>Artocarpus champeden</i>. Mitochondrial DNA Part B: Resources, 2021, 6, 3148-3150.	0.2	0
16370	The complete chloroplast genome of <i>Saussurea medusa</i> maxim. (Asteraceae), an alpine Tibetan herb. Mitochondrial DNA Part B: Resources, 2021, 6, 3144-3145.	0.2	1
16371	Phylogeography of cicadas on continental and oceanic islands in the northwestern Pacific region. Journal of Biogeography, 2021, 48, 3060-3071.	1.4	4
16372	Genome-wide identification and characterization of basic helix-loop-helix transcription factors in Spodoptera litura upon pathogen infection. Insect Science, 2021, , .	1.5	1
16373	A Mutation-Selection Model of Protein Evolution under Persistent Positive Selection. Molecular Biology and Evolution, 2022, 39, .	3.5	10
16374	Taxonomy and molecular phylogeny of a new freshwater ciliate Frontonia apoacuminata sp. nov. (Protista, Ciliophora, Oligohymenophorea) from Qingdao, PR China. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	4
16375	Complete mitochondrial genome of Teratoscincus przewalskii (Reptilia, Squamata, Sphaerodactylidae) and phylogenetic analysis. Mitochondrial DNA Part B: Resources, 2021, 6, 3166-3168.	0.2	1
16376	Thousands of Qatari genomes inform human migration history and improve imputation of Arab haplotypes. Nature Communications, 2021, 12, 5929.	5.8	18
16378	Variation and Evolution of the Whole Chloroplast Genomes of Fragaria spp. (Rosaceae). Frontiers in Plant Science, 2021, 12, 754209.	1.7	13
16380	Identification of Antimicrobial Peptide Genes in Black Rockfish Sebastes schlegelii and Their Responsive Mechanisms to Edwardsiella tarda Infection. Biology, 2021, 10, 1015.	1.3	14
16381	Methanogenesis and Salt Tolerance Genes of a Novel Halophilic Methanosarcinaceae Metagenome-Assembled Genome from a Former Solar Saltern. Genes, 2021, 12, 1609.	1.0	10

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16382	A versatile genetic toolbox for <i>Prevotella copri</i> enables studying polysaccharide utilization systems. <i>EMBO Journal</i> , 2021, 40, e108287.	3.5	18
16383	Whole genome based insights into the phylogeny and evolution of the Juglandaceae. <i>Bmc Ecology and Evolution</i> , 2021, 21, 191.	0.7	11
16384	AncestralClust: clustering of divergent nucleotide sequences by ancestral sequence reconstruction using phylogenetic trees. <i>Bioinformatics</i> , 2022, 38, 663-670.	1.8	3
16387	Duplication of spiralian-specific TALE genes and evolution of the blastomere specification mechanism in the bivalve lineage. <i>EvoDevo</i> , 2021, 12, 11.	1.3	4
16388	Characterization of the First Cultured Psychrotolerant Representative of <i>Legionella</i> from Antarctica Reveals Its Unique Genome Structure. <i>Microbiology Spectrum</i> , 2021, 9, e0042421.	1.2	7
16389	<i>Pluteus lauracearum</i> (Agaricales, Basidiomycota), a new species of <i>Pluteus</i> sect. <i>Hispidoderma</i> from thermophilic <i>Laurus</i> forests. <i>Phytotaxa</i> , 2021, 523, 126-140.	0.1	1
16390	The chromosome-scale genome assembly, annotation and evolution of <i>Rhododendron henanense</i> subsp. <i>lingbaoense</i> . <i>Molecular Ecology Resources</i> , 2022, 22, 988-1001.	2.2	14
16391	Comparative Genomics of <i>Mycobacterium avium</i> Complex Reveals Signatures of Environment-Specific Adaptation and Community Acquisition. <i>MSystems</i> , 2021, 6, e0119421.	1.7	7
16392	The complete chloroplast genome sequence of the Tibetan herb <i>Phlomis rotata</i> (Benth. ex) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.2	1
16393	Molecular Phylogeny and Taxonomy of the Genus <i>Spumella</i> (Chrysophyceae) Based on Morphological and Molecular Evidence. <i>Frontiers in Plant Science</i> , 2021, 12, 758067.	1.7	7
16394	Ancient volcanos as species pumps: A case study of freshwater amphipods in Northeast Asia. <i>Molecular Ecology</i> , 2022, 31, 343-355.	2.0	7
16395	Investigating mechanisms associated with emamectin benzoate resistance in the tomato borer <i>Tuta absoluta</i> . <i>Journal of Pest Science</i> , 2022, 95, 1163-1177.	1.9	7
16396	Draft genome and description of <i>Waterburya agarophytonicola</i> gen. nov. sp. nov. (Pleurocapsales,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.7	5
16397	Triple reassortment increases compatibility among viral ribonucleoprotein genes of contemporary avian and human influenza A viruses. <i>PLoS Pathogens</i> , 2021, 17, e1009962.	2.1	3
16398	A dated molecular phylogeny and biogeographical analysis reveals the evolutionary history of the trans-pacifically disjunct tropical tree genus <i>Ormosia</i> (Fabaceae). <i>Molecular Phylogenetics and Evolution</i> , 2022, 166, 107329.	1.2	10
16400	Role of Pleistocene climatic oscillations on genetic differentiation and evolutionary history of the Transvolcanic deer mouse <i>Peromyscus hylocetes</i> (Rodentia: Cricetidae) throughout the Mexican central highlands. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2021, 59, 2481-2499.	0.6	3
16401	Characterization of the complete chloroplast genome of <i>Astragalus galactites</i> (Fabaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 3278-3279.	0.2	4
16402	Raptor roosts as invasion archives: insights from the first black rat mitochondrial genome sequenced from the Caribbean. <i>Biological Invasions</i> , 2022, 24, 17.	1.2	0

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16403	Development of a database and standardized approach for <i>rpoB</i> sequence-based subtyping and identification of aerobic spore-forming Bacillales. <i>Journal of Microbiological Methods</i> , 2021, 191, 106350.	0.7	4
16404	First Genomic Evidence of Dual African Swine Fever Virus Infection: Case Report from Recent and Historical Outbreaks in Sardinia. <i>Viruses</i> , 2021, 13, 2145.	1.5	4
16405	Identification of a novel <i>Candida metapsilosis</i> isolate reveals multiple hybridization events. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	6
16406	A morphological and molecular survey of <i>Neoconidiobolus</i> reveals a new species and two new combinations. <i>Mycological Progress</i> , 2021, 20, 1233-1241.	0.5	4
16407	Natural Hybrid Origin of the Controversial "Species" <i>Clematis</i> <i>pinnata</i> (Ranunculaceae) Based on Multidisciplinary Evidence. <i>Frontiers in Plant Science</i> , 2021, 12, 745988.	1.7	4
16408	New data on the valvatiform-shelled Hydrobiidae (Caenogastropoda, Truncatelloidea) from southern Greece. <i>ZooKeys</i> , 2021, 1062, 31-47.	0.5	4
16409	Surveillance along the Rio Grande during the 2020 Vesicular Stomatitis Outbreak Reveals Spatio-Temporal Dynamics of and Viral RNA Detection in Black Flies. <i>Pathogens</i> , 2021, 10, 1264.	1.2	4
16410	Mitochondrial and karyotypic evidence reveals a lack of support for the genus <i>Nasuella</i> (Procyonidae). <i>Tj ETQq1 1 0,784314 rgBT /Overl</i>	0.4	2
16412	Depside and Depsidone Synthesis in Lichenized Fungi Comes into Focus through a Genome-Wide Comparison of the Olivetoric Acid and Physodic Acid Chemotypes of <i>Pseudevernia furfuracea</i> . <i>Biomolecules</i> , 2021, 11, 1445.	1.8	27
16413	Three new species of <i>Cylindrobasidium</i> (Physalacriaceae, Agaricales) from East Asia. <i>Mycological Progress</i> , 2021, 20, 1297-1308.	0.5	1
16414	Characterization of a pESI-like plasmid and analysis of multidrug-resistant <i>Salmonella enterica</i> <i>Infantis</i> isolates in England and Wales. <i>Microbial Genomics</i> , 2021, 7, .	1.0	14
16415	Genetic diversity of <i>Salmonella</i> <i>Paratyphi</i> A isolated from enteric fever patients in Bangladesh from 2008 to 2018. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009748.	1.3	10
16416	Plastid phylogenomics of the Gynoxoid group (Senecioneae, Asteraceae) highlights the importance of motif-based sequence alignment amid low genetic distances. <i>American Journal of Botany</i> , 2021, 108, 2235-2256.	0.8	8
16417	Phylogeography of the capybara, <i>Hydrochoerus hydrochaeris</i> , in a large portion of its distribution area in South America. <i>Journal of Mammalian Evolution</i> , 2022, 29, 191-206.	1.0	2
16418	New distributional opportunities with niche innovation in Eurasian snowfinches. <i>Journal of Avian Biology</i> , 2021, 52, .	0.6	3
16420	Viral genome wide association study identifies novel hepatitis C virus polymorphisms associated with sofosbuvir treatment failure. <i>Nature Communications</i> , 2021, 12, 6105.	5.8	11
16421	A dated phylogeny shows Pliocene-Pleistocene climates spurred evolution of antibrowsing defences in the New Zealand flora. <i>New Phytologist</i> , 2022, 233, 546-554.	3.5	4
16422	Similar heterotrophic communities but distinct interactions supported by red and green snow algae in the Antarctic Peninsula. <i>New Phytologist</i> , 2022, 233, 1358-1368.	3.5	7

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16423	Evolutionary history and divergence times of Odonata (dragonflies and damselflies) revealed through transcriptomics. <i>IScience</i> , 2021, 24, 103324.	1.9	25
16424	A Previously Undescribed Highly Prevalent Phage Identified in a Danish Enteric Virome Catalog. <i>MSystems</i> , 2021, 6, e0038221.	1.7	22
16425	Towards revealing the global diversity and community assembly of soil eukaryotes. <i>Ecology Letters</i> , 2022, 25, 65-76.	3.0	47
16426	The fungus <i>Kalmusia longispora</i> is able to cause vascular necrosis on <i>Vitis vinifera</i> . <i>PLoS ONE</i> , 2021, 16, e0258043.	1.1	4
16427	bHLH Transcription Factors Undergo Alternative Splicing During Cold Acclimation in a <i>Eucalyptus</i> hybrid. <i>Plant Molecular Biology Reporter</i> , 0, , 1.	1.0	2
16428	Ten millennia of hepatitis B virus evolution. <i>Science</i> , 2021, 374, 182-188.	6.0	64
16429	A single sulfatase is required to access colonic mucin by a gut bacterium. <i>Nature</i> , 2021, 598, 332-337.	13.7	87
16430	Ophiostomatoid species associated with pine trees (<i>Pinus</i> spp.) infested by <i>Cryphalus piceae</i> from eastern China, including five new species. <i>MycoKeys</i> , 2021, 83, 181-208.	0.8	5
16431	Four new species of <i>Russula</i> subsection <i>Roseinae</i> from tropical montane forests in western Panama. <i>PLoS ONE</i> , 2021, 16, e0257616.	1.1	5
16432	Chromosome-Level Genome Assembly of the Asian Red-Tail Catfish (<i>Hemibagrus wyckioides</i>). <i>Frontiers in Genetics</i> , 2021, 12, 747684.	1.1	12
16433	<i>Luteolibacter ambystomatis</i> sp. nov., isolated from the skin of an Anderson's salamander (<i>Ambystoma</i>)	0.8	9
16434	Characterization of the complete chloroplast genome of <i>Scrophularia cephalantha</i> endemic to Korea. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 3179-3180.	0.2	1
16435	The red flower wintersweet genome provides insights into the evolution of magnoliids and the molecular mechanism for tepal color development. <i>Plant Journal</i> , 2021, 108, 1662-1678.	2.8	12
16436	The origin of an extreme case of sister-species sympatry in a palm-pollinator mutualistic system. <i>Journal of Biogeography</i> , 2021, 48, 3158-3169.	1.4	9
16437	The complete chloroplast genome and phylogenetic analysis of <i>Gentiana arethusae</i> Burkill (<i>Gentianaceae</i>) from China. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 3132-3133.	0.2	0
16438	Do colour-morphs of an amphidromous goby represent different species? Taxonomy of <i>Lentipes</i> (<i>Gobiiformes</i>) from Japan and Palawan, Philippines, with phylogenomic approaches. <i>Systematics and Biodiversity</i> , 0, , 1-33.	0.5	4
16439	Molecular basis of a bacterial-amphibian symbiosis revealed by comparative genomics, modeling, and functional testing. <i>ISME Journal</i> , 2022, 16, 788-800.	4.4	15
16440	Comparative mitogenomics of <i>Drosophilidae</i> and the evolution of the <i>Zygothrica</i> genus group (<i>Diptera</i> , <i>Drosophilidae</i>). <i>Genetica</i> , 2021, 149, 267-281.	0.5	5

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16443	Clinical and Molecular Epidemiology of Crimean-Congo Hemorrhagic Fever in Humans in Uganda, 2013–2019. <i>American Journal of Tropical Medicine and Hygiene</i> , 2022, 106, 88-98.	0.6	9
16444	The first molecular insight into the genus <i>Turanium</i> Baeckmann, 1922 (Coleoptera: Cerambycidae: Tj ETQq1 1 0.784314 rgBT /Overlo... 0, 79, 465-484.	5.5	4
16445	Genome, Transcriptome, and Germplasm Sequencing Uncovers Functional Variation in the Warm-Season Grain Legume Horsegram <i>Macrotyloma uniflorum</i> (Lam.) Verdc.. <i>Frontiers in Plant Science</i> , 2021, 12, 758119.	1.7	7
16446	The durability of immunity against reinfection by SARS-CoV-2: a comparative evolutionary study. <i>Lancet Microbe</i> , The, 2021, 2, e666-e675.	3.4	147
16447	Evidence of cryptic diversity in <i>Podarcis peloponnesiacus</i> and re-evaluation of its current taxonomy; insights from genetic, morphological, and ecological data. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2021, 59, 2350-2370.	0.6	5
16448	RefPlantNLR is a comprehensive collection of experimentally validated plant disease resistance proteins from the NLR family. <i>PLoS Biology</i> , 2021, 19, e3001124.	2.6	81
16449	Palm Foliage as Pathways of Pathogenic Botryosphaeriaceae Fungi and Host of New <i>Lasiodiplodia</i> Species from Mexico. <i>Pathogens</i> , 2021, 10, 1297.	1.2	3
16450	Rapid evolutionary turnover of mobile genetic elements drives bacterial resistance to phages. <i>Science</i> , 2021, 374, 488-492.	6.0	96
16451	<i>Nitzschia anatoliensis</i> sp. nov., a cryptic diatom species from the highly alkaline Van Lake (Turkey). <i>PeerJ</i> , 2021, 9, e12220.	0.9	4
16452	Phylogenetics of Japanese <i>Geranium</i> (Geraniaceae) using chloroplast genome sequences and genome-wide single nucleotide polymorphisms. <i>Plant Systematics and Evolution</i> , 2021, 307, 1.	0.3	1
16453	Lower Statistical Support with Larger Data Sets: Insights from the Ochrophyta Radiation. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	7
16454	The complete chloroplast genome sequence of <i>Phalaenopsis wilsonii</i> (Orchidaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 3303-3305.	0.2	3
16455	Undiscovered Biodiversity of the European Moss Flora: <i>Neodicranella hamulosa</i> (Aongstroemiaceae), a New Genus and Species from SW Portugal. <i>Plants</i> , 2021, 10, 2289.	1.6	4
16456	Classification of uncultivated anammox bacteria and <i>Candidatus Uabimicrobium</i> into new classes and provisional nomenclature as <i>Candidatus Brocadiia classis nov.</i> and <i>Candidatus Uabimicrobiia classis nov.</i> of the phylum Planctomycetes and novel family <i>Candidatus Scalinduaceae fam. nov.</i> to accommodate the genus <i>Candidatus Scalindua</i> . <i>Systematic and Applied Microbiology</i> , 2021, 44, 126272.	1.2	22
16457	A paradigm for the recognition of cryptic trematode species in tropical Indo-west Pacific fishes: the problematic genus <i>Preptetos</i> (Trematoda: Lepocreadiidae). <i>International Journal for Parasitology</i> , 2022, 52, 169-203.	1.3	24
16458	Biphasic taxonomic approaches for generic relatedness and phylogenetic relationships of <i>Teichosporaceae</i> . <i>Fungal Diversity</i> , 2021, 110, 199-241.	4.7	2
16459	Mitochondrial and Plastid Genomes of the Monoraphid Diatom <i>Schizostauron trachyderma</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 11139.	1.8	5
16460	Sperm Cyst – Looping: A Developmental Novelty Enabling Extreme Male Ornament Evolution. <i>Cells</i> , 2021, 10, 2762.	1.8	3

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16461	Genome-wide association studies reveal the role of polymorphisms affecting factor H binding protein expression in host invasion by <i>Neisseria meningitidis</i> . <i>PLoS Pathogens</i> , 2021, 17, e1009992.	2.1	15
16462	Genetic Diversity and Phylogeny of the Genus <i>Euplotes</i> (Protozoa, Ciliophora) Revealed by the Mitochondrial CO1 and Nuclear Ribosomal Genes. <i>Microorganisms</i> , 2021, 9, 2204.	1.6	6
16463	Understudied, underrepresented, and unknown: Methodological biases that limit detection of early diverging fungi from environmental samples. <i>Molecular Ecology Resources</i> , 2022, 22, 1065-1085.	2.2	14
16464	Geographical isolation versus dispersal: Relictual alpine grasshoppers support a model of interglacial diversification with limited hybridization. <i>Molecular Ecology</i> , 2022, 31, 296-312.	2.0	14
16465	Deep sequencing across multiple host species tests pineâ€endophyte specificity. <i>American Journal of Botany</i> , 2021, , .	0.8	3
16466	Contributions to the phylogeny of <i>Lepraria</i> (Stereocaulaceae) species from the Southern Hemisphere, including three new species. <i>Bryologist</i> , 2021, 124, .	0.1	2
16469	Ancestral sequence reconstruction pinpoints adaptations that enable avian influenza virus transmission in pigs. <i>Nature Microbiology</i> , 2021, 6, 1455-1465.	5.9	7
16472	Ancient Mitogenomes Provide New Insights into the Origin and Early Introduction of Chinese Domestic Donkeys. <i>Frontiers in Genetics</i> , 2021, 12, 759831.	1.1	2
16473	The complete chloroplast genome and phylogenetic analysis of <i>Paris stigmatosa</i> (Melanthiaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 3204-3206.	0.2	0
16474	The origins and spread of domestic horses from the Western Eurasian steppes. <i>Nature</i> , 2021, 598, 634-640.	13.7	142
16475	Molecular evolution and convergence of the rhodopsin gene in <i>Gymnogobius</i> , a goby group having diverged into coastal to freshwater habitats. <i>Journal of Evolutionary Biology</i> , 2022, 35, 333-346.	0.8	5
16476	The first complete plastome sequence from family Flagellariaceae (<i>Flagellaria indica</i> L., Poales). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 3164-3165.	0.2	1
16477	The complete chloroplast genome and phylogenetic analysis of <i>Sida szechuensis matsuda</i> (Malvaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 3146-3147.	0.2	0
16478	Cenozoic climatic changes drive evolution and dispersal of coastal benthic foraminifera in the Southern Ocean. <i>Scientific Reports</i> , 2021, 11, 19869.	1.6	8
16480	The complete chloroplast genome of <i>Lonicera similis</i> Hemsl. and its phylogenetic analysis. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 3151-3153.	0.2	1
16481	The chloroplast genomes of four <i>Bupleurum</i> (Apiaceae) species endemic to Southwestern China, a diversity center of the genus, as well as their evolutionary implications and phylogenetic inferences. <i>BMC Genomics</i> , 2021, 22, 714.	1.2	17
16482	Complete Genome Sequence of SMBL-WEM22, a Halotolerant Strain of <i>Kosakonia cowanii</i> Isolated from Hong Kong Seawater. <i>Microbiology Resource Announcements</i> , 2021, 10, e0089121.	0.3	1
16483	Sulfur cycling and host-virus interactions in <i>Aquificales</i> -dominated biofilms from Yellowstoneâ€™s hottest ecosystems. <i>ISME Journal</i> , 2022, 16, 842-855.	4.4	8

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16484	Yunnanâ€™Guizhou Plateau: a mycological hotspot. <i>Phytotaxa</i> , 2021, 523, 1-31.	0.1	11
16485	Genomics-Based Phylogenetic and Population Genetic Analysis of Global Samples Confirms <i>Halophila johnsonii</i> Eiseman as <i>Halophila ovalis</i> (R.Br.) Hook.f.. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	6
16486	Molecular data elucidate cryptic diversity within the widespread Threadfin Shad (<i>Dorosoma</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 662 T	1.0	6
16489	Gene regulation of adult skeletogenesis in starfish and modifications during gene network co-option. <i>Scientific Reports</i> , 2021, 11, 20111.	1.6	6
16490	Molecular phylogenetic, morphological, and pathogenic analyses reveal a single clonal population of <i>Septoria lycopersici</i> with a narrower host range in Brazil. <i>Plant Pathology</i> , 2022, 71, 621-633.	1.2	1
16491	Fast and accurate distanceâ€based phylogenetic placement using divide and conquer. <i>Molecular Ecology Resources</i> , 2022, 22, 1213-1227.	2.2	25
16492	Kouprey (<i>Bos sauveli</i>) genomes unveil polytomic origin of wild Asian Bos. <i>IScience</i> , 2021, 24, 103226.	1.9	8
16493	Isolation of Novel Mycobacterium Species from Skin Infection in an Immunocompromised Person. <i>Emerging Infectious Diseases</i> , 2021, 27, 2944-2947.	2.0	0
16494	<i>Saccharopolyspora karakumensis</i> sp. nov., <i>Saccharopolyspora elongata</i> sp. nov., <i>Saccharopolyspora aridisoli</i> sp. nov., <i>Saccharopolyspora terrae</i> sp. nov. and their biotechnological potential revealed by genome analysis. <i>Systematic and Applied Microbiology</i> , 2021, 44, 126270.	1.2	20
16495	Virome analysis of three Ixodidae ticks species from Colombia: A potential strategy for discovering and surveying tick-borne viruses. <i>Infection, Genetics and Evolution</i> , 2021, 96, 105103.	1.0	5
16496	Shedding light on the functional role of the Ignavibacteria in Italian rice field soil: A meta-genomic/transcriptomic analysis. <i>Soil Biology and Biochemistry</i> , 2021, 163, 108444.	4.2	12
16497	Genome-wide identification of 216 G protein-coupled receptor (GPCR) genes from the marine water flea <i>Diaphanosoma celebensis</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2021, 40, 100922.	0.4	0
16498	The genome of the black cutworm <i>Agrotis ipsilon</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2021, 139, 103665.	1.2	8
16504	Relation between Insertion Sequences and Genome Rearrangements in <i>Pseudomonas aeruginosa</i> . <i>Lecture Notes in Computer Science</i> , 2015, , 426-437.	1.0	1
16512	Pylogeny: an open-source Python framework for phylogenetic tree reconstruction and search space heuristics. <i>PeerJ Computer Science</i> , 0, 1, e9.	2.7	1
16516	Occurrence and Molecular Phylogenetic Characteristics of Benthic Sand-dwelling Dinoflagellates in the Intertidal Flat of Dongho, West Coast of Korea. <i>Pada (Han'guk Haeyang Hakhoe)</i> , 2015, 20, 141-150.	0.3	0
16517	The genus <i>Scouleria</i> (Bryophyta) in Russia revisited. <i>Arctoa</i> , 2015, 24, 47-66.	0.3	7
16524	Phylogeography in Response to Reproductive Strategies and Ecogeographic Isolation in Ant Species on Madagascar: Genus <i>Mystrium</i> (Formicidae: Amblyoponinae). <i>PLoS ONE</i> , 2016, 11, e0146170.	1.1	2

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16525	Molecular phylogenetics reveals a new species of Prostanthera from tropical Queensland with links to more southerly taxa. <i>Telopea</i> , 0, 19, 13-22.	0.4	6
16527	Quantitative comparison of plasmodial networks of different slime molds. , 2016, , .		2
16543	<i>Parmotrema clavuliferum</i> and <i>P. reticulatum</i> are independent species. <i>Journal of Species Research</i> , 2016, 5, 254-260.	0.1	0
16545	On the morphology of <i>Plectrohyla chryses</i> (Anura: Hylidae; Hylini), with comments on some controversial characters, phylogenetic relationships, and diagnosis of this species. <i>Caldasia</i> , 2016, 38, 257.	0.1	1
16566	Comment on Falade et al. (2016) DNA-barcoding of <i>Clarias gariepinus</i> , <i>Coptedon zillii</i> and <i>Sarotherodon melanotheron</i> from Southwestern Nigeria. <i>F1000Research</i> , 0, 5, 2654.	0.8	0
16571	Species distinctness of <i>Litthabitella</i> Boeters, 1970 (Caenogastropoda: Truncatelloidea) from the Ionian Islands. <i>Folia Malacologica</i> , 2016, 24, 295-305.	0.1	1
16576	Whole genome sequencing to investigate a putative outbreak of the virulent community-associated methicillin-resistant <i>Staphylococcus aureus</i> ST93 clone in a remote Indigenous community. <i>Microbial Genomics</i> , 2016, 2, e000098.	1.0	1
16579	Revisiting the phylogeny of phylum Ctenophora: a molecular perspective. <i>F1000Research</i> , 0, 5, 2881.	0.8	0
16587	Bioinformatics Aspects of Foodborne Pathogen Research. , 2017, , 51-64.		0
16588	Improving Multiobjective Phylogenetic Searches by Using a Parallel ϵ -Dominance Based Adaptation of the Firefly Algorithm. <i>Lecture Notes in Computer Science</i> , 2017, , 384-396.	1.0	0
16589	Occurrence of <i>Belonolaimus</i> in Sinaloa, Northwestern Mexico: A New Report on Distribution and Host Range. <i>Journal of Nematology</i> , 2017, 49, 103-113.	0.4	0
16594	<i>Motilimonas eburnea</i> gen. nov., sp. nov., isolated from coastal sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 306-310.	0.8	12
16632	A new genus and species of uncertain phylogenetic position within the family Hydrobiidae (Caenogastropoda: Truncatelloidea) discovered in Tunisian springs. <i>European Journal of Taxonomy</i> , 2017, , .	0.6	2
16654	Revisiting the phylogeny of phylum Ctenophora: a molecular perspective. <i>F1000Research</i> , 0, 5, 2881.	0.8	0
16655	A new species of the genus <i>Rana</i> from Henan, central China (Anura, Ranidae). <i>ZooKeys</i> , 2017, 694, 95-108.	0.5	9
16664	Morphological observations and phylogenetic position of the parasitoid nanoflagellate <i>Pseudopirsonia</i> sp. (Cercozoa) infecting the marine diatom <i>Coscinodiscus wailesii</i> (Bacillariophyta). <i>Algae</i> , 2017, 32, 181-187.	0.9	3
16665	North-Western Palaearctic species of <i>Pristiphora</i> (Hymenoptera, Tenthredinidae). <i>Journal of Hymenoptera Research</i> , 0, 59, 1-190.	0.8	1
16680	Three-dimensional Modelling of the Voltage-gated Sodium Ion Channel from <i>Anopheles gambiae</i> Reveals Spatial Clustering of Evolutionarily Conserved Acidic Residues at the Extracellular Sites. <i>Current Neuropharmacology</i> , 2017, 15, 1062-1072.	1.4	1

#	ARTICLE	IF	CITATIONS
16879	Palaeogenome Reveals Genetic Contribution of Extinct Giant Panda to Extant Populations. SSRN Electronic Journal, 0, , .	0.4	0
16880	The Parallel Lives of Human Y Chromosome Lineages Across the Strait of Gibraltar. , 2019, , 217-231.		0
16887	Comparative Endocrinology, 2019, 45, 26-31.		0
16890	A Quantitative and Qualitative Characterization of k-mer Based Alignment-Free Phylogeny Construction. Lecture Notes in Computer Science, 2019, , 19-31.	1.0	1
16891	Morpho-molecular characterization of Colombian and Brazilian populations of <i>Rotylenchulus</i> associated with <i>Musa</i> spp. Journal of Nematology, 2019, 51, 1-13.	0.4	7
16894	Comparative Analyses of 35 Marine Mammal Genomes Provide Insights into the Evolution of Aquatic Life. SSRN Electronic Journal, 0, , .	0.4	0
16899	Protective Immunity in a Genetically Tractable Natural Mouse Model of Cryptosporidiosis. SSRN Electronic Journal, 0, , .	0.4	0
16900	Fully automated sequence alignment methods are comparable to, and much faster than, traditional methods in large data sets: an example with hepatitis B virus. PeerJ, 2019, 7, e6142.	0.9	3
16902	Aerobic Hydrocarbon-Degrading Gammaproteobacteria: Oleiphilaceae and Relatives. , 2019, , 1-14.		0
16915	Biodiversity Survey and Molecular Identification of the Phasiinae (Diptera: Tachinidae) of Great Smoky Mountains National Park, USA. Proceedings of the Entomological Society of Washington, 2019, 121, 1.	0.0	0
16922	Taxonomic Identity of <i>Arisaema pangii</i> (Araceae) Inferred from Molecular and Morphological Data with a Note on its Distribution. Annales Botanici Fennici, 2019, 56, 19.	0.0	0
16924	<i>Zavarzina aquatilis</i> sp. nov., isolated from a freshwater river. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 727-731.	0.8	7
16939	<i>Septonema lohmanii</i> G. Delgado & O. Koukol, sp. nov., a New Species in Mytilinidiales (Dothideomycetes) and the Phylogenetic Position of <i>S. fasciculare</i> (Corda) S. Hughes. Cryptogamie, Mycologie, 2019, 40, 3.	0.2	0
16946	The Third Species of <i>Darpa</i> Moore, 1865 in China and Some Notes on the Genus (Hesperiidae: Pyrginae:). Tj ETQq1 1 0.784314 1 rgBT /Over	0.1	1
16949	Genetic differentiation in the southern population of the Fathead Minnow <i>Pimephales promelas</i> Rafinesque (Actinopterygii: Cyprinidae). PeerJ, 2019, 7, e6224.	0.9	3
16953	Revision of the genus <i>Emphylica</i> Turner, 1913 based on morphology and molecular data (Lepidoptera,). Tj ETQq1 1 0.784314 4 rgBT /Over	0.5	4
16954	Every beach an island – deep population divergence and possible loss of genetic diversity in <i>Tylos granulatus</i> , a sandy shore isopod. Marine Ecology - Progress Series, 2019, 614, 111-123.	0.9	7
16961	Polysyncraton (Ascidiacea, Didemnidae): a re-examination of some specimens and descriptions of three new species. European Journal of Taxonomy, 2019, , .	0.6	1

#	ARTICLE	IF	CITATIONS
16962	rGUIDANCE “ alignment confidence score computation in R. <i>Journal of Open Source Software</i> , 2019, 4, 1350.	2.0	0
16969	Molecular and phenotypical studies on species diversity of <i>Hypotrachyna</i> (Parmeliaceae, Ascomycota) in Kenya, East Africa. <i>Bryologist</i> , 2019, 122, 140.	0.1	3
16987	<i>Syntrophotalea acetylenivorans</i> sp. nov., a diazotrophic, acetylenotrophic anaerobe isolated from intertidal sediments. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 71, .	0.8	9
16988	<i>Grimontia sedimenti</i> sp. nov., isolated from benthic sediments near coral reefs south of Kuwait. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 71, .	0.8	8
16994	<i>Pelistega ratti</i> sp. nov. from <i>Rattus norvegicus</i> of Hainan island. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 71, .	0.8	7
16995	Bloom-forming dinoflagellate <i>Akashiwo sanguinea</i> (Dinophyceae) in Jangmok Harbour of Geoje Island, Korea: Morphology, phylogeny and effects of temperature and salinity on growth. <i>Hangug Hwangyeong Saengmul Haghoeji</i> , 2019, 37, 119-128.	0.1	1
16999	<i>Sulfurovum indicum</i> sp. nov., a novel hydrogen- and sulfur-oxidizing chemolithoautotroph isolated from a deep-sea hydrothermal plume in the Northwestern Indian Ocean. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 71, .	0.8	17
17003	<i>Elbamycella rosea</i> gen. et sp. nov. (Juncigenaceae, Torpedosporales) isolated from the Mediterranean Sea. <i>MycKeys</i> , 2019, 55, 15-28.	0.8	4
17007	Proposal of <i>Enterococcus xinjiangensis</i> Ren et al. 2020 as a later heterotypic synonym of <i>Enterococcus lactis</i> Morandi et al. 2012. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 71, .	0.8	7
17008	<i>Pseudorhodobacter turbinis</i> sp. nov., isolated from the gut of the Korean turban shell, <i>Turbo cornutus</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 71, .	0.8	6
17009	<i>Entomobacter blattae</i> gen. nov., sp. nov., a new member of the Acetobacteraceae isolated from the gut of the cockroach <i>Gromphadorhina portentosa</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 71, .	0.8	19
17025	Description of a new species of <i>Paraplehnia</i> (Polycladida, Stylochoidea) from Japan, with inference on the phylogenetic position of Plehniidae. <i>ZooKeys</i> , 2019, 864, 1-13.	0.5	4
17035	Species of <i>Heterolepismatinae</i> (Zygentoma: Lepismatidae) found on some remote eastern Australian Islands. <i>Records of the Australian Museum</i> , 2019, 71, 139-181.	0.3	2
17036	<i>Nectria</i> -related fungi causing dieback and canker diseases in China, with <i>Neothyronectria citri</i> sp. nov. described. <i>MycKeys</i> , 2019, 56, 49-66.	0.8	3
17038	<i>Streptomyces altiplanensis</i> sp. nov., an alkalitolerant species isolated from Chilean Altiplano soil, and emended description of <i>Streptomyces chryseus</i> (Krasil'nikov et al. 1965) Pridham 1970. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 2498-2505.	0.8	12
17040	<i>Sculptolumina yunnanensis</i> , a new species of <i>Buellia</i> s.l. (lichenized Ascomycota, Caliciaceae) from Yunnan, China. <i>Bryologist</i> , 2019, 122, 404.	0.1	0
17044	The revised complete mitogenome sequence of the tree frog <i>Polypedates megacephalus</i> (Anura). <i>Tj ETQq0 0 0 rgBT /Overlock 10 T</i>	0.9	5
17045	First Genetic Data of the Critically Endangered Vietnamese Pond Turtle (<i>Mauremys annamensis</i>) from Known-locality Specimens. <i>Current Herpetology</i> , 2019, 38, 140.	0.5	0

#	ARTICLE	IF	CITATIONS
17047	Morphology, chemistry and molecular phylogeny revealed a new species and a new combination of <i>Myriolecis</i> (Lecanoraceae, Ascomycota) from China. <i>Bryologist</i> , 2019, 122, 375.	0.1	4
17054	Phylogenetic Relationships in <i>Arjona</i> (Schoepfiaceae), a Hemiparasitic Herb from Southern South America. <i>Systematic Botany</i> , 2019, 44, 592-599.	0.2	2
17063	A study of newly recorded genus and species for aerial cyanobacteria <i>Wilmottia murrayi</i> (Oscillatoriales, Cyanobacteria) in Korea. <i>Hangug Hwangyeong Saengmul Haghoeji</i> , 2019, 37, 260-267.	0.1	4
17072	Evaluaci3n de las regiones del cloroplasto matK e ycf1 como marcadores de diagn3stico para el g3nero Pinus. <i>Cuadernos De La Sociedad Espa3ola De Ciencias Forestales</i> , 2019, 45, 215-236.	0.1	0
17073	New morphological and DNA evidence supports the existence of <i>Calligonum jeminaicum</i> Z. M. Mao (Calligoneae, Polygonaceae) in China. <i>PhytoKeys</i> , 2019, 132, 53-73.	0.4	2
17077	A New Species of Plateau Pit Viper (Reptilia: Serpentes: Gloydius) from the Upper Lancang (=Mekong) Valley in the Hengduan Mountain Region, Tibet, China. <i>Journal of Herpetology</i> , 2019, 53, 224.	0.2	5
17078	<i>Alsidium oliveiranum</i> ; sp. nov. (Rhodomelaceae, Rhodophyta), an overlooked species from the southwestern Atlantic based on morphology and DNA sequence data. <i>Algae</i> , 2019, 34, 187-198.	0.9	4
17084	Genomic evolution and local epidemiology of <i>Klebsiella pneumoniae</i> from a major hospital in Beijing, China, over a 15 year period: dissemination of known and novel high-risk clones. <i>Microbial Genomics</i> , 2019, 7, .	1.0	5
17085	Junior Synonym of <i>Prosopocoilus blanchardi</i> (Coleoptera: Lucanidae) Proposed by the Integrated Taxonomic Approach. <i>Journal of Entomological Science</i> , 2019, 54, 430.	0.2	1
17091	Morphology and DNA Data Reveal a New Shrimp Species of Genus <i>Latreutes</i> Stimpson, 1860 (Decapoda: Tj ETQq1,1,0.784314 rgBT 0,3 1		
17101	Reappraisal of <i>Taxiphyllum arcuatum</i> (Bosch & Sande Lac.) S.He based on molecular and morphological data. <i>Bryologist</i> , 2019, 122, 559.	0.1	2
17103	<i>Toxicocladosporium aquimarinum</i> sp. nov. and <i>Toxicocladosporium qatarense</i> sp. nov., isolated from marine waters of the Arabian Gulf surrounding Qatar. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 2992-3000.	0.8	4
17109	<i>Alloscardovia theropithecii</i> sp. nov., isolated from the faeces of gelada baboon, the 'bleeding heart' monkey (<i>Theropithecus gelada</i>). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 3041-3048.	0.8	9
17110	Characterization and Phylogenetic Analysis of the Complete Chloroplast Genome of <i>Orinus kokonoricus</i> (Poaceae), an Endemic Species from the Qinghai-Tibet Plateau. <i>Cytology and Genetics</i> , 2019, 53, 510-514.	0.2	0
17137	<i>Zahora</i> , a new monotypic genus from tribe Brassiceae (Brassicaceae) endemic to the Moroccan Sahara. <i>PhytoKeys</i> , 2019, 135, 119-131.	0.4	5
17138	New Asian localities of <i>Hymenostylium xerophilum</i> and <i>H. gracillimum</i> . <i>Arctoa</i> , 2019, 28, 149-158.	0.3	3
17143	High mortality in <i>Bufo gargarizans</i> eggs associated with an undescribed <i>Saprolegnia ferax</i> strain in the Republic of Korea. <i>Diseases of Aquatic Organisms</i> , 2019, 137, 89-99.	0.5	4
17144	<i>Chaetomium</i> in Indoor Environment and Medically Important Species of <i>Chaetomium</i> . <i>Fungal Biology</i> , 2020, , 161-173.	0.3	2

#	ARTICLE	IF	CITATIONS
17157	On moss family Lembophyllaceae in the Russian Far East. <i>Arctoa</i> , 2019, 28, 179-192.	0.3	2
17159	Complementary description of <i>Africoseius lativentris</i> and placement of <i>Africoseius</i> in Podocinidae (Acari, Mesostigmata) based on molecular and morphological evidences <i>Systematic and Applied Acarology</i> , 2019, 24, 2369-2394.	0.5	1
17161	Patterns of MHC Polymorphism in Endangered San Joaquin Kit Foxes Living in Urban and Non-urban Environments. , 2020, , 269-298.		0
17163	A revised circumscription for <i>Siphonolejeunea</i> and a new species from New Zealand. <i>Australian Systematic Botany</i> , 2020, , .	0.3	1
17166	First report of <i>Meloidogyne javanica</i> infecting <i>Zinnia elegans</i> in CearÃ¡ State, Brazil. <i>Journal of Nematology</i> , 2020, 52, 1-4.	0.4	2
17167	Identification of a novel hybrid zone within the black-footed rock-wallaby (<i>Petrogale lateralis</i>) in Western Australia. <i>Australian Journal of Zoology</i> , 2020, 68, 98.	0.6	3
17168	Phylogenetic placement of the stone-nest orb-weaving spider <i>Nemoscolus</i> Simon, 1895 (Araneae :) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 262 Tc 893.	0.5	1
17169	Convergent evolution of sexually dimorphic glands in an amphi-Pacific harvestman family. <i>Invertebrate Systematics</i> , 2020, 34, 871.	0.5	2
17190	The new genus <i>Jocatoa</i> (Lecanoromycetes: Graphidaceae) and new insights into subfamily Redonographoideae. <i>Bryologist</i> , 2020, 123, 127.	0.1	5
17195	Identity of the <i>Calcarata</i> species complex in <i>Viola</i> sect. <i>Melanium</i> (Violaceae). <i>Willdenowia</i> , 2020, 50, 195.	0.5	6
17200	<i>Oleiliquidispirillum nitrogeniifigens</i> gen. nov., sp. nov., a new member of the family Rhodospirillaceae isolated from oil reservoir water. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 3468-3474.	0.8	11
17209	Cryptic diversity among Yazoo Darters (Percidae: <i>Etheostoma raneyi</i>) in disjunct watersheds of northern Mississippi. <i>PeerJ</i> , 2020, 8, e9014.	0.9	3
17212	A new species of buffalo leech in the genus <i>Hirudinaria</i> Whitman, 1886 (Arhynchobdellida,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 262 Tc 0.5	0.5	2
17213	A New Rupicolous Species of the <i>Pristimantis conspicillatus</i> Group (Anura: Brachycephaloidea:) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 262 Tc 0.2	0.2	4
17222	Species composition of <i>Saxifraga</i> sect. <i>Saxifraga</i> subsect. <i>Arachnoideae</i> (Saxifragaceae) based on DNA sequence evidence. <i>Willdenowia</i> , 2020, 50, 225.	0.5	4
17224	<i>Sarocladium graminicola</i> , a new endophytic species from tropical grasses. <i>Mycological Progress</i> , 2020, 19, 605-614.	0.5	6
17225	Characterization of <i>Peptacetobacter hominis</i> gen. nov., sp. nov., isolated from human faeces, and proposal for the reclassification of <i>Clostridium hiranonis</i> within the genus <i>Peptacetobacter</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 2988-2997.	0.8	18
17229	<i>Kwanghwana miscanthi</i> Karun., C.H.Kuo & K.D.Hyde, gen. et sp. nov. (Phaeosphaeriaceae,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 262 Tc 0.2	0.2	3
	<i>Cryptogamie, Mycologie</i> , 2020, 41, 119.		

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17230	Descriptions of five new species of the salamander genus <i>Chiropterotriton</i> (Caudata): <i>Tj ETQqO 0 0 rgBT /Overlock 10 Tf 50 747 T e8800</i> .	0.9	11
17231	<i>Sedum formosanum</i> subsp. <i>miyakojimense</i> (Crassulaceae), a new subspecies from Miyako-jima Island of the Ryukyu Islands, Japan. <i>PhytoKeys</i> , 2020, 148, 51-70.	0.4	1
17232	Cryptic species inside the genus <i>Hariotina</i> (Scenedesmaceae, Sphaeropleales), with descriptions of four new species in this genus. <i>European Journal of Phycology</i> , 2020, 55, 373-383.	0.9	4
17233	Phylogeny and Floral Character Evolution of <i>Mentzelia</i> Section <i>Bicuspidaria</i> (Loasaceae). <i>Systematic Botany</i> , 2020, 45, 306-314.	0.2	3
17236	<i>Lutibacter citreus</i> sp. nov., isolated from Arctic surface sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 3154-3161.	0.8	6
17238	A phylogenomic tree inferred with an inexpensive <i>scp</i> PCR-generated probe kit resolves higher-level relationships among <i>Neptis</i> butterflies (Nymphalidae: Limenitidinae). <i>Systematic Entomology</i> , 2020, 45, 924-934.	1.7	8
17244	<i>Caa</i> , a new South American genus of Gonolobinae (Apocynaceae: Asclepiadeae: Asclepiadoideae). <i>Lilloa</i> , 0, , 81-88.	0.1	3
17245	A novel polyubiquitin chain linkage formed by viral Ubiquitin is resistant to host deubiquitinating enzymes. <i>Biochemical Journal</i> , 2020, 477, 2193-2219.	1.7	2
17249	Disentangling Reticulate Evolution of North Temperate Haplostemonous <i>Ludwigia</i> (Onagraceae). <i>Annals of the Missouri Botanical Garden</i> , 2020, 105, 163-182.	1.3	5
17254	Molecular Species Delimitation of the Genus <i>Reishia</i> (Mollusca: Gastropoda) along the Coasts of China and Korea. <i>Zoological Science</i> , 2020, 37, 382.	0.3	1
17264	Diversity of the Genus <i>Calocybella</i> Vizzini, Consiglio & Setti in Kerala State, India. <i>Cryptogamie, Mycologie</i> , 2020, 41, 147.	0.2	1
17270	Taxonomic Revision of <i>Chironius bicarinatus</i> (Wied 1820) (Serpentes: Colubridae), with Description of a New Species. <i>Herpetological Monographs</i> , 2020, 34, 98.	1.1	0
17273	A New Species of <i>Pseudoeurycea</i> (Amphibia: Caudata) from the Mountains of Central Veracruz, Mexico. <i>Journal of Herpetology</i> , 2020, 54, 258.	0.2	2
17274	The Nucho-dorsal Glands of <i>Rhabdophis guangdongensis</i> (Squamata: Colubridae: Natricinae), with Notes on Morphological Variation and Phylogeny Based on Additional Specimens. <i>Current Herpetology</i> , 2020, 39, 108.	0.5	4
17276	<i>Prevotella vespertina</i> sp. nov., isolated from an abscess of a hospital patient. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 4576-4582.	0.8	9
17278	Molecular relationships of the Israeli shrews (Eulipotyphla: Soricidae) based on cytochrome b sequences. <i>Mammalia</i> , 2021, 85, 79-89.	0.3	5
17284	Two new combinations in <i>Oreocharis</i> (Gesneriaceae) based on morphological, molecular and cytological evidence. <i>PhytoKeys</i> , 2020, 157, 43-58.	0.4	10
17290	Reassessment of <i>Bournea</i> Oliver (Gesneriaceae) based on molecular and palynological evidence. <i>PhytoKeys</i> , 0, 157, 27-41.	0.4	7

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17297	Nesticus kosodensis Yaginuma, 1972 bona species. Molecular and morphological separation from N. laticapus Yaginuma, 1972 with notes on cave scaffold-web spiders subspecies in Japan (Araneae, Tj ETQq0 0 0 rgBTQOverlook 10 Tf 50		
17298	A New Species of Bathyal Nemertean, <i>Proamphiporus</i> <i>kaimeiae</i> sp. nov., off Tohoku, Japan, and Molecular Systematics of the Genus (Nemertea: Monostilifera). Species Diversity, 2020, 25, 183-188.	0.1	8
17299	<i>Cuscuta</i> sect. <i>Californicae</i> (Convolvulaceae) Revisited: â€˜Crypticâ€™ Speciation and Host Range Differentiation. Systematic Botany, 2020, 45, 638-651.	0.2	5
17300	Two new species of Leptographium associated with Tomicus spp. infesting Pinus spp. in Southwestern China. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 4798-4807.	0.8	2
17304	Morphological, Molecular, and Biogeographic Evidence for Specific Recognition of <i>Euthamia hirtipes</i> and <i>Euthamia scabra</i> (Asteraceae, Astereae). Systematic Botany, 2020, 45, 658-667.	0.2	1
17308	Lactococcus insecticola sp. nov. and Lactococcus hodotermopsidis sp. nov., isolated from the gut of the wood-feeding lower termite Hodotermopsis sjostedti. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 4515-4522.	0.8	10
17309	Revision of the genus Epiparbattia Caradja, 1925 (Lepidoptera, Crambidae, Pyraustinae), based on morphology and molecular data. ZooKeys, 2020, 960, 143-155.	0.5	4
17311	Cryptic genetic variation enhances primate L1 retrotransposon survival by enlarging the functional coiled coil sequence space of ORF1p. PLoS Genetics, 2020, 16, e1008991.	1.5	6
17312	Two new species of Microdochium from Indocalamus longiauritus in south-western China. MycoKeys, 2020, 72, 93-108.	0.8	9
17316	Phylogenetic position of Carex splendentissima, a Korean endemic sedge (Cyperaceae). Korean Journal of Plant Taxonomy, 2020, 50, 253-261.	0.3	0
17318	Organization of the 5s rDNA intergenic spacer of Quercus rubra L. and its relationship to the ukrainian Quercus species. Faktori Eksperimental Noi Evolucii Organizmiv, 0, 26, 125-131.	0.0	5
17321	Two new species in Iris series Chinenses (Iridaceae) from south-central China. PhytoKeys, 2020, 161, 41-60.	0.4	5
17322	Taxonomy of Verrucaria species characterised by large spores, perithecia leaving pits in the rock and a pale thin thallus in Finland. MycoKeys, 2020, 72, 43-92.	0.8	4
17323	Alicyclobacillus mali sp. nov., Alicyclobacillus suci sp. nov. and Alicyclobacillus fructus sp. nov., thermoacidophilic sporeforming bacteria isolated from fruit beverages. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	16
17324	Contribution of historical herbarium small RNAs to the reconstruction of a cassava mosaic geminivirus evolutionary history. Scientific Reports, 2021, 11, 21280.	1.6	8
17325	Pseudomonas alliivorans sp. nov., a plant-pathogenic bacterium isolated from onion foliage in Georgia, USA. Systematic and Applied Microbiology, 2022, 45, 126278.	1.2	14
17326	Multidrug Resistance Dynamics in Salmonella in Food Animals in the United States: An Analysis of Genomes from Public Databases. Microbiology Spectrum, 2021, 9, e0049521.	1.2	11
17327	Chromosome-Level Genome Assembly Reveals Significant Gene Expansion in the Toll and IMD Signaling Pathways of Dendrolimus kikuchii. Frontiers in Genetics, 2021, 12, 728418.	1.1	1

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17328	Floral Trait and Mycorrhizal Similarity between an Endangered Orchid and Its Natural Hybrid. <i>Diversity</i> , 2021, 13, 550.	0.7	5
17329	Establishment of a Publicly Available Core Genome Multilocus Sequence Typing Scheme for <i>Clostridium perfringens</i> . <i>Microbiology Spectrum</i> , 2021, 9, e0053321.	1.2	5
17330	<i>Bradyrhizobium altum</i> sp. nov., <i>Bradyrhizobium oropedii</i> sp. nov. and <i>Bradyrhizobium acaciae</i> sp. nov. from South Africa show locally restricted and pantropical nodA phylogeographic patterns. <i>Molecular Phylogenetics and Evolution</i> , 2022, 167, 107338.	1.2	9
17331	A new genus and species of tanager (Passeriformes, Thraupidae) from the lower Yungas of western Bolivia and southern Peru. <i>Auk</i> , 2021, 138, .	0.7	5
17332	Confirmed polyphyly, generic recircumscription and typification of <i>Dysoxylum</i> (Meliaceae), with revised disposition of currently accepted species. <i>Taxon</i> , 2021, 70, 1248-1272.	0.4	5
17333	<scp>PANTHER</scp>: Making genome-scale phylogenetics accessible to all. <i>Protein Science</i> , 2022, 31, 8-22.	3.1	467
17334	Evolutionary history of the Aztec shiner <i>Aztecula sallaei</i> (Günther, 1868) (Teleostei: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 507 Evolutionary Research, 2021, 59, 2103-2118.	0.6	2
17335	Phylogenetic relatedness, functional traits, and spatial scale determine herbivore co-occurrence in a subtropical forest. <i>Ecological Monographs</i> , 2022, 92, e01492.	2.4	8
17336	Infection Process and Genome Assembly Provide Insights into the Pathogenic Mechanism of Destructive Mycoparasite <i>Calcarisporium cordycipiticola</i> with Host Specificity. <i>Journal of Fungi</i> (Basel, Switzerland), 2021, 7, 918.	1.5	8
17337	Genomic Features of <i>Salmonella enterica</i> Subspecies <i>houtenae</i> Serotype 45:g,z51:- Isolated from Multiple Abdominal Abscesses of an African Fat-Tailed Gecko, United States, 2020. <i>Antibiotics</i> , 2021, 10, 1322.	1.5	6
17338	<i>Stypella mirabilis</i> , recollected after 24 years and transferred to the genus <i>Myxarium</i> following DNA barcoding. <i>Field Mycology</i> , 2021, 22, 113-116.	0.0	0
17339	Altered gut ecosystems plus the microbiota's potential for rapid evolution: A recipe for inevitable change with unknown consequences. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 5969-5977.	1.9	2
17340	A case of <i>Candida auris</i> candidemia in Xiamen, China, and a comparative analysis of clinical isolates in China. <i>Mycology</i> , 2022, 13, 68-75.	2.0	10
17341	A new species of free-living marine nematode, <i>Diplolaimella ariakensis</i> n. sp. (Nematoda: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 0.2 1	0.2	1
17342	Genomic analysis of group A <i>Streptococcus</i> isolated during a correctional facility outbreak of MRSA in 2004. <i>Jammi</i> , 0, .	0.3	0
17343	Molecular and Morphological Data Improve the Classification of Plantagineae (Lamiales). <i>Plants</i> , 2021, 10, 2299.	1.6	4
17344	Phylogeny of gracillariid leaf-mining moths: evolution of larval behaviour inferred from phylogenomic and Sanger data. <i>Cladistics</i> , 2022, 38, 277-300.	1.5	11
17345	Drivers of methicillin-resistant <i>Staphylococcus aureus</i> (MRSA) lineage replacement in China. <i>Genome Medicine</i> , 2021, 13, 171.	3.6	32

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17346	A phylogenomic framework for charting the diversity and evolution of giant viruses. <i>PLoS Biology</i> , 2021, 19, e3001430.	2.6	72
17347	A New Shrimp Genus (Crustacea: Decapoda) from the Deep Atlantic and an Unusual Cleaning Mechanism of Pelagic Decapods. <i>Diversity</i> , 2021, 13, 536.	0.7	4
17348	Diversity of Endophytic and Pathogenic Fungi of Saffron (<i>Crocus sativus</i>) Plants from Cultivation Sites in Italy. <i>Diversity</i> , 2021, 13, 535.	0.7	8
17349	The <i>Melastoma dodecandrum</i> genome and the evolution of Myrtales. <i>Journal of Genetics and Genomics</i> , 2022, 49, 120-131.	1.7	14
17350	Plastid phylogenomic insights into relationships of all flowering plant families. <i>BMC Biology</i> , 2021, 19, 232.	1.7	109
17351	<i>Mycobacterium intracellulare</i> subsp. <i>chimaera</i> from Cardio Surgery Heating-Cooling Units and from Clinical Samples in Israel Are Genetically Unrelated. <i>Pathogens</i> , 2021, 10, 1392.	1.2	3
17352	<i>Miracula einbuarlaekurica</i> sp. nov., a new holocarpic endoparasitoid species from pennate freshwater diatoms in Iceland. <i>Mycology</i> , 2022, 13, 153-161.	2.0	2
17353	Phylogenomics resolves ambiguous relationships within Aciculata (Errantia, Annelida). <i>Molecular Phylogenetics and Evolution</i> , 2022, 166, 107339.	1.2	16
17354	Highly Variable and Non-complex Diazotroph Communities in Corals From Ambient and High CO2 Environments. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	5
17355	A new species of <i>Galerina</i> (Hymenogastraceae, Agaricales) from northeast China. <i>Phytotaxa</i> , 2021, 524, 27-36.	0.1	1
17356	Biodiversity of Hawaiian Peyssonneliales (Peyssonneliaceae, Rhodophyta): new species in the genera <i>Incendia</i> and <i>Seiria</i> . <i>Phytotaxa</i> , 2021, 524, 14-26.	0.1	5
17357	Ruminal effects of excessive dietary sulphur in feedlot cattle. <i>Journal of Animal Physiology and Animal Nutrition</i> , 2021, , .	1.0	6
17358	Genomic analysis of shiga toxin-containing <i>Escherichia coli</i> O157:H7 isolated from Argentinean cattle. <i>PLoS ONE</i> , 2021, 16, e0258753.	1.1	4
17359	Anaeramoebae are a divergent lineage of eukaryotes that shed light on the transition from anaerobic mitochondria to hydrogenosomes. <i>Current Biology</i> , 2021, 31, 5605-5612.e5.	1.8	29
17360	Complete Genome Analysis of Undecylprodigiosin Pigment Biosynthesizing Marine <i>Streptomyces</i> Species Displaying Potential Bioactive Applications. <i>Microorganisms</i> , 2021, 9, 2249.	1.6	5
17361	Around the world in 40 million years: Phylogeny and biogeography of <i>Tecomeae</i> (Bignoniaceae). <i>Molecular Phylogenetics and Evolution</i> , 2021, 166, 107335.	1.2	1
17363	<i>Fusarium elaeidis</i> Causes Stem and Root Rot on <i>Alocasia longiloba</i> in South China. <i>Pathogens</i> , 2021, 10, 1395.	1.2	6
17365	The <i>Aphelenchus avenae</i> genome highlights evolutionary adaptation to desiccation. <i>Communications Biology</i> , 2021, 4, 1232.	2.0	19

#	ARTICLE	IF	CITATIONS
17366	SARS-CoV-2 surveillance in Italy through phylogenomic inferences based on Hamming distances derived from pan-SNPs, -MNP and -InDels. BMC Genomics, 2021, 22, 782.	1.2	12
17368	Emergence of Tigecycline Nonsusceptible and IMP-4 Carbapenemase-Producing K2-ST65 Hypervirulent Klebsiella pneumoniae in China. Microbiology Spectrum, 2021, 9, e0130521.	1.2	17
17369	In the Asia-Pacific region, the COI DNA test revealed the divergence of the bivalve mollusc <i>Macra chinensis</i> into three species; can these species be distinguished using shell coloration and sperm structure?. Helgoland Marine Research, 2021, 75, .	1.3	6
17370	Molecular Characterization Based on Whole-Genome Sequencing of <i>Streptococcus pneumoniae</i> in Children Living in Southwest China During 2017-2019. Frontiers in Cellular and Infection Microbiology, 2021, 11, 726740.	1.8	12
17371	Connected across the ocean: taxonomy and biogeography of deep-water Nudibranchia from the Northwest Pacific reveal trans-Pacific links and two undescribed species. Organisms Diversity and Evolution, 2021, 21, 753-782.	0.7	6
17372	Novel <i>Mucor</i> species (<i>Mucoromycetes</i> , <i>Mucoraceae</i>) from northern Thailand. MycoKeys, 2021, 84, 57-78.	0.8	5
17373	Diversification of <i>Escherichia albertii</i> H-Antigens and Development of H-Genotyping PCR. Frontiers in Microbiology, 2021, 12, 737979.	1.5	5
17374	Identification of potential new mosquito-associated viruses of adult <i>Aedes aegypti</i> mosquitoes from Tocantins state, Brazil. Brazilian Journal of Microbiology, 2022, 53, 51-62.	0.8	6
17375	Plant ecological genomics at the limits of life in the Atacama Desert. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	35
17376	The Genus <i>Chlorosplenium</i> (<i>Helotiales</i> , <i>Leotiomyces</i>) from China with Notes on <i>C. chlora</i> Complex. Life, 2021, 11, 1167.	1.1	0
17377	Draft Genome Sequences of Five Historical <i>Bacillus anthracis</i> Strains. Microbiology Resource Announcements, 2020, 9, .	0.3	0
17378	Genotypic Diversity and Host-Specificity of <i>Frankia</i> Bacteria Associated with Sympatric Populations of <i>Alnus rubra</i> and <i>Alnus rhombifolia</i> in Oregon. Northwest Science, 2020, 93, 244.	0.1	3
17380	Phylogenetic Analyses of Chemokine Receptors from Sequence Retrieval to Phylogenetic Trees. Methods in Molecular Biology, 2020, 2108, 313-343.	0.4	0
17384	Morphology, Morphogenesis and Phylogenetic Position of the Soil Hypotrichous Ciliate, <i>Parabistichella dieckmanni</i> (Foissner, 1998) Foissner, 2016 (Ciliophora, Hypotrichia), with Notes on the Phylogeny of <i>Parabistichella</i> . Journal of Eukaryotic Microbiology, 2021, 68, e12832.	0.8	4
17385	Taxonomic updates to <i>Artocarpus</i> subgenus <i>Pseudojaca</i> (<i>Moraceae</i>), with a particular focus on the taxa in Singapore. The Gardens' Bulletin Singapore, 2020, 72, 173-213.	0.1	1
17386	Morphological and Molecular Evidence for the Occurrence of <i>Hodophilus variabilipes</i> (<i>Clavariaceae</i>), Tj ETQq1 1 0.784314 rgBT /Overl	0.3	0
17387	Whole-genome sequencing from the New Zealand <i>Saccharomyces cerevisiae</i> population reveals the genomic impacts of novel microbial range expansion. G3: Genes, Genomes, Genetics, 2021, 11, 1-12.	0.8	3
17388	Swine Conjunctivitis Associated with a Novel <i>Mycoplasma</i> Species Closely Related to <i>Mycoplasma hyorhinis</i> . Pathogens, 2021, 10, 13.	1.2	5

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17389	Complete chloroplast genome comparisons for <i>Pityopsis</i> (Asteraceae). PLoS ONE, 2020, 15, e0241391.	1.1	7
17390	Identification and characterization of <i>Cercospora beticola</i> necrosis-inducing effector CbNip1. Molecular Plant Pathology, 2021, 22, 301-316.	2.0	14
17392	New genus of trichomatous coelomycete on <i>Myrcia feniziana</i> from the Brazilian Cerrado. Mycologia, 2021, 113, 231-244.	0.8	0
17393	<i>Hondaria</i> , a new genus of Collemataceae (Ascomycota lichenized) from South America. Acta Botanica Brasilica, 2020, 34, 615-622.	0.8	1
17395	Chasing breeding footprints through structural variations in <i>Cucumis melo</i> and wild relatives. G3: Genes, Genomes, Genetics, 2021, 11, 1-12.	0.8	7
17396	The First Draft Genome of a Cold-Water Coral <i>Trachythela</i> sp. (Alcyonacea: Stolonifera: Tj ETQq1 1 0.784314rgBT /Overlock 10	1.1	5
17397	<i>Saxiloba</i> : a new genus of placodioid lichens from the Caribbean and Hawaii shakes up the Porinaceae tree (lichenized Ascomycota: Gyalectales). Plant and Fungal Systematics, 2020, 65, 577-585.	0.7	2
17399	Taxonomy and Phylogeny of <i>Helenium scaposum</i> (Asteraceae, Helenieae, Gaillardinae).. Lundellia, 2020, 23, .	0.2	0
17402	Telomeric TART elements target the piRNA machinery in <i>Drosophila</i> . PLoS Biology, 2020, 18, e3000689.	2.6	7
17403	Diversification in the Arctic: Biogeography and Systematics of the North American <i>Micranthes</i> (Saxifragaceae). Systematic Botany, 2020, 45, 802-811.	0.2	5
17404	Species Identification of Shed Snake Skins by Scanning Electron Microscopy, with Verification of Intraspecific Variations and Phylogenetic Comparative Analyses of Microdermatoglyphics. Herpetological Monographs, 2020, 34, .	1.1	1
17406	Genome-based classification of <i>Calidifontibacillus erzurumensis</i> gen. nov., sp. nov., isolated from a hot spring in Turkey, with reclassification of <i>Bacillus azotoformans</i> as <i>Calidifontibacillus azotoformans</i> comb. nov. and <i>Bacillus oryztterrae</i> as <i>Calidifontibacillus oryztterrae</i> comb. nov.. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 6418-6427.	0.8	19
17407	The genus <i>Pylaisia</i> (Pylaisiaceae, Bryophyta) in Russia. Arctoa, 2020, 29, 135-178.	0.3	6
17408	A revision of the genus <i>Orthothecium</i> (Plagiotheciaceae, Bryophyta) in northern Eurasia. Arctoa, 2020, 29, 10-48.	0.3	7
17409	Bryophyte molecular barcoding records. 3. Arctoa, 2020, 29, 216-218.	0.3	0
17411	The Location of Substitutions and Bacterial Genome Arrangements. Genome Biology and Evolution, 2021, 13, .	1.1	2
17413	Redescription of Two <i>Psathyromyia</i> Species (Diptera: Psychodidae), Including Description of the Female of <i>Psathyromyia pradobarrientosi</i> Using Molecular and Morphological Approaches. Journal of Medical Entomology, 2021, 58, 1115-1125.	0.9	2
17414	Genetic diversity of clinical and environmental Mucorales isolates obtained from an investigation of mucormycosis cases among solid organ transplant recipients. Microbial Genomics, 2020, 6, .	1.0	10

#	ARTICLE	IF	CITATIONS
17415	Classification and phylogeny for the annotation of novel eukaryotic GNAT acetyltransferases. PLoS Computational Biology, 2020, 16, e1007988.	1.5	7
17417	Nocardiopsis dassonvillei subsp. crassaminis subsp. nov., isolated from freshwater sediment, and reappraisal of Nocardiopsis alborubida Grund and Kroppenstedt 1990 emend. Nouiouei et al. 2018. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 6172-6179.	0.8	7
17418	Homologous Recombination in Clostridioides difficile Mediates Diversification of Cell Surface Features and Transport Systems. MSphere, 2020, 5, .	1.3	4
17419	Haraldiophyllum hawaiiense sp. nov. (Delesseriaceae, Rhodophyta): a new mesophotic genus record for the Hawaiian Islands. Algae, 2020, 35, 337-347.	0.9	7
17420	Hymenidium pilosum (Apiaceae) is a synonym of H. apiolens based on morphology and molecular data. Nordic Journal of Botany, 2020, 38, .	0.2	1
17421	Genomic and Phenotypic Diversity of Carbapenemase-Producing Enterobacteriaceae Isolates from Bacteremia in China: A Multicenter Epidemiological, Microbiological, and Genetic Study. Engineering, 2022, 12, 90-100.	3.2	15
17425	Molecular insights into meningococcal carriage isolates from Burkina Faso 7 years after introduction of a serogroup A meningococcal conjugate vaccine. Microbial Genomics, 2020, 6, .	1.0	0
17427	Systematic revision of mountain dragons (Reptilia: Agamidae: Diploderma) in China, with descriptions of six new species and discussion on their conservation. Journal of Zoological Systematics and Evolutionary Research, 2021, 59, 222-263.	0.6	7
17429	On the genera Isopterygiopsis and Isopterygiella, gen. nov. (Plagiotheciaceae) in Russia. Arctoa, 2020, 29, 49-62.	0.3	1
17430	Species delimitation of North American Nyssa species. Journal of Systematics and Evolution, 0, , .	1.6	2
17431	Molecular Systematics of Eupines King, Including a New Genus and Notes on New Zealand Brachyglutini (Coleoptera: Staphylinidae: Pselaphinae: Goniaceritae). The Coleopterists Bulletin, 2020, 74, .	0.1	0
17432	Extremus adstrictus from a dolomite wall in Poland: the first report outside Mallorca. Plant and Fungal Systematics, 2020, 65, 624-630.	0.7	1
17436	Characterization of DNA methylation in Malawian <i>Mycobacterium tuberculosis</i> clinical isolates. PeerJ, 2020, 8, e10432.	0.9	4
17437	Two further new lichen species from the Atlantic Forest remnant Pedra Talhada (Alagoas, Brazil), with a species list. Bryologist, 2020, 123, .	0.1	4
17438	A New Species of New Guinea Worm-Eating Snake (Elapidae: Toxicocalamus Boulenger, 1896), with Comments on Postfrontal Bone Variation Based on Micro-computed Tomography. Journal of Herpetology, 2020, 54, .	0.2	2
17439	Phylogenetic structure of Salmonella Enteritidis provides context for a foodborne outbreak in Peru. Scientific Reports, 2020, 10, 22080.	1.6	5
17440	Sequencing of Complete Chloroplast Genomes. Methods in Molecular Biology, 2021, 2222, 89-105.	0.4	0
17441	Morphology of gemmae, an overlooked taxonomic trait in the genus Marchantia L. (Marchantiaceae). Bryologist, 2020, 123, .	0.1	3

#	ARTICLE	IF	CITATIONS
17444	Biogeography of succulent spurges from Brazilian Seasonally Dry Tropical Forest (SDTF). <i>Taxon</i> , 2021, 70, 153-169.	0.4	5
17445	Taxonomy and molecular phylogeny of four karyorelictid species belonging to the genera <i>Apotrachelocerca</i> and <i>Tracheloraphis</i> (Protozoa: Ciliophora), with descriptions of two new species. <i>Zoological Journal of the Linnean Society</i> , 2021, 192, 690-709.	1.0	9
17446	Molecular Phylogeny of the Subgenus <i>Karstomys</i> Reveals Genetic Signature of Post-Glacial Colonization of <i>Apodemus mystacinus</i> (Rodentia: Muridae) in the Zagros Mountains from Different Refugia. <i>Zoological Science</i> , 2020, 38, 72-81.	0.3	3
17449	On the phylogenetic position of the genus <i>Claopodium</i> : a revival of a 19th century idea. <i>Arctoa</i> , 2020, 29, 1-9.	0.3	0
17450	Using a GTR+ Γ substitution model for dating sequence divergence when stationarity and time-reversibility assumptions are violated. <i>Bioinformatics</i> , 2020, 36, i884-i894.	1.8	6
17451	Statistical Methods for Analyzing Tree-Structured Microbiome Data. <i>Frontiers in Probability and the Statistical Sciences</i> , 2021, , 193-220.	0.1	1
17452	Evaluating Selective Pressures Driving Clades Differentiation of the <i>Faecalibacterium prausnitzii</i> Complex. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
17453	The story of a rock-star: multilocus phylogeny and species delimitation in the starred or rough-tail rock agama, <i>Laudakia stellio</i> (Reptilia: Agamidae). <i>Zoological Journal of the Linnean Society</i> , 2022, 195, 195-219.	1.0	6
17454	A phylogenetic analysis between humans and <i>D. melanogaster</i> : A repertoire of solute carriers in humans and flies. <i>Gene</i> , 2022, 809, 146033.	1.0	2
17455	Dynamics of SARS-CoV-2 variants of concern (VOC) in Bangladesh during the first half of 2021. <i>Virology</i> , 2022, 565, 29-37.	1.1	7
17456	Deciphering reticulate evolution of the largest group of polyploid vertebrates, the subfamily cyprininae (Teleostei: Cypriniformes). <i>Molecular Phylogenetics and Evolution</i> , 2022, 166, 107323.	1.2	12
17457	Genes from oxidative phosphorylation complexes II-V and two dual-function subunits of complex I are transcribed in <i>Viscum album</i> despite absence of the entire mitochondrial holo-complex I. <i>Mitochondrion</i> , 2022, 62, 1-12.	1.6	7
17458	Characterization of cellular, biochemical and genomic features of the diazotrophic plant growth-promoting bacterium <i>Azospirillum</i> sp. UENF-412522, a novel member of the <i>Azospirillum</i> genus. <i>Microbiological Research</i> , 2022, 254, 126896.	2.5	5
17459	Denitrification and dissimilatory nitrate reduction to ammonia in long-term lake sediment microcosms with iron(II). <i>Science of the Total Environment</i> , 2022, 807, 150835.	3.9	20
17460	<i>Nocardioides guangzhouensis</i> sp. nov., an actinobacterium isolated from soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 112-119.	0.8	8
17461	<i>Flavobacterium macacae</i> sp. nov., isolated from <i>Macaca mulatta</i> faeces. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 51-57.	0.8	6
17463	Assessing Rapid Relaxed-Clock Methods for Phylogenomic Dating. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	7
17464	Variation in the <i>Myotis keaysi</i> complex (Chiroptera, Vespertilionidae), with description of a new species from Ecuador. <i>Journal of Mammalogy</i> , 2022, 103, 540-559.	0.6	7

#	ARTICLE	IF	CITATIONS
17467	Bioinformatics structural and phylogenetic characterization of Entamoeba histolytica alcohol dehydrogenase 2 (EhADH2). Bios, 2019, 90, 30.	0.0	0
17470	The more the merrier: unparalleled sympatric species richness in a sea spider genus (Pycnogonida :) Tj ETQq1 1 0.784314 rgBJ /Overlo	0.5	3
17476	An integrative approach to the study of Helicotylenchus (Nematoda: Hoplolaimidae) Colombian and Brazilian populations associated with Musa crops. Journal of Nematology, 2020, 52, 1-19.	0.4	4
17477	TNet: Phylogeny-Based Inference of Disease Transmission Networks Using Within-Host Strain Diversity. Lecture Notes in Computer Science, 2020, , 203-216.	1.0	8
17478	Towards a Phylogenetic Measure to Quantify HIV Incidence. Communications in Computer and Information Science, 2020, , 34-50.	0.4	0
17480	Gowardia zebrina sp. nov., a new species in a little-known genus of arctic-alpine lichens (Parmeliaceae). Plant and Fungal Systematics, 2020, 65, 219-226.	0.7	0
17481	Roseovarius spongiae sp. nov., a bacterium isolated from marine sponge. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 274-281.	0.8	9
17482	Analysis of phylogenetic diversity and in vitro adherence characteristics of respiratory syncytial virus and Streptococcus pneumoniae clinical isolates obtained during pediatric respiratory co-infections. Microbiology (United Kingdom), 2020, 166, 63-72.	0.7	4
17485	OUP accepted manuscript. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	1.4	8
17486	Sympatry between species of Juliomys (Rodentia: Sigmodontinae) along an altitudinal gradient in the Serra da Bocaina National Park. Biota Neotropica, 2020, 20, .	0.2	2
17487	Genomic analysis of Latin American-Mediterranean family of Mycobacterium tuberculosis clinical strains from Kazakhstan. Memorias Do Instituto Oswaldo Cruz, 2020, 115, e200215.	0.8	5
17488	Comprehensive Analyses of Copy Number Variations In DNA Repair Genes Reveal the Role of Poly(ADP-Ribose) Polymerase in Longevity in Trees. SSRN Electronic Journal, 0, , .	0.4	0
17489	RECONSTRUCTION OF NITROGENASE PREDECESSORS SUGGESTS ORIGIN FROM MATURASE-LIKE ENZYMES. , 2020, , .		0
17490	Taxonomy and systematics of Hyaloscyphaceae and Archnopezizaceae. Persoonia: Molecular Phylogeny and Evolution of Fungi, 2020, , .	1.6	6
17491	Integrative systematics unveils the controversial identity of Engraulidae fishing stocks in a Neotropical estuary, northeast Brazil. Neotropical Ichthyology, 2020, 18, .	0.5	3
17494	Locally Acquired Human Infection with Swine-Origin Influenza A(H3N2) Variant Virus, Australia, 2018. Emerging Infectious Diseases, 2020, 26, .	2.0	0
17495	Molecular Phylogenetics of Saw-scaled Viper (Echis carinatus) from Pakistan. Pakistan Journal of Zoology, 2020, 52, .	0.1	0
17496	Some noteworthy records of Helvella from Turkey based on morphology and DNA sequence data. Current Research in Environmental and Applied Mycology, 2020, 10, 290-299.	0.3	2

#	ARTICLE	IF	CITATIONS
17497	Effect of <i>Heterodera schachtii</i> female age on susceptibility to three fungal hyperparasites in the genus <i>Hyalorbilia</i> . <i>Journal of Nematology</i> , 2020, 52, 1-12.	0.4	2
17498	Multiple trans-Torres Strait colonisations by tree frogs in the <i>Litoria caerulea</i> group, with the description of a new species from New Guinea. <i>Australian Journal of Zoology</i> , 2020, 68, 25.	0.6	2
17499	Genome analysis reveals that <i>Nocardiopsis baichengensis</i> Li et al. 2006 is a later heterotypic synonym of <i>Nocardiopsis halophila</i> Al-Tai and Ruan 1994. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 89-92.	0.8	4
17500	Redescription of <i>Gyrinicola japonica</i> , a Tadpole-Endoparasitic Nematode from Japan, with Resurrection of the Family <i>Gyrinicolidae</i> (Nematoda: Oxyurina). <i>Zoological Science</i> , 2020, 37, 70.	0.3	3
17502	Rapid in-country sequencing of whole virus genomes to inform rabies elimination programmes. <i>Wellcome Open Research</i> , 2020, 5, 3.	0.9	26
17503	Recombination Potential of SARS-CoV-2 and MERS-CoV. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
17504	Performance Evaluation of Parallel Inference of Large Phylogenetic Trees in Santos Dumont Supercomputer: A Practical Approach. <i>Communications in Computer and Information Science</i> , 2020, , 448-463.	0.4	0
17506	Tuberculosis in Liberia: high multidrug-resistance burden, transmission and diversity modelled by multiple importation events. <i>Microbial Genomics</i> , 2020, 6, .	1.0	11
17507	<i>Candidatus</i> <i>Anthehtikosiphon siderophilum</i> OHK22, a New Member of the Chloroflexi Family <i>Herpetosiphonaceae</i> from Oku-okuhachikuro Onsen. <i>Microbes and Environments</i> , 2020, 35, n/a.	0.7	12
17519	<i>Salinibius halmophilus</i> gen. nov., sp. nov., isolated from a marine solar saltern. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 1079-1085.	0.8	7
17522	<i>Hydrogeniiclostidium mannosilyticum</i> gen. nov., sp. nov. isolated from human faeces. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 1210-1216.	0.8	14
17523	Gene expression patterns of novel visual and non-visual opsin families in immature and mature Japanese eel males. <i>PeerJ</i> , 2020, 8, e8326.	0.9	5
17524	Studies on Brazilian <i>Amauroderma</i> s.str. reveal a new species from the Atlantic Forest, <i>Amauroderma robledoi</i> sp. nov. (Polyporales, Ganodermataceae). <i>Journal of the Torrey Botanical Society</i> , 2020, 147, 199.	0.1	0
17532	DEN-IM: dengue virus genotyping from amplicon and shotgun metagenomic sequencing. <i>Microbial Genomics</i> , 2020, 6, .	1.0	0
17536	<i>Rariglobus hedericola</i> gen. nov., sp. nov., belonging to the Verrucomicrobia, isolated from a temperate freshwater habitat. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 1830-1836.	0.8	9
17542	<i>Pseudoderbesia Eckloniae</i> , sp. nov. (Bryopsidaceae, Ulvophyceae) from Western Australia. <i>Cryptogamie, Algologie</i> , 2020, 41, 19.	0.3	0
17546	Isolation and initial propagation of guinea pig adenovirus (GPA _{dv}) in <i>Cavia porcellus</i> cell lines. <i>F1000Research</i> , 2019, 8, 1597.	0.8	1
17549	Una especie nueva de <i>Lasiurus</i> (Chiroptera: Vespertilionidae) del suroeste de Perú. <i>Revista Mexicana De Biodiversidad</i> , 2020, 91, .	0.4	4

#	ARTICLE	IF	CITATIONS
17550	Rhodobacter flagellatus sp. nov., a thermophilic bacterium isolated from a hot spring. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 1541-1546.	0.8	11
17551	A giant new species of Enchiridium (Polycladida, Prosthiostomidae) from southwestern Japan. ZooKeys, 2020, 918, 15-28.	0.5	5
17552	Reproducible Containers. , 2020, , .		5
17555	Salt Tolerance Seedlings Derived from Putative Hybrid Pines (<i>Pinus</i> Å—) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 622 Td (0.1	0.1	0
17559	TWO NEW SPECIES OF STREPTANTHUS (BRASSICACEAE) IN SOUTHERN CALIFORNIA, AND NOTES ON THEIR CONSERVATION. MadroÃ±o, 2020, 67, 19.	0.3	0
17572	Phylogenetic analyses reveal that simian foamy virus isolated from Japanese Yakushima macaques (Macaca fuscata yakui) is distinct from most of Japanese Hondo macaques (Macaca fuscata fuscata). Gene, 2020, 734, 144382.	1.0	0
17576	Revision of the genus Hoplodrina Boursin, 1937 (Lepidoptera, Noctuidae, Xyleninae). I. Hoplodrina octogenaria (Goeze, 1781) and its sister species H. alsinides (Costantini, 1922) sp. rev. in Europe. ZooKeys, 2020, 927, 75-97.	0.5	5
17577	Adding missing vines to the tree: multilocus phylogeny of New World vine snakes (Serpentes:) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 622 Td (0.2	0.2	0
17578	A Revision of the Genus Agarum (Laminariaceae, Phaeophyceae) from the Far Eastern Seas with a Description of Agarum undulatum sp. nov. from the Kuril Islands. Russian Journal of Marine Biology, 2021, 47, 364-372.	0.2	0
17579	Analysis of rDNA reveals a high genetic diversity of Halophila major in the Wallacea region. PLoS ONE, 2021, 16, e0258956.	1.1	6
17580	A first inference of the phylogeography of the worldwide invader Xylosandrus compactus. Journal of Pest Science, 0, , 1.	1.9	10
17581	The chromosome-scale genomes of <i>Dipterocarpus turbinatus</i> and <i>Hopea hainanensis</i> (Dipterocarpaceae) provide insights into fragrant oleoresin biosynthesis and hardwood formation. Plant Biotechnology Journal, 2022, 20, 538-553.	4.1	21
17582	The mode of speciation during a recent radiation in open-ocean phytoplankton. Current Biology, 2021, 31, 5439-5449.e5.	1.8	22
17584	Characterization of the complete chloroplast genome of Zephyranthes phycelloides (Amaryllidaceae,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 622 Td (1.8	1.8	5
17585	Characterization of the complete chloroplast genome of <i>Salvia trijuga</i> Diels (Lamiaceae). Mitochondrial DNA Part B: Resources, 2021, 6, 3248-3249.	0.2	0
17587	The complete chloroplast genome sequence of <i>Polyalthiopsis verrucipes</i> (Annonaceae). Mitochondrial DNA Part B: Resources, 2021, 6, 3238-3239.	0.2	0
17588	Taxonomy and Relationships Within Polemonium foliosissimum (Polemoniaceae): Untangling a Clade of Colorful and Gynodioecious Herbs. Systematic Botany, 2021, 46, 519-537.	0.2	1
17589	Mitogenome-wide comparison and phylogeny reveal group I intron dynamics and intraspecific diversification within the phytopathogen Corynespora cassiicola. Computational and Structural Biotechnology Journal, 2021, 19, 5987-5999.	1.9	3

#	ARTICLE	IF	CITATIONS
17590	MtDNA species-level phylogeny and delimitation support significantly underestimated diversity and endemism in the largest Neotropical cichlid genus (<i>Cichlidae:Crenicichla</i>). PeerJ, 2021, 9, e12283.	0.9	6
17591	Type studies and fourteen new North American species of <i>Cortinarius</i> section <i>Anomali</i> reveal high continental species diversity. Mycological Progress, 2021, 20, 1399-1439.	0.5	5
17593	The Sulawesi Thrush (<i>Cataponera turdoides</i> ; Aves: Passeriformes) belongs to the genus <i>Turdus</i> . Zoologica Scripta, 2022, 51, 32.	0.7	2
17594	Expression analyses in <i>Ginkgo biloba</i> provide new insights into the evolution and development of the seed. Scientific Reports, 2021, 11, 21995.	1.6	8
17595	Type VI secretion system mutations reduced competitive fitness of classical <i>Vibrio cholerae</i> biotype. Nature Communications, 2021, 12, 6457.	5.8	15
17596	Complete mitochondrial genomes of <i>Conogethes punctiferalis</i> and <i>C. pinicolalis</i> (Lepidoptera: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Entomology, 2021, 24, 1179-1186.	0.4	7
17597	One in a Million: Genetic Diversity and Conservation of the Reference <i>Crassostrea angulata</i> Population in Europe from the Sado Estuary (Portugal). Life, 2021, 11, 1173.	1.1	2
17598	A whole genome duplication drives the genome evolution of <i>Phytophthora betacei</i> , a closely related species to <i>Phytophthora infestans</i> . BMC Genomics, 2021, 22, 795.	1.2	6
17599	Comparative Analysis of Complete Chloroplast Genomes of 13 Species in <i>Epilobium</i> , <i>Circaea</i> , and <i>Chamaenerion</i> and Insights Into Phylogenetic Relationships of Onagraceae. Frontiers in Genetics, 2021, 12, 730495.	1.1	6
17600	Simulated patterns of mitochondrial diversity are consistent with partial population turnover in Bronze Age Central Europe. American Journal of Biological Anthropology, 2022, 177, 134-146.	0.6	1
17601	Insights into the Ancient Adaptation to Intertidal Environments by Red Algae Based on a Genomic and Multiomics Investigation of <i>Neoporphyra haitanensis</i> . Molecular Biology and Evolution, 2022, 39, .	3.5	21
17602	A new potentially toxic dinoflagellate <i>Fukuyoa koreansis</i> sp. nov. (Gonyaulacales, Dinophyceae) from Korean coastal waters: Morphology, phylogeny, and effects of temperature and salinity on growth. Harmful Algae, 2021, 109, 102107.	2.2	11
17603	Genetic diversity in the <i>Diplosoma listerianum</i> complex (Asciacea: Didemnidae) from the Western Atlantic. Systematics and Biodiversity, 0, , 1-15.	0.5	1
17604	Five new species of <i>Neopestalotiopsis</i> associated with diseased <i>Eucalyptus</i> spp. in Portugal. Mycological Progress, 2021, 20, 1441-1456.	0.5	8
17605	Mining of Cyanobacterial Genomes Indicates Natural Product Biosynthetic Gene Clusters Located in Conjugative Plasmids. Frontiers in Microbiology, 2021, 12, 684565.	1.5	12
17606	Multidrug-resistant <i>Neisseria gonorrhoeae</i> infection in heterosexual men with reduced susceptibility to ceftriaxone, first report in Thailand. Scientific Reports, 2021, 11, 21659.	1.6	29
17607	Diversification of a Fucosyllactose Transporter within the Genus <i>Bifidobacterium</i> . Applied and Environmental Microbiology, 2022, 88, AEM0143721.	1.4	18
17608	The Wzi outer membrane protein mediates assembly of a tight capsular polysaccharide layer on the <i>Acinetobacter baumannii</i> cell surface. Scientific Reports, 2021, 11, 21741.	1.6	10

#	ARTICLE	IF	CITATIONS
17609	Acarosporaceae of the Chihuahuan Desert: four Magnusson species saved from synonymy and a new yellow species. <i>Bryologist</i> , 2021, 124, .	0.1	6
17610	High-quality reference genome sequences of two coconut cultivars provide insights into evolution of monocot chromosomes and differentiation of fiber content and plant height. <i>Genome Biology</i> , 2021, 22, 304.	3.8	32
17611	<i>Candida albicans</i> Isolates 529L and CHN1 Exhibit Stable Colonization of the Murine Gastrointestinal Tract. <i>MBio</i> , 2021, 12, e0287821.	1.8	21
17612	Gene Expression of Diverse <i>Cryptococcus</i> Isolates during Infection of the Human Central Nervous System. <i>MBio</i> , 2021, 12, e0231321.	1.8	23
17613	Genomic Epidemiology and Characterization of Methicillin-Resistant <i>Staphylococcus aureus</i> from Bloodstream Infections in China. <i>MSystems</i> , 2021, 6, e0083721.	1.7	27
17614	High rates of evolution preceded shifts to sex-biased gene expression in <i>Leucadendron</i> , the most sexually dimorphic angiosperms. <i>ELife</i> , 2021, 10, .	2.8	15
17615	Gene-tree misrooting drives conflicts in phylogenomic coalescent analyses of palaeognath birds. <i>Molecular Phylogenetics and Evolution</i> , 2022, 167, 107344.	1.2	16
17617	The effects of introgression across thousands of quantitative traits revealed by gene expression in wild tomatoes. <i>PLoS Genetics</i> , 2021, 17, e1009892.	1.5	9
17618	Independent evolutionary transitions to pueriparity across multiple timescales in the viviparous genus <i>Salamandra</i> . <i>Molecular Phylogenetics and Evolution</i> , 2022, 167, 107347.	1.2	3
17620	Viral Haplotypes in COVID-19 Patients Associated With Prolonged Viral Shedding. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 715143.	1.8	1
17621	Molecular Analysis of <i>bla</i> _{KPC-2} -Harboring Plasmids: Tn 4401a Interplasmid Transposition and Tn 4401a-Carrying ColRNAI Plasmid Mobilization from <i>Klebsiella pneumoniae</i> to <i>Citrobacter europaeus</i> and <i>Morganella morganii</i> in a Single Patient. <i>MSphere</i> , 2021, 6, e0085021.	1.3	5
17623	Phylogenetic and Ancestral Sequence Reconstruction of SARS-CoV-2 Reveals Latent Capacity to Bind Human ACE2 Receptor. <i>Journal of Molecular Evolution</i> , 2021, 89, 656-664.	0.8	5
17625	Splitting of RNA-dependent RNA polymerase is common in <i>Narnaviridae</i> : Identification of a type II divided RdRp from deep-sea fungal isolates. <i>Virus Evolution</i> , 2021, 7, .	2.2	7
17626	<i>Fibroporia gossypium</i> isolated from an indoor environment in Argentina. <i>Mycotaxon</i> , 2021, 136, 645-660.	0.1	0
17627	A Comprehensive Study of the Genus <i>Sanguisorba</i> (Rosaceae) Based on the Floral Micromorphology, Palynology, and Plastome Analysis. <i>Genes</i> , 2021, 12, 1764.	1.0	9
17628	Nuclear and plastid phylogenomic analyses provide insights into the reticulate evolution, species delimitation, and biogeography of the Sino-Japanese disjunctive <i>Diabelia</i> (<i>Caprifoliaceae</i>). <i>Journal of Systematics and Evolution</i> , 2022, 60, 1331-1343.	1.6	7
17629	Insecticide resistance by a host-symbiont reciprocal detoxification. <i>Nature Communications</i> , 2021, 12, 6432.	5.8	34
17630	The origin and impeded dissemination of the DNA phosphorothioation system in prokaryotes. <i>Nature Communications</i> , 2021, 12, 6382.	5.8	14

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17631	Evidence linking lifeâ€œform to a major shift in diversification rate in <i>Crassula</i> . <i>American Journal of Botany</i> , 2022, 109, 272-290.	0.8	11
17632	Profiling cellular diversity in sponges informs animal cell type and nervous system evolution. <i>Science</i> , 2021, 374, 717-723.	6.0	111
17633	Transmission patterns of a <i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i> clone within a single herd investigated by Whole Genome Sequencing. <i>Veterinary Microbiology</i> , 2021, 263, 109272.	0.8	3
17635	Phylogenomic and comparative analyses of <i>Rheum</i> (Polygonaceae, Polygonoideae). <i>Journal of Systematics and Evolution</i> , 2022, 60, 1229-1240.	1.6	11
17637	Phylogeography of <i>Agathistoma</i> (Turbinidae, Tegulinae) snails in tropical and southwestern Atlantic. <i>Zoologica Scripta</i> , 2022, 51, 76-90.	0.7	0
17639	A genome-phenome association study in native microbiomes identifies a mechanism for cytosine modification in DNA and RNA. <i>ELife</i> , 2021, 10, .	2.8	6
17640	Insights on Lulworthiales Inhabiting the Mediterranean Sea and Description of Three Novel Species of the Genus <i>Paralulworthia</i> . <i>Journal of Fungi</i> (Basel, Switzerland), 2021, 7, 940.	1.5	7
17641	Complete mitochondrial genomes of four species of praying mantises (Dictyoptera, Mantidae) with ribosomal second structure, evolutionary and phylogenetic analyses. <i>PLoS ONE</i> , 2021, 16, e0254914.	1.1	7
17642	<i>Antarctolichena onofrii</i> gen. nov. sp. nov. from Antarctic Endolithic Communities Untangles the Evolution of Rock-Inhabiting and Lichenized Fungi in Arthoniomycetes. <i>Journal of Fungi</i> (Basel, Switzerland), 2021, 7, 940.	1.5	7
17643	Isolation of Novel <i>Mycobacterium</i> Species from Skin Infection in an Immunocompromised Person. <i>Emerging Infectious Diseases</i> , 2021, 27, 2944-2947.	2.0	1
17644	New insights into the phylogeny and evolution of Podocarpaceae inferred from transcriptomic data. <i>Molecular Phylogenetics and Evolution</i> , 2022, 166, 107341.	1.2	9
17645	Uncertainty Regarding Species Delimitation, Geographic Distribution, and the Evolutionary History of South-Central Amazonian Titi Monkey Species (<i>Plecturocebus</i> , Pitheciidae). <i>International Journal of Primatology</i> , 2024, 45, 12-34.	0.9	6
17646	Genomic evidence of environmental and resident <i>Salmonella</i> Senftenberg and Montevideo contamination in the pistachio supply-chain. <i>PLoS ONE</i> , 2021, 16, e0259471.	1.1	11
17647	Not out of the woods yet: Signatures of the prolonged negative genetic consequences of a population bottleneck in a rapidly reâ€œexpanding wader, the blackâ€œfaced spoonbill <i>Platalea minor</i> . <i>Molecular Ecology</i> , 2022, 31, 529-545.	2.0	3
17648	Dispersal, not vicariance, explains the biogeographic origin of iguanas on Madagascar. <i>Molecular Phylogenetics and Evolution</i> , 2022, 167, 107345.	1.2	6
17650	An Evolutionary Study of <i>Carex</i> Subg. <i>Psyllophorae</i> (Cyperaceae) Sheds Light on a Strikingly Disjunct Distribution in the Southern Hemisphere, With Emphasis on Its Patagonian Diversification. <i>Frontiers in Plant Science</i> , 2021, 12, 735302.	1.7	3
17651	Biogeography of curimatid fishes reveals multiple lowlandâ€œupland river transitions and differential diversification in the Neotropics (Teleostei, Curimatidae). <i>Ecology and Evolution</i> , 2021, 11, 15815-15832.	0.8	8
17652	Universal activity-based labeling method for ammonia- and alkane-oxidizing bacteria. <i>ISME Journal</i> , 2022, 16, 958-971.	4.4	12

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17653	Integrative systematics illuminates the relationships in two sponge-associated hydrozoan families (Capitata: Sphaerocorynidae and Zancleopsidae). <i>Contributions To Zoology</i> , 2021, 90, 487-525.	0.2	7
17654	Description of the Himalayan newt <i>Tylototriton verrucosus</i> (Urodela: Salamandridae) in northern Thailand with its phylogenetic relationships, distribution, and conservation status. <i>Journal of Asia-Pacific Biodiversity</i> , 2021, 15, 30-30.	0.2	0
17655	Vermetid gastropods as key intermediate hosts for a lineage of marine turtle blood flukes (Digenea: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 Parasitology, 2022, 52, 225-241.	1.3	7
17656	A survey of substrate specificity among Auxiliary Activity Family 5 copper radical oxidases. <i>Cellular and Molecular Life Sciences</i> , 2021, 78, 8187-8208.	2.4	15
17657	<i>Fusibacter ferrireducens</i> sp. nov., an anaerobic, Fe(â€¦)- and sulphur-reducing bacterium isolated from mangrove sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	12
17658	<i>Txikijspora philomaios</i> n. sp., n. g., a microâ€œkaryotic pathogen of amphipods, reveals parasitism and hidden diversity in Class Filasterea. <i>Journal of Eukaryotic Microbiology</i> , 2022, 69, e12875.	0.8	6
17659	Molecular and structural basis of olfactory sensory neuron axon coalescence by Kirrel receptors. <i>Cell Reports</i> , 2021, 37, 109940.	2.9	7
17660	FIRST REPORT OF <i>Meloidogyne incognita</i> PARASITIZING <i>Momordica charantia</i> L. IN PERNAMBUCO, BRAZIL. <i>Revista CiÃancia AgrÃcola</i> , 2020, 18, 43.	0.1	1
17663	<i>Frigidibacter oleivorans</i> sp. nov., isolated from a deep well with oil reservoir water. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 4339-4344.	0.8	5
17666	Morpho-molecular diversity of <i>Linocarpaceae</i> (Chaetosphaeriales): <i>Claviformispora</i> gen. nov. from decaying branches of <i>Phyllostachys heteroclada</i> . <i>MycKeys</i> , 0, 69, 113-129.	0.8	1
17667	<i>Pulverulina</i> , a New Genus of Agaricales for <i>Clitocybe ulmicola</i> . <i>Southeastern Naturalist</i> , 2020, 19, 447.	0.2	3
17668	Bacteriocytes and <i>Blattabacterium</i> Endosymbionts of the German Cockroach <i>Blattella germanica</i> , the Forest Cockroach <i>Blattella nipponica</i> , and Other Cockroach Species. <i>Zoological Science</i> , 2020, 37, 1.	0.3	7
17674	Taxonomic Revision of <i>Chironius bicarinatus</i> (Wied 1820) (Serpentes: Colubridae), with Description of a New Species. <i>Herpetological Monographs</i> , 2020, 34, 98.	1.1	5
17675	<i>Vaginimicrobium propionicum</i> gen. nov., sp. nov., a novel propionic acid bacterium derived from human vaginal discharge. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 4091-4097.	0.8	11
17685	Genomics of Atlantic Forest <i>Mycobacteriaceae</i> strains unravels a mobilome diversity with a novel integrative conjugative element and plasmids harbouring T7SS. <i>Microbial Genomics</i> , 2020, 6, .	1.0	3
17686	<i>Archernis humilis</i> (Swinhoe) (Lepidoptera: Crambidae) Rediscovered Feeding on Skunk Vine (<i>Paederia</i>) Tj ETQq1 1 0,784314 rgBT /Over	0,0	0,0
17689	Additions to <i>Phaeosphaeriaceae</i> (Pleosporales): <i>Elongaticollum</i> gen. nov., <i>Ophiosphaerella taiwanensis</i> sp. nov., <i>Phaeosphaeriopsis beaucarneae</i> sp. nov. and a new host record of <i>Neosetophoma poaceicola</i> from Musaceae. <i>MycKeys</i> , 2020, 70, 59-88.	0.8	11
17692	Hidden in our pockets: building of a DNA barcode library unveils the first record of <i>Myotis alcaethoe</i> for Portugal. <i>Biodiversity Data Journal</i> , 2020, 8, e54479.	0.4	4

#	ARTICLE	IF	CITATIONS
17693	Genomic epidemiology of methicillin-resistant <i>Staphylococcus aureus</i> ST22 widespread in communities of the Gaza Strip, 2009. <i>Eurosurveillance</i> , 2018, 23, .	3.9	0
17694	Isolation and molecular characterization of Fowl adenovirus strains in Black grouse: First reported case in Poland. <i>PLoS ONE</i> , 2020, 15, e0234532.	1.1	5
17695	Crossing Lydekker's Line: Northern Water Dragons (<i>Tropicagama temporalis</i>) Colonized the Mollucan Islands of Indonesia from New Guinea. <i>Herpetologica</i> , 2020, 76, 344.	0.2	0
17710	Hidden or unnoticed? <sc>Multiple</sc> lines of evidence support the recognition of a new species of <sc><i>Pseudocorynopoma</i></sc> (Characidae: Corynopomini) </sc>. <i>Journal of Fish Biology</i> , 2021, 98, 219-236.	0.7	6
17711	Patterns of acquired HIV-1 drug resistance mutations and predictors of virological failure in Moshi, Northern Tanzania. <i>PLoS ONE</i> , 2020, 15, e0232649.	1.1	11
17712	Complete Genome Sequence of <i>Arcanobacterium</i> sp. Strain 2701, Isolated from a Harbor Seal. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	2
17713	Phylogeny and species delimitation in <i>Silene</i> sect. <i>Arenosae</i> (Caryophyllaceae): a new section. <i>PhytoKeys</i> , 2020, 159, 1-34.	0.4	6
17714	A new record of critically endangered <i>Saussurea bogedaensis</i> (Asteraceae) from Dzungarian Gobi, Mongolia. <i>PhytoKeys</i> , 2020, 160, 109-121.	0.4	6
17715	Revisiting the taxonomy of <i>Dioclea</i> and related genera (Leguminosae, Papilionoideae), with new generic circumscriptions. <i>PhytoKeys</i> , 2020, 164, 67-114.	0.4	5
17716	<i>Salinimicrobium nanhaiense</i> sp. nov. and <i>Salinimicrobium oceani</i> sp. nov., two novel species of the family Flavobacteriaceae isolated from the South China Sea. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 5263-5270.	0.8	10
17717	<i>Cerasibacillus terrae</i> sp. nov., isolated from maize field, and emended description of <i>Cerasibacillus quisquiliarum</i> Nakamura et al. 2004. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 5725-5733.	0.8	7
17718	<i>Nocardioides flavescens</i> sp. nov., isolated from soil of Gaoligong Mountain, PR China. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 5740-5746.	0.8	6
17719	Genomic analysis of cardiac surgery-associated <i>Mycobacterium chimaera</i> infections in Italy. <i>PLoS ONE</i> , 2020, 15, e0239273.	1.1	8
17720	Species delimitation, environmental cline and phylogeny for a new Neotropical genus of Cryptinae (Ichneumonidae). <i>PLoS ONE</i> , 2020, 15, e0237233.	1.1	4
17732	Fungal infection, decline and persistence in the only obligate troglodytic Neotropical salamander. <i>PeerJ</i> , 2020, 8, e9763.	0.9	5
17733	A new species of Rain Frog (<i>Brevicipitidae</i> , <i>Breviceps</i>) endemic to Angola. <i>ZooKeys</i> , 2020, 979, 133-160.	0.5	6
17735	Siblings or doppelgÄngers? Deciphering the evolution of structured cis-regulatory RNAs beyond homology. <i>Biochemical Society Transactions</i> , 2020, 48, 1941-1951.	1.6	3
17736	Expression of Genes Involved in Offensive and Defensive Phenotype Induction in the Pituitary Gland of the Hokkaido Salamander (<i>Hynobius retardatus</i>). <i>Zoological Science</i> , 2020, 37, 563-574.	0.3	2

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17737	Wide Distribution but Low Differentiation: Phylogenetic Relationships and Phylogeography of <i>Hynobius nigrescens</i> (Amphibia: Caudata). <i>Zoological Science</i> , 2020, 37, 529-537.	0.3	4
17755	Genome-Wide Analyses Provide Insights into the Scavenging Lifestyle of the Striped Hyena (<i>Hyaena</i>)	1.0	3
17756	Türkiye'de Baklagil Nodüllerinden İzole Edilen Bitki Gelişimini Destekleyici Aktinobakterilerin Filogenisi. <i>Yuzuncu Yil University Journal of Agricultural Sciences</i> , 0, , 611-619.	0.1	0
17757	Two New Species of <i>Pseudojuloides</i> from Western Australia and Southern Japan, with a Redescription of <i>Pseudojuloides elongatus</i> (Teleostei: Labridae). <i>Copeia</i> , 2020, 108, .	1.4	1
17758	Two New Species of Pencil Wrasses (Teleostei: Labridae: <i>Pseudojuloides</i>) from Micronesia and the Marquesan Islands. <i>Copeia</i> , 2020, 108, .	1.4	1
17759	New records and phylogenetic position of <i>Ornithodoros knoxjonesi</i> (Ixodida: Argasidae). <i>Ticks and Tick-borne Diseases</i> , 2020, 11, 101473.	1.1	0
17760	Pan-genomics of <i>Ochrobactrum</i> species from clinical and environmental origins reveals distinct populations and possible links. <i>Genomics</i> , 2020, 112, 3003-3012.	1.3	8
17761	The complete chloroplast genome of <i>Stephania tetrandra</i> (Menispermaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 3819-3820.	0.2	2
17762	The complete chloroplast genome of <i>Turpinia arguta</i> (Staphyleaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 3825-3826.	0.2	0
17763	Two new species of the freshwater-crab genus <i>Demanietta</i> Bott, 1966 (Decapoda: Brachyura)	1.0	3
17794	Identifying Evolutionary Origins of Repeat Domains in Protein Families. , 2020, , .		0
17795	Using B cell receptor lineage structures to predict affinity. <i>PLoS Computational Biology</i> , 2020, 16, e1008391.	1.5	13
17796	Molecular analysis confirms <i>Laurenciella marilzae</i> (Rhodophyta, Rhodomelaceae) in the Mediterranean Sea, a species often misidentified as <i>Laurencia dendroidea</i> . <i>Botanica Marina</i> , 2020, 63, 527-535.	0.6	0
17797	A New Amazonian Species of the Diminutive Frog Genus <i>Adelophryne</i> (Anura: Brachycephaloidea)	1.0	1
17798	Molecular Genetics Supports a Potential Fifth Asian Pangolin Species (Mammalia, Pholidota, Manis). <i>Zoological Science</i> , 2020, 37, 538-543.	0.3	4
17799	Phylogeographic Patterns in a Semi-Lithophilous Burrowing Scorpion, <i>Opisthophthalmus pallipes</i> , from South Africa. <i>Zoological Science</i> , 2020, 38, 36-44.	0.3	3
17800	A new bathyal tubulanid nemertean, <i>Tubulanus izuensis</i> sp. nov. (Nemertea: Palaeonemertea), from Japanese waters. <i>Proceedings of the Biological Society of Washington</i> , 2020, 133, .	0.3	3
17801	The taxonomy of the model filamentous fungus <i>Podospira anserina</i> . <i>MycKeys</i> , 2020, 75, 51-69.	0.8	6

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17802	Integrative taxonomy and analysis of species richness patterns of nocturnal Darwin wasps of the genus <i>Enicospilus</i> Stephens (Hymenoptera, Ichneumonidae, Ophioninae) in Japan. <i>ZooKeys</i> , 2020, 990, 1-144.	0.5	8
17803	The land flatworm <i>Amaga expatria</i> (Geoplanidae) in Guadeloupe and Martinique: new reports and molecular characterization including complete mitogenome. <i>PeerJ</i> , 2020, 8, e10098.	0.9	6
17804	Genome-wide identification and analysis of the thiolase family in insects. <i>PeerJ</i> , 2020, 8, e10393.	0.9	4
17805	The effects of evolutionary and environmental variance on estimates of phylogenetic diversity in temperate forest plots. <i>Journal of Plant Ecology</i> , 2021, 14, 96-107.	1.2	2
17806	Complete Chloroplast Genome of <i>Psammochloa villosa</i> (Poaceae), a Pioneer Grass Endemic to Sand Dunes in Northwest China. <i>Cytology and Genetics</i> , 2020, 54, 582-587.	0.2	1
17807	H7N1 Low Pathogenicity Avian Influenza Viruses in Poultry in the United States During 2018. <i>Avian Diseases</i> , 2020, 65, 59-62.	0.4	1
17808	Morphology, morphogenesis and molecular phylogeny of the new soil ciliate <i>Sterkiella paratricirrata</i> n. sp. (Ciliophora, Hypotrichia, Oxytrichidae). <i>Journal of Natural History</i> , 2020, 54, 2471-2488.	0.2	0
17809	Remarkable cases of parallel evolution of the placodioid thallus growth form in the Lecanographaceae (Arthoniales) with the description of a new species of <i>Alyxoria</i> from Mexico. <i>Lichenologist</i> , 2020, 52, 415-424.	0.5	1
17811	Selective Sweeps in a Nutshell: The Genomic Footprint of Rapid Insecticide Resistance Evolution in the Almond Agroecosystem. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	19
17812	Comprehensive Analysis of the Jellyfish (<i>Goette</i> , 1886) (Semaestomeae: Pelagiidae) with Description of the Complete rDNA Sequence. <i>Zoological Studies</i> , 2018, 57, e51.	0.3	2
17813	Sensitivity of Ribosomal RNA Character Sampling in the Phylogeny of Rhabditida. <i>Journal of Nematology</i> , 2015, 47, 337-55.	0.4	11
17814	Evolution and phylogenetic application of the MC1R gene in the Cobitoidea (Teleostei: Cypriniformes). <i>Zoological Research</i> , 2016, 37, 281-9.	0.9	4
17816	Whole-Genome Sequencing of Russian <i>Neisseria Gonorrhoeae</i> Isolates Related to ST 1407 Genogroup. <i>Acta Naturae</i> , 2018, 10, 68-76.	1.7	2
17817	A new species of the lichenised genus (<i>Baeomycetaceae</i> , <i>Baeomycetales</i>) from Tengger Desert of China. <i>MycKeys</i> , 2018, , 107-118.	0.8	0
17818	Reassessment of <i>Oliver</i> (Gesneriaceae) based on molecular and palynological evidence. <i>PhytoKeys</i> , 2020, 157, 27-41.	0.4	1
17819	Complete mitochondrial genome of (<i>Duchassaing & Michelotti</i> , 1860) (Octocorallia: Alcyonacea): Tj ETQq1 1 0.784314 rgBT 0Overloc	0.2	0
17820	Lacydoniidae (Annelida) Off the Coast of North-eastern Japan: A Description of sp. nov. <i>Zoological Studies</i> , 2020, 59, e28.	0.3	0
17821	Pyrolocin A, a 3-Decalinoyltetramic Acid with Selective Biological Activity, Isolated from Amazonian Cultures of the Novel Endophyte <i>Diaporthea</i> sp. E6927E. <i>Natural Product Communications</i> , 2015, 10, 1649-54.	0.2	2

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17822	The complete chloroplast genome of (Rosaceae: Potentilleae). Mitochondrial DNA Part B: Resources, 2020, 5, 2036-2037.	0.2	0
17823	Revision and phylogeny of the genus Hampson, 1896 (Lepidoptera, Crambidae, Pyraustinae), based on morphology and molecular data. ZooKeys, 2021, 1036, 75-98.	0.5	0
17824	Molecular Approach to Identifying Three Closely Related Slug Species of the genus (Gastropoda:) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50 6	0.3	0
17825	Phylogeography of (Nemacheilidae): Responded to the Mid-Pleistocene Climate Transition in the Qinghai-Tibetan Plateau. Zoological Studies, 2020, 59, e67.	0.3	0
17826	Three new species (Agaricales, Basidiomycota) from north-eastern China, supported by morphological and molecular data. MycoKeys, 2021, 80, 133-148.	0.8	1
17827	Molecular phylogeny of the orb-weaving spider genus Leucauge and the intergeneric relationships of Leucauginae (Araneae, Tetragnathidae). Invertebrate Systematics, 2021, 35, 922-939.	0.5	2
17828	Reconstruction of the Doradinae (Siluriformes-Doradidae) ancestral diploid number and NOR pattern reveals new insights about the karyotypic diversification of the Neotropical thorny catfishes. Genetics and Molecular Biology, 2021, 44, e20200068.	0.6	1
17829	Ophiostomatoid fungi including a new species associated with Asian larch bark beetle <i>Ips subelongatus</i> , in Heilongjiang (Northeast China). Fungal Systematics and Evolution, 2021, 8, 155-161.	0.9	1
17830	Contribution of plant-bacteria interactions to horizontal gene transfer in plants. Biotechnology and Biotechnological Equipment, 2021, 35, 1587-1592.	0.5	1
17831	Anchoring the species <i>Rhizophagus intraradices</i> (formerly <i>Glomus intraradices</i>). Fungal Systematics and Evolution, 2021, 8, 179-201.	0.9	8
17832	Mitochondrial capture and subsequent genetic divergence generates a novel haplogroup: evidence from ancient and ongoing hybridization in mule and white-tailed deer. Journal of Mammalogy, 2022, 103, 723-736.	0.6	8
17833	Genomic Epidemiology of Typhoid Highlights the Need for Lineage Resolution Diagnosis in Treatment Decisions. SSRN Electronic Journal, 0, , .	0.4	0
17835	A new order of fishes as hosts of blood flukes (Aporocotylidae); description of a new genus and three new species infecting squirrelfishes (Holocentridae, Holocentridae) on the Great Barrier Reef. Parasite, 2021, 28, 76.	0.8	3
17836	Chloroplast genome characteristics and phylogenetic analysis of the medicinal plant <i>Blumea balsamifera</i> (L.) DC. Genetics and Molecular Biology, 2021, 44, e20210095.	0.6	2
17837	A Reference Genome Assembly of Hybrid-Derived California Wild Radish (<i>Raphanus sativus</i> × <i>R. raphanistrum</i>) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50 6	1.0	1
17838	Genomic diversity and distribution of <i>Mesorhizobium nodulating chickpea</i> (<i>Cicer arietinum</i> L.) from low pH soils of Ethiopia. Systematic and Applied Microbiology, 2022, 45, 126279.	1.2	6
17839	Insights into equine piroplasmiasis in Venezuelan sport horses: Molecular diagnosis, clinical, and cardiovascular findings. Veterinary Parasitology: Regional Studies and Reports, 2022, 27, 100666.	0.3	0
17840	How challenging RADseq data turned out to favor coalescent-based species tree inference. A case study in <i>Aichryson</i> (Crassulaceae). Molecular Phylogenetics and Evolution, 2022, 167, 107342.	1.2	14

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17841	Genome-wide ultraconserved elements resolve phylogenetic relationships and biogeographic history among Neotropical leaf-nosed bats in the genus <i>Anoura</i> (Phyllostomidae). <i>Molecular Phylogenetics and Evolution</i> , 2022, 167, 107356.	1.2	3
17842	Host phylogeny is the primary determinant of ectomycorrhizal fungal community composition in the permafrost ecosystem of eastern Siberia at a regional scale. <i>Fungal Ecology</i> , 2022, 55, 101117.	0.7	5
17843	Progress in understanding the phylogeny of the <i>Plasmodium vivax</i> lineage. <i>Parasitology International</i> , 2022, 87, 102507.	0.6	4
17844	<i>Lysimachia brevianthera</i> (Primulaceae), a New Species from the Daba Mountains in Hubei and Shaanxi, China. <i>Annales Botanici Fennici</i> , 2021, 58, .	0.0	1
17845	DNA barcoding of Iranian leeches (Annelida: Clitellata: Hirudinida). <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2021, 59, 1438-1452.	0.6	6
17846	Abundance and Diversity of Ophiostomatoid Fungi Associated With the Great Spruce Bark Beetle (<i>Dendroctonus micans</i>) in the Northeastern Qinghai-Tibet Plateau. <i>Frontiers in Microbiology</i> , 2021, 12, 721395.	1.5	3
17847	Chironomidae (Diptera: Insecta) of Qeshlagh River, Kurdistan: DNA and morphology reveal new genus, species, and faunistic records for Iran. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2021, 59, 1416-1437.	0.6	2
17848	Molecular phylogeny of <i>Aplosporella abexaminans</i> : a novel species revealing the second report of sexual-asexual connection in Aplosporellaceae (Botryosphaeriales) from India. <i>Phytotaxa</i> , 2021, 525, 205-222.	0.1	0
17849	Initial Phylotranscriptomic Confirmation of Homoplastic Evolution of the Conspicuous Coloration and Bufoniform Morphology of Pumpkin-Toadlets in the Genus <i>Brachycephalus</i> . <i>Toxins</i> , 2021, 13, 816.	1.5	3
17850	Nonstarter Bacterial Communities in Aged Cheddar Cheese: Patterns on Two Timescales. <i>Applied and Environmental Microbiology</i> , 2022, 88, AEM0193921.	1.4	3
17852	Contrasting variation patterns in <i>Austroplaca hookeri</i> and <i>Rusavskia elegans</i> (Teloschistaceae, Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 34	0.5	1
17853	Unexpected myriad of co-occurring viral strains and species in one of the most abundant and microdiverse viruses on Earth. <i>ISME Journal</i> , 2022, 16, 1025-1035.	4.4	8
17854	Morphological and molecular analyses of parasitic barnacles (Crustacea: Cirripedia: Rhizocephala) in Korea: preliminary data for the taxonomy and host ranges of Korean species. <i>PeerJ</i> , 2021, 9, e12281.	0.9	2
17855	Molecular mechanisms and topological consequences of drastic chromosomal rearrangements of muntjac deer. <i>Nature Communications</i> , 2021, 12, 6858.	5.8	23
17859	Chromosome-level de novo genome assembly and whole-genome resequencing of the threatened species <i>Acanthochlamys bracteata</i> (Velloziaceae) provide insights into alpine plant divergence in a biodiversity hotspot. <i>Molecular Ecology Resources</i> , 2022, 22, 1582-1595.	2.2	5
17860	5S rDNA in wind-pollinated trees (<i>Fagus</i> L.) encapsulates 55 million years of reticulate evolution and hybrid origins of modern species. <i>Plant Journal</i> , 2022, 109, 909-926.	2.8	16
17861	Chromosome Genome Assembly of <i>Cromileptes altivelis</i> Reveals Loss of Genome Fragment in <i>Cromileptes</i> Compared with <i>Epinephelus</i> Species. <i>Genes</i> , 2021, 12, 1873.	1.0	4
17862	Re-Evaluation of the Taxonomy of <i>Talaromyces minioluteus</i> . <i>Journal of Fungi</i> (Basel, Switzerland), 2021, 7, 993.	1.5	6

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17863	<i>Listeria monocytogenes</i> faecal carriage is common and depends on the gut microbiota. <i>Nature Communications</i> , 2021, 12, 6826.	5.8	25
17865	Phylogeography and morphometric variation in the Cinnamon Hummingbird complex: <i>Amazilia rutila</i> (Aves: Trochilidae). <i>Avian Research</i> , 2021, 12, .	0.5	3
17866	Origin, genetic diversity, adaptive evolution and transmission dynamics of Getah virus. <i>Transboundary and Emerging Diseases</i> , 2022, 69, .	1.3	9
17867	Heme auxotrophy in abundant aquatic microbial lineages. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	20
17868	Species diversity, taxonomy and multi-gene phylogeny of phlebioid clade (Phanerochaetaceae,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 58	4.7	23
17869	Draft genome sequences of strains CBS6241 and CBS6242 of the basidiomycetous yeast <i>Filobasidium floriforme</i> . <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	0
17870	Microbial diversity in a military impacted lagoon (Vieques, Puerto Rico) and description of <i>Candidatus Biekeibacterium resiliens</i> gen. nov., sp. nov. comprising a new bacterial family. <i>Systematic and Applied Microbiology</i> , 2022, 45, 126288.	1.2	1
17871	The genome of the diatom <i>Chaetoceros tenuissimus</i> carries an ancient integrated fragment of an extant virus. <i>Scientific Reports</i> , 2021, 11, 22877.	1.6	10
17872	Deep phylogeographic splits but no taxonomic structure in the disjointly distributed <i>Draba pacheri</i> (Brassicaceae), a subendemic of the Eastern Alps. <i>Folia Geobotanica</i> , 2021, 56, 179-192.	0.4	0
17873	A phylogeny of the genus <i>Limia</i> (Teleostei: Poeciliidae) suggests a single-lake radiation nested in a Caribbean-wide allopatric speciation scenario. <i>BMC Research Notes</i> , 2021, 14, 425.	0.6	4
17874	Protein innovation through template switching in the <i>Saccharomyces cerevisiae</i> lineage. <i>Scientific Reports</i> , 2021, 11, 22558.	1.6	1
17875	A New Species of Night Lizard of the Genus <i>Lepidophyma</i> (Xantusiidae) from Southern Mexico. <i>Herpetologica</i> , 2021, 77, .	0.2	2
17876	Comparative genome sequence and phylogenetic analysis of chloroplast for evolutionary relationship among <i>Pinus</i> species. <i>Saudi Journal of Biological Sciences</i> , 2022, 29, 1618-1627.	1.8	6
17877	A Systematic Study of the Antibacterial Activity of Basidiomycota Crude Extracts. <i>Antibiotics</i> , 2021, 10, 1424.	1.5	7
17878	Genome-wide analysis of long terminal repeat retrotransposons from the cranberry <i>Vaccinium macrocarpon</i> . <i>Journal of Berry Research</i> , 2022, 12, 165-185.	0.7	2
17879	Characterization of a Novel Hypotrich Ciliate From Heavy Metal-Contaminated Industrial Outlet in Onsan, Ulsan, South Korea. <i>Frontiers in Microbiology</i> , 2021, 12, 761961.	1.5	1
17880	Evolutionary Divergence of the Novel Staphylococcal Species <i>Staphylococcus argenteus</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 769642.	1.5	4
17881	Assessing candidate DNA barcodes for Chinese and internationally traded timber species. <i>Molecular Ecology Resources</i> , 2022, 22, 1478-1492.	2.2	9

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17883	Long-Read Assembly and Annotation of the Parasitoid Wasp <i>Muscidifurax raptorellus</i> , a Biological Control Agent for Filth Flies. <i>Frontiers in Genetics</i> , 2021, 12, 748135.	1.1	3
17885	<i>Staphylococcus aureus</i> injection drug use-associated bloodstream infections are propagated by community outbreaks of diverse lineages. <i>Communications Medicine</i> , 2021, 1, .	1.9	9
17887	Ancient hybridization patterns between bighorn and thorn sheep. <i>Molecular Ecology</i> , 2021, 30, 6273-6288.	2.0	4
17888	Punctuated evolution in the learned songs of African sunbirds. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2021, 288, 20212062.	1.2	5
17889	Extensive Interspecific Gene Flow Shaped Complex Evolutionary History and Underestimated Species Diversity in Rapidly Radiated Dolphins. <i>Journal of Mammalian Evolution</i> , 2022, 29, 353-367.	1.0	6
17890	Molecular phylogenetic analyses based on the complete plastid genomes and nuclear sequences reveal <i>Daphne</i> (Thymelaeaceae) to be non-monophyletic as current circumscription. <i>Plant Diversity</i> , 2022, 44, 279-289.	1.8	10
17891	Identification, pathogenicity and effects of plant extracts on <i>Neopestalotiopsis</i> and <i>Pseudopestalotiopsis</i> causing fruit diseases. <i>Scientific Reports</i> , 2021, 11, 22606.	1.6	11
17892	Real-time kinetic studies of <i>Mycobacterium tuberculosis</i> LexA-DNA interaction. <i>Bioscience Reports</i> , 2021, 41, .	1.1	2
17893	Genomic expansion of <i>Aldh1a1</i> protects beavers against high metabolic aldehydes from lipid oxidation. <i>Cell Reports</i> , 2021, 37, 109965.	2.9	7
17894	Two new species of <i>Diaporthe</i> (Diaporthaceae, Diaporthales) associated with tree cankers in the Netherlands. <i>MycKeys</i> , 2021, 85, 31-56.	0.8	15
17895	Intraspecific antagonism through viral toxin encoded by chronic <i>Sulfolobus</i> spindle-shaped virus. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2022, 377, 20200476.	1.8	3
17896	<i>Hoyosella suaedae</i> sp. nov., a novel bacterium isolated from rhizosphere soil of <i>Suaeda aralocaspica</i> (Bunge) Freitag & SchÄtze. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	9
17897	Metabolomics of the wild mushroom <i>Gymnopilus imperialis</i> (Agaricomycetes, Basidiomycota) by UHPLC-HRMS/MS analysis and molecular network. <i>Fungal Biology</i> , 2022, 126, 132-138.	1.1	5
17898	Strong trait correlation and phylogenetic signal in North American ground beetle (Carabidae) morphology. <i>Ecosphere</i> , 2021, 12, .	1.0	3
17899	The complete chloroplast genome sequence of <i>Athrotaxis cupressoides</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 3468-3470.	0.2	0
17900	MAGUS+eHMMs: improved multiple sequence alignment accuracy for fragmentary sequences. <i>Bioinformatics</i> , 2022, 38, 918-924.	1.8	12
17902	Phylogenomic analyses of the genus <i>Drosophila</i> reveals genomic signals of climate adaptation. <i>Molecular Ecology Resources</i> , 2022, 22, 1559-1581.	2.2	15
17903	Molecular phylogeny and macroevolution of Chaitophorinae aphids (Insecta) Tj ETQq1 1 0,784314rgBT /Over	1.7	4

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17904	Chloranthus genome provides insights into the early diversification of angiosperms. <i>Nature Communications</i> , 2021, 12, 6930.	5.8	44
17905	A morphological and molecular reinvestigation of <i>Janickina pigmentifera</i> (Grassi, 1881) Chatton 1953 " an amoebozoan parasite of arrow-worms (Chaetognatha). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	4
17907	The maintenance of standing genetic variation: Gene flow vs. selective neutrality in Atlantic stickleback fish. <i>Molecular Ecology</i> , 2022, 31, 811-821.	2.0	4
17908	Whole genome sequencing and <i>de novo</i> assembly of <i>Staphylococcus pseudintermedius</i> : a pangenome approach to unravelling pathogenesis of canine pyoderma. <i>Veterinary Dermatology</i> , 2021, 32, 654-663.	0.4	7
17909	Weak population genetic structure of a widely distributed nematode parasite of frogs in the western Palearctic. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2021, 59, 1689.	0.6	2
17910	Sage Insights Into the Phylogeny of <i>Salvia</i> : Dealing With Sources of Discordance Within and Across Genomes. <i>Frontiers in Plant Science</i> , 2021, 12, 767478.	1.7	10
17911	The First Two Complete Mitochondrial Genomes of Neophemeridae (Ephemeroptera): Comparative Analysis and Phylogenetic Implication for Furcatergalia. <i>Genes</i> , 2021, 12, 1875.	1.0	6
17912	Regional Variation in Dengue Virus Serotypes in Sri Lanka and Its Clinical and Epidemiological Relevance. <i>Diagnostics</i> , 2021, 11, 2084.	1.3	2
17913	Characterization of the MYB Genes Reveals Insights Into Their Evolutionary Conservation, Structural Diversity, and Functional Roles in Magnaporthe oryzae. <i>Frontiers in Microbiology</i> , 2021, 12, 721530.	1.5	9
17914	Convergent adaptation of <i>Saccharomyces uvarum</i> to sulfite, an antimicrobial preservative widely used in human-driven fermentations. <i>PLoS Genetics</i> , 2021, 17, e1009872.	1.5	11
17915	Description of a New Hamatipeda Species, with an 18S Molecular Phylogeny (Crustacea: Tanaidacea: Tj ETQq0 0 0 rgBT /Overlock 10 TF	0.8	5
17916	A high-resolution genome of an euryhaline and eurythermal rhinogoby (<i>Rhinogobius similis</i> Gill 1895). <i>G3: Genes, Genomes, Genetics</i> , 2021, , .	0.8	1
17917	Phylogenetic Relatedness and Genome Structure of <i>Yersinia ruckeri</i> Revealed by Whole Genome Sequencing and a Comparative Analysis. <i>Frontiers in Microbiology</i> , 2021, 12, 782415.	1.5	1
17918	Interactions among Escovopsis, Antagonistic Microfungi Associated with the Fungus-Growing Ant Symbiosis. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 1007.	1.5	3
17919	Genomic characterization and production of antimicrobial lipopeptides by <i>Bacillus velezensis</i> P45 growing on feather by-products. <i>Journal of Applied Microbiology</i> , 2022, 132, 2067-2079.	1.4	4
17920	A new endemic species of <i>Sesuvium</i> (Aizoaceae: Sesuvioideae) from the Caribbean Basin, with further notes on the genus composition in the West Indies. <i>Kew Bulletin</i> , 0, , 1.	0.4	2
17923	Using the Evolutionary History of Proteins to Engineer Insertion-Deletion Mutants from Robust, Ancestral Templates Using Graphical Representation of Ancestral Sequence Predictions (GRASP). <i>Methods in Molecular Biology</i> , 2022, 2397, 85-110.	0.4	9
17924	Three New Records of Marine Macroalgae from Viet Nam based on Morphological Observations and Molecular Analyses. <i>Pacific Science</i> , 2021, 75, .	0.2	3

#	ARTICLE	IF	CITATIONS
17925	Morphological and phylogenetic analyses reveal a new genus and two new species of Tubakiaceae from China. MycoKeys, 2021, 84, 185-201.	0.8	2
17927	<i>Adiantum japonicum</i> , a new species of the <i>Adiantum pedatum</i> complex (Pteridaceae) from Japan. Phytotaxa, 2021, 525, 1-14.	0.1	0
17928	Morphological Variety in <i>Distoseptispora</i> and Introduction of Six Novel Species. Journal of Fungi (Basel, Switzerland), 2021, 7, 945.	1.5	11
17929	Genome-Wide Analysis of the Cyclin-Dependent Kinases (CDK) and Cyclin Family in Molluscs. Journal of Ocean University of China, 2021, 20, 1469-1482.	0.6	0
17931	Divergence time estimation of Galliformes based on the best gene shopping scheme of ultraconserved elements. BMC Ecology and Evolution, 2021, 21, 209.	0.7	17
17932	The complete chloroplast genome of <i>Petasites japonicus</i> (Siebold & Zucc.) Maxim. (Asteraceae). Mitochondrial DNA Part B: Resources, 2021, 6, 3503-3505.	0.2	0
17933	The complete chloroplast genome of <i>Flemingia macrophylla</i> (Willd.) Prain (Fabaceae) from Guangxi, China. Mitochondrial DNA Part B: Resources, 2021, 6, 3378-3380.	0.2	1
17934	History, demography and genetic status of Balkan and Caucasian <i>Lynx lynx</i> (Linnaeus, 1758) populations revealed by genome-wide variation. Diversity and Distributions, 2022, 28, 65-82.	1.9	9
17935	Complete chloroplast genome of <i>Dactylicapnos torulosa</i> (Hook. & Thoms.) Hutch., a medicinal plant from southwest China and its phylogeny. Mitochondrial DNA Part B: Resources, 2021, 6, 3423-3425.	0.2	0
17936	The complete chloroplast genome sequence of <i>Sedum lineare</i> (Crassulaceae). Mitochondrial DNA Part B: Resources, 2021, 6, 3338-3339.	0.2	1
17937	The discovery of multidrug resistant <i>Staphylococcus aureus</i> harboring novel SaRI isolated from retail foods. Food Control, 2022, 135, 108739.	2.8	3
17938	<i>Enterococcus faecium</i> Regulates Honey Bee Developmental Genes. International Journal of Molecular Sciences, 2021, 22, 12105.	1.8	12
17939	Comparative Chloroplast Genome Analyses of the Winter-Blooming Eastern Asian Endemic Genus <i>Chimonanthus</i> (Calycanthaceae) With Implications For Its Phylogeny and Diversification. Frontiers in Genetics, 2021, 12, 709996.	1.1	1
17940	Whole-genome sequence analysis unveils different origins of European and Asiatic mouflon and domestication-related genes in sheep. Communications Biology, 2021, 4, 1307.	2.0	38
17943	Pan-genome analysis identifies intersecting roles for <i>Pseudomonas</i> specialized metabolites in potato pathogen inhibition. ELife, 2021, 10, .	2.8	25
17944	Completing the Genome Sequence of <i>Chlamydia pecorum</i> Strains MC/MarsBar and DBDeUG: New Insights into This Enigmatic Koala (<i>Phascolarctos cinereus</i>) Pathogen. Pathogens, 2021, 10, 1543.	1.2	6
17945	<i>Campylocarpon fasciculare</i> (Nectriaceae, Sordariomycetes); Novel Emergence of Black-Foot Causing Pathogen on Young Grapevines in China. Pathogens, 2021, 10, 1555.	1.2	3
17946	Two Complete Mitogenomes of Chalcididae (Hymenoptera: Chalcidoidea): Genome Description and Phylogenetic Implications. Insects, 2021, 12, 1049.	1.0	3

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17947	<i>Paralysiella testudinis</i> gen. nov., sp. nov., isolated from the cloaca of a toad-headed turtle (<i>Mesoclemmys nasuta</i>). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	9
17948	Metagenomics of Antarctic Marine Sediment Reveals Potential for Diverse Chemolithoautotrophy. <i>MSphere</i> , 2021, 6, e0077021.	1.3	5
17949	Morphology, Life Cycle, and SSU rDNA-based Phylogeny of Two Folliculinid Ciliates (Ciliophora,) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 66</i> 172, 125844.	0.6	2
17950	Complex adaptive architecture underlies adaptation to quantitative host resistance in a fungal plant pathogen. <i>Molecular Ecology</i> , 2021, , .	2.0	0
17951	Phylogenomics, introgression, and demographic history of South American true toads (<i>Rhinella</i>). <i>Molecular Ecology</i> , 2022, 31, 978-992.	2.0	14
17952	Old origin for an Europeanâ€African amphitropical disjunction pattern: New insights from a case study on wingless darkling beetles. <i>Journal of Biogeography</i> , 0, , .	1.4	11
17953	Molecular epidemiology of extended-spectrum beta-lactamaseâ€producing extra-intestinal pathogenic <i>Escherichia coli</i> strains over a 2-year period (2017â€2019) from Zimbabwe. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2021, , 1.	1.3	5
17954	Genetic Characterization of Novel H7Nx Low Pathogenic Avian Influenza Viruses from Wild Birds in South Korea during the Winter of 2020â€2021. <i>Viruses</i> , 2021, 13, 2274.	1.5	2
17955	Integrative taxonomy unveils a new species of <i>Dugesia</i> (Platyhelminthes, Tricladida, Dugesiidae) from the southern portion of the Taihang Mountains in northern China, with the description of its complete mitogenome and an exploratory analysis of mitochondrial gene order as a taxonomic character. <i>Integrative Zoology</i> , 2022, 17, 1193-1214.	1.3	7
17956	Chloroplast morphology and pyrenoid ultrastructural analyses reappraise the diversity of the lichen phycobiont genus <i>Trebouxia</i> (Chlorophyta). <i>Algal Research</i> , 2022, 61, 102561.	2.4	16
17958	Resurrecting Enzymes by Ancestral Sequence Reconstruction. <i>Methods in Molecular Biology</i> , 2022, 2397, 111-136.	0.4	13
17959	Resurrection of <i>Plocamium pusillum</i> Sonder (Plocamiaceae, Rhodophyta) from Australia. <i>Cryptogamie, Algologie</i> , 2021, 42, .	0.3	1
17961	Large-scale geography survey provides insights into the colonization history of a major aphid pest on its cultivated apple host in Europe, North America and North Africa. , 0, 1, .		0
17962	Whole-genome epidemiology and characterisation of <i>mcr-1</i> -encoding <i>Escherichia coli</i> in aquatic bird farms from the Pearl River Delta, China, 2019â€2020. <i>International Journal of Antimicrobial Agents</i> , 2022, 59, 106478.	1.1	3
17963	The Baltic Sea methane pockmark microbiome: The new insights into the patterns of relative abundance and ANME niche separation. <i>Marine Environmental Research</i> , 2022, 173, 105533.	1.1	17
17964	Chromosomeâ€level genome assembly of the Chinese threeâ€keeled pond turtle (<i>Mauremys reevesii</i>) provides insights into freshwater adaptation. <i>Molecular Ecology Resources</i> , 2022, 22, 1596-1605.	2.2	8
17965	Origin, evolution and diversification of plant ARGONAUTE proteins. <i>Plant Journal</i> , 2022, 109, 1086-1097.	2.8	24
17966	Comparative genomic analysis reveals varying levels of mammalian adaptation to coronavirus infections. <i>PLoS Computational Biology</i> , 2021, 17, e1009560.	1.5	5

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17967	Evolution of Beak and Feather Disease Virus across Three Decades of Conservation Intervention for Population Recovery of the Mauritius Parakeet. <i>Diversity</i> , 2021, 13, 584.	0.7	8
17970	Genetic and Phenotypic Diversity of <i>Morganella morganii</i> Isolated From Cheese. <i>Frontiers in Microbiology</i> , 2021, 12, 738492.	1.5	8
17972	Comparative Genomic and Pan-Genomic Characterization of <i>Staphylococcus epidermidis</i> From Different Sources Unveils the Molecular Basis and Potential Biomarkers of Pathogenic Strains. <i>Frontiers in Microbiology</i> , 2021, 12, 770191.	1.5	4
17973	Genetic Characterization of <i>Salmonella infantis</i> with Multiple Drug Resistance Profiles Isolated from a Poultry-Farm in Chile. <i>Microorganisms</i> , 2021, 9, 2370.	1.6	9
17974	Mongoose (<i>Urva auropunctata</i>) as reservoir hosts of <i>Leptospira</i> species in the United States Virgin Islands, 2019–2020. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009859.	1.3	8
17975	Functional diversification gave rise to allelic specialization in a rice NLR immune receptor pair. <i>ELife</i> , 2021, 10, .	2.8	28
17976	Using Oxidative Electrodes to Enrich Novel Members in the Desulfobulbaceae Family from Intertidal Sediments. <i>Microorganisms</i> , 2021, 9, 2329.	1.6	4
17977	The rhodopsin-retinochrome system for retinal re-isomerization predates the origin of cephalopod eyes. <i>Bmc Ecology and Evolution</i> , 2021, 21, 215.	0.7	7
17978	Evolutionary genomics of APSE: a tailed phage that lysogenically converts the bacterium <i>Hamiltonella defensa</i> into a heritable protective symbiont of aphids. <i>Virology Journal</i> , 2021, 18, 219.	1.4	11
17980	Prevalence, transmission, and molecular epidemiology of tet(X)-positive bacteria among humans, animals, and environmental niches in China: An epidemiological, and genomic-based study. <i>Science of the Total Environment</i> , 2022, 818, 151767.	3.9	18
17982	Oxygen-deficient water zones in the Baltic Sea promote uncharacterized Hg methylating microorganisms in underlying sediments. <i>Limnology and Oceanography</i> , 2022, 67, 135-146.	1.6	15
17983	Development of a real-time RT-PCR assay for the detection of pan-human parechoviruses. <i>Virology Journal</i> , 2021, 18, 227.	1.4	2
17984	Clinical outcomes and bacterial characteristics of carbapenem-resistant <i>Klebsiella pneumoniae</i> complex among patients from different global regions (CRACKLE-2): a prospective, multicentre, cohort study. <i>Lancet Infectious Diseases</i> , The, 2022, 22, 401-412.	4.6	122
17985	Epidemiological associations with genomic variation in SARS-CoV-2. <i>Scientific Reports</i> , 2021, 11, 23023.	1.6	5
17986	Phylosymbiosis in the Rhizosphere Microbiome Extends to Nitrogen Cycle Functional Potential. <i>Microorganisms</i> , 2021, 9, 2476.	1.6	2
17987	A comprehensive appraisal of evolutionary diversity in venomous Asian coralsnakes of the genus <i>Sinomicrurus</i> (Serpentes: Elapidae) using Bayesian coalescent inference and supervised machine learning. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2021, 59, 2212-2277.	0.6	4
17988	Domestication obscures genomic estimates of population history. <i>Molecular Ecology</i> , 2022, 31, 752-766.	2.0	6
17990	Unexpected cryptic species among streptophyte algae most distant to land plants. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2021, 288, 20212168.	1.2	22

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17991	Characterization of the complete chloroplast genome of <i>Salvia leucantha</i> (Lamiaceae). Mitochondrial DNA Part B: Resources, 2021, 6, 3406-3408.	0.2	2
17992	The complete plastome of the South African species, <i>Amaryllis belladonna</i> L. (Amaryllidaceae). Mitochondrial DNA Part B: Resources, 2021, 6, 3393-3395.	0.2	2
17993	The complete chloroplast genome sequence of <i>Trollius macropetalus</i> . Mitochondrial DNA Part B: Resources, 2021, 6, 3501-3502.	0.2	0
17994	Specialization on <i>Ficus</i> Supported by Genetic Divergence and Morphometrics in Sympatric Host-Populations of the Camellia Aphid, <i>Aphis aurantii</i> . <i>Frontiers in Ecology and Evolution</i> , 2021, 9, .	1.1	4
17995	Comparative Phylogeography and Phylogeny of Pennah Croakers (Teleostei: Sciaenidae) in Southeast Asian Waters. <i>Genes</i> , 2021, 12, 1926.	1.0	1
17996	Seasonal Dynamics of Bathyarchaeota-Dominated Benthic Archaeal Communities Associated with Seagrass (<i>Zostera japonica</i>) Meadows. <i>Journal of Marine Science and Engineering</i> , 2021, 9, 1304.	1.2	6
17997	Oil and Gas Wastewater Components Alter Streambed Microbial Community Structure and Function. <i>Frontiers in Microbiology</i> , 2021, 12, 752947.	1.5	4
17998	Genomic investigation of a suspected <i>Klebsiella pneumoniae</i> outbreak in a neonatal care unit in sub-Saharan Africa. <i>Microbial Genomics</i> , 2021, 7, .	1.0	8
17999	The complete genome sequence of Indian sheeppox vaccine virus and comparative analysis with other capripoxviruses. <i>Gene</i> , 2022, 810, 146085.	1.0	4
18000	Eye-Transcriptome and Genome-Wide Sequencing for Scolecophidia: Implications for Inferring the Visual System of the Ancestral Snake. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	8
18002	The first high-quality chromosomal genome assembly of a medicinal and edible plant <i>Arctium lappa</i> . <i>Molecular Ecology Resources</i> , 2021, , .	2.2	11
18003	Hopping or Jumping on the Cliffs: The Unusual Phylogeographical and Demographic Structure of an Extremely Narrow Endemic Mediterranean Plant. <i>Frontiers in Plant Science</i> , 2021, 12, 737111.	1.7	1
18004	Mitochondrial genomes of two parasitic <i>Cuscuta</i> species lack clear evidence of horizontal gene transfer and retain unusually fragmented ccmFC genes. <i>BMC Genomics</i> , 2021, 22, 816.	1.2	11
18005	High-throughput sequencing of faeces provides evidence for dispersal of parasites and pathogens by migratory waterbirds. <i>Molecular Ecology Resources</i> , 2022, 22, 1303-1318.	2.2	8
18006	Chromosome-level assembly of the <i>Neolamarckia cadamba</i> genome provides insights into the evolution of cadambine biosynthesis. <i>Plant Journal</i> , 2022, 109, 891-908.	2.8	19
18007	Evolutionary innovations through gain and loss of genes in the ectomycorrhizal Boletales. <i>New Phytologist</i> , 2022, 233, 1383-1400.	3.5	19
18008	Comparative plastomics of Amaryllidaceae: inverted repeat expansion and the degradation of the <i>ndh</i> genes in <i>Strumaria truncata</i> Jacq.. <i>PeerJ</i> , 2021, 9, e12400.	0.9	4
18009	The Gene Rearrangement, Loss, Transfer, and Deep Intronic Variation in Mitochondrial Genomes of <i>Conidiobolus</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 765733.	1.5	5

#	ARTICLE	IF	CITATIONS
18010	Honey bee sHSP are responsive to diverse proteostatic stresses and potentially promising biomarkers of honey bee stress. <i>Scientific Reports</i> , 2021, 11, 22087.	1.6	15
18011	Comparative Genomics Analyses Support the Reclassification of Bisgaard Taxon 40 as <i>Mergibacter</i> gen. nov., With <i>Mergibacter septicus</i> sp. nov. as Type Species: Novel Insights Into the Phylogeny and Virulence Factors of a Pasteurellaceae Family Member Associated With Mortality Events in Seabirds. <i>Frontiers in Microbiology</i> , 2021, 12, 667356.	1.5	4
18012	High-Quality Genomes and High-Density Genetic Map Facilitate the Identification of Genes From a Weedy Rice. <i>Frontiers in Plant Science</i> , 2021, 12, 775051.	1.7	7
18013	Multispecies Populations of Methanotrophic <i>Methyloprofundus</i> and Cultivation of a Likely Dominant Species from the Iheya North Deep-Sea Hydrothermal Field. <i>Applied and Environmental Microbiology</i> , 2022, 88, AEM0075821.	1.4	12
18014	In depth analysis of Cyprus-specific mutations of SARS-CoV-2 strains using computational approaches. <i>BMC Genomic Data</i> , 2021, 22, 48.	0.7	4
18015	Evolution of diverse host infection mechanisms delineates an adaptive radiation of lampsiline freshwater mussels centered on their larval ecology. <i>PeerJ</i> , 2021, 9, e12287.	0.9	5
18016	Telomere-to-telomere genome assembly of asparaginase-producing <i>Trichoderma simmonsii</i> . <i>BMC Genomics</i> , 2021, 22, 830.	1.2	9
18017	Antimicrobial Resistance in <i>Enterococcus</i> Spp. Isolated from a Beef Processing Plant and Retail Ground Beef. <i>Microbiology Spectrum</i> , 2021, 9, e0198021.	1.2	10
18019	Antimicrobial resistance determinants are associated with <i>Staphylococcus aureus</i> bacteraemia and adaptation to the healthcare environment: a bacterial genome-wide association study. <i>Microbial Genomics</i> , 2021, 7, .	1.0	15
18020	Vertical Inheritance Facilitates Interspecies Diversification in Biosynthetic Gene Clusters and Specialized Metabolites. <i>MBio</i> , 2021, 12, e0270021.	1.8	23
18021	Soil microbial community response to winter climate change is phylogenetically conserved and highly resilient in a cool-temperate forest. <i>Soil Biology and Biochemistry</i> , 2022, 165, 108499.	4.2	15
18022	Phylogeographic pattern of a cryptoviviparous mangrove, <i>Aegiceras corniculatum</i> , in the Indo-West Pacific, provides insights for conservation actions. <i>Planta</i> , 2022, 255, 7.	1.6	2
18023	Pattern of New Gene Origination in a Special Fish Lineage, the Flatfishes. <i>Genes</i> , 2021, 12, 1819.	1.0	2
18024	Endogenic upregulations of HIF/VEGF signaling pathway genes promote air breathing organ angiogenesis in bimodal respiration fish. <i>Functional and Integrative Genomics</i> , 2022, 22, 65-76.	1.4	2
18025	Complete chloroplast genome of <i>Baccaurea ramiflora</i> (phyllanthaceae), a promising underutilized species. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 3362-3363.	0.2	0
18026	The complete chloroplast genome of <i>Callicarpa longifolia</i> Lamk. var. <i>floccosa</i> Schauer (Lamiaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 3473-3474.	0.2	1
18028	Parallel evolution of a new sympatric species pair of <i>Crenicichla</i> (Teleostei: Cichlidae) from Misiones, Argentina with a review of biogeography and mitonuclear discordance in the <i>C. mandelburgeri</i> species complex. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2021, 59, 2134-2149.	0.6	4
18031	A new nomenclature for the livestock-associated <i>Mycobacterium tuberculosis</i> complex based on phylogenomics. <i>Open Research Europe</i> , 0, 1, 100.	2.0	14

#	ARTICLE	IF	CITATIONS
18032	Taxonomic and phylogenetic studies on two new freshwater Amphileptus species (Ciliophora,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 747 125854.	0.5	6
18033	Colonization of the Southern Hemisphere by Sagina and Colobanthus (Caryophyllaceae). Plant Systematics and Evolution, 2022, 308, 1.	0.3	4
18034	A rodent anchored hybrid enrichment probe set for a range of phylogenetic utility: From order to species. Molecular Ecology Resources, 2021, , .	2.2	0
18035	Diversity, distribution, and evolutionary history of the most studied African rodents, multimammate mice of the genus <i>Mastomys</i> : An overview after a quarter of century of using DNA sequencing. Journal of Zoological Systematics and Evolutionary Research, 2021, 59, 2500-2518.	0.6	7
18036	In vitro interaction network of a synthetic gut bacterial community. ISME Journal, 2022, 16, 1095-1109.	4.4	66
18037	Species diversity in Penicillium and Acaulium from herbivore dung in China, and description of Acaulium stercorarius sp. nov. Mycological Progress, 2021, 20, 1539-1551.	0.5	0
18039	Distribution, Function, and Evolution of a Gene Essential for Trichothecene Toxin Biosynthesis in Trichoderma. Frontiers in Microbiology, 2021, 12, 791641.	1.5	10
18040	Genomic insights into Salmonella Choleraesuis var. Kunzendorf outbreak reveal possible interspecies transmission. Veterinary Microbiology, 2021, 263, 109282.	0.8	5
18041	Rhythmic Clock Gene Expression in Atlantic Salmon Parr Brain. Frontiers in Physiology, 2021, 12, 761109.	1.3	6
18043	Evaluating the morphological and molecular challenges in identifying the afrotropical Atylotus species (Diptera: Tabanidae). Acta Tropica, 2022, 226, 106262.	0.9	1
18044	Identification and characterization of homeobox gene clusters in harpacticoid and calanoid copepods. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2022, 338, 215-224.	0.6	2
18045	Phylogenetic analysis reveals the new genus <i>Amoenoboletus</i> from Asia and New Zealand. Mycologia, 2022, 114, 144-156.	0.8	3
18046	A Conserved Histophilus somni 23S Intervening Sequence Yields Functional, Fragmented 23S rRNA. Microbiology Spectrum, 2021, 9, e0143121.	1.2	1
18047	Oreocharis xieyongii, an unusual new species of Gesneriaceae from western Hunan, China. Plant Diversity, 2022, 44, 222-230.	1.8	3
18048	Revisiting proboscidean phylogeny and evolution through total evidence and palaeogenetic analyses including Notiomastodon ancient DNA. IScience, 2022, 25, 103559.	1.9	13
18049	Establishing community-wide DNA barcode references for conserving mangrove forests in China. BMC Plant Biology, 2021, 21, 571.	1.6	1
18050	Histone acetylation regulates the expression of genes involved in worker reproduction in the ant Temnothorax rugatulus. BMC Genomics, 2021, 22, 871.	1.2	10
18051	The chromosome-level genome provides insight into the molecular mechanism underlying the tortuous branch phenotype of <i>Prunus mume</i> . New Phytologist, 2022, 235, 141-156.	3.5	15

#	ARTICLE	IF	CITATIONS
18052	H9N2 virus-derived M1 protein promotes H5N6 virus release in mammalian cells: Mechanism of avian influenza virus inter-species infection in humans. <i>PLoS Pathogens</i> , 2021, 17, e1010098.	2.1	10
18053	New Data Define the Molecular Phylogeny and Taxonomy of Four Freshwater Suctorian Ciliates With Redefinition of Two Families Heliophryidae and Cyclophryidae (Ciliophora, Phyllopharyngea, Suctorina). <i>Frontiers in Microbiology</i> , 2021, 12, 768724.	1.5	3
18055	<i>Vannella mustalahtiana</i> sp. nov. (Amoebozoa, Vannellida) and rainbow trout nodular gill disease (NGD) in Russia. <i>Diseases of Aquatic Organisms</i> , 2022, 148, 29-41.	0.5	5
18056	Checking Phylogenetics Decisiveness in Theory and in Practice. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, PP, 1-1.	1.9	0
18058	Chloroplast genome characteristics and phylogenetic analysis of the medicinal plant <i>Blumea balsamifera</i> (L.) DC. <i>Genetics and Molecular Biology</i> , 2021, 44, .	0.6	1
18059	Fungal Planet description sheets: 1284–1382. <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2021, 47, 178-374.	1.6	44
18060	Phyllodes and bipinnate leaves of. <i>Australian Systematic Botany</i> , 2021, 34, 595-608.	0.3	4
18061	Molecular species delimitation of the genera <i>Anodus</i> , <i>Argonectes</i> , <i>Bivibranchia</i> and <i>Micromischodus</i> (Ostariophysi: Characiformes). <i>Neotropical Ichthyology</i> , 2021, 19, .	0.5	2
18062	Phylogenetic inference of Ericales based on plastid genomes and implication of cp-SSRs. <i>Biotechnologia</i> , 2021, 102, 277-283.	0.3	2
18063	The new genus <i>Aglaona</i> : the first abyssal aglajid (Heterobranchia: Cephalaspidea: Aglajidae) with a description of two new species from the north-western Pacific Ocean. <i>Zoological Journal of the Linnean Society</i> , 2022, 196, 198-214.	1.0	2
18064	16S rRNA gene sequences of <i>Candidatus Methylumidiphilus</i> (Methylococcales), a putative methanotrophic genus in lakes and ponds. <i>Aquatic Microbial Ecology</i> , 2022, 88, 25-30.	0.9	0
18065	Uncertainty Quantification Using Subsampling for Assembly-Free Estimates of Genomic Distance and Phylogenetic Relationships. <i>SSRN Electronic Journal</i> , 0, , .	0.4	2
18066	Cytochrome P450 monooxygenase of <i>Acanthamoeba castellanii</i> participates in resistance to polyhexamethylene biguanide treatment. <i>Parasite</i> , 2021, 28, 77.	0.8	3
18067	A new genus of frenulates (Annelida: Siboglinidae) from shallow waters of the Yenisey River estuary, Kara Sea. <i>Invertebrate Systematics</i> , 2021, 35, 857-875.	0.5	7
18068	Molecular epidemiology and pathogenicity of H5N1 and H9N2 avian influenza viruses in clinically affected chickens on farms in Bangladesh. <i>Emerging Microbes and Infections</i> , 2021, 10, 2223-2234.	3.0	10
18069	Visualization of the Evolutionary Path: an Influenza Case Study. , 2021, , .		1
18070	Niche conservatism, divergence and polyploidy in <i>Senna</i> series <i>Aphyllae</i> (Fabaceae: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 10 199, 773-789.	0.8	0
18071	High-level taxonomic splitting in allopatric taxa causes confusion downstream: a revision of the nudibranch family <i>Đjoryphellidae</i> . <i>Zoological Journal of the Linnean Society</i> , 2022, 196, 215-249.	1.0	6

#	ARTICLE	IF	CITATIONS
18072	The Complete Genome of <i>Chelonus insularis</i> Reveals Dynamic Arrangement of Genome Components in Parasitoid Wasps That Produce Bracoviruses. <i>Journal of Virology</i> , 2022, 96, JV0157321.	1.5	6
18073	Characterization of the complete chloroplast genome of a Peruvian landrace of <i>Capsicum chinense</i> Jacq. (Solanaceae), arnaucho chili pepper. <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 156-158.	0.2	1
18075	<i>Allochromatium tepidum</i> , sp. nov., a hot spring species of purple sulfur bacteria. <i>Archives of Microbiology</i> , 2022, 204, 115.	1.0	9
18076	Co-option of the limb patterning program in cephalopod eye development. <i>BMC Biology</i> , 2022, 20, 1.	1.7	34
18077	Phylogeographic Relationships among <i>Bombyx mandarina</i> (Lepidoptera: Bombycidae) Populations and Their Relationships to <i>B. mori</i> Inferred from Mitochondrial Genomes. <i>Biology</i> , 2022, 11, 68.	1.3	6
18078	Comparative and Phylogenetic Analysis of Complete Plastomes among Aristidoideae Species (Poaceae). <i>Biology</i> , 2022, 11, 63.	1.3	6
18080	Two divergent haplotypes from a highly heterozygous lychee genome suggest independent domestication events for early and late-maturing cultivars. <i>Nature Genetics</i> , 2022, 54, 73-83.	9.4	88
18081	Prevalence and conservation of <i>ebp</i> genes in <i>Enterococcus faecalis</i> originated from animals. <i>Journal of Applied Microbiology</i> , 2022, 132, 3293-3301.	1.4	2
18082	The changing molecular epidemiology of <i>Enterococcus faecium</i> harbouring the <i>van</i> operon at a teaching hospital in Western Australia: A fifteen-year retrospective study. <i>International Journal of Medical Microbiology</i> , 2022, 312, 151546.	1.5	0
18083	Extensive species diversification and marked geographic phylogenetic structure in the Mesoamerican genus <i>Stenopelmatus</i> (Orthoptera: Stenopelmatidae: Stenopelmatinae) revealed by mitochondrial and nuclear 3RAD data. <i>Invertebrate Systematics</i> , 2022, , .	0.5	0
18084	Convergent evolution of venom gland transcriptomes across Metazoa. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	15
18085	Unlocking the Complete Chloroplast Genome of a Native Tree Species from the Amazon Basin, <i>Capirona</i> (<i>Calycophyllum Spruceanum</i> , Rubiaceae), and Its Comparative Analysis with Other Ixoroideae Species. <i>Genes</i> , 2022, 13, 113.	1.0	9
18086	Evolutionary Ecology of Natural Comammox <i>Nitrospira</i> Populations. <i>MSystems</i> , 2022, 7, e0113921.	1.7	14
18087	Providing a phylogenetic framework for trait-based analyses in brown algae: Phylogenomic tree inferred from 32 nuclear protein-coding sequences. <i>Molecular Phylogenetics and Evolution</i> , 2022, 168, 107408.	1.2	2
18088	What ancient DNA reveals about the ubiquitous rockfish of the Pacific Coast of North America. <i>Archaeological and Anthropological Sciences</i> , 2022, 14, 1.	0.7	1
18089	A new tapeworm from <i>Compsophis infralineatus</i> (Pseudoxyrhopiidae), an endemic snake of Madagascar: Scratching the surface of undiscovered reptilian parasite diversity. <i>Parasitology International</i> , 2022, 88, 102538.	0.6	2
18090	Native and foreign mitochondrial and nuclear encoded proteins conform the OXPHOS complexes of a holoparasitic plant. <i>Gene</i> , 2022, 817, 146176.	1.0	6
18091	A simple guide to <i>de novo</i> transcriptome assembly and annotation. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	42

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18092	Whence Came These Plants Most Foul? Phylogenomics and Biogeography of Lowiaceae (Zingiberales). <i>Frontiers in Ecology and Evolution</i> , 2022, 9, .	1.1	1
18093	<i>Ischnura praematura</i> sp. nov. (Odonata: Zygoptera: Coenagrionidae): a species from Yunnan (China) whose females mate in the teneral state. <i>Zootaxa</i> , 2022, 5087, 59-74.	0.2	2
18096	Genomic epidemiology and characterisation of penicillin-sensitive <i>Staphylococcus aureus</i> isolates from invasive bloodstream infections in China: an increasing prevalence and higher diversity in genetic typing be revealed. <i>Emerging Microbes and Infections</i> , 2022, 11, 326-336.	3.0	8
18097	Genome sequences of five <i>Sitopsis</i> species of <i>Aegilops</i> and the origin of polyploid wheat B subgenome. <i>Molecular Plant</i> , 2022, 15, 488-503.	3.9	84
18099	Hidden Diversity—A New Speciose Gall Midge Genus (Diptera: Cecidomyiidae) Associated with Succulent Aizoaceae in South Africa. <i>Insects</i> , 2022, 13, 75.	1.0	2
18100	Highly diverged lineages of <i>Saccharomyces paradoxus</i> in temperate to subtropical climate zones in China. <i>Yeast</i> , 2021, , .	0.8	8
18101	Multi-Gene Phylogeny and Taxonomy of <i>Hypoxylon</i> (Hypoxylaceae, Ascomycota) from China. <i>Diversity</i> , 2022, 14, 37.	0.7	9
18103	A high-quality chromosome-level genome of the endangered roughskin sculpin provides insights into its evolution and adaptation. <i>Molecular Ecology Resources</i> , 2022, 22, 1892-1905.	2.2	1
18104	Whole-genome analysis of carbapenem-resistant <i>Acinetobacter baumannii</i> from clinical isolates in Southern Thailand. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 545-558.	1.9	12
18105	Plastome structure, evolution, and phylogeny of <i>Selaginella</i> . <i>Molecular Phylogenetics and Evolution</i> , 2022, 169, 107410.	1.2	11
18106	Expression profiles and functional prediction of ionotropic receptors in Asian corn borer, (Lepidoptera: Crambidae). <i>Journal of Integrative Agriculture</i> , 2022, 21, 474-485.	1.7	4
18107	Evolutionary insights and brief review of <i>Loxodes Ehrenberg, 1830</i> (Ciliophora, Karyorelictea). <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10</i> 125856.	0.5	4
18108	Examining the Relationship Between the Testate Amoeba <i>Hyalosphenia papilio</i> (Arcellinida, Amoebozoa) and its Associated Intracellular Microalgae Using Molecular and Microscopic Methods. <i>Protist</i> , 2022, 173, 125853.	0.6	2
18109	Bioinformatics of virus taxonomy: foundations and tools for developing sequence-based hierarchical classification. <i>Current Opinion in Virology</i> , 2022, 52, 48-56.	2.6	13
18110	Sex pheromone receptors of the light brown apple moth, <i>Epiphyas postvittana</i> , support a second major pheromone receptor clade within the Lepidoptera. <i>Insect Biochemistry and Molecular Biology</i> , 2022, 141, 103708.	1.2	15
18111	Occurrence and chemotaxonomical analysis of amatoxins in <i>Lepiota</i> spp. (Agaricales). <i>Phytochemistry</i> , 2022, 195, 113069.	1.4	7
18112	Comparative phylotranscriptomics reveals putative sex differentiating genes across eight diverse bivalve species. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2022, 41, 100952.	0.4	7
18113	Pathogenicity of Shiga toxin-producing <i>Escherichia coli</i> (STEC) from wildlife: Should we care?. <i>Science of the Total Environment</i> , 2022, 812, 152324.	3.9	8

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18114	Phylogenomic analysis, reclassification, and evolution of South American nemesioid burrowing mygalomorph spiders. <i>Molecular Phylogenetics and Evolution</i> , 2022, 168, 107377.	1.2	11
18115	Genetic divergence and range expansion in a western North Pacific coral. <i>Science of the Total Environment</i> , 2022, 813, 152423.	3.9	22
18116	Ancestral sequence reconstruction of ancient lipase from family I.3 bacterial lipolytic enzymes. <i>Molecular Phylogenetics and Evolution</i> , 2022, 168, 107381.	1.2	13
18117	Transcriptome analysis reveals infection strategies employed by <i>Fusarium graminearum</i> as a root pathogen. <i>Microbiological Research</i> , 2022, 256, 126951.	2.5	7
18118	Detection and genetic diversity of Mopeia virus in <i>Mastomys natalensis</i> from different habitats in the Limpopo National Park, Mozambique. <i>Infection, Genetics and Evolution</i> , 2022, 98, 105204.	1.0	3
18119	Characterization of the mitochondrial genome of <i>Tetrameres grusi</i> and insights into the phylogeny of Spirurina. <i>International Journal for Parasitology: Parasites and Wildlife</i> , 2022, 17, 35-42.	0.6	4
18120	Scalable Phylogeny Reconstruction with Disaggregated Near-memory Processing. <i>ACM Transactions on Reconfigurable Technology and Systems</i> , 2022, 15, 1-32.	1.9	1
18121	<i>Trema domingensis</i> rises like a Phoenix from the ashes of <i>Trema integerrima</i> : a reassessment of the entire-leaved species of neotropical Tream (Cannabaceae). <i>Journal of the Botanical Research Institute of Texas</i> , 2018, 12, 555-577.	0.0	1
18122	Molecular phylogeny and chromosomal evolution of endemic species of Sri Lankan Anacardiaceae. <i>Journal of the National Science Foundation of Sri Lanka</i> , 2020, 48, 289.	0.1	0
18123	Exploring Modern FPGA Platforms for Faster Phylogeny Reconstruction with RAxML. , 2020, , .		4
18124	Molecular data and updated morphological description of <i>Flabellina rubrolineata</i> (Nudibranchia: Flabellinidae) from the Red and Arabian seas. <i>Ruthenica</i> , 2020, 30, 183-194.	0.2	9
18125	<i>Litoria aplini</i> sp. nov., a new species of treefrog (Pelodyadidae) from Papua New Guinea. <i>Records of the Australian Museum</i> , 2020, 72, 325-337.	0.3	3
18127	First records and a new genus of comb-tailed spiders (Araneae: Hahniidae) from Thailand with comments on the six-eyed species of this family. <i>European Journal of Taxonomy</i> , 0, 724, .	0.6	1
18128	DNA Barcoding and Phylogenetic Placement of the Genus <i>Euphorbia</i> L. (Euphorbiaceae) in Egypt. , 2020, 4, .		2
18129	Revision of the genus <i>Plexaurella</i> KÅlliker, 1865 (Anthozoa: Octocorallia) and resurrection of <i>Plexaurellidae</i> Verrill, 1912 new rank. <i>Invertebrate Systematics</i> , 2021, , .	0.5	1
18130	Gene Regulatory Networks Shape Developmental Plasticity of Root Cell Types Under Water Extremes. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1
18131	Molecular characterization and phylogenetic assessment of agricultural-related noctuids (Lepidoptera: Noctuidae) of South America. <i>Revista Brasileira De Entomologia</i> , 2021, 65, .	0.1	3
18132	Étude g�n�tologique de la diversit� et de lâ€™alimentation de lâ€™hy�ne des cavernes Å partir de coprolithes de six sites du sud de la France. <i>Quaternaire</i> , 2021, , 153-171.	0,1	1

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18133	Revision of <i>Cerinomyces</i> (<i>Dacrymycetes</i> , <i>Basidiomycota</i>) with notes on morphologically and historically related taxa. <i>Studies in Mycology</i> , 2021, 99, 100117-100117.	4.5	6
18134	A phylogenetic overview of the <i>Hydnaceae</i> (<i>Cantharellales</i> , <i>Basidiomycota</i>) with new taxa from China. <i>Studies in Mycology</i> , 2021, 99, 100121-100121.	4.5	22
18135	A panel of diverse <i>Pseudomonas aeruginosa</i> clinical isolates for research and development. <i>JAC-Antimicrobial Resistance</i> , 2021, 3, dlab179.	0.9	13
18136	<i>Bryoerythrophyllum campylocarpum</i> (M&A1/4ll.Hal.) H.A.Crum, a tropical and subtropical moss new to Ireland and Britain. <i>Journal of Bryology</i> , 2021, 43, 321-329.	0.4	2
18137	Morphology and phylogeny of <i>Teratoramularia rumicis</i> a new foliar pathogen of <i>Rumex crispus</i> from India and diversity of Ramularioid complex on <i>Rumex</i> spp.. <i>Phytotaxa</i> , 2021, 523, 208-228.	0.1	1
18138	<i>Rhodobacter amnigenus</i> sp. nov. and <i>Rhodobacter ruber</i> sp. nov., isolated from freshwater habitats. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	8
18139	Complete mitochondrial genomes of two sand diver species (Perciformes, Trichonotidae): novel gene orders and phylogenetic position within Gobiiformes. <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 12-14.	0.2	1
18140	First Comparative Analysis of <i>Clostridium septicum</i> Genomes Provides Insights Into the Taxonomy, Species Genetic Diversity, and Virulence Related to Gas Gangrene. <i>Frontiers in Microbiology</i> , 2021, 12, 771945.	1.5	5
18141	Applicability of several rooted phylogenetic network algorithms for representing the evolutionary history of SARS-CoV-2. <i>Bmc Ecology and Evolution</i> , 2021, 21, 220.	0.7	2
18143	Chromosome-Level Genome Assembly Provides New Insights into Genome Evolution and Tuberos Root Formation of <i>Potentilla anserina</i> . <i>Genes</i> , 2021, 12, 1993.	1.0	8
18145	Mining the Genome of <i>Bacillus velezensis</i> VB7 (CP047587) for MAMP Genes and Non-Ribosomal Peptide Synthetase Gene Clusters Conferring Antiviral and Antifungal Activity. <i>Microorganisms</i> , 2021, 9, 2511.	1.6	22
18146	Genomic insights into the circulation of pandemic fluoroquinolone-resistant extra-intestinal pathogenic <i>Escherichia coli</i> ST1193 in Vietnam. <i>Microbial Genomics</i> , 2021, 7, .	1.0	8
18147	Chromosomal-level genome and multi-omics dataset of <i>Pueraria lobata</i> var. <i>thomsonii</i> provide new insights into legume family and the isoflavone and puerarin biosynthesis pathways. <i>Horticulture Research</i> , 2022, 9, .	2.9	10
18148	Bacterial Biofilm Thickness and Fungal Inhibitory Bacterial Richness Both Prevent Establishment of the Amphibian Fungal Pathogen <i>Batrachochytrium dendrobatidis</i> . <i>Applied and Environmental Microbiology</i> , 2022, 88, AEM0160421.	1.4	7
18149	Genomic and Phenotypic Evolution of Tigecycline-Resistant <i>Acinetobacter baumannii</i> in Critically Ill Patients. <i>Microbiology Spectrum</i> , 2022, 10, e0159321.	1.2	7
18150	Phylogenetics and the evolution of terrestriality in mudskippers (Gobiidae: Oxudercinae). <i>Molecular Phylogenetics and Evolution</i> , 2022, 169, 107416.	1.2	15
18151	<i>Pterocладиella xiae</i> sp. nov. (Gelidiales, Rhodophyta), a new species from southern China. <i>Phycologia</i> , 0, , 1-9.	0.6	1
18152	Chloroplast phylogenomics in <i>Camelina</i> (Brassicaceae) reveals multiple origins of polyploid species and the maternal lineage of <i>C. sativa</i> . <i>Horticulture Research</i> , 2022, 9, .	2.9	14

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18153	Genomic Comparison, Phylogeny and Taxonomic Reevaluation of the Ectothiorhodospiraceae and Description of Halorhodospiraceae fam. nov. and Halochlorospira gen. nov.. <i>Microorganisms</i> , 2022, 10, 295.	1.6	10
18154	Nosocomial Outbreak of Carbapenemase-Producing <i>Proteus mirabilis</i> With Two Novel Salmonella Genomic Island 1 Variants Carrying Different bla _{NDM-1} Gene Copies in China. <i>Frontiers in Microbiology</i> , 2021, 12, 800938.	1.5	5
18155	The genome of low-chill Chinese plum (<i>Prunus salicina</i> Lindl.) provides insights into the regulation of the chilling requirement of flower buds. <i>Molecular Ecology Resources</i> , 2022, 22, 1919-1938.	2.2	11
18156	Whole-genome sequencing elucidates the species-wide diversity and evolution of fungicide resistance in the early blight pathogen <i>Alternaria solani</i> . <i>Evolutionary Applications</i> , 2022, 15, 1605-1620.	1.5	6
18157	World Travelers: Parthenogenesis and Ecological Tolerance Enable Multiple Colonization Events by the Widespread Short-Tailed Whipscorpion, <i>Stenochrus portoricensis</i> (Schizomida: Tj ETQq0 0 0 rgBT /Overdoxk 10 Tf150 577 Td		
18158	Hybridization boosts dispersal of two contrasted ecotypes in a grass species. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2022, 289, 20212491.	1.2	3
18160	Amino Acid Specificity of Ancestral Aminoacyl-tRNA Synthetase Prior to the Last Universal Common Ancestor Commonote commonote. <i>Journal of Molecular Evolution</i> , 2022, 90, 73-94.	0.8	2
18161	Phylogenomic Analysis of the Phylum Nematoda: Conflicts and Congruences With Morphology, 18S rRNA, and Mitogenomes. <i>Frontiers in Ecology and Evolution</i> , 2022, 9, .	1.1	28
18162	Frequencies and characteristics of genome-wide recombination in <i>Streptococcus agalactiae</i> , <i>Streptococcus pyogenes</i> , and <i>Streptococcus suis</i> . <i>Scientific Reports</i> , 2022, 12, 1515.	1.6	5
18163	Pantropical diversification of padauk trees and relatives was influenced by biome-switching and long-distance dispersal. <i>Journal of Biogeography</i> , 0, , .	1.4	4
18164	Comparative Genomics Reveals Evolutionary Drivers of Sessile Life and Left-right Shell Asymmetry in Bivalves. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 1078-1091.	3.0	8
18165	Deleterious Mutations Accumulate Faster in Allopolyploid Than Diploid Cotton (<i>Gossypium</i>) and Unequally between Subgenomes. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	16
18166	The promiscuous and highly mobile resistome of <i>Acinetobacter baumannii</i> . <i>Microbial Genomics</i> , 2022, 8, .	1.0	18
18167	Loss of the IR region in conifer plastomes: Changes in the selection pressure and substitution rate of protein-coding genes. <i>Ecology and Evolution</i> , 2022, 12, e8499.	0.8	4
18168	<i>Leucoagaricus taniae</i> sp. nov. (Agaricaceae), a sand-dwelling mushroom from Brazil. <i>Brittonia</i> , 2022, 74, 18-29.	0.8	1
18169	Development of an Anti- <i>Acinetobacter baumannii</i> Biofilm Phage Cocktail: Genomic Adaptation to the Host. <i>Antimicrobial Agents and Chemotherapy</i> , 2022, 66, AAC0192321.	1.4	12
18170	Phylogeography and population genetics reveal ring species patterns in a highly polymorphic California lily. <i>Journal of Biogeography</i> , 2022, 49, 416-430.	1.4	5
18171	A classification of the aquatic Podostemaceae subfamily Tristichoideae, with a new genus based on <i>ITS</i> and <i>matK</i> phylogeny and morphological characters. <i>Taxon</i> , 2022, 71, 307-320.	0.4	1

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18173	Diversity of cultivable bacteria from deep-sea sediments of the Colombian Caribbean and their potential in bioremediation. <i>Antonie Van Leeuwenhoek</i> , 2022, 115, 421-431.	0.7	7
18174	End-to-end learning of evolutionary models to find coding regions in genome alignments. <i>Bioinformatics</i> , 2022, 38, 1857-1862.	1.8	0
18175	Proteomics, phylogenetics, and coexpression analyses indicate novel interactions in the plastid CLP chaperone-protease system. <i>Journal of Biological Chemistry</i> , 2022, 298, 101609.	1.6	7
18176	Multiple Cases of Bacterial Sequence Erroneously Incorporated Into Publicly Available Chloroplast Genomes. <i>Frontiers in Genetics</i> , 2021, 12, 821715.	1.1	4
18177	Genome-wide insights into adaptive hybridisation across the <i>Schistosoma haematobium</i> group in West and Central Africa. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010088.	1.3	5
18178	Antenna-Biased Odorant Receptor <i>HvarOR25</i> in <i>Hippodamia variegata</i> Tuned to Allelochemicals from Hosts and Habitat Involved in Perceiving Preys. <i>Journal of Agricultural and Food Chemistry</i> , 2022, 70, 1090-1100.	2.4	13
18179	<i>Streptomyces apricus</i> sp. nov., isolated from soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	4
18180	<i>Sphingomonas arenae</i> sp. nov., isolated from desert soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	11
18181	Marine and terrestrial nitrifying bacteria are sources of diverse bacteriohopanepolyols. <i>Geobiology</i> , 2022, 20, 399-420.	1.1	8
18183	Phylogenomics and Fossil Data Inform the Systematics and Geographic Range Evolution of a Diverse Neotropical Ant Lineage. <i>Insect Systematics and Diversity</i> , 2022, 6, .	0.7	8
18184	A New Monotypic Genus from the American Southwest to accommodate <i>Semiothisa ruscuscha</i> (Geometridae: Ennominae). <i>Zootaxa</i> , 2022, 5093, 67-74.	0.2	1
18185	HIV-2/SIV Vpx antagonises NF- κ B activation by targeting p65. <i>Retrovirology</i> , 2022, 19, 2.	0.9	7
18186	DNA barcoding validates new sightings of <i>Tridacna elongatissima</i> in Tanzania and Mozambique (Western Indian Ocean). <i>Coral Reefs</i> , 2022, 41, 837-842.	0.9	1
18187	Synthesis of Nuclear and Chloroplast Data Combined With Network Analyses Supports the Polyploid Origin of the Apple Tribe and the Hybrid Origin of the Maleae "Gillenieae" Clade. <i>Frontiers in Plant Science</i> , 2021, 12, 820997.	1.7	16
18188	Genome biology of the darkedged splitfin, <i>Girardinichthys multiradiatus</i> , and the evolution of sex chromosomes and placentation. <i>Genome Research</i> , 2022, 32, 583-594.	2.4	9
18190	Chromosome-level genome assembly of the shuttles hoptfish, <i>Periophthalmus modestus</i> . <i>GigaScience</i> , 2022, 11, .	3.3	4
18192	CellPhy: accurate and fast probabilistic inference of single-cell phylogenies from scDNA-seq data. <i>Genome Biology</i> , 2022, 23, 37.	3.8	28
18194	<i>Staphylococci</i> . , 2022, , 169-192.		1

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18195	Genomic Analysis and Antimicrobial Resistance of <i>Campylobacter jejuni</i> and <i>Campylobacter coli</i> in Peru. <i>Frontiers in Microbiology</i> , 2021, 12, 802404.	1.5	18
18196	Comparing Partitioned Models to Mixture Models: Do Information Criteria Apply?. <i>Systematic Biology</i> , 2022, 71, 1541-1548.	2.7	11
18197	DNA Barcode of Tilapia Fish Fillet from the Brazilian Market and a Standardized Coi Haplotyping for Molecular Identification of <i>Oreochromis Spp.</i> (Actinopterygii, Cichlidae). <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
18198	Diversity and Phylogeny of Novel Cord-Forming Fungi from Borneo. <i>Microorganisms</i> , 2022, 10, 239.	1.6	0
18199	Anchored phylogenomics and a revised classification of the planidial larva clade of jewel wasps (Hymenoptera: Chalcidoidea). <i>Systematic Entomology</i> , 2022, 47, 329-353.	1.7	9
18200	<i>Thecamoeba vumurta</i> n. sp. (Amoebozoa, Discosea, Thecamoebida) from freshwater pond sediment â€œ a sibling species of <i>T. striata</i> (Penard, 1890) Schaeffer, 1926. <i>European Journal of Protistology</i> , 2022, 83, 125866.	0.5	2
18201	Mitochondrial Genetic Diversity and Structure of the Langur Population in a Complex Landscape of the Nepal Himalaya. <i>Diversity</i> , 2022, 14, 69.	0.7	0
18202	Genetic relatedness and association mapping of horticulturally valuable traits for the <i>Ceiba</i> plants using ddRAD sequencing. <i>Horticultural Plant Journal</i> , 2023, 9, 826-836.	2.3	2
18203	Genomic Characterization of SARS-CoV-2 Isolated from Patients with Distinct Disease Outcomes in Mexico. <i>Microbiology Spectrum</i> , 2022, , e0124921.	1.2	5
18204	The genetic identity of the earliest human-made hybrid animals, the kungas of Syro-Mesopotamia. <i>Science Advances</i> , 2022, 8, eabm0218.	4.7	14
18205	Down, then up: non-parallel genome size changes and a descending chromosome series in a recent radiation of the Australian allotetraploid plant species, <i>Nicotiana</i> section <i>Suaveolentes</i> (Solanaceae). <i>Annals of Botany</i> , 2023, 131, 123-142.	1.4	16
18206	Revision of the coral reef crab genus <i>Tweedieia</i> Ward, 1935 (Decapoda: Brachyura: Xanthidae). <i>Journal of Crustacean Biology</i> , 2022, 42, .	0.3	3
18208	Specificities and Commonalities of Carbapenemase-Producing <i>Escherichia coli</i> Isolated in France from 2012 to 2015. <i>MSystems</i> , 2022, 7, e0116921.	1.7	7
18209	¸Molecular phylogeny and taxonomy of the <i>Hydrangea serrata</i> complex (Hydrangeaceae) in western Japan, including a new subspecies of <i>H. acuminata</i> from Yakushima. <i>PhytoKeys</i> , 2022, 188, 49-71.	0.4	6
18210	Rapid alignment updating with Extensiphy. <i>Methods in Ecology and Evolution</i> , 2022, 13, 682-693.	2.2	0
18212	Comparative genome analysis of plant ascomycete fungal pathogens with different lifestyles reveals distinctive virulence strategies. <i>BMC Genomics</i> , 2022, 23, 34.	1.2	13
18213	Heterogeneous genetic structure in eastern North American peat mosses (<i>Sphagnum</i>). <i>Biological Journal of the Linnean Society</i> , 0, , .	0.7	3
18214	Activity-Based Protein Profiling for the Identification of Novel Carbohydrate-Active Enzymes Involved in Xylan Degradation in the Hyperthermophilic Euryarchaeon <i>Thermococcus</i> sp. Strain 2319x1E. <i>Frontiers in Microbiology</i> , 2021, 12, 734039.	1.5	6

#	ARTICLE	IF	CITATIONS
18215	Phylogenetic relationships of Indian Memecylon L. (Melastomataceae) based on nrDNA ITS and cpDNA rbcL sequence data. Journal of Genetics, 2022, 101, 1.	0.4	0
18216	Lichens from the littoral zone host diverse ulvophycean photobionts. Journal of Phycology, 2022, , .	1.0	3
18217	Global diversity and distribution of aerobic anoxygenic phototrophs in the tropical and subtropical oceans. Environmental Microbiology, 2022, 24, 2222-2238.	1.8	10
18218	Leapfrog dynamics in phage-bacteria coevolution revealed by joint analysis of cross-infection phenotypes and whole genome sequencing. Ecology Letters, 2022, 25, 876-888.	3.0	10
18219	Trypanosomes of the Trypanosoma theileri Group: Phylogeny and New Potential Vectors. Microorganisms, 2022, 10, 294.	1.6	8
18220	Phylotranscriptomics Reveals Discordance in the Phylogeny of Hawaiian <i>Drosophila</i> and <i>Scaptomyza</i> (Diptera: Drosophilidae). Molecular Biology and Evolution, 2022, 39, .	3.5	8
18221	The mitochondrial genome of <i>Chelonus formosanus</i> (Hymenoptera: Braconidae) with novel gene orders and phylogenetic implications. Archives of Insect Biochemistry and Physiology, 2022, , e21870.	0.6	4
18222	Genome-resolved evidence for functionally redundant communities and novel nitrogen fixers in the deyin-1 hydrothermal field, Mid-Atlantic Ridge. Microbiome, 2022, 10, 8.	4.9	5
18223	Prevalence, Antimicrobial Resistance, and Whole Genome Sequencing Analysis of Shiga Toxin-Producing <i>Escherichia coli</i> (STEC) and Enteropathogenic <i>Escherichia coli</i> (EPEC) from Imported Foods in China during 2015-2021. Toxins, 2022, 14, 68.	1.5	10
18224	Chromosome-Level Assembly of the Chinese Hooksnout Carp (<i>Opsariichthys bidens</i>) Genome Using PacBio Sequencing and Hi-C Technology. Frontiers in Genetics, 2021, 12, 788547.	1.1	3
18225	Connection between two historical tuberculosis outbreak sites in Japan, Honshu, by a new ancestral <i>Mycobacterium tuberculosis</i> L2 sublineage. Epidemiology and Infection, 2022, 150, 1-25.	1.0	7
18227	Genomic Analysis Reveals Subdivision of Black Rats (<i>Rattus rattus</i>) in India, Origin of the Worldwide Species Spread. Genes, 2022, 13, 267.	1.0	2
18228	The highly continuous reference genome of a leaf-chimeric red pineapple (<i>Ananas comosus</i> var.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 2022, 12, .	0.8	1
18229	Molecular phylogeny of the subgenus <i>Syrhophus</i> (Amphibia: Anura: Eleutherodactylidae), with the description of a new species from Eastern Mexico. Systematics and Biodiversity, 2022, 20, 1-20.	0.5	6
18231	The complete chloroplast genome sequence and phylogenetic analysis of <i>Nanhaia speciosa</i> (Fabaceae). Mitochondrial DNA Part B: Resources, 2022, 7, 266-268.	0.2	0
18233	Characterization of the complete mitochondrial genome of <i>Haemadipsa tianmushana</i> Song 1977 (Hirudiniformes, Haemadipsidae) and its phylogenetic analysis. Mitochondrial DNA Part B: Resources, 2022, 7, 103-105.	0.2	0
18234	The complete mitochondrial genome of a tropical midge <i>Chironomus kiiensis</i> Tokunaga, 1936 (Diptera: Chironomidae). Mitochondrial DNA Part B: Resources, 2022, 7, 211-212.	0.2	4
18235	Effects of Periodontal Treatment in Patients with Periodontitis and Kidney Failure: A Pilot Study. International Journal of Environmental Research and Public Health, 2022, 19, 1533.	1.2	2

#	ARTICLE	IF	CITATIONS
18236	Phylogenomics of the World's Otters: Evolutionary Insights from Whole-Genome Sequences. SSRN Electronic Journal, 0, , .	0.4	0
18237	Ornithinimicrobium laminariae sp. nov., isolated from the kelp Laminaria japonica. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	6
18238	High-resolution genomic surveillance elucidates a multilayered hierarchical transfer of resistance between WWTP- and human/animal-associated bacteria. Microbiome, 2022, 10, 16.	4.9	18
18239	Genome-wide identification and expression profile of YABBY genes in <i>Averrhoa carambola</i> . PeerJ, 2022, 9, e12558.	0.9	7
18240	Digenean Metacercariae Parasitic in a Staurozoan Cnidarian. Zoological Science, 2022, 39, 215-218.	0.3	2
18241	The Role of Photobionts as Drivers of Diversification in an Island Radiation of Lichen-Forming Fungi. Frontiers in Microbiology, 2021, 12, 784182.	1.5	9
18242	Phylogenetic evidence for an independent origin of extreme sexual size dimorphism in a genus of araneid spiders (Araneae: Araneidae). Invertebrate Systematics, 2022, 36, 48-62.	0.5	3
18243	Phylogeography of ancient and modern brown bears from eastern Eurasia. Biological Journal of the Linnean Society, 2022, 135, 722-733.	0.7	4
18244	How to Tackle Phylogenetic Discordance in Recent and Rapidly Radiating Groups? Developing a Workflow Using Loricaria (Asteraceae) as an Example. Frontiers in Plant Science, 2021, 12, 765719.	1.7	12
18245	Description of a New Species of Sulcospira (Gastropoda: Pachychilidae) From Guangxi, China Based on Morphology and Molecular Evidence. Zoological Science, 2022, 39, 219-224.	0.3	1
18246	NDM-1 carbapenemase resistance gene vehicles emergent on distinct plasmid backbones from the IncL/M family. Journal of Antimicrobial Chemotherapy, 2022, 77, 620-624.	1.3	6
18248	Quantitative Insights into the Contribution of Nematocysts to the Adaptive Success of Cnidarians Based on Proteomic Analysis. Biology, 2022, 11, 91.	1.3	2
18249	Horizontal and vertical distribution of Gambierdiscus spp. (Dinophyceae) including novel phylotypes in Japan identified by 18S rDNA metabarcoding. Harmful Algae, 2022, 111, 102163.	2.2	7
18250	Placing Ancient DNA Sequences into Reference Phylogenies. Molecular Biology and Evolution, 2022, 39, .	3.5	23
18251	Large-scale WGS of carbapenem-resistant <i>Acinetobacter baumannii</i> isolates reveals patterns of dissemination of ST clades associated with antibiotic resistance. Journal of Antimicrobial Chemotherapy, 2022, 77, 934-943.	1.3	5
18252	Sulfuriroseicoccus oceanibius gen. nov., sp. nov., a representative of the phylum Verrucomicrobia with a special cytoplasmic membrane. Antonie Van Leeuwenhoek, 2022, 115, 337-352.	0.7	0
18254	Updating species diversity of <i>Colletotrichum</i> , with a phylogenomic overview. Studies in Mycology, 2022, 101, 1-56.	4.5	71
18255	A new species of the genus <i>Coryphella</i> (Gastropoda: Nudibranchia) from the Kuril Islands. Ruthenica, 2022, 32, 41-48.	0.2	2

#	ARTICLE	IF	CITATIONS
18256	Comparative Genomics of <i>Pseudomonas stutzeri</i> Complex: Taxonomic Assignments and Genetic Diversity. <i>Frontiers in Microbiology</i> , 2021, 12, 755874.	1.5	6
18257	The skull of <i>Sanajeh indicus</i> , a Cretaceous snake with an upper temporal bar, and the origin of ophidian wide-gaped feeding. <i>Zoological Journal of the Linnean Society</i> , 2023, 197, 656-697.	1.0	6
18258	Comparative genomics reveals electron transfer and syntrophic mechanisms differentiating methanotrophic and methanogenic archaea. <i>PLoS Biology</i> , 2022, 20, e3001508.	2.6	62
18260	DNA Methylation in <i>Ensifer</i> Species during Free-Living Growth and during Nitrogen-Fixing Symbiosis with <i>Medicago</i> spp.. <i>MSystems</i> , 2022, 7, e0109221.	1.7	7
18261	Hyphal compartmentalization and sporulation in <i>Streptomyces</i> require the conserved cell division protein SepX. <i>Nature Communications</i> , 2022, 13, 71.	5.8	9
18262	A scaffold-level genome assembly of a minute pirate bug, <i>Orius laevigatus</i> (Hemiptera: Anthocoridae), and a comparative analysis of insecticide resistance-related gene families with hemipteran crop pests. <i>BMC Genomics</i> , 2022, 23, 45.	1.2	14
18263	A global phylogeny of the deep-sea gastropod family Scaphandridae (Heterobranchia: Cephalaspidea): Redefinition and generic classification. <i>Molecular Phylogenetics and Evolution</i> , 2022, 169, 107415.	1.2	1
18264	A Pre-Vaccination Baseline of SARS-CoV-2 Genetic Surveillance and Diversity in the United States. <i>Viruses</i> , 2022, 14, 104.	1.5	1
18265	<i>Gracilaria parva</i> sp. nov. (Gracilariales, Rhodophyta) a Diminutive Species from the Tropical Eastern Pacific. <i>Taxonomy</i> , 2022, 2, 48-56.	0.4	1
18266	Complete Chloroplast Genome Sequence of <i>Fagus longipetiolata</i> Seemen (Fagaceae): Genome Structure, Adaptive Evolution, and Phylogenetic Relationships. <i>Life</i> , 2022, 12, 92.	1.1	15
18267	Whole genome sequence of bacteremic <i>Clostridium tertium</i> in a World War I soldier, 1914. <i>Current Research in Microbial Sciences</i> , 2022, 3, 100089.	1.4	2
18269	Taxonomy and phylogeny of the novel rhytidhysterion-like collections in the Greater Mekong Subregion. <i>Mycology</i> , 2022, 86, 65-85.	0.8	8
18270	Combined data analysis of fossil and living mammals: a Paleogene sister taxon of Placentalia and the antiquity of Marsupialia. <i>Cladistics</i> , 2022, 38, 359-373.	1.5	10
18271	A description of <i>Dendronotus shpataki</i> sp. nov. (Gastropoda: Nudibranchia) from the Sea of Japan: a contribution of citizen science to marine zoology. <i>Zoosystematica Rossica</i> , 2022, 31, 3-19.	0.2	0
18272	When the tail shakes the snake: phylogenetic affinities and morphology of <i>Atractus badius</i> (Serpentes). <i>Revista Colombiana de Ciencias</i> , 2022, 94, e20191254.	0.3	4
18273	Wheat stem rust recorded for the first time in decades in Ireland. <i>Plant Pathology</i> , 2022, 71, 890-900.	1.2	7
18274	Phenolic degradation by catechol dioxygenases is associated with pathogenic fungi with a necrotrophic lifestyle in the Ceratocystidaceae. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	2
18275	A Superior Contiguous Whole Genome Assembly for Shrimp (<i>Penaeus indicus</i>). <i>Frontiers in Marine Science</i> , 2022, 8, .	1.2	6

#	ARTICLE	IF	CITATIONS
18277	Discovery of <i>Kerivoula kachinensis</i> and a validity of <i>K.Âtitania</i> (Chiroptera): Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 742 Td (V	0.3	2
18278	The phylogeny of <i>Salix</i> revealed by whole genome re-sequencing suggests different sex-determination systems in major groups of the genus. <i>Annals of Botany</i> , 2022, 129, 485-498.	1.4	15
18281	Overview of the Americasâ€™ First Peopling from a Patrilineal Perspective: New Evidence from the Southern Continent. <i>Genes</i> , 2022, 13, 220.	1.0	5
18282	Interplay between <i>Klebsiella pneumoniae</i> producing KPC-31 and KPC-3 under treatment with high dosage meropenem: a case report. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2022, 41, 495-500.	1.3	10
18283	Replication initiator proteins of <i>Acinetobacter baumannii</i> plasmids: An update note. <i>Plasmid</i> , 2022, 119-120, 102616.	0.4	6
18284	Assessment of marine benthic diatom communities: insights from a combined morphologicalâ€™ metabarcoding approach in Mediterranean shallow coastal waters. <i>Marine Pollution Bulletin</i> , 2022, 174, 113183.	2.3	13
18285	A new subgenus of <i>Epeorus</i> and its five species from China (Ephemeroptera: Heptageniidae). <i>Insect Systematics and Evolution</i> , 2022, -1, 1-40.	0.2	2
18286	Generic revision of the species formerly belonging to the genus <i>Carangoides</i> and its related genera (Carangiformes: Carangidae). <i>Ichthyological Research</i> , 2022, 69, 433-487.	0.5	4
18287	â€™Spider Monkey Cottonâ€™ Bridging Waiwai and Scientific Ontologies to Characterize Spider Monkey (<i>Ateles paniscus</i>) Filariasis in the Konashen Community Owned Conservation Area, Guyana. <i>International Journal of Primatology</i> , 2022, 43, 253-272.	0.9	7
18288	Patterns and Predictors of Small Mammal Phylogenetic and Functional Diversity in Contrasting Elevational Gradients in Kenya. <i>Frontiers in Ecology and Evolution</i> , 2022, 9, .	1.1	5
18289	DNA barcoding and morphological identification of spiny lobsters in South Korean waters: a new record of <i>Panulirus longipes</i> and <i>Panulirus homarus homarus</i> . <i>PeerJ</i> , 2022, 10, e12744.	0.9	2
18290	Microbiome analyses of 12 psyllid species of the family Psyllidae identified various bacteria including <i>Fukatsuia</i> and <i>Serratia symbiotica</i> , known as secondary symbionts of aphids. <i>BMC Microbiology</i> , 2022, 22, 15.	1.3	17
18291	Rodents of the Afar Triangle (Ethiopia): geographical isolation causes high level of endemism. <i>Biodiversity and Conservation</i> , 2022, 31, 629-650.	1.2	7
18293	Southeast Asian Dipterocarp origin and diversification driven by Africa-India floristic interchange. <i>Science</i> , 2022, 375, 455-460.	6.0	27
18294	Methylphosphonate Degradation and Salt-Tolerance Genes of Two Novel Halophilic <i>Marivita</i> Metagenome-Assembled Genomes from Unrestored Solar Salterns. <i>Genes</i> , 2022, 13, 148.	1.0	4
18295	A Metagenomics Investigation of Intergenerational Effects of Non-nutritive Sweeteners on Gut Microbiome. <i>Frontiers in Nutrition</i> , 2021, 8, 795848.	1.6	13
18296	Hyper-aerotolerant <i>Campylobacter coli</i> , an emerging foodborne pathogen, shows differential expressions of oxidative stress-related genes. <i>Veterinary Microbiology</i> , 2022, 264, 109308.	0.8	1
18298	A well-supported nuclear phylogeny of Poaceae and implications for the evolution of C4 photosynthesis. <i>Molecular Plant</i> , 2022, 15, 755-777.	3.9	47

#	ARTICLE	IF	CITATIONS
18300	A new species of <i>Auriculostoma</i> (Digenea: Allocreadiidae) in South America: life cycle and phylogenetic relationships. <i>Anais Da Academia Brasileira De Ciencias</i> , 2022, 94, e20200538.	0.3	2
18303	Genome of the parasitoid wasp <i>Dinocampus coccinellae</i> reveals extensive duplications, accelerated evolution, and independent origins of thelytokous parthenogeny and solitary behavior. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	4
18304	Loss of phylogenetic diversity under landscape change. <i>Science of the Total Environment</i> , 2022, 822, 153595.	3.9	2
18305	Systematics of Afrotropical <i>Eristalinae</i> (Diptera: Syrphidae) using mitochondrial phylogenomics. <i>Systematic Entomology</i> , 0, , .	1.7	4
18307	The Diesel Tree <i>Sindora glabra</i> Genome Provides Insights Into the Evolution of Oleoresin Biosynthesis. <i>Frontiers in Plant Science</i> , 2021, 12, 794830.	1.7	0
18308	Traits and phylogenies modulate the environmental responses of wood-inhabiting fungal communities across spatial scales. <i>Journal of Ecology</i> , 2022, 110, 784-798.	1.9	5
18309	Characterization of <i>Fusarium nirenbergiae</i> and <i>F. elaeidis</i> causing diseases on <i>Dipladenia</i> and <i>Grevillea</i> plants. <i>European Journal of Plant Pathology</i> , 2022, 162, 885-896.	0.8	4
18310	Multilocus sequence based identification and adaptational strategies of <i>Pseudomonas</i> sp. from the supraglacial site of Sikkim Himalaya. <i>PLoS ONE</i> , 2022, 17, e0261178.	1.1	7
18311	No link between population isolation and speciation rate in squamate reptiles. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	13
18312	Improved 93-11 Genome and Time-Course Transcriptome Expand Resources for Rice Genomics. <i>Frontiers in Plant Science</i> , 2021, 12, 769700.	1.7	4
18313	Taxonomic Review of the Genus <i>Herpetoreas</i> (Serpentes: Natricidae), with the Description of a New Species from Tibet, China. <i>Diversity</i> , 2022, 14, 79.	0.7	7
18314	<i>Balamuthia spinosa</i> n. sp. (Amoebozoa, Discosea) from the brackish-water sediments of NivÅ¥ Bay (Baltic) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 Research, 2022, 121, 713-724.	0.6	3
18315	Three new species of <i>Helicometroides</i> Yamaguti, 1934 from Japan and Australia, with new molecular evidence of a widespread species. <i>Parasitology</i> , 2022, , 1-18.	0.7	3
18316	New considerations of the systematics of the family Holophryidae (Protozoa, Ciliophora,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 <i>Pelagothrix plancticola</i>. <i>Systematics and Biodiversity</i> , 2022, 20, 1-15.	0.5	5
18317	The reference genome of <i>Camellia chekiangoleosa</i> provides insights into <i>Camellia</i> evolution and tea oil biosynthesis. <i>Horticulture Research</i> , 2022, 9, .	2.9	30
18318	Description of <i>Tubulanus misakiensis</i> sp. nov. (Nemertea: Palaeonemertea) from Sagami Bay, Japan. <i>Zoological Science</i> , 2022, 39, 81-86.	0.3	1
18319	A New Species of Acoela Possessing a Middorsal Appendage with a Possible Sensory Function. <i>Zoological Science</i> , 2022, 39, 147-156.	0.3	2
18320	The complete chloroplast genome sequence of chaya (<i>Cnidoscolus aconitifolius</i>) and phylogenetic analysis. <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 269-270.	0.2	0

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18321	The complete chloroplast genome sequence of <i>Begonia gulongshanensis</i> (Begoniaceae). Mitochondrial DNA Part B: Resources, 2022, 7, 191-193.	0.2	2
18322	Basic chloroplast genome characterization of <i>Phalaenopsis stobartiana</i> (Orchidaceae) from China. Mitochondrial DNA Part B: Resources, 2022, 7, 257-258.	0.2	2
18323	The complete chloroplast genome of <i>Rubus setchuenensis</i> , an edible and medicinal dual-purpose wild plant. Mitochondrial DNA Part B: Resources, 2022, 7, 228-230.	0.2	2
18324	Molecular characterisation and updated description of <i>Neoechinorhynchus aldrichettae</i> Edmonds, 1971 (Acanthocephala: Neoechinorhynchidae), based on material from <i>Aldrichetta forsteri</i> (Valenciennes) collected in Tasmania, Australia. Systematic Parasitology, 2022, 99, 241.	0.5	2
18325	Two novel species of <i>Arthroderma</i> isolated from domestic cats with dermatophytosis in the United States. Medical Mycology, 2022, 60, .	0.3	3
18326	Insights into the geographical origin and phylogeographical patterns of <i>Paradisaea</i> birds-of-paradise. Zoological Journal of the Linnean Society, 2022, 196, 1394-1407.	1.0	1
18327	Organelle Phylogenomics and Extensive Conflicting Phylogenetic Signals in the Monocot Order Poales. Frontiers in Plant Science, 2021, 12, 824672.	1.7	9
18328	A chromosome-level genome assembly of an alpine plant <i>Crucihimalaya lasiocarpa</i> provides insights into high-altitude adaptation. DNA Research, 2022, 29, .	1.5	13
18329	The Caspase Homologues in Scallop <i>Chlamys farreri</i> and Their Expression Responses to Toxic Dinoflagellates Exposure. Toxins, 2022, 14, 108.	1.5	3
18330	Mutations that adapt SARS-CoV-2 to mink or ferret do not increase fitness in the human airway. Cell Reports, 2022, 38, 110344.	2.9	46
18332	A description of <i>Dendronotus shpataki</i> sp. nov. (Gastropoda: Nudibranchia) from the Sea of Japan: a contribution of citizen science to marine zoology. Zoosystematica Rossica, 2022, 31, 3-19.	0.2	1
18333	Diversification of tiny toads (Bufonidae: <i>Amazophrynella</i>) sheds light on ancient landscape dynamism in Amazonia. Biological Journal of the Linnean Society, 2022, 136, 75-91.	0.7	9
18334	<i>Lacydonia shohoensis</i> (Annelida, Lacydoniidae) sp. nov. – a new lacydonid species from deep-sea sunken wood discovered at the Nishi-Shichito Ridge, North-western Pacific Ocean. Journal of the Marine Biological Association of the United Kingdom, 0, , 1-7.	0.4	1
18336	Evolution of two-component quorum sensing systems. Access Microbiology, 2022, 4, 000303.	0.2	6
18337	Site-and-branch-heterogeneous analyses of an expanded dataset favour mitochondria as sister to known Alphaproteobacteria. Nature Ecology and Evolution, 2022, 6, 253-262.	3.4	48
18338	Mitogenomic phylogeny resolves <i>Cuneopsis</i> (Bivalvia: Unionidae) as polyphyletic: The description of two new genera and a new species. Zoologica Scripta, 2022, 51, 173-184.	0.7	8
18339	<i>Merodon chalybeus</i> Subgroup: An Additional Piece of the <i>M. aureus</i> Group (Diptera, Syrphidae) Puzzle. Annales Zoologici Fennici, 2022, 59, .	0.2	3
18340	A new red alga from Japan, <i>Dasya japonovillosa</i> sp. nov. (Delesseriaceae, Ceramiales). Phycological Research, 2022, 70, 118-128.	0.8	4

#	ARTICLE	IF	CITATIONS
18341	Chloroplast Genome Evolution in Four Montane Zingiberaceae Taxa in China. <i>Frontiers in Plant Science</i> , 2021, 12, 774482.	1.7	16
18342	Description of two new bird species from the Meratus Mountains of southeast Borneo, Indonesia. <i>Journal of Ornithology</i> , 2022, 163, 575-588.	0.5	2
18343	Tissue specific expression of UMAMIT amino acid transporters in wheat. <i>Scientific Reports</i> , 2022, 12, 348.	1.6	4
18344	Isolation and Characterization of Lignocellulose-Degrading <i>Geobacillus thermoleovorans</i> from Yellowstone National Park. <i>Applied and Environmental Microbiology</i> , 2022, 88, AEM0095821.	1.4	2
18346	Phylotranscriptomics of Theaceae: generic-level relationships, reticulation and whole-genome duplication. <i>Annals of Botany</i> , 2022, 129, 457-471.	1.4	23
18347	RNA Virosphere in a Marine Zooplankton Community in the Subtropical Western North Pacific. <i>Microbes and Environments</i> , 2022, 37, n/a.	0.7	3
18348	High prevalence of <i>Paramarteilia canceri</i> infecting velvet swimming crabs <i>Necora puber</i> in Ireland. <i>Diseases of Aquatic Organisms</i> , 2022, 148, 167-181.	0.5	3
18349	Development and evaluation of a meat mitochondrial metagenomic (3MG) method for composition determination of meat from fifteen mammalian and avian species. <i>BMC Genomics</i> , 2022, 23, 36.	1.2	4
18350	Archaeal and Bacterial Metagenome-Assembled Genome Sequences Derived from Pig Feces. <i>Microbiology Resource Announcements</i> , 2022, 11, e0114221.	0.3	6
18351	The PIWI/piRNA response is relaxed in a rodent that lacks mobilizing transposable elements. <i>Rna</i> , 2022, 28, 609-621.	1.6	3
18352	Comparative Genomics of <i>Clostridium baratii</i> Reveals Strain-Level Diversity in Toxin Abundance. <i>Microorganisms</i> , 2022, 10, 213.	1.6	6
18353	Reappraisal of the Genus <i>Exsudoporus</i> (Boletaceae) Worldwide Based on Multi-Gene Phylogeny, Morphology and Biogeography, and Insights on <i>Amoenoboletus</i> . <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 101.	1.5	5
18354	Negevirus isolated from mosquitoes in the Brazilian Amazon. <i>Virology Journal</i> , 2022, 19, 17.	1.4	4
18355	Drainage rearrangements and in situ diversification of an endemic freshwater fish genus from northeastern Brazilian rivers. <i>Freshwater Biology</i> , 2022, 67, 759-773.	1.2	7
18356	Development of a Genomics-Based Approach To Identify Putative Hypervirulent Nontyphoidal <i>Salmonella</i> Isolates: <i>Salmonella enterica</i> Serovar Saintpaul as a Model. <i>MSphere</i> , 2022, 7, e0073021.	1.3	5
18357	Complete chloroplast genomes of <i>Rubus</i> species (Rosaceae) and comparative analysis within the genus. <i>BMC Genomics</i> , 2022, 23, 32.	1.2	17
18358	The complete mitochondrial genome of <i>Hymenopus coronatus</i> (Mantodea: Hymenopodidae) from Xishuangbanna, China. <i>International Journal of Transgender Health</i> , 2022, 15, 50-53.	1.1	1
18359	Deep distributed computing to reconstruct extremely large lineage trees. <i>Nature Biotechnology</i> , 2022, 40, 566-575.	9.4	14

#	ARTICLE	IF	CITATIONS
18382	Complete chloroplast genome of <i>Geum aleppicum</i> (Rosaceae). Mitochondrial DNA Part B: Resources, 2022, 7, 234-235.	0.2	4
18383	Complete chloroplast genome of <i>Baccaurea ramiflora</i> and its phylogenetic analysis. Mitochondrial DNA Part B: Resources, 2022, 7, 206-207.	0.2	1
18384	Evidence for niche conservatism in alpine beetles under a climate-driven species pump model. Journal of Biogeography, 2022, 49, 364-377.	1.4	9
18385	Exploring the diversity of andean berries from northern Peru based on molecular analyses. Heliyon, 2022, 8, e08839.	1.4	2
18386	Biogeographical Importance of the Livingstone Mountains in Southern Tanzania: Comparative Genetic Structure of Small Non-volant Mammals. Frontiers in Ecology and Evolution, 2022, 9, .	1.1	8
18387	Beyond RuBisCO: convergent molecular evolution of multiple chloroplast genes in C_4 plants. PeerJ, 2022, 10, e12791.	0.9	2
18388	Molecular barcoding reveals unexpected diversity in eastern North American stitchworts (Caryophyllaceae). Botanical Journal of the Linnean Society, 2022, 200, 75-84.	0.8	2
18389	Speciation process on Brazilian continental islands, with the description of a new insular lancehead of the genus <i>Bothrops</i> (Serpentes, Viperidae). Systematics and Biodiversity, 2022, 20, 1-25.	0.5	7
18390	Two New Amanita Species in Section Amanita from Thailand. Diversity, 2022, 14, 101.	0.7	5
18391	Between a Rock and a Hard Polytoxy: Phylogenomics of the Rock-Dwelling Mbuna Cichlids of Lake Malawi. Systematic Biology, 2022, 71, 741-757.	2.7	17
18392	Balancing Selection of the Intracellular Pathogen Response in Natural <i>Caenorhabditis elegans</i> Populations. Frontiers in Cellular and Infection Microbiology, 2021, 11, 758331.	1.8	7
18393	Environmental identification of arbuscular mycorrhizal fungi using the LSU rDNA gene region: an expanded database and improved pipeline. Mycorrhiza, 2022, 32, 145-153.	1.3	16
18394	Vps501, a novel vacuolar SNX-BAR protein cooperates with the SEA complex to regulate TORC1 signaling. Traffic, 2022, , .	1.3	3
18396	The molecular phylogenetic position of <i>Mariplanella piscadera</i> sp. nov. reveals a new major group of rhabdocoel flatworms: Mariplanellida status novus (Platyhelminthes: Rhabdocoela). Organisms Diversity and Evolution, 2022, 22, 577-584.	0.7	4
18397	Five New Species of the Lichen-Forming Fungal Genus <i>Peltula</i> from China. Journal of Fungi (Basel), 2022, 8, 1010.	1.5	3
18399	Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa. Nature, 2022, 603, 679-686.	13.7	1,210
18400	Genome Sequencing of a Gray Wolf from Peninsular India Provides New Insights into the Evolution and Hybridization of Gray Wolves. Genome Biology and Evolution, 2022, 14, .	1.1	5
18401	A Broad Survey of Gene Body and Repeat Methylation in Cnidaria Reveals a Complex Evolutionary History. Genome Biology and Evolution, 2022, 14, .	1.1	1

#	ARTICLE	IF	CITATIONS
18402	Sal-type ABC-F proteins: intrinsic and common mediators of pleuromutilin resistance by target protection in staphylococci. <i>Nucleic Acids Research</i> , 2022, 50, 2128-2142.	6.5	16
18403	Whole-genome sequencing of Kaposi sarcoma-associated herpesvirus (KSHV/HHV8) reveals evidence for two African lineages. <i>Virology</i> , 2022, 568, 101-114.	1.1	6
18404	Integrated Analysis of Transcriptome and Proteome to Reveal Pupal Color Switch in <i>Papilio xuthus</i> Butterflies. <i>Frontiers in Genetics</i> , 2021, 12, 795115.	1.1	1
18405	Machinery and Developmental Role of Retinoic Acid Signaling in Echinoderms. <i>Cells</i> , 2022, 11, 523.	1.8	3
18406	Panoramic Insights into Microevolution and Macroevolution of A <i>Prevotella copri</i> -containing Lineage in Primate Guts. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 334-349.	3.0	3
18407	Gut microbiome of the largest living rodent harbors unprecedented enzymatic systems to degrade plant polysaccharides. <i>Nature Communications</i> , 2022, 13, 629.	5.8	26
18408	Taxonomy and Phylogeny of Novel and Extant Taxa in Pleosporales Associated with <i>Mangifera indica</i> from Yunnan, China (Series I). <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 152.	1.5	12
18409	Hammerhead flatworms (Platyhelminthes, Geoplanidae, Bipaliinae): mitochondrial genomes and description of two new species from France, Italy, and Mayotte. <i>PeerJ</i> , 2022, 10, e12725.	0.9	10
18410	A robust approach to estimate relative phytoplankton cell abundances from metagenomes. <i>Molecular Ecology Resources</i> , 2023, 23, 16-40.	2.2	29
18411	The Vampyrellid Amoebae (Vampyrellida, Rhizaria). <i>Protist</i> , 2022, 173, 125854.	0.6	20
18412	The interplay between community and hospital <i>Enterococcus faecium</i> clones within health-care settings: a genomic analysis. <i>Lancet Microbe, The</i> , 2022, 3, e133-e141.	3.4	17
18413	Large-Scale Phylogenetic Analysis Reveals a New Genetic Clade among <i>Escherichia coli</i> O26 Strains. <i>Microbiology Spectrum</i> , 2022, 10, e0252521.	1.2	1
18414	Ecological traits drive genetic structuring in two open-habitat birds from the morphologically cryptic genus <i>Elaenia</i> (Aves: Tyrannidae). <i>Journal of Avian Biology</i> , 2022, 2022, .	0.6	1
18416	Morphogenesis and molecular phylogeny of a freshwater ciliate, <i>Oxytricha multilineata</i> n. sp. (Ciliophora, Hypotrichia). <i>European Journal of Protistology</i> , 2022, 82, 125864.	0.5	5
18417	Isolated by dry lands: integrative analyses unveil the existence of a new species and a previously unknown evolutionary lineage of Brazilian Lanceheads (Serpentes: Viperidae: <i>Bothrops</i>) from a Caatinga moist-forest enclave. <i>Canadian Journal of Zoology</i> , 2022, 100, 147-159.	0.4	4
18418	Large dataset of octocoral mitochondrial genomes provides new insights into mt-mutS evolution and function. <i>DNA Repair</i> , 2022, 110, 103273.	1.3	16
18419	Differential Response of Bacterial Microdiversity to Simulated Global Change. <i>Applied and Environmental Microbiology</i> , 2022, 88, aem0242921.	1.4	7
18420	Functionally characterized arthropod pest and pollinator cytochrome P450s associated with xenobiotic metabolism. <i>Pesticide Biochemistry and Physiology</i> , 2022, 181, 105005.	1.6	18

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18421	Ancient introgression underlying the unusual mitochondrial nuclear discordance and coat phenotypic variation in the Moupin pika. <i>Diversity and Distributions</i> , 2022, 28, 2593-2609.	1.9	4
18422	Evolutionary characteristics and immune mutation of hepatitis C virus genotype 1b among intravenous drug users in mainland, China. <i>Journal of Viral Hepatitis</i> , 2022, , .	1.0	0
18423	Molecular evolution of hatching enzymes and their paralogous genes in vertebrates. <i>Bmc Ecology and Evolution</i> , 2022, 22, 9.	0.7	4
18424	The complete chloroplast genome sequence of <i>Ligularia stenocephala</i> (Maxim.) Matsum. & Koidz. (Asteraceae: Senecioneae). <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 336-338.	0.2	0
18425	Phylogeny, Age, and Evolution of Tribe Lilieae (Liliaceae) Based on Whole Plastid Genomes. <i>Frontiers in Plant Science</i> , 2021, 12, 699226.	1.7	10
18426	Dissemination Routes of Carbapenem and Pan-Aminoglycoside Resistance Mechanisms in Hospital and Urban Wastewater Canalizations of Ghana. <i>MSystems</i> , 2022, 7, e0101921.	1.7	7
18427	Detection and population genetic analysis of kdr L1014F variant in eastern Ethiopian <i>Anopheles stephensi</i> . <i>Infection, Genetics and Evolution</i> , 2022, 99, 105235.	1.0	5
18428	<i>Phytophthora</i> species associated with red alder dieback in British Columbia, Canada. <i>Canadian Journal of Plant Pathology</i> , 2022, 44, 549-558.	0.8	2
18429	Species delimitation and mitonuclear discordance within a species complex of biting midges. <i>Scientific Reports</i> , 2022, 12, 1730.	1.6	14
18430	<i>Buxus</i> and Tetracentron genomes help resolve eudicot genome history. <i>Nature Communications</i> , 2022, 13, 643.	5.8	24
18432	Evolving in the darkness: Phylogenomics of <i>Sinocyclocheilus</i> cavefishes highlights recent diversification and cryptic diversity. <i>Molecular Phylogenetics and Evolution</i> , 2022, 168, 107400.	1.2	12
18433	Conflicting nuclear and mitogenome phylogenies reveal ancient mitochondrial replacement between two North American species of collared lemmings (<i>Dicrostonyx groenlandicus</i> , <i>D. hudsonius</i>). <i>Molecular Phylogenetics and Evolution</i> , 2022, 168, 107399.	1.2	4
18434	Phylotranscriptomics reveals the evolutionary history of subtropical East Asian white pines: further insights into gymnosperm diversification. <i>Molecular Phylogenetics and Evolution</i> , 2022, 168, 107403.	1.2	12
18435	From continental Asia into the world: Global historical biogeography of the saltbush genus <i>Atriplex</i> (Chenopodieae, Chenopodioideae, Amaranthaceae). <i>Perspectives in Plant Ecology, Evolution and Systematics</i> , 2022, 54, 125660.	1.1	13
18436	Phylogenomic classification and synteny network analyses deciphered the evolutionary landscape of aldo-keto reductase (AKR) gene superfamily in the plant kingdom. <i>Gene</i> , 2022, 816, 146169.	1.0	4
18437	Genetic diversity, gene flow and hybridization in fan-shaped sponges (<i>Phakellia</i> spp.) in the North-East Atlantic deep sea. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2022, 181, 103685.	0.6	6
18438	Two new pseudocryptic species in the medium-sized common European land snails, <i>Fruticicola</i> Held, 1838; as a result of phylogeographic analysis of <i>Fruticicola fruticum</i> (O. F. Müller, 1774) (Gastropoda: Tj ETQq0 D rgBT /overlock 1		
18439	Gene duplication and rate variation in the evolution of plastid ACCase and Clp genes in angiosperms. <i>Molecular Phylogenetics and Evolution</i> , 2022, 168, 107395.	1.2	2

#	ARTICLE	IF	CITATIONS
18440	Plastid phylogenomics of the Sansevieria Clade of Dracaena (Asparagaceae) resolves a recent radiation. <i>Molecular Phylogenetics and Evolution</i> , 2022, 169, 107404.	1.2	4
18441	Escovopsioides nivea is a non-specific antagonistic symbiont of ant-fungal crops. <i>Fungal Ecology</i> , 2022, 56, 101140.	0.7	1
18442	Deciphering phylogenetic relationships in class Karyorelictea (Protista, Ciliophora) based on updated multi-gene information with establishment of a new order Wilbertomorphida n. ord.. <i>Molecular Phylogenetics and Evolution</i> , 2022, 169, 107406.	1.2	12
18443	Morphological and molecular reinvestigation of acanthoecid species I. "Enibas urnula (Thomsen,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 125865.	0.5	5
18444	Historical biogeographical analysis of the Udoteaceae (Bryopsidales, Chlorophyta) elucidates origins of high species diversity in the Central Indo-Pacific, Western Indian Ocean and Greater Caribbean regions. <i>Molecular Phylogenetics and Evolution</i> , 2022, 169, 107412.	1.2	1
18445	Molecular characterization of Dipetalonema yatesi from the black-faced spider monkey (Ateles) Tj ETQq1 1 0.784314 rgBT /Overlock 10 International Journal for Parasitology: Parasites and Wildlife, 2022, 17, 152-157.	0.6	4
18446	Polyphyly, asexual reproduction and dual trophic mode in Buchwaldoboletus. <i>Fungal Ecology</i> , 2022, 56, 101141.	0.7	3
18447	Phylogeny and secondary sexual trait evolution in Schizocosa wolf spiders (Araneae, Lycosidae) shows evidence for multiple gains and losses of ornamentation and species delimitation uncertainty. <i>Molecular Phylogenetics and Evolution</i> , 2022, 169, 107397.	1.2	8
18448	Rickettsia spp. in ticks from a tropical dry forest reserve on Mexico's Pacific Coast. <i>Ticks and Tick-borne Diseases</i> , 2022, 13, 101911.	1.1	3
18449	Origin and evolutionary analysis of the SARS-CoV-2 Omicron variant. <i>Journal of Biosafety and Biosecurity</i> , 2022, 4, 33-37.	1.4	75
18450	Champagne: Automated Whole-Genome Phylogenomic Character Matrix Method Using Large Genomic Indels for Homoplasy-Free Inference. <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	3
18451	Biological Classification. , 2024, , 579-593.		0
18452	Characterization and Phylogenetic Analysis of the Complete Chloroplast Genome of Xanthopappus subcaulis (Asteraceae), an Endemic Species from the Qinghai-Tibet Plateau in China. <i>Cytology and Genetics</i> , 2022, 56, 77-83.	0.2	0
18453	Analyzing Phylogenetic Trees with a Tree Lattice Coordinate System and a Graph Polynomial. <i>Systematic Biology</i> , 2022, 71, 1378-1390.	2.7	7
18454	Chromosome-Level Genome Assemblies of Two Hypnales (Mosses) Reveal High Intergeneric Synteny. <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	11
18455	KaruBioNet: a network and discussion group for a better collaboration and structuring of bioinformatics in Guadeloupe (French West Indies). <i>Bioinformatics Advances</i> , 2022, 2, .	0.9	7
18456	OUP accepted manuscript. <i>DNA Research</i> , 2022, , .	1.5	4
18457	New information about the toxicological profile of <sc><i>Prorocentrum panamense</i></sc> (<sc>Prorocentrales</sc>, <sc>Dinophyceae</sc>) and its global distribution. <i>Phycological Research</i> , 2022, 70, 81-88.	0.8	1

#	ARTICLE	IF	CITATIONS
18458	Exceptional evolutionary lability of flower-like inflorescences (pseudanthia) in Apiaceae subfamily Apioideae. <i>American Journal of Botany</i> , 2022, , .	0.8	6
18459	Genomic insights into the evolution of <i>Echinochloa</i> species as weed and orphan crop. <i>Nature Communications</i> , 2022, 13, 689.	5.8	26
18460	Morphology and phylogeny of two anaerobic freshwater ciliates: <i>Brachonella comma</i> sp. nov. and the widely distributed but little-known caenomorphid, <i>Ludio parvulus</i> Penard, 1922. <i>Journal of Eukaryotic Microbiology</i> , 2022, 69, e12892.	0.8	4
18461	Diversity of <i>Fusarium</i> associated banana wilt in northern Viet Nam. <i>MycKeys</i> , 2022, 87, 53-76.	0.8	4
18462	Exploration of Diverse Secondary Metabolites From <i>Streptomyces</i> sp. YINM00001, Using Genome Mining and One Strain Many Compounds Approach. <i>Frontiers in Microbiology</i> , 2022, 13, 831174.	1.5	10
18463	The Carbon Footprint of Bioinformatics. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	29
18464	A transcriptomic reevaluation of the accessory olfactory organ in Bichir (<i>Polypterus senegalus</i>). <i>Zoological Letters</i> , 2022, 8, 5.	0.7	2
18465	Overlooked and widespread pennate diatom-diazotroph symbioses in the sea. <i>Nature Communications</i> , 2022, 13, 799.	5.8	26
18466	The distinction between <i>Sagina apetala</i> and <i>S. micropetala</i> (Caryophyllaceae: Sagineae), their phylogenetic relationships, and a note on the coastal origin of some widespread ruderals. <i>Willdenowia</i> , 2022, 52, .	0.5	1
18467	Complete mitochondrial genomes of three fairy shrimps from snowmelt pools in Japan. <i>BMC Zoology</i> , 2022, 7, .	0.3	3
18468	Sonogenetic control of mammalian cells using exogenous Transient Receptor Potential A1 channels. <i>Nature Communications</i> , 2022, 13, 600.	5.8	53
18469	Population genetics, demographic and evolutionary history of the Dudley's lousewort (<i>Pedicularis</i>) Tj ETQq1 1 0,784314 gBT / Overl	0.8	1
18471	Distribution of membrane trafficking system components across ciliate diversity highlights heterogenous <i>organelle-associated</i> machinery. <i>Traffic</i> , 2022, , .	1.3	6
18472	Phylogenomics and biogeography of <i>Torreya</i> (Taxaceae) Integrating data from three organelle genomes, morphology, and fossils and a practical method for reducing missing data from RADseq. <i>Journal of Systematics and Evolution</i> , 2022, 60, 1241-1262.	1.6	7
18473	Target sequence capture of Barnadesioideae (Compositae) demonstrates the utility of low coverage loci in phylogenomic analyses. <i>Molecular Phylogenetics and Evolution</i> , 2022, 169, 107432.	1.2	9
18474	Seasonal abundance of stem-boring insects associated with the invasive <i>Senecio madagascariensis</i> in its native range (KwaZulu-Natal, South Africa) and their potential for biological control. <i>Biocontrol Science and Technology</i> , 0, , 1-17.	0.5	3
18475	Genomic Analysis of <i>Stropharia rugosoannulata</i> Reveals Its Nutritional Strategy and Application Potential in Bioremediation. <i>Journal of Fungi</i> (Basel, Switzerland), 2022, 8, 162.	1.5	5
18476	A 638-gene phylogeny supports the recognition of twice as many species in the Malagasy endemic genus <i>Capurodendron</i> (Sapotaceae). <i>Taxon</i> , 2022, 71, 360-395.	0.4	6

#	ARTICLE	IF	CITATIONS
18477	Molecular phylogeny of the threadfin fishes (Polynemidae) using ultraconserved elements. <i>Journal of Fish Biology</i> , 2022, 100, 793-810.	0.7	5
18478	Adaptive evolution of major histocompatibility complex class I immune genes and disease associations in coastal juvenile sea turtles. <i>Royal Society Open Science</i> , 2022, 9, 211190.	1.1	8
18479	Comparative Analysis of the Complete Chloroplast Genomes of Nine Paphiopedilum Species. <i>Frontiers in Genetics</i> , 2021, 12, 772415.	1.1	10
18480	Biochemical and functional characterization of a thermostable RecJ exonuclease from <i>Thermococcus gammatolerans</i> . <i>International Journal of Biological Macromolecules</i> , 2022, 204, 617-626.	3.6	3
18482	Comparison of Genetic Features and Evolution of Global and Chinese Strains of Community-Associated Methicillin-Resistant <i>Staphylococcus aureus</i> ST22. <i>Microbiology Spectrum</i> , 2022, 10, e0203721.	1.2	15
18484	Endogenous CRISPR-Cas Systems in Group I <i>Clostridium botulinum</i> and <i>Clostridium sporogenes</i> Do Not Directly Target the Botulinum Neurotoxin Gene Cluster. <i>Frontiers in Microbiology</i> , 2021, 12, 787726.	1.5	8
18485	Out of the shadows: Multilocus systematics and biogeography of night monkeys suggest a Central Amazonian origin and a very recent widespread southeastward expansion in South America. <i>Molecular Phylogenetics and Evolution</i> , 2022, 170, 107426.	1.2	4
18486	Transmission dynamics of low pathogenicity avian influenza (H2N2) viruses in live bird markets of the Northeast United States of America, 2013–2019. <i>Virus Evolution</i> , 2022, 8, veac009.	2.2	2
18487	Evidence that nuclear receptors are related to terpene synthases. <i>Journal of Molecular Endocrinology</i> , 2022, 68, 153-166.	1.1	0
18488	Effect of pneumococcal conjugate vaccine availability on <i>Streptococcus pneumoniae</i> infections and genetic recombination in Zhejiang, China from 2009 to 2019. <i>Emerging Microbes and Infections</i> , 2022, 11, 606-615.	3.0	7
18489	Reaching the Monophyly: Re-Evaluation of the Enigmatic Species <i>Tenuibiotus hyperonyx</i> (Maucci, 1983) and the Genus <i>Tenuibiotus</i> (Eutardigrada). <i>Animals</i> , 2022, 12, 404.	1.0	8
18490	The genome of the rice variety LTH provides insight into its universal susceptibility mechanism to worldwide rice blast fungal strains. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 1012-1026.	1.9	16
18491	Accessory Genome Dynamics of Local and Global <i>Staphylococcus pseudintermedius</i> Populations. <i>Frontiers in Microbiology</i> , 2022, 13, 798175.	1.5	7
18492	Diversity and Ecological Guild Analysis of the Oil Palm Fungal Microbiome Across Root, Rhizosphere, and Soil Compartments. <i>Frontiers in Microbiology</i> , 2022, 13, 792928.	1.5	7
18493	A large accessory genome and high recombination rates may influence global distribution and broad host range of the fungal plant pathogen <i>Claviceps purpurea</i> . <i>PLoS ONE</i> , 2022, 17, e0263496.	1.1	8
18494	Evolution of Guanylate Binding Protein (GBP) Genes in Muroid Rodents (Muridae and Cricetidae) Reveals an Outstanding Pattern of Gain and Loss. <i>Frontiers in Immunology</i> , 2022, 13, 752186.	2.2	7
18495	A new species of <i>Sabuloglossum</i> (Geoglossaceae, Ascomycota) from montane areas. <i>Plant Biosystems</i> , 0, 1-11.	0.8	0
18496	RF-Net 2: fast inference of virus reassortment and hybridization networks. <i>Bioinformatics</i> , 2022, 38, 2144-2152.	1.8	5

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18497	Complete Genome Sequencing and Comparative Analysis of the Clinically-Derived <i>Apiotrichum</i> mycotoxinivorans Strain GMU1709. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 834015.	1.8	3
18498	Mega-fire in redwood tanoak forest reduces bacterial and fungal richness and selects for pyrophilous taxa that are phylogenetically conserved. <i>Molecular Ecology</i> , 2022, 31, 2475-2493.	2.0	19
18500	When Morphology and Biogeography Approximate Nuclear ITS but Conflict with Plastid Phylogeny: Phylogeography of the <i>Lotus dorycnium</i> Species Complex (Leguminosae). <i>Plants</i> , 2022, 11, 410.	1.6	1
18501	Genome-wide data reveal paraphyly in the sand plover complex (<i>Charadrius</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50.622 Td (m	0.7	5
18502	The complete chloroplast genome sequence of <i>Opuntia sulphurea</i> (Cactaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 361-362.	0.2	2
18503	Chemosensory Receptors in the Larval Maxilla of <i>Papilio hospiton</i> . <i>Frontiers in Ecology and Evolution</i> , 2022, 9, .	1.1	6
18504	The complete chloroplast genome of <i>Ficus pumila</i> , a functional plant in East Asia. <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 326-327.	0.2	2
18505	A high-quality functional genome assembly of <i>Delia radicum</i> L. (Diptera: Anthomyiidae) annotated from egg to adult. <i>Molecular Ecology Resources</i> , 2022, 22, 1954-1971.	2.2	6
18507	Comparative genomics and phylogenetic perspectives of six fertile <i>Lycoris</i> species endemic to East Asia based on plastome characterization. <i>Nordic Journal of Botany</i> , 2022, 2022, .	0.2	5
18508	The complete chloroplast genome of <i>Hylotelephium erythrostictum</i> (Miq.) H. Ohba (Crassulaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 365-366.	0.2	2
18509	Molecular identification and post-prandial regulation of glucose carrier proteins in the hindgut of Pacific hagfish, <i>Eptatretus stoutii</i> . <i>American Journal of Physiology - Regulatory Integrative and Comparative Physiology</i> , 2022, , .	0.9	1
18511	<i>Pythium</i> and <i>Phytopythium</i> species associated with weeds collected in vegetable production fields in Brazil. <i>Letters in Applied Microbiology</i> , 2022, 74, 796-808.	1.0	4
18513	Taxonomic reevaluation of the Japanese <i>Marchantia</i> taxa belonging to sect. <i>Papillatae</i> of subg. <i>Chlamidium</i> (Marchantiaceae). <i>Bryologist</i> , 2022, 125, .	0.1	5
18514	Freshwater Microbial Eukaryotic Core Communities, Open-Water and Under-Ice Specialists in Southern Victoria Island Lakes (Ekaluktutiak, NU, Canada). <i>Frontiers in Microbiology</i> , 2021, 12, 786094.	1.5	3
18515	<i>Lactobacillus huangpiensis</i> sp. nov. and <i>Lactobacillus laiwuensis</i> sp. nov., isolated from the gut of honeybee (<i>Apis mellifera</i>). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	11
18516	A highly virulent variant of HIV-1 circulating in the Netherlands. <i>Science</i> , 2022, 375, 540-545.	6.0	39
18517	Using Ultraconserved Elements to Unravel Lagomorph Phylogenetic Relationships. <i>Journal of Mammalian Evolution</i> , 2022, 29, 395-411.	1.0	7
18520	Detection and diversity of the mannosylerythritol lipid (MEL) gene cluster and lipase A and B genes of <i>Moesziomyces antarcticus</i> isolated from terrestrial sites chronically contaminated with crude oil in Trinidad. <i>BMC Microbiology</i> , 2022, 22, 43.	1.3	4

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18521	ACE2 binding is an ancestral and evolvable trait of sarbecoviruses. <i>Nature</i> , 2022, 603, 913-918.	13.7	109
18523	Phylogenomics and Biogeography of <i>Populus</i> Based on Comprehensive Sampling Reveal Deep-Level Relationships and Multiple Intercontinental Dispersals. <i>Frontiers in Plant Science</i> , 2022, 13, 813177.	1.7	11
18524	A bacterial endosymbiont of the fungus <i>Rhizopus microsporus</i> drives phagocyte evasion and opportunistic virulence. <i>Current Biology</i> , 2022, 32, 1115-1130.e6.	1.8	22
18525	<i>Sciaromiopsis sinensis</i> (Amblystegiaceae), revised to a member of <i>Brachythecium</i> (Brachytheciaceae). <i>Bryologist</i> , 2022, 125, .	0.1	0
18526	Landscape Genetics and Species Delimitation in the Andean Palm Rocket Frog (<i>Aromobatidae</i>), Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 58.	0.6	0
18527	A Burst of Numt Insertion in the Dasyuridae Family During Marsupial Evolution. <i>Frontiers in Ecology and Evolution</i> , 2022, 10, .	1.1	6
18529	A curated dataset of peste des petits ruminants virus sequences for molecular epidemiological analyses. <i>PLoS ONE</i> , 2022, 17, e0263616.	1.1	5
18530	Phylogenetics of global <i>Camellia</i> (<i>Theaceae</i>) based on three nuclear regions and its implications for systematics and evolutionary history. <i>Journal of Systematics and Evolution</i> , 2023, 61, 356-368.	1.6	12
18532	A Case Study of the Morphological and Molecular Variation within a Ciliate Genus: Taxonomic Descriptions of Three <i>Dysteria</i> Species (<i>Ciliophora</i> , <i>Cyrtophoria</i>), with the Establishment of a New Species. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1764.	1.8	3
18533	Genomic insights into the evolution of the critically endangered soft-shelled turtle <i>Rafetus swinhoei</i> . <i>Molecular Ecology Resources</i> , 2022, 22, 1972-1985.	2.2	9
18534	Differential gene expression associated with a floral scent polymorphism in the evening primrose <i>Oenothera harringtonii</i> (<i>Onagraceae</i>). <i>BMC Genomics</i> , 2022, 23, 124.	1.2	2
18535	Volcanic events coincide with plant dispersal across the Northern Andes. <i>Global and Planetary Change</i> , 2022, 210, 103757.	1.6	5
18536	Human-induced loss of functional and phylogenetic diversity is mediated by concomitant deterministic processes in subtropical aquatic insect communities. <i>Ecological Indicators</i> , 2022, 136, 108600.	2.6	7
18537	Out of the Himalaya-Hengduan Mountains: Phylogenomics, biogeography and diversification of <i>Polygonatum</i> Mill. (<i>Asparagaceae</i>) in the Northern Hemisphere. <i>Molecular Phylogenetics and Evolution</i> , 2022, 169, 107431.	1.2	28
18539	<i>Alteriqingyuania abyssalis</i> sp. nov., a Novel Member of the Class Alphaproteobacteria Isolated from Sponge, and Emended Description of the Genus <i>Alteriqingyuania</i> . <i>Diversity</i> , 2021, 13, 670.	0.7	11
18540	Reinvestigating the phylogeny of Myriapoda with more extensive taxon sampling and novel genetic perspective. <i>PeerJ</i> , 2021, 9, e12691.	0.9	3
18541	Molecular Analysis Reveals a High Diversity of Anopheline Mosquitoes in Yanomami Lands and the Pantanal Region of Brazil. <i>Genes</i> , 2021, 12, 1995.	1.0	2
18542	The evolutionary history of <i>Shigella flexneri</i> serotype 6 in Asia. <i>Microbial Genomics</i> , 2021, 7, .	1.0	3

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18543	Genomic Analysis of 18th-Century Kazakh Individuals and Their Oral Microbiome. <i>Biology</i> , 2021, 10, 1324.	1.3	2
18544	ï»¿A new combination in <i>Pseudolappula</i> (Boraginaceae, Rochelieae) based on morphological, molecular and palynological evidence. <i>PhytoKeys</i> , 2021, 187, 77-92.	0.4	1
18545	Exploring the multifunctionality of SR proteins. <i>Biochemical Society Transactions</i> , 2022, 50, 187-198.	1.6	15
18546	Toward quantifying the adaptive role of bacterial pangenomes during environmental perturbations. <i>ISME Journal</i> , 2022, 16, 1222-1234.	4.4	13
18547	The emergence, genomic diversity and global spread of SARS-CoV-2. <i>Nature</i> , 2021, 600, 408-418.	13.7	249
18548	Fast and accurate metagenotyping of the human gut microbiome with GT-Pro. <i>Nature Biotechnology</i> , 2022, 40, 507-516.	9.4	18
18549	Convergent evolution of bacterial ceramide synthesis. <i>Nature Chemical Biology</i> , 2022, 18, 305-312.	3.9	36
18550	Comparative Population Genomics of Cryptic Speciation and Adaptive Divergence in Bicknellâ€™s and Gray-Cheeked Thrushes (<i>Aves</i> : <i>Catharus bicknelli</i> and <i>Catharus minimus</i>). <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	7
18551	Evolution of Olfactory Receptors Tuned to Mustard Oils in Herbivorous Drosophilidae. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	18
18552	Introduction and adaptation of an emerging pathogen to olive trees in Italy. <i>Microbial Genomics</i> , 2021, 7, .	1.0	14
18554	Drivers of neutral and adaptive differentiation in pike (<i>Esox lucius</i>) populations from contrasting environments. <i>Molecular Ecology</i> , 2022, 31, 1093-1110.	2.0	15
18555	End of a mystery: Integrative approach reveals the phylogenetic position of an enigmatic Antarctic tardigrade genus <i>Ramajendas</i> (Tardigrada, Eutardigrada). <i>Zoologica Scripta</i> , 2022, 51, 217-231.	0.7	5
18556	Genetic diversity of <i>Anopheles stephensi</i> in Ethiopia provides insight into patterns of spread. <i>Parasites and Vectors</i> , 2021, 14, 602.	1.0	18
18557	Long-term adaptation following influenza A virus host shifts results in increased within-host viral fitness due to higher replication rates, broader dissemination within the respiratory epithelium and reduced tissue damage. <i>PLoS Pathogens</i> , 2021, 17, e1010174.	2.1	7
18558	Pandoraâ€™s Box in the Deep Sea â€“ Intraspecific Diversity Patterns and Distribution of Two Congeneric Scavenging Amphipods. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	11
18559	<i>Amycolatopsis aidingensis</i> sp. nov., a Halotolerant Actinobacterium, Produces New Secondary Metabolites. <i>Frontiers in Microbiology</i> , 2021, 12, 743116.	1.5	11
18560	Lateral Transmission of Yeast Symbionts Among Lucanid Beetle Taxa. <i>Frontiers in Microbiology</i> , 2021, 12, 794904.	1.5	3
18561	Multilocus Phylogeography of the <i>Tuber mesentericum</i> Complex Unearths Three Highly Divergent Cryptic Species. <i>Journal of Fungi</i> (Basel, Switzerland), 2021, 7, 1090.	1.5	1

#	ARTICLE	IF	CITATIONS
18562	Molecular analysis reveals <i>Latonius planus</i> Kononova to be a derived species of <i>Trissolcus</i> Ashmead. <i>Journal of Hymenoptera Research</i> , 0, 87, 267-289.	0.8	2
18563	A new subspecies of <i>Stellaria alsine</i> (Caryophyllaceae) from Yakushima, Japan. <i>PhytoKeys</i> , 2021, 187, 177-188.	0.4	6
18564	Species recognition in social amoebae. <i>Journal of Biosciences</i> , 2018, 43, 1025-1036.	0.5	2
18565	Integrative taxonomy of commercially important deep water penaeoid shrimps from India. <i>Journal of Genetics</i> , 2019, 98, .	0.4	0
18566	Characterization of the complete chloroplast genome of , a desert shrub. <i>Journal of Genetics</i> , 2019, 98, .	0.4	4
18567	Mitogenome analysis of dwarf pufferfish () endemic to southwest India and its implications in the phylogeny of Tetraodontidae. <i>Journal of Genetics</i> , 2019, 98, .	0.4	0
18568	Complete plastid genome of <i>L.</i> (Surianaceae) and its implications in phylogenetic reconstruction of Fabales. <i>Journal of Genetics</i> , 2019, 98, .	0.4	0
18569	Global phylogeny and taxonomic reassessment of the lichen genus <i>Dendrioscicta</i> (Ascomycota: Peltigerales). <i>Taxon</i> , 2022, 71, 256-287.	0.4	3
18570	Redescription of Two Free-Swimming Peritrichs, <i>Hastatella</i> and <i>Hastatella</i> ; <i>Hastatella</i> and <i>Hastatella</i> (Ciliophora, Peritrichia), With Note on the Phylogeny of the Genus <i>Hastatella</i> . <i>SSRN Electronic Journal</i> , 0, .	0.4	0
18571	Phylogenetic relationships of the zokor genus <i>Eospalax</i> (Mammalia, Rodentia.) <i>Tj ETQq1 1 0.784314 rgBT /Overlock</i> <i>Zoological Research</i> , 2022, 43, 331-342.	0.9	7
18572	A phylogenetic assessment of <i>Endocalyx</i> (Cainiaceae, Xylariales) with <i>E. grossus</i> comb. et stat. nov.. <i>Mycological Progress</i> , 2022, 21, 221-242.	0.5	4
18573	Phylogenetic position of the deep-sea snail family Haloceratidae and new insights into caenogastropod relationships. <i>Journal of Molluscan Studies</i> , 2022, 88, .	0.4	5
18574	Chromosome-level genome assembly, annotation, and phylogenomics of the gooseneck barnacle <i>Pollicipes pollicipes</i> . <i>GigaScience</i> , 2022, 11, .	3.3	8
18576	Generic boundaries in the <i>Ophiostomatales</i> reconsidered and revised. <i>Studies in Mycology</i> , 2022, 101, 57-120.	4.5	33
18577	Convergence and vicariance: speciation of chameleons in the Cape Fold Mountains, South Africa, and the description of three new species of <i>Bradypodion</i> Fitzinger, 1843. <i>African Journal of Herpetology</i> , 2022, 71, 14-38.	0.3	7
18578	DNA barcode reveals candidate species of <i>Scinax</i> and <i>Ololygon</i> (Anura: Hylidae) in Atlantic Forest. <i>Genetics and Molecular Biology</i> , 2022, 45, e20210177.	0.6	2
18579	Macrofungal conservation in Canada and target species for assessment: a starting point. <i>Facets</i> , 2022, 7, 448-463.	1.1	2
18580	Richness of <i>Cladosporium</i> in a tropical bat cave with the description of two new species. <i>Mycological Progress</i> , 2022, 21, 345-357.	0.5	13

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18581	High-quality reference genomes of swallowtail butterflies provide insights into their coloration evolution. <i>Zoological Research</i> , 2022, 43, 367-379.	0.9	6
18582	Diversity of Growth Patterns in the Alphaproteobacteria. , 2022, , 185-220.		1
18583	New species and new records of <i>Peltula</i> (Lichinales, Ascomycota lichenized) from Mato Grosso do Sul, Brazil. <i>Rodriguesia</i> , 0, 73, .	0.9	0
18584	<i>Calonectria</i> species, including four novel taxa, associated with Eucalyptus in Malaysia. <i>Mycological Progress</i> , 2022, 21, 181-197.	0.5	11
18585	Chromosome-level genome of the globe skimmer dragonfly (<i>Pantala flavescens</i>). <i>GigaScience</i> , 2022, 11, .	3.3	9
18586	Taming the beast: a revised classification of Cortinariaceae based on genomic data. <i>Fungal Diversity</i> , 2022, 112, 89-170.	4.7	24
18587	Fungal diversity in the tropics: <i>Entoloma</i> spp. in Panama. <i>Mycological Progress</i> , 2022, 21, 93-145.	0.5	2
18588	Morpho-molecular characterization of <i>Brunneofissuraceae</i> fam. nov., <i>Cirsosia mangiferae</i> sp. nov., and <i>Asterina neomangiferae</i> nom. nov. <i>Mycological Progress</i> , 2022, 21, 279-295.	0.5	1
18590	Geography-Dependent Horizontal Gene Transfer from Vertebrate Predators to Their Prey. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	7
18592	<i>Wenhuisporus taiwanensis</i> gen. et sp. nov., a peculiar setose hyphomycete from submerged wood in Taiwan. <i>Mycological Progress</i> , 2022, 21, 409-426.	0.5	1
18593	<i>Aleurodiscus bicornis</i> and <i>A. formosanus</i> spp. nov. (Basidiomycota) with smooth basidiospores, and redescription of <i>A. parvisporus</i> . <i>Mycological Progress</i> , 2022, 21, 147-157.	0.5	2
18594	<i>Seimatosporium marivanicum</i> , <i>Sporocadus kurdistanicus</i> , and <i>Xenoseimatosporium kurdistanicum</i> : three new pestalotioid species associated with grapevine trunk diseases from the Kurdistan Province, Iran. <i>Mycological Progress</i> , 2022, 21, 427-446.	0.5	4
18595	The emergence and transmission dynamics of HIV-1 CRF07_BC in Mainland China. <i>Virus Evolution</i> , 2022, 8, veac014.	2.2	5
18596	A worldwide key to species of <i>Carbacanthographis</i> (<i>Graphidaceae</i>), with 17 species new to science. <i>Lichenologist</i> , 2022, 54, 45-70.	0.5	6
18597	Population structure of bla _{KPC} -harbouring IncN plasmids at a New York City medical centre and evidence for multi-species horizontal transmission. <i>Journal of Antimicrobial Chemotherapy</i> , 2022, 77, 1873-1882.	1.3	7
18598	Co-Infection of Peruvian Horse Sickness Virus and West Nile Virus Associated with Neurological Diseases in Horses from Brazil. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
18599	Fungi Are What They Secrete: Evolution of Zygomycete Secretomes and the Origins of Terrestrial Fungal Ecologies. <i>SSRN Electronic Journal</i> , 0, , .	0.4	4
18600	<i>Ormyrus labotus</i> (Hymenoptera: Ormyridae): Another Generalist That Should not be a Generalist is not a Generalist. <i>Insect Systematics and Diversity</i> , 2022, 6, .	0.7	7

#	ARTICLE	IF	CITATIONS
18601	Comparative mitochondrial genome analyses reveal conserved gene arrangement but massive expansion/contraction in two closely related Exserohilum pathogens. Computational and Structural Biotechnology Journal, 2022, 20, 1456-1469.	1.9	4
18602	First molecular phylogeny and species delimitation of West Palaearctic <i>Pollenia</i> (Diptera: Tj ETQq1 1 0.784314 rgBT /Overlock 10 TF	1.0	5
18603	The monophyly of Crenuchinae and description of two new species of <i>Poecilocharax</i> (Teleostei: Tj ETQq0 0 0 rgBT /Overlock 10 TF 2023, 197, 442-473.	1.0	1
18604	Prevalence of carbapenem resistance and its potential association with antimicrobial use in humans and animals in rural communities in Vietnam. JAC-Antimicrobial Resistance, 2022, 4, dlac038.	0.9	5
18606	<i>Umbilicaria meizospora</i> comb. nov., a south-western European endemic species of the subgenus <i>Papillophora</i> . Lichenologist, 2022, 54, 1-12.	0.5	1
18607	Extensive Diversity and Prevalent Fluconazole Resistance among Environmental Yeasts from Tropical China. Genes, 2022, 13, 444.	1.0	5
18608	A New Approach Using Targeted Sequence Capture for Phylogenomic Studies across Cactaceae. Genes, 2022, 13, 350.	1.0	13
18609	<i>Pacificimonas pallium</i> sp. nov., an Isolated Bacterium from the Mantle of Pacific Oyster <i>Crassostrea gigas</i> in Germany, and Prediction of One-Carbon Metabolism. Diversity, 2022, 14, 181.	0.7	7
18610	Convergent consequences of parthenogenesis on stick insect genomes. Science Advances, 2022, 8, eabg3842.	4.7	27
18611	The Peptide Hormone CNMa Influences Egg Production in the Mosquito <i>Aedes aegypti</i> . Insects, 2022, 13, 230.	1.0	3
18612	Supergene origin and maintenance in Atlantic cod. Nature Ecology and Evolution, 2022, 6, 469-481.	3.4	46
18613	The complete chloroplast genome of <i>Caroxylon passerinum</i> (Chenopodiaceae), an annual desert plant. Mitochondrial DNA Part B: Resources, 2022, 7, 426-427.	0.2	0
18614	Comparative Analysis and Phylogenetic Relationships of <i>Ceriops</i> Species (Rhizophoraceae) and <i>Avicennia lanata</i> (Acanthaceae): Insight into the Chloroplast Genome Evolution between Middle and Seaward Zones of Mangrove Forests. Biology, 2022, 11, 383.	1.3	10
18615	DNA Barcoding of Invertebrates Inhabiting Olive Orchards and Vineyards Accelerates Understudied Mediterranean Biodiversity Assessment. Diversity, 2022, 14, 182.	0.7	4
18616	Transcriptomes across fertilization and seed development in the water lily <i>Nymphaea thermarum</i> (Nymphaeales): evidence for epigenetic patterning during reproduction. Plant Reproduction, 2022, 35, 161-178.	1.3	3
18617	Genome of the Rio Pearlfish (<i>Nematolebias whitei</i>), a bi-annual killifish model for Eco-Evo-Devo in extreme environments. G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	6
18618	The complete chloroplast genome of <i>Rubus lambertianus</i> var. <i>paykouangensis</i> , an edible wild plant. Mitochondrial DNA Part B: Resources, 2022, 7, 414-416.	0.2	0
18620	Wolbachia in <i>Aedes koreicus</i> : Rare Detections and Possible Implications. Insects, 2022, 13, 216.	1.0	8

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18622	Two new <i>Russula</i> species (fungi) from dry dipterocarp forest in Thailand suggest niche specialization to this habitat type. <i>Scientific Reports</i> , 2022, 12, 2826.	1.6	5
18623	First report of any species of the red algal order Nemaliales from mainland Ecuador: <i>Neoizziella asiatica</i> (Liagoraceae, Rhodophyta). <i>Botanica Marina</i> , 2022, 65, 135-139.	0.6	0
18625	Effects of synthetic nitrification inhibitor (3,4-dimethylpyrazole phosphate; DMPP) and biological nitrification inhibitor (methyl 3-(4-hydroxyphenyl) propionate; MHPP) on the gross N nitrification rate and ammonia oxidizers in two contrasting soils. <i>Biology and Fertility of Soils</i> , 2022, 58, 333-344.	2.3	15
18626	Diversifying of Two <i>Pampus</i> Species across the Indo-Pacific Barrier and the Origin of the Genus. <i>Diversity</i> , 2022, 14, 180.	0.7	1
18628	Episodes of Diversification and Isolation in Island Southeast Asian and Near Oceanian Male Lineages. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	9
18629	Population genomics of <i>Bacillus anthracis</i> from an anthrax hyperendemic area reveals transmission processes across spatial scales and unexpected within-host diversity. <i>Microbial Genomics</i> , 2022, 8, .	1.0	5
18630	Chloroplast genome structure and phylogenetic position of <i>Syringodium isoetifolium</i> (Asch.) Dandy. <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 370-371.	0.2	0
18631	Circulation, genomic characteristics, and evolutionary dynamics of class I Newcastle disease virus in China. <i>Virulence</i> , 2022, 13, 414-427.	1.8	4
18632	Catabolic protein degradation in marine sediments confined to distinct archaea. <i>ISME Journal</i> , 2022, 16, 1617-1626.	4.4	12
18633	IMA Genome - F16. <i>IMA Fungus</i> , 2022, 13, 3.	1.7	4
18634	Pelagic larval polyclads that practice macrophagous carnivory. <i>Invertebrate Biology</i> , 2022, 141, .	0.3	2
18635	Molecular characterization and expression profiling of <i>transformer 2</i> and <i>fruitless</i> -like homologs in the black tiger shrimp, <i>Penaeus monodon</i> . <i>PeerJ</i> , 2022, 10, e12980.	0.9	2
18636	Transcription Factors Evolve Faster Than Their Structural Gene Targets in the Flavonoid Pigment Pathway. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	23
18637	Does monitoring of saproxylic beetles benefit from inclusion of larvae?. <i>Insect Conservation and Diversity</i> , 2022, 15, 555-571.	1.4	3
18638	The genome of the forest insect pest <i>Pissodes strobi</i> reveals genome expansion and evidence of a <i>Wolbachia</i> endosymbiont. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	4
18639	Comparative mitogenomic analysis of two earwigs (Insecta, Dermaptera) and the preliminary phylogenetic implications. <i>ZooKeys</i> , 2022, 1087, 105-122.	0.5	3
18640	Phylogenomic discordance suggests polytomies along the backbone of the large genus <i>Solanum</i> . <i>American Journal of Botany</i> , 2022, 109, 580-601.	0.8	36
18642	Leg length and bristle density, both necessary for water surface locomotion, are genetically correlated in water striders. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	2

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18643	Niche partitioning of the ubiquitous and ecologically relevant NS5 marine group. ISME Journal, 2022, 16, 1570-1582.	4.4	11
18644	Toll-Like Receptor Evolution: Does Temperature Matter?. Frontiers in Immunology, 2022, 13, 812890.	2.2	9
18646	<i>Thermus brevis</i> sp. nov., a moderately thermophilic bacterium isolated from a hot spring microbial mat. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	7
18648	The complete chloroplast genome of <i>Rubus ellipticus</i> var. <i>obcordatus</i> , an edible and medicinal dual-purpose plant. Mitochondrial DNA Part B: Resources, 2022, 7, 406-408.	0.2	1
18649	Antimicrobial Susceptibility, Virulence, and Genomic Features of a Hypervirulent Serotype K2, ST65 <i>Klebsiella pneumoniae</i> Causing Meningitis in Italy. Antibiotics, 2022, 11, 261.	1.5	8
18650	Distinct Expansion of Group II Introns During Evolution of Prokaryotes and Possible Factors Involved in Its Regulation. Frontiers in Microbiology, 2022, 13, 849080.	1.5	4
18651	Diversity of Endophytes in the Botryosphaeriaceae Differs on Anacardiaceae in Disturbed and Undisturbed Ecosystems in South Africa. Forests, 2022, 13, 341.	0.9	1
18652	Neotropical Studies on Hymenochaetaceae: Unveiling the Diversity and Endemicity of Phellinotus. Journal of Fungi (Basel, Switzerland), 2022, 8, 216.	1.5	1
18653	Rapid SARS-CoV-2 Intra-Host and Within-Household Emergence of Novel Haplotypes. Viruses, 2022, 14, 399.	1.5	5
18654	Reconstruction of Nitrogenase Predecessors Suggests Origin from Maturase-Like Proteins. Genome Biology and Evolution, 2022, 14, .	1.1	12
18656	Phylogenetic analysis of forkhead transcription factors in the Panarthropoda. Development Genes and Evolution, 2022, 232, 39-48.	0.4	4
18657	The complete mitochondrial genome of <i>Linnemannia amoeboidea</i> (W. Gams) Vandepol & Bonito (<i>Mortierellales</i> : <i>Mortierellaceae</i>). Mitochondrial DNA Part B: Resources, 2022, 7, 374-376.	0.2	3
18658	Host ecology regulates interspecies recombination in bacteria of the genus <i>Campylobacter</i> . ELife, 2022, 11, .	2.8	17
18659	Vegetation of the supralittoral and upper sublittoral zones of the Western German Baltic Sea coast: a phytosociological study. Botanica Marina, 2022, 65, 121-133.	0.6	2
18660	Genomic variation from an extinct species is retained in the extant radiation following speciation reversal. Nature Ecology and Evolution, 2022, 6, 461-468.	3.4	12
18661	The complete mitochondrial genome sequence of <i>Clam</i> (<i>Corbicula fluminea</i>). F1000Research, 0, 11, 226.	0.8	0
18662	The complete chloroplast genome of the Chinese banyan tree <i>Ficus microcarpa</i> . Mitochondrial DNA Part B: Resources, 2022, 7, 423-425.	0.2	1
18663	Characterizations of an Emerging Disease: Apple Blotch Caused by <i>Diplocarpon coronariae</i> (syn.) Tj ETQq1 1_0,784314 rgBT / Ove	0.7	8

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18664	Diversification of the orchid genus <i>Tridactyle</i> : Origin of endemism on the oceanic islands of São Tomé & Príncipe in the Gulf of Guinea. <i>Journal of Biogeography</i> , 2022, 49, 523-536.	1.4	1
18665	Librator: a platform for the optimized analysis, design, and expression of mutable influenza viral antigens. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	2
18666	The phylogeographic history of <i>Megistostegium</i> (Malvaceae) in the dry, spiny thickets of southwestern Madagascar using RADseq data and ecological niche modeling. <i>Ecology and Evolution</i> , 2022, 12, e8632.	0.8	3
18667	Protease activities of vaginal <i>Porphyromonas</i> species disrupt coagulation and extracellular matrix in the cervicovaginal niche. <i>Npj Biofilms and Microbiomes</i> , 2022, 8, 8.	2.9	10
18668	Chromosome-level genome assembly of a xerophytic plant, <i>Haloxylon ammodendron</i> . <i>DNA Research</i> , 2022, 29, .	1.5	15
18669	Application of Matrix-Assisted Laser Desorption/Ionization Time-of-Flight Mass Spectrometry for the Rapid Identification of Yeast Species From Polar Regions. <i>Frontiers in Microbiology</i> , 2022, 13, 832893.	1.5	2
18670	DNA Barcoding and Phylogenomic Analysis of the Genus <i>Fritillaria</i> in China Based on Complete Chloroplast Genomes. <i>Frontiers in Plant Science</i> , 2022, 13, 764255.	1.7	17
18671	Phylogenetic signal of subarctic beetle communities. <i>Ecology and Evolution</i> , 2022, 12, e8520.	0.8	0
18672	Three New Species of <i>Absidia</i> (Mucoromycota) from China Based on Phylogeny, Morphology and Physiology. <i>Diversity</i> , 2022, 14, 132.	0.7	6
18673	Comparative Genomics Reveals Evolutionary Traits, Mating Strategies, and Pathogenicity-Related Genes Variation of <i>Botryosphaeriaceae</i> . <i>Frontiers in Microbiology</i> , 2022, 13, 800981.	1.5	9
18675	Long-Term Persistence of Arbuscular Mycorrhizal Fungi in the Rhizosphere and Bulk Soils of Non-host <i>Brassica napus</i> and Their Networks of Co-occurring Microbes. <i>Frontiers in Plant Science</i> , 2022, 13, 828145.	1.7	10
18676	Comparative Genome Analysis Reveals Cis-Regulatory Elements on Gene-Sized Chromosomes of Ciliated Protists. <i>Frontiers in Microbiology</i> , 2022, 13, 775646.	1.5	5
18677	Molecular epidemiology and microbiological characteristics of <i>Cryptococcus gattii</i> VGII isolates from China. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010078.	1.3	3
18678	<i>Legionella pneumophila</i> in Municipal Shower Systems in Stavanger, Norway; A Longitudinal Surveillance Study Using Whole Genome Sequencing in Risk Management. <i>Microorganisms</i> , 2022, 10, 536.	1.6	3
18679	Complex patterns of ploidy in a holocentric plant clade (<i>Schoenus</i> , Cyperaceae) in the Cape biodiversity hotspot. <i>Annals of Botany</i> , 2023, 131, 143-156.	1.4	7
18680	Molecular Typing of Ukrainian <i>Bacillus anthracis</i> Strains by Combining Whole-Genome Sequencing Techniques. <i>Microorganisms</i> , 2022, 10, 461.	1.6	7
18681	Phylotranscriptomic and Evolutionary Analyses of <i>Oedogoniales</i> (Chlorophyceae, Chlorophyta). <i>Diversity</i> , 2022, 14, 157.	0.7	2
18682	<i>Nicotiana gandarela</i> (Solanaceae), a new species of "tobacco" highly endangered from the Quadrilátero Ferrífero in Brazil. <i>PhytoKeys</i> , 2022, 190, 113-129.	0.4	2

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18683	The Genome of the Marine Rotifer <i>Brachionus manjavacas</i> : Genome-Wide Identification of 310 G Protein-Coupled Receptor (GPCR) Genes. <i>Marine Biotechnology</i> , 2022, 24, 226-242.	1.1	5
18684	Using natural history to guide supervised machine learning for cryptic species delimitation with genetic data. <i>Frontiers in Zoology</i> , 2022, 19, 8.	0.9	13
18685	Phylogeography and transmission of <i>M. tuberculosis</i> in Moldova: A prospective genomic analysis. <i>PLoS Medicine</i> , 2022, 19, e1003933.	3.9	16
18686	A myxozoan genome reveals mosaic evolution in a parasitic cnidarian. <i>BMC Biology</i> , 2022, 20, 51.	1.7	8
18687	Incorporating Within-Host Diversity in Phylogenetic Analyses for Detecting Clusters of New HIV Diagnoses. <i>Frontiers in Microbiology</i> , 2021, 12, 803190.	1.5	3
18688	Whole-genome resequencing of <i>Coffea arabica</i> L. (Rubiaceae) genotypes identify SNP and unravels distinct groups showing a strong geographical pattern. <i>BMC Plant Biology</i> , 2022, 22, 69.	1.6	7
18689	Redescription of the giant Southeast Asian millipede <i>Spirobolus macrurus</i> Pocock, 1893 and its assignment to the new genus <i>Macrurobolus</i> gen. nov. (Diplopoda, Spirobolida, Pachybolidae). <i>ZooKeys</i> , 2022, 1087, 1-18.	0.5	1
18690	Biogeographical and seasonal dynamics of the marine <i>Roseobacter</i> community and ecological links to DMSP-producing phytoplankton. <i>ISME Communications</i> , 2022, 2, .	1.7	6
18691	The complete chloroplast genome of <i>Chimonobambusa angustifolia</i> C. D. Chu et C. S. Chao, a fiber and bamboo shoot species in Poaceae. <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 399-400.	0.2	1
18692	Plastid genome sequences are consistent with introduction of <i>Phormium tenax</i> to Norfolk Island and Chatham Islands by early East Polynesian voyagers but not vicariance explanations. <i>New Zealand Journal of Botany</i> , 2022, 60, 429-447.	0.8	5
18693	A new species of <i>Mindomys</i> (Rodentia, Cricetidae) with remarks on external traits as indicators of arboreality in sigmodontine rodents. <i>Evolutionary Systematics</i> , 2022, 6, 35-55.	0.2	2
18694	<i>Phytochytrium</i> and <i>Sparrowiella</i> , two new polycentric genera in Cladochytriales. <i>Mycological Progress</i> , 2022, 21, 1.	0.5	2
18695	Was the Last Bacterial Common Ancestor a Monoderm after All?. <i>Genes</i> , 2022, 13, 376.	1.0	6
18696	Combining mitochondrial DNA and morphological data to delineate four new millipede species and provisional assignment to the genus. <i>Invertebrate Systematics</i> , 2022, 36, 91-112.	0.5	3
18697	Ten new species of <i>Ulva</i> (Ulvophyceae, Chlorophyta) discovered in New Caledonia: genetic and morphological diversity, and bloom potential. <i>European Journal of Phycology</i> , 2022, 57, 458-478.	0.9	13
18698	Using RDNA sequences to define dinoflagellate species. <i>PLoS ONE</i> , 2022, 17, e0264143.	1.1	8
18700	Molecular phylogenetics and character evolution in <i>Haplanthodes</i> (Acanthaceae), an endemic genus from peninsular India. <i>Nordic Journal of Botany</i> , 2022, 2022, .	0.2	0
18701	Genome assembly of the JD17 soybean provides a new reference genome for comparative genomics. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	7

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18702	Ancestral Chromosomes for Family Peronosporaceae Inferred from a Telomere-to-Telomere Genome Assembly of <i>Peronospora effusa</i> . <i>Molecular Plant-Microbe Interactions</i> , 2022, 35, 450-463.	1.4	9
18703	The complete chloroplast genome sequence of <i>Zanthoxylum undulatifolium</i> Hemsl. (Rutaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 382-384.	0.2	0
18704	Genome-Annotated Bacterial Collection of the Barley Rhizosphere Microbiota. <i>Microbiology Resource Announcements</i> , 2022, 11, e0106421.	0.3	3
18706	Pufferfish (<i>Tetraodon cutcutia</i>) Sampled from a Freshwater River Serves as an Intermediate Reservoir of a Sucrose Nonfermenting Variant of <i>Vibrio cholerae</i> PS-4. <i>Microbiology Spectrum</i> , 2022, 10, e0122121.	1.2	5
18707	Phylogenetic inference of changes in amino acid propensities with single-position resolution. <i>PLoS Computational Biology</i> , 2022, 18, e1009878.	1.5	0
18708	Phylogenomics of paleoendemic lampshade spiders (Araneae, Hypochilidae, Hypochilus), with the description of a new species from montane California. <i>ZooKeys</i> , 2022, 1086, 163-204.	0.5	5
18710	Comparison of structural variants in the whole genome sequences of two <i>Medicago truncatula</i> ecotypes: Jemalong A17 and R108. <i>BMC Plant Biology</i> , 2022, 22, 77.	1.6	8
18711	Genomic Bootstrap Barcodes and Their Application to Study the Evolution of Sarbecoviruses. <i>Viruses</i> , 2022, 14, 440.	1.5	7
18712	Gene age shapes the transcriptional landscape of sexual morphogenesis in mushroom-forming fungi (Agaricomycetes). <i>ELife</i> , 2022, 11, .	2.8	18
18713	Circumscription and Phylogenetic Position of Two Propagulose Species of <i>Syntrichia</i> (Pottiaceae). <i>Tj ETQq1 1 0.784314 rgBT₂Overlo</i>	1.6	0
18714	Regulation of Eye Determination and Regionalization in the Spider <i>Parasteatoda tepidariorum</i> . <i>Cells</i> , 2022, 11, 631.	1.8	6
18715	Phylogenomic and comparative analyses of Coffeae alliance (Rubiaceae): deep insights into phylogenetic relationships and plastome evolution. <i>BMC Plant Biology</i> , 2022, 22, 88.	1.6	17
18716	No genomic repercussions of assortative pairing in a colour polymorphic lizard. <i>Journal of Evolutionary Biology</i> , 2022, 35, 648-656.	0.8	0
18717	Pharmacological Evaluation of Melanocortin 2 Receptor Accessory Protein 2 on Axolotl Neural Melanocortin Signaling. <i>Frontiers in Endocrinology</i> , 2022, 13, 820896.	1.5	2
18718	<i>Benna alternifolia</i> (Melastomataceae: Sonerileae), a new herbaceous genus and species from Guinea, West Africa. <i>Willdenowia</i> , 2022, 52, .	0.5	3
18719	Delimiting 33 <i>Carpinus</i> (Betulaceae) species with a further phylogenetic inference. <i>AoB PLANTS</i> , 2022, 14, .	1.2	1
18720	<i>Curtobacterium</i> spp. and <i>Curtobacterium flaccumfaciens</i> : Phylogeny, Genomics-Based Taxonomy, Pathogenicity, and Diagnostics. <i>Current Issues in Molecular Biology</i> , 2022, 44, 889-927.	1.0	15
18721	The Chromosome-Scale Reference Genome of <i>Macadamia tetraphylla</i> Provides Insights Into Fatty Acid Biosynthesis. <i>Frontiers in Genetics</i> , 2022, 13, 835363.	1.1	4

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18722	The mostly cavernicolous millipede genus <i>Stygiulus</i> Verhoeff, 1929, stat. nov.: taxonomy, distribution and phylogenetic relationships (Diplopoda, Julida, Julidae). <i>European Journal of Taxonomy</i> , 0, 798, 30-69.	0.6	1
18723	Historical mitochondrial genome introgression confounds species delimitation: evidence from phylogenetic inference in the <i>Odorrana grahami</i> species complex. <i>Environmental Epigenetics</i> , 2023, 69, 82-90.	0.9	2
18724	<i>Valentiella maceioensis</i> gen. et sp. nov. (Herpotrichiellaceae, Chaetothyriales), a new black yeast-like fungus isolated from bromeliads in Brazil. <i>Mycological Progress</i> , 2022, 21, 1.	0.5	2
18725	Taxonomic Reappraisal of Periconiaceae with the Description of Three New Periconia Species from China. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 243.	1.5	6
18726	Biogeography and systematics of <i>Carex</i> subgenus <i>Uncinia</i> (Cyperaceae): A unique radiation for the genus <i>Carex</i> in the Southern Hemisphere. <i>Taxon</i> , 2022, 71, 587-607.	0.4	4
18727	Offshore Marine Sediment Microbiota Breathe Structurally Distinct Organohalide Pollutants. <i>Environmental Science & Technology</i> , 2022, 56, 3065-3075.	4.6	30
18728	RevTiculate: An R framework for interaction with RevBayes. <i>Methods in Ecology and Evolution</i> , 2022, 13, 1177-1184.	2.2	1
18729	Plant migration under long-lasting hyperaridity – phylogenomics unravels recent biogeographic history in one of the oldest deserts on Earth. <i>New Phytologist</i> , 2022, 234, 1863-1875.	3.5	9
18730	Past climate cooling promoted global dispersal of amphipods from Tian Shan montane lakes to circumboreal lakes. <i>Global Change Biology</i> , 2022, 28, 3830-3845.	4.2	10
18731	Characterization of Atypical Shiga Toxin Gene Sequences and Description of Stx2j, a New Subtype. <i>Journal of Clinical Microbiology</i> , 2022, 60, jcm0222921.	1.8	21
18732	Molecular and Genomic Characterization of the <i>Pseudomonas syringae</i> Phylogroup 4: An Emerging Pathogen of <i>Arabidopsis thaliana</i> and <i>Nicotiana benthamiana</i> . <i>Microorganisms</i> , 2022, 10, 707.	1.6	3
18733	Transposable element insertion: a hidden major source of domesticated phenotypic variation in <i>Brassica rapa</i> . <i>Plant Biotechnology Journal</i> , 2022, 20, 1298-1310.	4.1	29
18735	Pan-Genome Analysis of <i>Laribacter hongkongensis</i> : Virulence Gene Profiles, Carbohydrate-Active Enzyme Prediction, and Antimicrobial Resistance Characterization. <i>Frontiers in Microbiology</i> , 2022, 13, 862776.	1.5	2
18736	Genome-Wide Identification and Expression Analysis of the R2R3-MYB Transcription Factor Family Revealed Their Potential Roles in the Flowering Process in Longan (<i>Dimocarpus longan</i>). <i>Frontiers in Plant Science</i> , 2022, 13, 820439.	1.7	8
18738	<i>Phytophthora tropicalis</i> : Causal agent of persimmon fruit rot in Brazil. <i>Journal of Phytopathology</i> , 2022, 170, 428-436.	0.5	1
18739	The Phlorizin-Degrading <i>Bacillus licheniformis</i> XNRB-3 Mediates Soil Microorganisms to Alleviate Apple Replant Disease. <i>Frontiers in Microbiology</i> , 2022, 13, 839484.	1.5	6
18740	Morphology and spicules elemental composition of <i>Marophrys nikolaevi</i> spec. nov. (Haptista: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 102	0.5	3
18741	Aerobic Methoxydotrophy: Growth on Methoxylated Aromatic Compounds by Methylobacteriaceae. <i>Frontiers in Microbiology</i> , 2022, 13, 849573.	1.5	4

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18742	Comparative Analysis of Codon Bias in the Chloroplast Genomes of Theaceae Species. <i>Frontiers in Genetics</i> , 2022, 13, 824610.	1.1	22
18743	Disentangle genus microdiversity within a complex microbial community by using a multi- ϵ distance long-read binning method: example of <i>Candidatus</i> <i>Accumulibacter</i> . <i>Environmental Microbiology</i> , 2022, 24, 2136-2156.	1.8	4
18744	Characterization of the complete chloroplast genome of <i>Rumex dentatus</i> L. (Polygonaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 546-547.	0.2	1
18745	Complete chloroplast genome sequence of the Tibetan catnip <i>Nepeta hemsleyana</i> Oliver ex Prain (Lamiaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 552-553.	0.2	1
18746	Associating life stages and sexes of Nearctic <i>Polycentropus</i> Curtis, 1835 (Trichoptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 582	0.8	5
18747	Phylogeographic relationships and the evolutionary history of the <i>Carassius auratus</i> complex with a newly born homodiploid raw fish (2nNCRC). <i>BMC Genomics</i> , 2022, 23, 242.	1.2	8
18748	Bacteriophage Control of <i>Pseudomonas</i> Δ <i>avastanoi</i> pv. <i>glycinea</i> in Soybean. <i>Plants</i> , 2022, 11, 938.	1.6	8
18749	Taxonomic synopsis of <i>Berberis</i> (Berberidaceae) from the northern Hengduan mountains region in China, with descriptions of seven new species. <i>Plant Diversity</i> , 2022, 44, 505-517.	1.8	3
18750	Transcriptional Regulation of Pine Male and Female Cone Initiation and Development: Key Players Identified Through Comparative Transcriptomics. <i>Frontiers in Genetics</i> , 2022, 13, 815093.	1.1	1
18751	Cervicovaginal DNA Virome Alterations Are Associated with Genital Inflammation and Microbiota Composition. <i>MSystems</i> , 2022, 7, e0006422.	1.7	14
18753	<i>Thesea pyrrha</i> sp. nov., a new shallow-water octocoral (Cnidaria, Anthozoa) from southwestern Atlantic, and implications on the systematics of the genus. <i>Zootaxa</i> , 2022, 5116, 89-106.	0.2	0
18754	Genomic and Phenotypic Insights for Toxigenic Clinical <i>Vibrio cholerae</i> O141. <i>Emerging Infectious Diseases</i> , 2022, 28, 617-624.	2.0	3
18755	<i>Colletotrichum truncatum</i> causing anthracnose disease of <i>Iris lactea</i> in Beijing, China. <i>Journal of Phytopathology</i> , 2022, 170, 391-398.	0.5	2
18756	Comparison of <i>Auxenochlorella protothecoides</i> and <i>Chlorella</i> spp. Chloroplast Genomes: Evidence for Endosymbiosis and Horizontal Virus-like Gene Transfer. <i>Life</i> , 2022, 12, 458.	1.1	0
18757	Based on morphology and molecular data, <i>Palisada rigida</i> comb. nov. and <i>Laurencia decussata</i> comb. et stat. nov. (Rhodophyta, Rhodomelaceae) are proposed. <i>Algae</i> , 2022, 37, 15-32.	0.9	2
18758	Fungal Biodiversity Profiles 111-120. <i>Cryptogamie, Mycologie</i> , 2022, 43, .	0.2	4
18759	Anaerobic derivatives of mitochondria and peroxisomes in the free-living amoeba <i>Pelomyxa schiedti</i> revealed by single-cell genomics. <i>BMC Biology</i> , 2022, 20, 56.	1.7	13
18760	The genome of <i>Hibiscus hamabo</i> reveals its adaptation to saline and waterlogged habitat. <i>Horticulture Research</i> , 2022, 9, uhac067.	2.9	12

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18761	The Enigmatic Dead-Leaf Miner <i>Geochus Broun</i> (Coleoptera: Curculionidae): Phylogenetic Placement, a New Species, and Lectotype Designations. <i>The Coleopterists Bulletin</i> , 2022, 76, .	0.1	2
18762	Unraveling the Genotypic and Phenotypic Diversity of the Psychrophilic <i>Clostridium estertheticum</i> Complex, a Meat Spoilage Agent. <i>Frontiers in Microbiology</i> , 2022, 13, 856810.	1.5	4
18763	<i>Geosmithia</i> Species Associated With Bark Beetles From China, With the Description of Nine New Species. <i>Frontiers in Microbiology</i> , 2022, 13, 820402.	1.5	2
18764	Taxonomy and Phylogeny of Two Spirotrichean Ciliates (Alveolata, Protista, and Ciliophora) From a Plateau Saline "Alkaline Lake in Tibet, China, Including Description of a New Species. <i>Frontiers in Marine Science</i> , 2022, 9, .	1.2	8
18765	Chromosome-level pepino genome provides insights into genome evolution and anthocyanin biosynthesis in Solanaceae. <i>Plant Journal</i> , 2022, 110, 1128-1143.	2.8	9
18766	Human infection with avian-origin H5N6 influenza A virus after exposure to slaughtered poultry. <i>Emerging Microbes and Infections</i> , 2022, 11, 807-810.	3.0	12
18767	Cryptic Species Diversification of the <i>Pedicularis siphonantha</i> Complex (Orobanchaceae) in the Mountains of Southwest China Since the Pliocene. <i>Frontiers in Plant Science</i> , 2022, 13, 811206.	1.7	5
18768	Genome and cuticular hydrocarbon-based species delimitation shed light on potential drivers of speciation in a Neotropical ant species complex. <i>Ecology and Evolution</i> , 2022, 12, e8704.	0.8	0
18769	The unresolved phylogenomic tree of butterflies and moths (Lepidoptera): Assessing the potential causes and consequences. <i>Systematic Entomology</i> , 2022, 47, 531-550.	1.7	14
18770	<i>Paraphlomis longicalyx</i> (Lamiaceae), a New Species from the Limestone Area of Guangxi and Guizhou Provinces, Southern China. <i>Systematic Botany</i> , 2022, 47, 251-258.	0.2	5
18771	On the origin of TSAR: morphology, diversity and phylogeny of <i>Telonemia</i> . <i>Open Biology</i> , 2022, 12, 210325.	1.5	7
18772	<i>Sporobolomyces lactucae</i> sp. nov. (Pucciniomycotina, Microbotryomycetes, Sporidiobolales): An Abundant Component of Romaine Lettuce Phylloplanes. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 302.	1.5	0
18773	Beneath a hairy problem: Phylogeny, morphology, and biogeography circumscribe the new <i>Miconia</i> supersection <i>Discolores</i> (Melastomataceae: Miconieae). <i>Molecular Phylogenetics and Evolution</i> , 2022, 171, 107461.	1.2	4
18775	Recurrent allopolyploidization, Y-chromosome introgression and the evolution of sexual systems in the plant genus <i>Mercurialis</i> . <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2022, 377, 20210224.	1.8	10
18776	Comparative Mitogenome Analysis of Gerbils and the Mitogenome Phylogeny of Gerbillinae (Rodentia: Tj ETQq0 0 0 rgBT /Overlock 10	0.8	3
18777	Global diversity and systematics of Hymenochaetaceae with poroid hymenophore. <i>Fungal Diversity</i> , 2022, 113, 1-192.	4.7	57
18778	<i>Hemiaustroboletus</i> , a new genus in the subfamily Austroboletoidae (Boletaceae, Boletales). <i>MycKeys</i> , 2022, 88, 55-78.	0.8	3
18779	Varied diversification patterns and distinct demographic trajectories in Ethiopian montane forest bird (Aves: Passeriformes) populations separated by the Great Rift Valley. <i>Molecular Ecology</i> , 2022, 31, 2664-2678.	2.0	3

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18781	WGS-Based Phenotyping and Molecular Characterization of the Resistome, Virulome and Plasmid Replicons in <i>Klebsiella pneumoniae</i> Isolates from Powdered Milk Produced in Germany. <i>Microorganisms</i> , 2022, 10, 564.	1.6	3
18782	Prolonged silent carriage, genomic virulence potential and transmission between staff and patients characterize a neonatal intensive care unit (NICU) outbreak of methicillin-resistant <i>Staphylococcus aureus</i> (MRSA). <i>Infection Control and Hospital Epidemiology</i> , 2023, 44, 40-46.	1.0	7
18783	Colonization rather than fragmentation explains the geographical distribution and diversification of treefrogs endemic to Brazilian shield sky islands. <i>Journal of Biogeography</i> , 2022, 49, 682-698.	1.4	5
18784	Chromosome-Level Genome Assembly for <i>Acer pseudosieboldianum</i> and Highlights to Mechanisms for Leaf Color and Shape Change. <i>Frontiers in Plant Science</i> , 2022, 13, 850054.	1.7	7
18785	Mineral Protection and Resource Limitations Combine to Explain Profileâ€Scale Soil Carbon Persistence. <i>Journal of Geophysical Research G: Biogeosciences</i> , 2022, 127, .	1.3	5
18786	The fern genus <i>Saccoloma</i> (Saccolomataceae) in Brazil, including new species and new combinations. <i>Brittonia</i> , 0, , 1.	0.8	2
18788	Unveiling the diversity of Giant Neotropical Torrent frogs (Hylodidae): phylogenetic relationships, morphology, and the description of two new species. <i>Systematics and Biodiversity</i> , 2022, 20, 1-31.	0.5	2
18789	Comparative Genome Analysis of the Photosynthetic Betaproteobacteria of the Genus <i>Rhodocyclus</i> : Heterogeneity within Strains Assigned to <i>Rhodocyclus tenuis</i> and Description of <i>Rhodocyclus gracilis</i> sp. nov. as a New Species. <i>Microorganisms</i> , 2022, 10, 649.	1.6	11
18790	Shared antibiotic resistance and virulence genes in <i>Staphylococcus aureus</i> from diverse animal hosts. <i>Scientific Reports</i> , 2022, 12, 4413.	1.6	23
18791	Diversification of <i>SEC15a</i> and <i>SEC15b</i> isoforms of an exocyst subunit in seed plants is manifested in their specific roles in <i>Arabidopsis</i> sporophyte and male gametophyte. <i>Plant Journal</i> , 2022, 110, 1382-1396.	2.8	3
18792	Population structure and phylogeography of <i>Elymus mutabilis</i> and its genetic relationships with <i>E. transbaicalensis</i> (Poaceae). <i>Nordic Journal of Botany</i> , 2022, 2022, .	0.2	1
18793	Effects of operational taxonomic unit inference methods on soil microeukaryote community analysis using long-read metabarcoding. <i>Ecology and Evolution</i> , 2022, 12, e8676.	0.8	3
18794	Multigene phylogeny reveals the ribbed shell morphotypes in the land snail genus <i>Sarika</i> (Eupulmonata: Ariophantidae), with description of two new species from Thailand and Myanmar. <i>Contributions To Zoology</i> , 2022, 91, 97-132.	0.2	2
18795	Gut Commensal <i>Bacteroidetes</i> Encode a Novel Class of Vitamin B ₁₂ -Binding Proteins. <i>MBio</i> , 2022, 13, e0284521.	1.8	8
18796	Host Shift Speciation of the Ectomycorrhizal Genus <i>Suillus</i> (Suillineae, Boletales) and Biogeographic Comparison With Its Host Pinaceae. <i>Frontiers in Microbiology</i> , 2022, 13, 831450.	1.5	4
18797	Chickensplash! Exploring the health concerns of washing raw chicken. <i>Physics of Fluids</i> , 2022, 34, 031910.	1.6	2
18798	An urban soil environmental <i>E. coli</i> ST354 isolate co-harboring <i>mcr-1</i> and <i>bla</i> NDM-9. <i>Journal of Global Antimicrobial Resistance</i> , 2022, 29, 173-175.	0.9	2
18799	Coevolutionary Analysis Implicates Toll-Like Receptor 9 in Papillomavirus Restriction. <i>MBio</i> , 2022, 13, e0005422.	1.8	5

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18800	Deep Genomic Divergence and Phenotypic Admixture of the Treefrog <i>Dendropsophus elegans</i> (Hylidae: Tj ETQq0 0 0 rgBT /Overlock 10 Evolution, 2022, 10, .	1.1	4
18801	Phylogeny and biogeography of the northern temperate genus <i>Dracocephalum</i> s.l. (Lamiaceae). <i>Cladistics</i> , 2022, 38, 429-451.	1.5	6
18802	Biogeography and Diversification of Bumblebees (Hymenoptera: Apidae), with Emphasis on Neotropical Species. <i>Diversity</i> , 2022, 14, 238.	0.7	7
18803	A serious shoot and leaf disease caused by <i>Colletotrichum theobromicola</i> discovered on eucalypts in South Africa. <i>Southern Forests</i> , 2022, 84, 8-20.	0.2	1
18804	Three novel species of <i>Distoseptispora</i> (Distoseptisporaceae) isolated from bamboo in Jiangxi Province, China. <i>MycKeys</i> , 0, 88, 35-54.	0.8	10
18805	Molecular characterization of hepatitis B virus (HBV) isolated from a pediatric case of acute lymphoid leukemia, with a delayed response to antiviral treatment: a case report. <i>BMC Pediatrics</i> , 2022, 22, 168.	0.7	2
18806	Fungus-insect symbiosis: Diversity and negative ecological role of the hypocrealean fungus <i>Trichoderma harzianum</i> in colonies of neotropical termites (Blattodea: Termitidae). <i>Fungal Ecology</i> , 2022, 57-58, 101152.	0.7	2
18807	The numbers of fungi: are the most speciose genera truly diverse?. <i>Fungal Diversity</i> , 2022, 114, 387-462.	4.7	52
18808	Species Persistence with Hybridization in Toad-Headed Lizards Driven by Divergent Selection and Low Recombination. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	3
18809	Phylogenomics of the Aphididae: Deep relationships between subfamilies clouded by gene tree discordance, introgression and the gene tree anomaly zone. <i>Systematic Entomology</i> , 2022, 47, 470-486.	1.7	7
18810	Convergent Evolution of Antibiotic Tolerance in Patients with Persistent Methicillin-Resistant <i>Staphylococcus aureus</i> Bacteremia. <i>Infection and Immunity</i> , 2022, 90, e0000122.	1.0	8
18811	Genetic Characteristics of the Transmissible Locus of Stress Tolerance (tLST) and tLST Harboring <i>Escherichia coli</i> as Revealed by Large-Scale Genomic Analysis. <i>Applied and Environmental Microbiology</i> , 2022, 88, e0218521.	1.4	10
18812	Haplotype Analysis of Chloroplast Genomes for Jujube Breeding. <i>Frontiers in Plant Science</i> , 2022, 13, 841767.	1.7	11
18813	Antigenic Evolution Characteristics and Immunological Evaluation of H9N2 Avian Influenza Viruses from 1994–2019 in China. <i>Viruses</i> , 2022, 14, 726.	1.5	12
18815	An Exception to the Rule? Could Photobiont Identity Be a Better Predictor of Lichen Phenotype than Mycobiont Identity?. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 275.	1.5	7
18816	Exploring statistical weight estimates for mitochondrial DNA matches involving heteroplasmy. <i>International Journal of Legal Medicine</i> , 2022, 136, 671-685.	1.2	5
18817	Enhancing Meningococcal Genomic Surveillance in the Meningitis Belt Using High-Resolution Culture-Free Whole-Genome Sequencing. <i>Journal of Infectious Diseases</i> , 2022, 226, 729-737.	1.9	6
18818	New plastomes of eight <i>Ipomoea</i> species and four putative hybrids from Eastern Amazon. <i>PLoS ONE</i> , 2022, 17, e0265449.	1.1	2

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18819	Sequence Capture of Mitochondrial Genome with PCR-Generated Baits Provides New Insights into the Biogeography of the Genus <i>Abies</i> Mill.. <i>Plants</i> , 2022, 11, 762.	1.6	4
18820	A near-chromosome level genome assembly of the European hoverfly, <i>Sphaerophoria rueppellii</i> (Diptera: Syrphidae), provides comparative insights into insecticide resistance-related gene family evolution. <i>BMC Genomics</i> , 2022, 23, 198.	1.2	2
18821	Assessing the vulnerability of habitats through plant rarity patterns in the Pyrenean range. <i>Conservation Science and Practice</i> , 2022, 4, .	0.9	3
18822	Establishment, Genetic Diversity, and Habitat Suitability of <i>Aedes albopictus</i> Populations from Ecuador. <i>Insects</i> , 2022, 13, 305.	1.0	5
18824	An isolated population of the secretive, endemic Aztec Rail (<i>Rallus tenuirostris</i>) in Chihuahua, Mexico. <i>Wilson Journal of Ornithology</i> , 2022, 133, .	0.1	0
18825	Complete mitogenomes reveal limited genetic variability in the garden dormouse <i>Eliomys quercinus</i> of the Iberian Peninsula. <i>Animal Biodiversity and Conservation</i> , 2022, , 107-122.	0.3	0
18826	Phylogeographic analysis of <i>Ligidium japonicum</i> (Isopoda: Ligiidae) and its allied species reveals high biodiversity and genetic differentiation in the Kanto region, Japan. <i>Entomological Science</i> , 2022, 25, .	0.3	2
18828	Amino acid sensor conserved from bacteria to humans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2110415119.	3.3	31
18829	Metagenomic Assessment of the Pathogenic Risk of Microorganisms in Sputum of Postoperative Patients With Pulmonary Infection. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 855839.	1.8	5
18830	A chromosome-scale genome assembly of the false clownfish, <i>Amphiprion ocellaris</i> . <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	11
18831	Investigation into a Superspreading Event of the German 2020â€“2021 Avian Influenza Epidemic. <i>Pathogens</i> , 2022, 11, 309.	1.2	3
18832	Diversity and Evolution of Pigment Types in Marine <i>Synechococcus</i> Cyanobacteria. <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	15
18833	Molecular and Morphological Analysis Supports the Separation of <i>Robrichia</i> as a Genus Distinct from <i>Enterolobium</i> (Leguminosae: Caesalpinioideae: Mimosoid Clade). <i>Systematic Botany</i> , 2022, 47, 268-277.	0.2	3
18834	DNA Barcoding and New Records of Odonates (Insecta: Odonata) from Para�ba State, Brazil. <i>Diversity</i> , 2022, 14, 203.	0.7	3
18835	<i>Flavobacterium ammonificans</i> sp. nov. and <i>Flavobacterium ammoniigenes</i> sp. nov., ammonifying bacteria isolated from surface river water. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	12
18836	Host species is linked to pathogen genotype for the amphibian chytrid fungus (<i>Batrachochytrium</i>) Tj ETQq1 1 0.784314 rgBT ₇ /Overlook	1.1	11
18838	Methanethiol Consumption and Hydrogen Sulfide Production by the Thermoacidophilic Methanotroph <i>Methylacidiphilum fumarolicum</i> SolV. <i>Frontiers in Microbiology</i> , 2022, 13, 857442.	1.5	15
18839	DNA barcoding of the National Museum of Natural History reptile tissue holdings raises concerns about the use of natural history collections and the responsibilities of scientists in the molecular age. <i>PLoS ONE</i> , 2022, 17, e0264930.	1.1	17

#	ARTICLE	IF	CITATIONS
18840	Molecular basis of cycloheximide resistance in the Ophiostomatales revealed. <i>Current Genetics</i> , 2022, 68, 505-514.	0.8	3
18841	First elucidation of a didymozoid life cycle: <i>Saccularina magnacetabula</i> n. gen. n. sp. infecting an arcid bivalve. <i>International Journal for Parasitology</i> , 2022, 52, 407-425.	1.3	14
18844	<i>Carex borealifujianica</i> (Cyperaceae), a new species of the core <i>Carex</i> clade from Fujian, southeastern China. <i>PLoS ONE</i> , 2022, 17, e0264419.	1.1	1
18845	Phylogenetic analyses and reclassification of the oleaginous marine species <i>Nannochloris</i> sp. "desiccata" (Trebouxiophyceae, Chlorophyta), formerly <i>Chlorella desiccata</i> , supported by a high-quality genome assembly. <i>Journal of Phycology</i> , 2022, 58, 436-448.	1.0	4
18846	Hybridization fuelled diversification in <i>Spialia</i> butterflies. <i>Molecular Ecology</i> , 2022, , .	2.0	6
18847	SHOOT: phylogenetic gene search and ortholog inference. <i>Genome Biology</i> , 2022, 23, 85.	3.8	28
18848	Phylogenomic conflict analyses in the apple genus <i>Malus</i> s.l. reveal widespread hybridization and allopolyploidy driving diversification, with insights into the complex biogeographic history in the Northern Hemisphere. <i>Journal of Integrative Plant Biology</i> , 2022, 64, 1020-1043.	4.1	31
18849	Global population structure of the <i>Serratia marcescens</i> complex and identification of hospital-adapted lineages in the complex. <i>Microbial Genomics</i> , 2022, 8, .	1.0	8
18850	Genome Sequences of <i>Marichromatium gracile</i> HOL-1 and Its Purple Photosynthetic Coisolate, <i>Afifella</i> sp. H1R. <i>Microbiology Resource Announcements</i> , 2022, , e0003322.	0.3	1
18851	Mitochondrial phylogeny of the brittle star genus <i>Ophioderma</i> . <i>Scientific Reports</i> , 2022, 12, 5304.	1.6	2
18852	Three new species of arbuscular mycorrhizal fungi of the genus <i>Diversispora</i> from maritime dunes of Poland. <i>Mycologia</i> , 2022, 114, 453-466.	0.8	6
18853	Novel Low Pathogenic Avian Influenza H6N1 in Backyard Chicken in Easter Island (Rapa Nui), Chilean Polynesia. <i>Viruses</i> , 2022, 14, 718.	1.5	2
18854	Phylogeny, diversification, and biogeography of a hemiclinal hybrid system of native Australian freshwater fishes (Gobiiformes: Gobioidae: Eleotridae: <i>Hypseleotris</i>). <i>Bmc Ecology and Evolution</i> , 2022, 22, 22.	0.7	5
18855	Novel viral RNA genomes of the vine mealybug <i>Planococcus ficus</i> . <i>Journal of General Virology</i> , 2022, 103, .	1.3	3
18856	Biogeography and character mapping of <i>Hiptage</i> (Malpighiaceae) corroborate Indochina's rainforests as one of the main sources of plant diversity in southeastern Asia. <i>Nordic Journal of Botany</i> , 2022, 2022, .	0.2	2
18858	A global analysis of mosses reveals low phylogenetic endemism and highlights the importance of long-distance dispersal. <i>Journal of Biogeography</i> , 2022, 49, 654-667.	1.4	7
18859	AutoCoEv: A High-Throughput In Silico Pipeline for Predicting Inter-Protein Coevolution. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3351.	1.8	1
18861	PowerBacGWAS: a computational pipeline to perform power calculations for bacterial genome-wide association studies. <i>Communications Biology</i> , 2022, 5, 266.	2.0	4

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18862	Phylogenetic position of <i>Ligusticopsis</i> (Apiaceae, Apioideae): evidence from molecular data and carpalogical characters. <i>AoB PLANTS</i> , 2022, 14, plac008.	1.2	10
18863	Biogeographic reconstruction of the migratory Neotropical fish family Prochilodontidae (Teleostei: Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.7	4
18864	Comprehensive Genomic Profiling of Neuroendocrine Carcinomas of the Gastrointestinal System. <i>Cancer Discovery</i> , 2022, 12, 692-711.	7.7	58
18865	A <i>Mel Wolbachia</i> variant in <i>Aedes aegypti</i> from field-collected <i>Drosophila melanogaster</i> with increased phenotypic stability under heat stress. <i>Environmental Microbiology</i> , 2022, 24, 2119-2135.	1.8	11
18866	Persistence and multi-ward dissemination of vancomycin-resistant <i>Enterococcus faecium</i> ST17 clone in hospital settings in Slovakia 2017–2020. <i>International Journal of Antimicrobial Agents</i> , 2022, 59, 106561.	1.1	1
18867	Phase variation in the glycosyltransferase genes of <i>Pasteurella multocida</i> associated with outbreaks of fowl cholera on free-range layer farms. <i>Microbial Genomics</i> , 2022, 8, .	1.0	1
18868	New phylogenetic insights into the African catfish families <i>Mochokidae</i> and <i>Austroglanididae</i> . <i>Journal of Fish Biology</i> , 2022, 100, 1171-1186.	0.7	5
18869	Epidemiology and Genetic Diversity of PCV2 Reveals That PCV2e Is an Emerging Genotype in Southern China: A Preliminary Study. <i>Viruses</i> , 2022, 14, 724.	1.5	6
18870	New contribution to the peritrichous genus <i>Ophrydium</i> (Protista, Ciliophora) with notes on the morphology, taxonomy, and phylogeny of a well-known species <i>Ophrydium crassicaule</i> Penard, 1922. <i>Journal of Eukaryotic Microbiology</i> , 2022, , e12900.	0.8	5
18871	Dissemination Dynamics of HIV-1 Subtype B Pandemic and Non-pandemic Lineages Circulating in Amazonas, Brazil. <i>Frontiers in Microbiology</i> , 2022, 13, 835443.	1.5	0
18872	The complete chloroplast genome of <i>Chimonobambusa utilis</i> (Keng) P. C. Keng, known as “the king of bamboo shoots”™. <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 492-494.	0.2	0
18873	Phylogenetics of Historical Host Switches in a Bacterial Plant Pathogen. <i>Applied and Environmental Microbiology</i> , 2022, 88, e0235621.	1.4	6
18874	Identification of a protein responsible for the synthesis of archaeal membrane-spanning GDGT lipids. <i>Nature Communications</i> , 2022, 13, 1545.	5.8	33
18875	Genotyping-by-Sequencing Analysis Shows That Siberian Lindens Are Nested within <i>Tilia cordata</i> Mill. <i>Diversity</i> , 2022, 14, 256.	0.7	1
18876	<i>Saprolegnia atlantica</i> sp. nov. (Oomycota, Saprolegniaceae) from Brazil, and new synonymizations and epitypifications in the genus <i>Saprolegnia</i> . <i>Mycological Progress</i> , 2022, 21, 1.	0.5	3
18877	Microbiomes in the Challenger Deep slope and bottom-axis sediments. <i>Nature Communications</i> , 2022, 13, 1515.	5.8	31
18878	Incongruent latitudinal patterns of taxonomic, phylogenetic and functional diversity reveal different drivers of caddisfly community assembly across spatial scales. <i>Global Ecology and Biogeography</i> , 2022, 31, 1006-1020.	2.7	13
18880	Co-expression network analyses of anthocyanin biosynthesis genes in <i>Ruellia</i> (Wild Petunias; Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.7	2

#	ARTICLE	IF	CITATIONS
18881	Comparative plastome analysis of Musaceae and new insights into phylogenetic relationships. BMC Genomics, 2022, 23, 223.	1.2	11
18882	Taxonomy of Rhizobiaceae revisited: proposal of a new framework for genus delimitation. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	125
18885	Phylogeny, Antifungal Susceptibility, and Point Mutations of SQLE Gene in Major Pathogenic Dermatophytes Isolated From Clinical Dermatophytosis. Frontiers in Cellular and Infection Microbiology, 2022, 12, 851769.	1.8	10
18886	Reassessment of the Phylogeny and Systematics of Chinese Parnassia (Celastraceae): A Thorough Investigation Using Whole Plastomes and Nuclear Ribosomal DNA. Frontiers in Plant Science, 2022, 13, 855944.	1.7	1
18887	Classification of 27 <i>Corynebacterium kroppenstedtii</i> -Like Isolates Associated with Mastitis in China and Descriptions of <i>C. parakroppenstedtii</i> sp. nov. and <i>C. pseudokroppenstedtii</i> sp. nov. Microbiology Spectrum, 2022, 10, e0137221.	1.2	12
18888	Fungal endophytic community associated with Hevea spp.: diversity, enzymatic activity, and biocontrol potential. Brazilian Journal of Microbiology, 2022, , .	0.8	2
18889	Integrated metagenomics identifies a crucial role for trimethylamine-producing Lachnoclostridium in promoting atherosclerosis. Npj Biofilms and Microbiomes, 2022, 8, 11.	2.9	41
18890	Identifying large-scale recombination and capsular switching events in Streptococcus agalactiae strains causing disease in adults in the UK between 2014 and 2015. Microbial Genomics, 2022, 8, .	1.0	4
18891	The Land-Sea Connection: Insights Into the Plant Lineage from a Green Algal Perspective. Annual Review of Plant Biology, 2022, 73, 585-616.	8.6	14
18892	A high-quality reference genome for the fish pathogen Streptococcus iniae. Microbial Genomics, 2022, 8, .	1.0	0
18893	Comparative Analysis of Bacillus cereus Group Isolates' Resistance Using Disk Diffusion and Broth Microdilution and the Correlation between Antimicrobial Resistance Phenotypes and Genotypes. Applied and Environmental Microbiology, 2022, 88, aem0230221.	1.4	8
18894	The arginine deaminase system plays distinct roles in Borrelia burgdorferi and Borrelia hermsii. PLoS Pathogens, 2022, 18, e1010370.	2.1	4
18895	Chromosome-Scale Assembly of the Dendrobium nobile Genome Provides Insights Into the Molecular Mechanism of the Biosynthesis of the Medicinal Active Ingredient of Dendrobium. Frontiers in Genetics, 2022, 13, 844622.	1.1	21
18896	Vasopressin-oxytocin-type signaling is ancient and has a conserved water homeostasis role in euryhaline marine planarians. Science Advances, 2022, 8, eabk0331.	4.7	2
18897	The evolution and competitive strategies of Akkermansia muciniphila in gut. Gut Microbes, 2022, 14, 2025017.	4.3	25
18898	Lepidodactylus browni (Squamata, Gekkonidae) Placed in the Synonymy of L. orientalis. Journal of Herpetology, 2022, 56, .	0.2	2
18899	Phylogenomics and integrative taxonomy reveal two new species of Amana (Liliaceae). Plant Diversity, 2023, 45, 54-68.	1.8	6
18900	Stability in the South, Turbulence Toward the North: Evolutionary History of Aurinia saxatilis (Brassicaceae) Revealed by Phylogenomic and Climatic Modelling Data. Frontiers in Plant Science, 2022, 13, 822331.	1.7	3

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18901	Long-distance dispersal of pigeons and doves generated new ecological opportunities for host-switching and adaptive radiation by their parasites. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2022, 289, 20220042.	1.2	13
18902	Genomic characterization of multidrug-resistant <i>Salmonella</i> serovar Kentucky ST198 isolated in poultry flocks in Spain (2011–2017). <i>Microbial Genomics</i> , 2022, 8, .	1.0	7
18903	Genome Characterisation of an Isoprene-Degrading <i>Alcaligenes</i> sp. Isolated from a Tropical Restored Forest. <i>Biology</i> , 2022, 11, 519.	1.3	4
18904	<i>Hypotrachyna neohorrescens</i> , a new species in the subgenus <i>Parmelinopsis</i> (<i>Parmeliaceae</i>) from Brazil. <i>Lichenologist</i> , 2022, 54, 107-115.	0.5	0
18905	Diversity of Lepidoptera associated with macadamia nut damage in South Africa and development of molecular tools to monitor pest populations. <i>Agricultural and Forest Entomology</i> , 2022, 24, 332-343.	0.7	2
18906	New Species and New Records of <i>Otidea</i> from China Based on Molecular and Morphological Data. <i>Journal of Fungi</i> (Basel, Switzerland), 2022, 8, 272.	1.5	2
18907	Phylogenetic and morphological analyses of <i>Pilosocereus leucocephalus</i> group s.s. (Cactaceae) reveal new taxonomical implications. <i>Journal of Plant Research</i> , 2022, 135, 423-442.	1.2	3
18908	Chromosomal-level genome of a sheet-web spider provides insight into the composition and evolution of venom. <i>Molecular Ecology Resources</i> , 2022, 22, 2333-2348.	2.2	10
18909	Phylogenetic analysis confirms the taxonomic placement of the marine flagellate <i>Hermesinum adriaticum</i> (Thecofilosea, Cercozoa, Rhizaria). <i>Journal of Eukaryotic Microbiology</i> , 2022, , e12905.	0.8	0
18910	Comparative genomic analysis of high-altitude adaptation for Mongolia Mastiff, Tibetan Mastiff, and <i>Canis Lupus</i> . <i>Genomics</i> , 2022, , 110359.	1.3	0
18911	Genome and proteome analyses show the gaseous alkane degrader <i>Desulfosarcina</i> sp. strain <i>BuS5</i> as an extreme metabolic specialist. <i>Environmental Microbiology</i> , 2022, 24, 1964-1976.	1.8	10
18912	Geographically dispersed zoonotic tuberculosis in pre-contact South American human populations. <i>Nature Communications</i> , 2022, 13, 1195.	5.8	22
18913	Cytoneuclear coevolution in a holoparasitic plant with highly disparate organellar genomes. <i>Plant Molecular Biology</i> , 2022, 109, 673-688.	2.0	5
18914	Taxonomic notes on the New Zealand moss flora: a new combination and a new species in the genus <i>Tridontium</i> (<i>Pottiaceae</i>). <i>New Zealand Journal of Botany</i> , 0, , 1-7.	0.8	0
18915	Integrative Taxonomy Reveals a New <i>Melitaea</i> (Lepidoptera: Nymphalidae) Species Widely Distributed in the Iberian Peninsula. <i>Insect Systematics and Diversity</i> , 2022, 6, .	0.7	4
18916	Genomic Fishing and Data Processing for Molecular Evolution Research. <i>Methods and Protocols</i> , 2022, 5, 26.	0.9	4
18917	Embracing Green Computing in Molecular Phylogenetics. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	10
18918	The complete chloroplast genome sequence of <i>Anaphalis margaritacea</i> var. <i>yedoensis</i> (<i>Asteraceae</i>) and phylogenetic relationships within <i>Gnaphalieae</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 563-565.	0.2	0

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18919	The complete mitochondrial genome of <i>Philus pallescens</i> Bates, 1866 (Coleoptera: Vesperidae) and its phylogenetic implications. <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 448-450.	0.2	0
18920	Phylogenetics of Archerfishes (Toxotidae) and Evolution of the Toxotid Shooting Apparatus. <i>Integrative Organismal Biology</i> , 2022, 4, .	0.9	4
18921	An Extended Reservoir of Class-D Beta-Lactamases in Non-Clinical Bacterial Strains. <i>Microbiology Spectrum</i> , 2022, 10, e0031522.	1.2	4
18922	Chromosome-Level Genome Assembly of <i>Bupleurum chinense</i> DC Provides Insights Into the Saikosaponin Biosynthesis. <i>Frontiers in Genetics</i> , 2022, 13, 878431.	1.1	0
18923	Variation in intraspecific demography drives localised concordance but species-wide discordance in response to past climatic change. <i>Bmc Ecology and Evolution</i> , 2022, 22, 35.	0.7	2
18924	A Systematic Phylogenomic Classification of the Multidrug and Toxic Compound Extrusion Transporter Gene Family in Plants. <i>Frontiers in Plant Science</i> , 2022, 13, 774885.	1.7	8
18925	Reunion of Australasian Possums by Shared SINE Insertions. <i>Systematic Biology</i> , 2022, , .	2.7	14
18926	Aridification-driven evolution of a migratory fish revealed by niche modelling and coalescence simulations. <i>Journal of Biogeography</i> , 0, , .	1.4	1
18927	Using molecular data to test the generic placement of a new and unusual ginger species from the Philippines. <i>Nordic Journal of Botany</i> , 0, , .	0.2	0
18928	Integrative taxonomy solves taxonomic impasses: a case study from Epyrinae (Hymenoptera,) Tj ETQq1 1 0.784314 rBT /Overlock 10 T	1.7	11
18929	The complete plastomes of seven <i>Peucedanum</i> plants: comparative and phylogenetic analyses for the <i>Peucedanum</i> genus. <i>BMC Plant Biology</i> , 2022, 22, 101.	1.6	25
18931	Dynamics of Antibodies to Ebolaviruses in an <i>Eidolon helvum</i> Bat Colony in Cameroon. <i>Viruses</i> , 2022, 14, 560.	1.5	7
18932	A new microsporidian parasite, <i>Ordospora pajunii</i> sp. nov (Ordosporidae), of <i>Daphnia longispina</i> highlights the value of genomic data for delineating species boundaries. <i>Journal of Eukaryotic Microbiology</i> , 2022, 69, e12902.	0.8	7
18933	Sequential development of several RT-PCR tests using LNA nucleotides and dual probe technology to differentiate SARS-CoV-2 from influenza A and B. <i>Microbial Biotechnology</i> , 2022, 15, 1995-2021.	2.0	6
18934	Lack of genetic structure suggests high connectivity of <i>Parnassius phoebus</i> between nearby valleys in the Alps. <i>Alpine Entomology</i> , 0, 6, 1-6.	0.2	2
18935	Deep Insights into the Specific Evolution of Fungal Hybrid B Heme Peroxidases. <i>Biology</i> , 2022, 11, 459.	1.3	4
18936	Bacterial community structure and metabolic potential in microbialite-forming mats from South Australian saline lakes. <i>Geobiology</i> , 2022, 20, 546-559.	1.1	3
18937	Revealing the species diversity of <i>Neolyngbya</i> (Cyanobacteria, Oscillatoriales) from subtropical coastal regions of Okinawa, Japan, with descriptions of <i>Neolyngbya intertidalis</i> sp. nov. and <i>Neolyngbya lata</i> sp. nov.. <i>Phycological Research</i> , 2022, 70, 69-80.	0.8	2

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18938	Worldwide Population Structure of the Coffee Rust Fungus <i>Hemileia vastatrix</i> Is Strongly Shaped by Local Adaptation and Breeding History. <i>Phytopathology</i> , 2022, 112, 1998-2011.	1.1	5
18939	Towards the plastome evolution and phylogeny of <i>Cycas</i> L. (Cycadaceae): molecular-morphology discordance and gene tree space analysis. <i>BMC Plant Biology</i> , 2022, 22, 116.	1.6	7
18940	The adaptive evolution of <i>Euryale ferox</i> to the aquatic environment through paleo-hexaploidization. <i>Plant Journal</i> , 2022, 110, 627-645.	2.8	12
18941	Novel linear plasmids carrying vanA cluster drives the spread of vancomycin resistance in <i>Enterococcus faecium</i> in India. <i>Journal of Global Antimicrobial Resistance</i> , 2022, 29, 168-172.	0.9	6
18942	Phylogeny of Marsdenieae (Apocynaceae, Asclepiadoideae) based on chloroplast and nuclear loci, with a conspectus of the genera. <i>Taxon</i> , 2022, 71, 833-875.	0.4	9
18943	Plastid phylogenomics shed light on intergeneric relationships and spatiotemporal evolutionary history of Melocanninae (Poaceae: Bambusoideae). <i>Journal of Systematics and Evolution</i> , 2022, 60, 640-652.	1.6	12
18944	Testing the Taxonomy of Amphidorini Leconte (Coleoptera: Tenebrionidae): A Molecular Phylogeny Leveraging Museum Sequencing. <i>Annales Zoologici</i> , 2022, 72, .	0.1	3
18945	Discovery of <i>Fusarium proliferatum</i> f. sp. <i>malus domestica</i> Causing Apple Replant Disease in China. <i>Plant Disease</i> , 2022, 106, 2958-2966.	0.7	13
18947	Emending <i>Gymnopus</i> sect. <i>Gymnopus</i> (Agaricales, Omphalotaceae) by including two new species from southern China. <i>MycKeys</i> , 2022, 87, 183-204.	0.8	1
18948	New Species of <i>Mallocybe</i> and <i>Pseudosperma</i> from North China. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 256.	1.5	7
18951	Mitochondrial Transcription of Entomopathogenic Fungi Reveals Evolutionary Aspects of Mitogenomes. <i>Frontiers in Microbiology</i> , 2022, 13, 821638.	1.5	0
18952	The First Deep-Sea Stylasterid (Hydrozoa, Stylasteridae) of the Red Sea. <i>Diversity</i> , 2022, 14, 241.	0.7	5
18953	The first complete mitochondrial genome of Dufouriellini (Hemiptera: Anthocoridae) and implications for its phylogenetic position. <i>Archives of Insect Biochemistry and Physiology</i> , 2022, , e21885.	0.6	3
18954	Avian Louse Flies and Their Trypanosomes: New Vectors, New Lineages and Host-Parasite Associations. <i>Microorganisms</i> , 2022, 10, 584.	1.6	10
18955	Recurrent evolution of an inhibitor of ESCRT-dependent virus budding and LINE-1 retrotransposition in primates. <i>Current Biology</i> , 2022, 32, 1511-1522.e6.	1.8	2
18956	The symmetry spectrum in a hybridising, tropical group of rhododendrons. <i>New Phytologist</i> , 2022, 234, 1491-1506.	3.5	3
18958	Detection and characterisation of 16S rRNA methyltransferase-producing <i>Pseudomonas aeruginosa</i> from the UK and Republic of Ireland from 2003-2015. <i>International Journal of Antimicrobial Agents</i> , 2022, 59, 106550.	1.1	8
18959	Applying biochemical and structural characterization of hydroxycinnamate catabolic enzymes from soil metagenome for lignin valorization strategies. <i>Applied Microbiology and Biotechnology</i> , 2022, 106, 2503-2516.	1.7	5

#	ARTICLE	IF	CITATIONS
18960	Whole genome sequence analysis of Salmonella Typhi in Papua New Guinea reveals an established population of genotype 2.1.7 sensitive to antimicrobials. PLoS Neglected Tropical Diseases, 2022, 16, e0010306.	1.3	6
18961	CIAlign: A highly customisable command line tool to clean, interpret and visualise multiple sequence alignments. PeerJ, 2022, 10, e12983.	0.9	32
18962	A new Amazonian species of <i>Allobates</i> Zimmermann & Zimmermann, 1988 (Aromobatidae) with a trilled advertisement call. PeerJ, 2022, 10, e13026.	0.9	3
18963	Candida auris on Apples: Diversity and Clinical Significance. MBio, 2022, 13, e0051822.	1.8	29
18964	Amazonocrinis thailandica sp. nov. (Nostocales, Cyanobacteria), a novel species of the previously monotypic Amazonocrinis genus from Thailand. Algae, 2022, 37, 1-14.	0.9	4
18966	Microbial communities of Auka hydrothermal sediments shed light on vent biogeography and the evolutionary history of thermophily. ISME Journal, 2022, 16, 1750-1764.	4.4	16
18967	Geographic Population Genetic Structure of the New World Screwworm, <i>Cochliomyia hominivorax</i> (Diptera: Calliphoridae), Using SNPs. Journal of Medical Entomology, 2022, 59, 874-882.	0.9	3
18968	Diversification Rate is Associated with Rate of Molecular Evolution in Ray-Finned Fish (Actinopterygii). Journal of Molecular Evolution, 2022, 90, 200-214.	0.8	2
18969	A Rhesus channel in the coral symbiosome membrane suggests a novel mechanism to regulate NH ₃ and CO ₂ delivery to algal symbionts. Science Advances, 2022, 8, eabm0303.	4.7	19
18970	Divergence time estimation using ddRAD data and an isolation-with-migration model applied to water vole populations of Arvicola. Scientific Reports, 2022, 12, 4065.	1.6	9
18971	A Genomic Perspective on the Evolutionary Diversification of Turtles. Systematic Biology, 2022, 71, 1331-1347.	2.7	2
18972	Isolation and Characterization of Lytic Bacteriophages Targeting Diverse <i>Enterobacter</i> spp. Clinical Isolates. Phage, 2022, 3, 50-58.	0.8	1
18973	A new contribution to the taxonomy and phylogeny of the ciliate genus Spirostomum (Alveolata), Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 2022, 1, 100031.		9
18974	Non-human primate papillomavirus E6-mediated p53 degradation reveals ancient evolutionary adaptation of carcinogenic phenotype to host niche. PLoS Pathogens, 2022, 18, e1010444.	2.1	7
18975	The complete chloroplast genome sequence of <i>Trigonotis peduncularis</i> (Boraginaceae). Mitochondrial DNA Part B: Resources, 2022, 7, 456-457.	0.2	6
18976	Characterization of the complete chloroplast genome of <i>Achnatherum pekinense</i> (Poaceae), a widespread weed. Mitochondrial DNA Part B: Resources, 2022, 7, 537-538.	0.2	0
18978	Penicillium Ochrochloron RLS11 Secretome Containing Carbohydrate-Active Enzymes Improves Commercial Enzyme Mixtures During Sugarcane Straw Saccharification. Applied Biochemistry and Biotechnology, 2022, 194, 2946-2967.	1.4	1
18980	Complete mitochondrial genome of Conus lischkeanus Weinkauff, 1875 (Neogastropoda, Conidae) and phylogenetic implications of the evolutionary diversification of dietary types of Conus species. ZooKeys, 2022, 1088, 173-185.	0.5	0

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18981	Phylogeography of the endangered orchids <i>Cypripedium japonicum</i> and <i>Cypripedium formosanum</i> in East Asia: Deep divergence at intra- and interspecific levels. <i>Taxon</i> , 2022, 71, 733-757.	0.4	4
18983	The complete chloroplast genome sequence of the monotypic and enigmatic genus <i>Cavea</i> (tribe Tj ETQq1 1 0.784314 rgBT 1/2 Overlock	0.4	2
18985	Reclassification of the Main Causal Agent of Glomerella Leaf Spot on Apple into <i>Colletotrichum chrysophilum</i> in Southern Brazil and Uruguay. <i>Phytopathology</i> , 2022, 112, 1825-1832.	1.1	4
18986	Microbial Consortia of Putative Degradors of Low-Density Polyethylene-Associated Compounds in the Ocean. <i>MSystems</i> , 2022, 7, e0141521.	1.7	7
18987	Phylogenetic Structure and Comparative Genomics of Multi-National Invasive <i>Haemophilus influenzae</i> Serotype a Isolates. <i>Frontiers in Microbiology</i> , 2022, 13, 856884.	1.5	3
18988	96 North American taxa sorted "Peck's <i>Hebeloma</i> revisited. <i>Mycologia</i> , 2022, 114, 337-387.	0.8	7
18989	<i>Nematostella vectensis</i> exhibits an enhanced molecular stress response upon co-exposure to highly weathered oil and surface UV radiation. <i>Marine Environmental Research</i> , 2022, 175, 105569.	1.1	2
18990	Genome-Wide Association Study Reveals Host Factors Affecting Conjugation in <i>Escherichia coli</i> . <i>Microorganisms</i> , 2022, 10, 608.	1.6	3
18991	Virulome and genome analyses identify associations between antimicrobial resistance genes and virulence factors in highly drug-resistant <i>Escherichia coli</i> isolated from veal calves. <i>PLoS ONE</i> , 2022, 17, e0265445.	1.1	17
18992	Whole-genome sequencing for the characterization of resistance mechanisms and epidemiology of colistin-resistant <i>Acinetobacter baumannii</i> . <i>PLoS ONE</i> , 2022, 17, e0264335.	1.1	6
18993	Morphological and Phylogenetic Evidence Reveal Five New Telamonioid Species of <i>Cortinarius</i> (Agaricales) from East Asia. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 257.	1.5	3
18995	The TCP transcription factor HvTB2 heterodimerizes with VRS5 and controls spike architecture in barley. <i>Plant Reproduction</i> , 2022, 35, 205-220.	1.3	5
18996	<i>Neisseria meningitidis</i> Serogroup C Clonal Complex 10217 Outbreak in West Kpendjal Prefecture, Togo 2019. <i>Microbiology Spectrum</i> , 2022, , e0192321.	1.2	1
18997	Unifying the known and unknown microbial coding sequence space. <i>ELife</i> , 2022, 11, .	2.8	41
18998	Novel viruses discovered in the transcriptomes of agnathan fish. <i>Journal of Fish Diseases</i> , 2022, 45, 931-938.	0.9	3
18999	Phylogenomics and Comparative Genomics Highlight Specific Genetic Features in <i>Ganoderma</i> Species. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 311.	1.5	10
19000	Comparative analysis of the kinomes of <i>Plasmodium falciparum</i> , <i>Plasmodium vivax</i> and their host <i>Homo sapiens</i> . <i>BMC Genomics</i> , 2022, 23, 237.	1.2	9
19001	Diverse Subclade Differentiation Attributed to the Ubiquity of <i>Prochlorococcus</i> High-Light-Adapted Clade II. <i>MBio</i> , 2022, 13, e0302721.	1.8	3

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19002	Role of mobile genetic elements in the global dissemination of the carbapenem resistance gene blaNDM. <i>Nature Communications</i> , 2022, 13, 1131.	5.8	72
19003	Rapid Parallel Morphological and Mechanical Diversification of South American Pike Cichlids (<i>Crenicichla</i>). <i>Systematic Biology</i> , 2023, 72, 120-133.	2.7	6
19004	Phylogenetic network analysis of South and North American <i>Corynespora cassiicola</i> isolates from tomato, cucumber, and novel hosts. <i>European Journal of Plant Pathology</i> , 2022, 163, 657-671.	0.8	3
19006	Inter-species geographic signatures for tracing horizontal gene transfer and long-term persistence of carbapenem resistance. <i>Genome Medicine</i> , 2022, 14, 37.	3.6	15
19007	Chromosome-Scale Assembly and Characterization of the Albino Northern Snakehead, <i>Channa argus</i> var. (Teleostei: Channidae) Genome. <i>Frontiers in Marine Science</i> , 2022, 9, .	1.2	1
19008	Relationship and distribution of <i>Salmonella enterica</i> serovar I 4,[5],12:i:- strain sequences in the NCBI Pathogen Detection database. <i>BMC Genomics</i> , 2022, 23, 268.	1.2	3
19010	New data in Porotheleaceae and Cyphellaceae: epitypification of <i>Prunulus scabripes</i> Murrill, the status of <i>Mycopan Redhead</i> , Moncalvo & Vilgalys and a new combination in <i>Pleurella</i> Horak emend.. <i>Mycological Progress</i> , 2022, 21, 1.	0.5	6
19011	The complete mitochondrial genome of <i>Asteroschema tubiferum</i> (Ophiuroidea: Euryalida): Tj ETQq1 1 0.784314 rgBT / Overl... 0.2	0.2	0
19012	Newly designed foraminifera primers identify habitat-specific lineages through metabarcoding analyses. <i>Journal of Eukaryotic Microbiology</i> , 2022, 69, e12913.	0.8	0
19014	Genome sequencing of a predominant clonal lineage of the grain aphid <i>Sitobion avenae</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2022, 143, 103742.	1.2	4
19016	The impact of tandem duplication on gene evolution in Solanaceae species. <i>Journal of Integrative Agriculture</i> , 2022, 21, 1004-1014.	1.7	17
19017	Neotropical Monogenoidea 64. <i>Cosmetocleithrum falsunilatum</i> sp. n. (Monogenoidea, Dactylogyridae) parasite of the gills of <i>Megalodoras uranoscopus</i> (Siluriformes, Doradidae) from the Solimões river, near Iquitos, Peru. <i>Systematic Parasitology</i> , 2022, 99, 341-346.	0.5	6
19018	Insight into the biotechnology potential of <i>Alicyclobacillus tolerans</i> from whole genome sequence analysis and genome-scale metabolic network modeling.. <i>Journal of Microbiological Methods</i> , 2022, 197, 106459.	0.7	4
19019	On the hybrid origin of the <i>C₂</i> <i>Salsola divaricata</i> agg. (Amaranthaceae) from <i>C₃</i> and <i>C₄</i> parental lineages. <i>New Phytologist</i> , 2022, 234, 1876-1890.	3.5	2
19020	Mitochondrial genome structure, phylogenetic analyses and substitution rate estimation of the Oedogoniales. <i>European Journal of Phycology</i> , 0, , 1-12.	0.9	2
19021	Identification of a recombinant equine coronavirus in donkey, China. <i>Emerging Microbes and Infections</i> , 2022, 11, 1010-1013.	3.0	4
19022	Chromosome-level genome assembly of grass carp (<i>Ctenopharyngodon idella</i>) provides insights into its genome evolution. <i>BMC Genomics</i> , 2022, 23, 271.	1.2	21
19024	The complete chloroplast genome sequence of <i>Actinidia chinensis</i> Planch. "Hongyang", a typical red core pulp in China. <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 593-595.	0.2	0

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19025	A chromosome-scale genome assembly of the Mongolian oak (<i>Quercus mongolica</i>). <i>Molecular Ecology Resources</i> , 2022, 22, 2396-2410.	2.2	25
19026	Description of the female, nymph and larva and mitochondrial genome, and redescription of the male of <i>Ixodes barkeri</i> Barker, 2019 (Acari: Ixodidae), from the short-beaked echidna, <i>Tachyglossus aculeatus</i> , with a consideration of the most suitable subgenus for this tick. <i>Parasites and Vectors</i> , 2022, 15, 117.	1.0	4
19027	Residual risk of mother-to-child transmission of hepatitis B virus infection despite timely birth-dose vaccination in Cameroon (ANRS 12303): a single-centre, longitudinal observational study. <i>The Lancet Global Health</i> , 2022, 10, e521-e529.	2.9	24
19028	<i>Verticillium</i> diseases of vegetable crops in Brazil: Host range, microsclerotia production, molecular haplotype network, and pathogen species determination. <i>Plant Pathology</i> , 2022, 71, 1417-1430.	1.2	3
19029	Genetic Variation in <i>Rhipicephalus sanguineus</i> s.l. Ticks across Arizona. <i>International Journal of Environmental Research and Public Health</i> , 2022, 19, 4223.	1.2	7
19030	Comparative analyses of American and Asian lotus genomes reveal insights into petal color, carpel thermogenesis and domestication. <i>Plant Journal</i> , 2022, 110, 1498-1515.	2.8	21
19031	A snapshot of progenitor-derivative speciation in <i>Iberodes</i> (Boraginaceae). <i>Molecular Ecology</i> , 2022, 31, 3192-3209.	2.0	11
19032	From rags to enriched: metagenomic insights into ammonia-oxidizing archaea following ammonia enrichment of a denuded oligotrophic soil ecosystem. <i>Environmental Microbiology</i> , 2022, 24, 3097-3110.	1.8	4
19033	Population status and genetic diversity of two endangered giant clams (<i>Tridacna squamosa</i> and <i>T. squamosa</i>) and conservation: Marine and Freshwater Ecosystems, 2022, 32, 1005-1021.	0.9	1
19034	Zoonotic origin of the human malaria parasite <i>Plasmodium malariae</i> from African apes. <i>Nature Communications</i> , 2022, 13, 1868.	5.8	9
19035	Systematic revision of <i>Hydnum</i> species in Japan. <i>Mycologia</i> , 2022, 114, 413-452.	0.8	7
19036	<i>Darksidea phi</i> , sp. nov., a dark septate root-associated fungus in foundation grasses in North American Great Plains. <i>Mycologia</i> , 2022, 114, 254-269.	0.8	6
19037	<i>Neckera</i> , <i>Forsstroemia</i> and <i>Alleniella</i> (Neckeraceae, Bryophyta) redefined based on phylogenetic analyses. <i>Bryologist</i> , 2022, 125, .	0.1	1
19038	Two new species of the marine flatworm <i>Pericelis</i> (Platyhelminthes: Polycladida) from southwestern Japan with an amendment of the generic diagnosis based on phylogenetic inference. <i>Marine Biology Research</i> , 2021, 17, 946-959.	0.3	3
19039	A cytosolic pentatricopeptide repeat protein is essential for tapetal plastid development by regulating <i>Osgl1</i> transcript levels in rice. <i>New Phytologist</i> , 2022, 234, 1678-1695.	3.5	10
19040	The complete mitochondrial genome of <i>Sinopodisma hengshanica</i> (Orthoptera: Acrididae) and its phylogenetic implication. <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 616-618.	0.2	0
19041	Novel insights into the dissemination route of Japanese apricot (<i>Prunus mume</i>) Sieb. et Zucc.) based on genomics. <i>Plant Journal</i> , 2022, 110, 1182-1197.	2.8	12
19042	Isolation, characterization, and comparative genomic analysis of vB_PlaM_Pd22F, a new bacteriophage of the family Myoviridae. <i>Archives of Virology</i> , 2022, , 1.	0.9	0

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19044	Comparative and phylogenetic analyses of six Kenya <i>Polystachya</i> (Orchidaceae) species based on the complete chloroplast genome sequences. <i>BMC Plant Biology</i> , 2022, 22, 177.	1.6	37
19045	A Chromosome-Level Reference Genome of Chinese Balloon Flower (<i>Platycodon grandiflorus</i>). <i>Frontiers in Genetics</i> , 2022, 13, 869784.	1.1	7
19046	Establishment of the Y-linked <i>Dmrt1Y</i> as the candidate sex determination gene in spotbanded scat (<i>Selenotoca multifasciata</i>). <i>Aquaculture Reports</i> , 2022, 23, 101085.	0.7	0
19047	Pollinator sharing, copollination, and speciation by host shifting among six closely related dioecious fig species. <i>Communications Biology</i> , 2022, 5, 284.	2.0	11
19048	<i>Lophosiphonia obscura</i> and <i>Polysiphonia sukatarii</i> sp. nov. (Rhodomelaceae, Rhodophyta) from mesohaline Lake Bafa, Turkey. <i>Phycologia</i> , 0, , 1-9.	0.6	2
19050	The complete sequence of a human genome. <i>Science</i> , 2022, 376, 44-53.	6.0	1,222
19051	Segmental duplications and their variation in a complete human genome. <i>Science</i> , 2022, 376, eabj6965.	6.0	130
19052	Genomic insights into the genotypeâ€environment mismatch and conservation units of a Qinghaiâ€Tibet Plateau endemic cypress under climate change. <i>Evolutionary Applications</i> , 2022, 15, 919-933.	1.5	7
19053	Putting small and big pieces together: a genome assembly approach reveals the largest Lamiid plastome in a woody vine. <i>PeerJ</i> , 2022, 10, e13207.	0.9	3
19054	Soil Fungi Exposed to Warming Temperatures and Shrinking Snowpack in a Northern Hardwood Forest Have Lower Capacity for Growth and Nutrient Cycling. <i>Frontiers in Forests and Global Change</i> , 2022, 5, .	1.0	2
19056	Genome Wide Analysis of the Potato Soft Rot Pathogen <i>Pectobacterium carotovorum</i> Strain ICMP 5702 to Predict Novel Insights into Its Genetic Features. <i>Plant Pathology Journal</i> , 2022, 38, 102-114.	0.7	1
19057	Relationships Between Soil Microbial Diversities Across an Aridity Gradient in Temperate Grasslands. <i>Microbial Ecology</i> , 2023, 85, 1013-1027.	1.4	7
19059	Insight into the Taxonomic Resolution of the Pleosporalean Species Associated with Dead Woody Litter in Natural Forests from Yunnan, China. <i>Journal of Fungi</i> (Basel, Switzerland), 2022, 8, 375.	1.5	9
19060	Purification and characterization of antifungal lipopeptide produced by <i>Bacillus velezensis</i> isolated from raw honey. <i>PLoS ONE</i> , 2022, 17, e0266470.	1.1	12
19061	Extensive epigenetic modification with large-scale chromosomal and plasmid recombination characterise the <i>Legionella longbeachae</i> serogroup 1 genome. <i>Scientific Reports</i> , 2022, 12, 5810.	1.6	0
19062	Salinity and host drive <i>Ulva</i> -associated bacterial communities across the Atlanticâ€Baltic Sea gradient. <i>Molecular Ecology</i> , 2023, 32, 6260-6277.	2.0	6
19063	Phylogeny and spatiotemporal dynamics of hepatitis E virus infections in wild boar and deer from six areas of Germany during 2013â€2017. <i>Transboundary and Emerging Diseases</i> , 2022, 69, .	1.3	14
19064	Comparative mitogenomics and phylogenetics of the family Carangidae with special emphasis on the mitogenome of the Indian Scad <i>Decapterus russelli</i> . <i>Scientific Reports</i> , 2022, 12, 5642.	1.6	2

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19065	Pathogenomes and variations in Shiga toxin production among geographically distinct clones of <i>Escherichia coli</i> O113:H21. <i>Microbial Genomics</i> , 2022, 8, .	1.0	4
19066	A new species, new host records and life cycle data for lepecreadiids (Digenea) of pomacentrid fishes from the Great Barrier Reef, Australia. <i>Systematic Parasitology</i> , 2022, 99, 375-397.	0.5	6
19067	The chromosome-level genome assembly of <i>Gentiana dahurica</i> (Gentianaceae) provides insights into gentiopicroside biosynthesis. <i>DNA Research</i> , 2022, 29, .	1.5	12
19068	Phylogenetic conservatism of mycoparasitism and its contribution to pathogen antagonism. <i>Molecular Ecology</i> , 2022, 31, 3018-3030.	2.0	7
19069	Identification of QTL and underlying genes for root system architecture associated with nitrate nutrition in hexaploid wheat. <i>Journal of Integrative Agriculture</i> , 2022, 21, 917-932.	1.7	6
19070	Distribution and the evolutionary history of G-protein components in plant and algal lineages. <i>Plant Physiology</i> , 2022, 189, 1519-1535.	2.3	9
19071	Characterization of the complete mitogenome of brown-spotted locust, <i>Cyrtacanthacris tatarica</i> (Orthoptera: Acrididae: Cyrtacanthacridinae). <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 613-615.	0.2	0
19072	Molecular characterization of <i>Burkholderia mallei</i> strains isolated from horses in Brazil (2014–2017). <i>Infection, Genetics and Evolution</i> , 2022, 99, 105250.	1.0	6
19073	The complete mitochondrial genome of <i>Trichoderma simmonsii</i> (Hypocreales: Hypocreaceae) from the Southern Coast of Korea. <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 640-641.	0.2	3
19074	<i>Natronosporangium hydrolyticum</i> gen. nov., sp. nov., a haloalkaliphilic polyhydrolytic actinobacterium from a soda solonchak soil in Central Asia. <i>Systematic and Applied Microbiology</i> , 2022, 45, 126307.	1.2	2
19075	<i>Haplosporidium acetes</i> n. sp. infecting the hepatopancreas of jelly prawns <i>Acetes sibogae australis</i> from Moreton Bay, Australia. <i>Journal of Invertebrate Pathology</i> , 2022, 190, 107751.	1.5	1
19076	Genome-wide SNPs reveal the fine-scale population structure of <i>Laodelphax striatellus</i> in China using double-digest restriction site-associated DNA sequencing. <i>Genomics</i> , 2022, 114, 110329.	1.3	2
19077	Comparative mitochondrial genomes of the <i>Rhus</i> gall aphid <i>Kaburagia rhusicola</i> subspecies with variable gall shapes. <i>Gene</i> , 2022, 824, 146379.	1.0	0
19078	Insights into the genetic diversity, antibiotic resistance and pathogenic potential of <i>Klebsiella pneumoniae</i> from the Norwegian marine environment using whole-genome analysis. <i>International Journal of Hygiene and Environmental Health</i> , 2022, 242, 113967.	2.1	11
19079	An ancient, Antarctic-specific species complex: large divergences between multiple Antarctic lineages of the tardigrade genus <i>Mesobiotus</i> . <i>Molecular Phylogenetics and Evolution</i> , 2022, 170, 107429.	1.2	13
19080	Genome-wide mining of <i>gpx</i> gene family provides new insights into cadmium stress responses in common carp (<i>Cyprinus carpio</i>). <i>Gene</i> , 2022, 821, 146291.	1.0	4
19081	Evidence for local and international spread of <i>Mycobacterium avium</i> subspecies <i>paratuberculosis</i> through whole genome sequencing of isolates from the island of Ireland. <i>Veterinary Microbiology</i> , 2022, 268, 109416.	0.8	11
19082	Analysis of carbohydrate-active enzymes and sugar transporters in <i>Penicillium echinulatum</i> : A genome-wide comparative study of the fungal lignocellulolytic system. <i>Gene</i> , 2022, 822, 146345.	1.0	6

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19083	Diversity, biogeography, and reproductive evolution in the genus <i>Pipa</i> (Amphibia: Anura: Pipidae). <i>Molecular Phylogenetics and Evolution</i> , 2022, 170, 107442.	1.2	11
19084	Re-description and molecular phylogeny of the free-swimming peritrichs <i>Hastatella radians</i> Erlanger, 1890 and <i>H. aesculacantha</i> Jarocki & Jakubowska, 1927 (Ciliophora, Peritrichia) from China. <i>European Journal of Protistology</i> , 2022, 84, 125891.	0.5	9
19085	Evolutionary relationships of anglerfishes (Lophiiformes) reconstructed using ultraconserved elements. <i>Molecular Phylogenetics and Evolution</i> , 2022, 171, 107459.	1.2	6
19086	Site pattern probabilities under the multispecies coalescent and a relaxed molecular clock: Theory and applications. <i>Journal of Theoretical Biology</i> , 2022, 542, 111078.	0.8	2
19087	Phylogenomic analysis of the Neotropical fish subfamily Characinae using ultraconserved elements (Teleostei: Characidae). <i>Molecular Phylogenetics and Evolution</i> , 2022, 171, 107462.	1.2	5
19088	Genome-wide identification of 194 G protein-coupled receptor (GPCR) genes from the water flea <i>Daphnia magna</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2022, 42, 100983.	0.4	0
19089	PASTA with many application-aware optimization criteria for alignment based phylogeny inference. <i>Computational Biology and Chemistry</i> , 2022, 98, 107661.	1.1	0
19090	Secondary metabolites produced by solid-state fermentation of a neotropical <i>Aspergillus flavus</i> strain confer anti-mosquito activity with long shelf-life. <i>Industrial Crops and Products</i> , 2022, 180, 114743.	2.5	2
19091	Molecular evolutionary analyses of tooth genes support sequential loss of enamel and teeth in baleen whales (Mysticeti). <i>Molecular Phylogenetics and Evolution</i> , 2022, 171, 107463.	1.2	12
19092	The role of nitrogen metabolism on polyethylene biodegradation. <i>Journal of Hazardous Materials</i> , 2022, 432, 128682.	6.5	2
19093	Morphology, cell division, and phylogeny of <i>Notohymena antarctica</i> Foissner, 1996 and <i>Engelmanniella mobilis</i> (Engelmann, 1862) Foissner, 1982 (Ciliophora, Hypotrichia). <i>European Journal of Protistology</i> , 2022, 84, 125879.	0.5	3
19094	New collections of blood flukes (Aporocotylidae) from fishes of the tropical Indo-west Pacific, including a new genus, two new species and molecular evidence that <i>Elaphrobates chaetodontis</i> (Yamaguti, 1970) is widespread in the region. <i>Parasitology International</i> , 2022, 88, 102565.	0.6	8
19095	Gypsum content influences culturable soil fungal communities in semi-arid steppes from central Spain. <i>Journal of Arid Environments</i> , 2022, 202, 104756.	1.2	2
19096	Four new monorchids from marine teleost fishes of Moreton Bay and the Great Barrier Reef, Australia, including the proposal of a new genus. <i>Parasitology International</i> , 2022, 89, 102566.	0.6	3
19097	Rediscovery of <i>Ixodes confusus</i> in Australia with the first description of the male from Australia, a redescription of the female and the mitochondrial (mt) genomes of five species of <i>Ixodes</i> . <i>International Journal for Parasitology: Parasites and Wildlife</i> , 2022, 18, 1-11.	0.6	2
19098	Genomic surveillance of <i>Acinetobacter baumannii</i> in the Philippines, 2013–2014. <i>Western Pacific Surveillance and Response Journal: WPSAR</i> , 2021, 12, 46-60.	0.3	1
19099	Olfactory receptor subgenome and expression in a highly olfactory procellariiform seabird. <i>Genetics</i> , 2022, 220, .	1.2	8
19100	A new species of <i>Cyrtodactylus</i> Gray (Squamata: Gekkonidae) from Manipur State, northeast India, with a critical review highlighting extensive errors in literature covering bent-toed geckos of the Indo-Burma region. <i>Journal of Natural History</i> , 2021, 55, 2445-2480.	0.2	5

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19101	A taxonomically complex catfish group from an underrepresented geographic area: Systematics and species limits in <i>Hypostomus</i> Lac��p��de, 1803 (Siluriformes, Loricariidae) from Eastern South America. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2021, 59, 1994-2009.	0.6	2
19102	Genome assembly, annotation, and comparative analysis of the cattail <i>Typha latifolia</i> . <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	6
19103	Molecular Identification of Sceloporus Lizards in the Laramie Mountains, Wyoming. <i>Western North American Naturalist</i> , 2021, 81, .	0.2	0
19104	Phylogeographic study of the <i>Bufo gargarizans</i> species complex, with emphasis on Northeast Asia. <i>Animal Cells and Systems</i> , 2021, 25, 434-444.	0.8	6
19105	Multilocus-phylogeny of the lichen-forming genus <i>Bacidia</i> s. str. (<i>Ramalinaceae</i>), <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 582</i>	0.5	1
19106	Fungal diversity notes 1387��1511: taxonomic and phylogenetic contributions on genera and species of fungal taxa. <i>Fungal Diversity</i> , 2021, 111, 1-335.	4.7	88
19107	New Dothideomycetes from Freshwater Habitats in Spain. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 1102.	1.5	7
19108	Novel strain of <i>Pseudoruminococcus massiliensis</i> possesses traits important in gut adaptation and host-microbe interactions. <i>Gut Microbes</i> , 2022, 14, 2013761.	4.3	0
19109	Using Transcript Levels of Nitrate Transporter 2 as Molecular Indicators to Estimate the Potentials of Nitrate Transport in Symbiodinium, Cladocopium, and Durusdinium of the Fluted Giant Clam, <i>Tridacna squamosa</i> . <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	4
19111	Variation in Plastome Sizes Accompanied by Evolutionary History in Monogenomic Triticeae (Poaceae.) <i>Tj ETQq1 1 0,784314,rgBT /Over</i>	1.7	7
19113	Morphological and molecular evidence reveals three new species of <i>Lithocarpus</i> (Fagaceae) from Bidoup-Nui Ba National Park, Vietnam. <i>PhytoKeys</i> , 2021, 186, 73-92.	0.4	6
19114	Correlation between acoustic divergence and phylogenetic distance in soniferous European gobiids (Gobiidae; Gobiinae). <i>PLoS ONE</i> , 2021, 16, e0260810.	1.1	6
19115	Comparative genomics reveal the convergent evolution of CYP82D and CYP706X members related to flavone biosynthesis in Lamiaceae and Asteraceae. <i>Plant Journal</i> , 2022, 109, 1305-1318.	2.8	12
19117	Unique roles of vaginal <i>Megasphaera</i> phylotypes in reproductive health. <i>Microbial Genomics</i> , 2021, 7, .	1.0	6
19119	Novel and extendable genotyping system for human respiratory syncytial virus based on whole-genome sequence analysis. <i>Influenza and Other Respiratory Viruses</i> , 2022, 16, 492-500.	1.5	14
19120	Evolutionary Processes Driving the Rise and Fall of <i>Staphylococcus aureus</i> ST239, a Dominant Hybrid Pathogen. <i>MBio</i> , 2021, 12, e0216821.	1.8	9
19121	Rates of Protein Evolution across the Marsupial Phylogeny: Heterogeneity and Link to Life-History Traits. <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	4
19122	<i>Zooshikella harenae</i> sp. nov., Isolated from Pacific Oyster <i>Crassostrea gigas</i> , and Establishment of <i>Zooshikella ganghwensis</i> subsp. marina subsp. nov. and <i>Zooshikella ganghwensis</i> subsp. ganghwensis subsp. nov.. <i>Diversity</i> , 2021, 13, 641.	0.7	15

#	ARTICLE	IF	CITATIONS
19123	The complete chloroplast genome of <i>Vandenboschia striata</i> , a common and widespread filmy fern (Hymenophyllaceae). Mitochondrial DNA Part B: Resources, 2022, 7, 128-129.	0.2	1
19124	<i>Benthodytes palauta</i> , a new species of deep-sea holothuroid (Elasipodida: Psychropotidae) from the western Pacific Ocean. Acta Oceanologica Sinica, 2021, 40, 50-54.	0.4	3
19125	Phylogenetic Reassessment, Taxonomy, and Biogeography of Codinaea and Similar Fungi. Journal of Fungi (Basel, Switzerland), 2021, 7, 1097.	1.5	11
19126	<i>Pseudocochlodinium profundisulcus</i> Resting Cysts Detected in the Ballast Tank Sediment of Ships Arriving in the Ports of China and North America and the Implications in the Species' Geographic Distribution and Possible Invasion. International Journal of Environmental Research and Public Health, 2022, 19, 299.	1.2	3
19127	Survival of climate warming through niche shifts: Evidence from frogs on tropical islands. Global Change Biology, 2022, 28, 1268-1286.	4.2	3
19128	Lineage-specific energy and carbon metabolism of sponge symbionts and contributions to the host carbon pool. ISME Journal, 2022, 16, 1163-1175.	4.4	13
19129	Intraspecific variation of some brown Parmeliae (in Poland) – a comparison of ITS rDNA and non-molecular characters. MycoKeys, 2021, 85, 127-160.	0.8	4
19130	A dual endosymbiosis supports nutritional adaptation to hematophagy in the invasive tick <i>Hyalomma marginatum</i> . ELife, 2021, 10, .	2.8	32
19131	Are Palmer's Elm-Leaf Goldenrod and the Smooth Elm-Leaf Goldenrod Real? The Angiosperms353 Kit Provides Within-Species Signal in <i>Solidago ulmifolia</i> s. l.. Systematic Botany, 2021, 46, 1107-1113.	0.2	3
19132	Phylogeny and Biogeography of <i>Acaena</i> (Rosaceae) and its Relatives: Evidence of Multiple Long-Distance Dispersal Events Across the Globe. Systematic Botany, 2021, 46, 998-1010.	0.2	2
19134	Semi-quantitative metabarcoding reveals how climate shapes arthropod community assembly along elevation gradients on Hawaii Island. Molecular Ecology, 2022, 31, 1416-1429.	2.0	10
19136	On Time and Environment of <i>Stephanorhinus kirchbergensis</i> Jäger 1839 (Mammalia, Rhinocerotidae) in Altai and Northeastern Russia. Biology Bulletin, 2021, 48, 1674-1687.	0.1	1
19137	Overall phylogenetic relationships of <i>Scutellaria</i> (Lamiaceae) shed light on the origin of the predominantly Caucasian and Irano-Turanian <i>S. orientalis</i> group. Willdenowia, 2021, 51, .	0.5	3
19139	Variation and transmission of the human gut microbiota across multiple familial generations. Nature Microbiology, 2022, 7, 87-96.	5.9	32
19140	Genomic adaptations of <i>Campylobacter jejuni</i> to long-term human colonization. Gut Pathogens, 2021, 13, 72.	1.6	5
19141	Complete Mitogenomes of Two Aragoa Species and Phylogeny of Plantagineae (Plantaginaceae.) Tj ETQq1 1 0.784314 rgBT (Overlock	1.6	3
19143	Island Biogeography Revisited: Museomics Reveals Affinities of Shelf Island Birds Determined by Bathymetry and Paleo-Rivers, Not by Distance to Mainland. Molecular Biology and Evolution, 2022, 39, .	3.5	8
19144	<i>Xerophorus donadinii</i> (Callistosporiaceae: Agaricales) From Mediterranean Region of Turkey. Sinop Üniversitesi Fen Bilimleri Dergisi, 0, , .	0.4	0

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19145	Chromosome-Level Genome Assembly and HazelOmics Database Construction Provides Insights Into Unsaturated Fatty Acid Synthesis and Cold Resistance in Hazelnut (<i>Corylus heterophylla</i>). <i>Frontiers in Plant Science</i> , 2021, 12, 766548.	1.7	7
19146	Global Emergence and Dissemination of <i>Neisseria gonorrhoeae</i> ST-9363 Isolates with Reduced Susceptibility to Azithromycin. <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	5
19147	The complete chloroplast genome sequence of <i>Artabotrys pilosus</i> (Annonaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 19-20.	0.2	1
19148	Evolutionary patterns of host type and chasmothecial appendage morphology in obligate plant parasites belonging to Cystothecaceae (powdery mildew, Erysiphaceae). <i>Mycologia</i> , 2022, 114, 35-45.	0.8	2
19150	<i>Castela senticosa</i> (Simaroubaceae: Sapindales), a New Species from the Caribbean Clade Endemic to Seasonally Dry Tropical Forest on Hispaniola. <i>Systematic Botany</i> , 2021, 46, 1033-1041.	0.2	2
19151	Transposable Prophages in <i>Leptospira</i> : An Ancient, Now Diverse, Group Predominant in Causative Agents of Weil's Disease. <i>International Journal of Molecular Sciences</i> , 2021, 22, 13434.	1.8	4
19152	<i>Gammarinema scyllae</i> sp. n. and <i>Monhysterium mangrovi</i> sp. n. (Nematoda: Monhysteridae) from land crabs from New Caledonia. <i>Systematic Parasitology</i> , 2022, 99, 83-101.	0.5	2
19153	<i>Mesorhizobium comanense</i> sp. nov., isolated from groundwater. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	10
19154	Living on the edge: genetic structure and geographic distribution in the threatened Markham's Storm-Petrel (<i>Hydrobates markhami</i>). <i>PeerJ</i> , 2021, 9, e12669.	0.9	1
19155	Phylogenetic Relationships, Speciation, and Origin of <i>Armillaria</i> in the Northern Hemisphere: A Lesson Based on rRNA and Elongation Factor 1-Alpha. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 1088.	1.5	8
19156	Genome placement of alpha-haemolysin cluster is associated with alpha-haemolysin sequence variation, adhesin and iron acquisition factor profile of <i>Escherichia coli</i> . <i>Microbial Genomics</i> , 2021, 7, .	1.0	2
19157	Intra-Alpine Islands: Population genomic inference reveals high degree of isolation between freshwater spring habitats. <i>Diversity and Distributions</i> , 2022, 28, 291-305.	1.9	11
19158	Evaluating the Genetic Capacity of <i>Mycoplasmas</i> for Coenzyme A Biosynthesis in a Search for New Anti-mycoplasma Targets. <i>Frontiers in Microbiology</i> , 2021, 12, 791756.	1.5	2
19159	SNPPar: identifying convergent evolution and other homoplasies from microbial whole-genome alignments. <i>Microbial Genomics</i> , 2021, 7, .	1.0	5
19160	<i>Paraneptunicella aestuarii</i> gen. nov., sp. nov., a member of the family Alteromonadaceae isolated from seawater in East China Sea. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	7
19161	Morphology, Individual Age, DNA and Sex of the Yuka Mammoth (<i>Mammuthus primigenius</i>) from Northern Yakutia, Russia. <i>Paleontological Journal</i> , 2021, 55, 1230-1259.	0.2	2
19162	Novel <i>Klebsiella pneumoniae</i> virulent bacteriophage KPPK108.1 capable of infecting the K108 serotype strains. <i>Bulletin of Russian State Medical University</i> , 2021, , .	0.3	1
19163	Phylogeny and Character Evolution of the Neotropical Fern Genus <i>Cyclodium</i> (Dryopteridaceae). <i>Systematic Botany</i> , 2021, 46, 916-928.	0.2	1

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19164	A New and Expanded Phylogenetic Analysis of Hyptidinae (Ocimeae-Lamiaceae). <i>Systematic Botany</i> , 2021, 46, 1086-1094.	0.2	4
19165	Functional Genomics and Comparative Lineage-Specific Region Analyses Reveal Novel Insights into Race Divergence in <i>Verticillium dahliae</i> . <i>Microbiology Spectrum</i> , 2021, 9, e0111821.	1.2	7
19166	The ties of brotherhood between japonica and indica rice for regional adaptation. <i>Science China Life Sciences</i> , 2022, 65, 1369-1379.	2.3	7
19167	Genetic differentiation of <i>Xylella fastidiosa</i> following the introduction into Taiwan. <i>Microbial Genomics</i> , 2021, 7, .	1.0	2
19168	The control of compound inflorescences: insights from grasses and legumes. <i>Trends in Plant Science</i> , 2022, 27, 564-576.	4.3	11
19170	The aggregate-forming pili (AFP) mediates the aggregative adherence of a hybrid-pathogenic <i>Escherichia coli</i> (UPEC/EPEC) isolated from a urinary tract infection. <i>Virulence</i> , 2021, 12, 3073-3093.	1.8	9
19171	<i>Octospora oscarii</i> spec. nov. (Pezizales), a bryophilous ascomycete on the pleurocarpous moss <i>Pseudotaxiphyllum elegans</i> (Hypnales). <i>Herzogia</i> , 2021, 34, .	0.1	4
19172	<i>Lentilactobacillus fungorum</i> sp. nov., isolated from spent mushroom substrates. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	6
19173	Comparative Analysis of <i>Apocellia endiviifolia</i> Plastomes Reveals a Strikingly High Level of Differentiation between Its Terrestrial and Water Form. <i>Diversity</i> , 2021, 13, 674.	0.7	5
19175	Seed traits matter—Endozoochoric dispersal through a pervasive mobile linker. <i>Ecology and Evolution</i> , 2021, 11, 18477-18491.	0.8	2
19176	A masculinizing supergene underlies an exaggerated male reproductive morph in a spider. <i>Nature Ecology and Evolution</i> , 2022, 6, 195-206.	3.4	18
19177	Evolutionary footprints of a cold relic in a rapidly warming world. <i>ELife</i> , 2021, 10, .	2.8	5
19178	Genetic structure and evolutionary diversity of mating-type (MAT) loci in <i>Hypsizygus marmoreus</i> . <i>IMA Fungus</i> , 2021, 12, 35.	1.7	9
19179	Biodiversity Patterns and Ecological Preferences of the Photobionts Associated With the Lichen-Forming Genus <i>Parmelia</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 765310.	1.5	6
19180	Amsterdam urban canals contain novel niches for methane-cycling microorganisms. <i>Environmental Microbiology</i> , 2022, 24, 82-97.	1.8	8
19181	VasH Contributes to Virulence of <i>Aeromonas hydrophila</i> and Is Necessary to the T6SS-mediated Bactericidal Effect. <i>Frontiers in Veterinary Science</i> , 2021, 8, 793458.	0.9	6
19182	Climate change and biocrust disturbance synergistically decreased taxonomic, functional and phylogenetic diversity in annual communities on gypsiferous soils. <i>Oikos</i> , 2022, 2022, .	1.2	7
19183	Parallel genomic responses to historical climate change and high elevation in East Asian songbirds. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	12

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19184	Comparative transcriptomic analysis of apple and peach fruits: insights into fruit type specification. <i>Plant Journal</i> , 2022, 109, 1614-1629.	2.8	4
19185	Performance and Agreement Between WGS Variant Calling Pipelines Used for Bovine Tuberculosis Control: Toward International Standardization. <i>Frontiers in Veterinary Science</i> , 2021, 8, 780018.	0.9	3
19187	Transcriptomic analysis of resistance and short-term induction response to pyrethroids, in <i>Anopheles coluzzii</i> legs. <i>BMC Genomics</i> , 2021, 22, 891.	1.2	11
19189	Morphological and Phylogenetic Analyses Reveal a New Species of <i>Ceratocystiopsis</i> (Ophiostomataceae, Ophiostomatales) Associated with <i>Ips subelongatus</i> in Inner Mongolia (China) with Weak Host Pathogenicity. <i>Forests</i> , 2021, 12, 1795.	0.9	4
19190	The Madeiran laurel forest endemic <i>Goodyera macrophylla</i> (Orchidaceae) is related to American orchids. <i>Anales Del Jardin Botanico De Madrid</i> , 2021, 78, e116.	0.2	2
19191	The complete chloroplast genome of <i>Sedum tricarpum</i> Makino. (Crassulaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 15-16.	0.2	1
19192	The Edible Plant Microbiome represents a diverse genetic reservoir with functional potential in the human host. <i>Scientific Reports</i> , 2021, 11, 24017.	1.6	14
19193	Draft Genome Sequence of a New <i>Fusarium</i> Isolate Belonging to <i>Fusarium tricinctum</i> Species Complex Collected From Hazelnut in Central Italy. <i>Frontiers in Plant Science</i> , 2021, 12, 788584.	1.7	6
19195	<i>Cryptosporidium felis</i> differs from other <i>Cryptosporidium</i> spp. in codon usage. <i>Microbial Genomics</i> , 2021, 7, .	1.0	3
19196	Pan-Resistome Characterization of Uropathogenic <i>Escherichia coli</i> and <i>Klebsiella pneumoniae</i> Strains Circulating in Uganda and Kenya, Isolated from 2017–2018. <i>Antibiotics</i> , 2021, 10, 1547.	1.5	11
19197	Palaeoecological and genetic analyses of Late Pleistocene bears in Asiatic Russia. <i>Boreas</i> , 2022, 51, 465-480.	1.2	3
19198	Prey life history influences the evolution of egg mass and indirectly reproductive investment in a group of free-living insect predators. <i>Ecology and Evolution</i> , 2022, 12, e8438.	0.8	2
19199	Delineation of the Ancestral Tus-Dependent Replication Fork Trap. <i>International Journal of Molecular Sciences</i> , 2021, 22, 13533.	1.8	4
19201	Another case of colour pattern polymorphism in Earth Snakes of the genus <i>Geophis</i> (Dipsadidae) from southern Mexico. <i>Journal of Natural History</i> , 2021, 55, 2985-2997.	0.2	2
19202	A Review of the Emerging White Chick Hatchery Disease. <i>Viruses</i> , 2021, 13, 2435.	1.5	6
19203	Reactivation of transposable elements following hybridization in fission yeast. <i>Genome Research</i> , 2022, 32, 324-336.	2.4	13
19204	The Dynamics of NO ₃ ⁻ and NH ₄ ⁺ Uptake in Duckweed Are Coordinated with the Expression of Major Nitrogen Assimilation Genes. <i>Plants</i> , 2022, 11, 11.	1.6	20
19205	The genomic basis of high-elevation adaptation in wild house mice (<i>Mus musculus domesticus</i>) from South America. <i>Genetics</i> , 2022, 220, .	1.2	7

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19206	A species-level timeline of mammal evolution integrating phylogenomic data. <i>Nature</i> , 2022, 602, 263-267.	13.7	84
19207	A new and very spiny lizard (<i>Gymnophthalmidae</i> : <i>Echinosaura</i>) from the Andes in northwestern Ecuador. <i>PeerJ</i> , 2021, 9, e12523.	0.9	1
19208	The complete mitogenome of <i>Chrysopogon zizanioides</i> (L.) Roberty (Poaceae), with its phylogenetic analysis. <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 25-27.	0.2	0
19209	<i>Shewanella nanhaiensis</i> sp. nov., a marine bacterium isolated from sediment of South China Sea, and emended descriptions of <i>Shewanella woodyi</i> , <i>Shewanella hanedai</i> and <i>Shewanella canadensis</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	14
19210	Identification and Antimicrobial Activity of Actinobacteria Isolated from Rhizosphere of the Local Endemic Plants. <i>Yuzuncu Yil University Journal of Agricultural Sciences</i> , 0, , 876-885.	0.1	0
19211	High genome plasticity and frequent genetic exchange in <i>Leishmania tropica</i> isolates from Afghanistan, Iran and Syria. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0010110.	1.3	8
19212	A new species of red toad, <i>Schismaderma</i> Smith, 1849 (Anura: Bufonidae), from central Angola. <i>Zootaxa</i> , 2021, 5081, 301-332.	0.2	3
19213	The first complete mitogenome of skin beetles <i>Omorgus chinensis</i> (Coleoptera: Trogidae) with the phylogenetic implications. <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 70-73.	0.2	1
19214	Characterization of the complete mitochondrial genome of <i>Aspergillus terricola</i> (Aspergillaceae, Eurotiales), isolated from soy sauce fermentation system. <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 76-78.	0.2	1
19215	A new eyeless species of <i>Nicon</i> (Annelida: Nereididae) from the deep Northwest Pacific Ocean. <i>Acta Oceanologica Sinica</i> , 2021, 40, 20-26.	0.4	5
19216	DNA Barcoding of <i>Adiantum</i> (Pteridaceae: Vittarioideae) in Puerto Rico. <i>Caribbean Journal of Science</i> , 2021, 51, .	0.2	1
19217	<i>Callistosporium luteo-olivaceum</i> (Callistosporiaceae: Basidiomycota), an agaric fungi new to Turkey. <i>Anatolian Journal of Botany</i> , 0, , .	0.5	1
19218	Update of Genetic Diversity of Porcine Circovirus Type 2 in Chile Evidences the Emergence of PCV2d Genotype. <i>Frontiers in Veterinary Science</i> , 2021, 8, 789491.	0.9	5
19220	<i>Notoligotrichum</i> synonymised with <i>Atrichopsis</i> (Polytrichaceae, Bryophyta), with two new species from South Africa. <i>Taxon</i> , 2022, 71, 11-24.	0.4	0
19221	Linkage of Whole Genome Sequencing, Epidemiological, and Clinical Data to Understand the Genetic Diversity and Clinical Outcomes of <i>Shigella flexneri</i> among Men Who Have Sex with Men in England. <i>Microbiology Spectrum</i> , 2021, 9, e0121321.	1.2	3
19222	Molecular phylogeny and diversity of <i>Laburnicola</i> (Didymosphaeriaceae): a new species from Uzbekistan. <i>Phytotaxa</i> , 2021, 527, 177-190.	0.1	2
19224	The complete chloroplast and mitochondrial genomes of <i>Scopelophila cataractae</i> (Mitt.) Broth. (Pottiaceae, Bryophyta). <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 125-127.	0.2	1
19225	<i>Streptococcus sputorum</i> , a Novel Member of <i>Streptococcus</i> with Multidrug Resistance, Exhibits Cytotoxicity. <i>Antibiotics</i> , 2021, 10, 1532.	1.5	0

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19226	Vineibacter terrae gen. nov., sp. nov., an ammonium-assimilating and nitrate-reducing bacterium isolated from vineyard soil. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	9
19227	Natural rodent model of viral transmission reveals biological features of virus population dynamics. Journal of Experimental Medicine, 2022, 219, .	4.2	18
19229	Source Tracking and Global Distribution of the Tigecycline Non-Susceptible <i>tet(X)</i> . Microbiology Spectrum, 2021, 9, e0116421.	1.2	16
19231	Evolutionary and Ecological Explanations for the Elevational Flexibility of Several East African Bird Species Complexes. Frontiers in Ecology and Evolution, 2021, 9, .	1.1	6
19232	The Importance of Glycerophospholipid Production to the Mutualist Symbiosis of Trypanosomatids. Pathogens, 2022, 11, 41.	1.2	5
19233	Whole-Genome Sequencing Highlights Conservative Genomic Strategies of a Stress-Tolerant, Long-Lived Scleractinian Coral, <i>Porites australiensis</i> Vaughan, 1918. Genome Biology and Evolution, 2021, 13, .	1.1	16
19234	Genomic evidence for the parallel regression of melatonin synthesis and signaling pathways in placental mammals. Open Research Europe, 0, 1, 75.	2.0	2
19235	One more piece to the puzzle: <i>Diadorimia</i> , a new monotypic genus in the Spermacoceae (Rubiaceae), endemic to the campo rupestre of Minas Gerais, southeastern Brazil. Taxon, 2022, 71, 396-419.	0.4	5
19236	Eastern Yellow Wagtail <i>Motacilla tschutschensis</i> and Western Yellow Wagtail <i>M. flava</i> in Sri Lanka with comments on their status in South Asia. Bulletin of the British Ornithologists' Club, 2021, 141, .	0.1	0
19237	In situ visualization of glycoside hydrolase family 92 genes in marine flavobacteria. ISME Communications, 2021, 1, .	1.7	1
19238	The complete mitochondrial genome of <i>Fopius arisanus</i> (Sonan 1932) (Hymenoptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 342	0.2	0
19239	Morphological and molecular phylogenetic analyses reveal three species of <i>Colletotrichum</i> in Shandong province, China. MycoKeys, 2021, 85, 57-71.	0.8	6
19240	Detecting the phylogenetic signal of glacial refugia in a bryodiversity hotspot outside the tropics. Diversity and Distributions, 2022, 28, 2681-2695.	1.9	5
19241	Identity of <i>Gymnophthalmus</i> (Squamata: Gymnophthalmidae) from northeastern Amazonia with evidence for <i>G. underwoodi</i> as invasive in BelĂ©m. Acta Amazonica, 2021, 51, 291-297.	0.3	0
19243	<i>Colletotrichum pereskiae</i> sp. nov. causing anthracnose on <i>Pereskia aculeata</i> in Brazil. Mycological Progress, 2021, 20, 1583-1593.	0.5	2
19245	Network science inspires novel tree shape statistics. PLoS ONE, 2021, 16, e0259877.	1.1	7
19246	Phylogeography of <i>Artemisia frigida</i> (Anthemideae, Asteraceae) based on genotyping-by-sequencing and plastid DNA data: Migration through Beringia. Journal of Evolutionary Biology, 2022, 35, 64-80.	0.8	4
19247	Diversification of ergot alkaloids and heritable fungal symbionts in morning glories. Communications Biology, 2021, 4, 1362.	2.0	12

#	ARTICLE	IF	CITATIONS
19248	Three new species of <i>Byrsopteryx</i> Flint microcaddisflies from Peru (Insecta: Trichoptera) including DNA-based larval associations. PeerJ, 2021, 9, e12645.	0.9	1
19250	Thrice out of Asia and the adaptive radiation of the western honey bee. Science Advances, 2021, 7, eabj2151.	4.7	33
19251	Genome-Wide Sequence-Based Genotyping Supports a Nonhybrid Origin of <i>Castanea alabamensis</i> . Systematic Botany, 2021, 46, 973-984.	0.2	3
19253	The Genetic Population Structure of Lake Tanganyika's <i>Lates</i> Species Flock, an Endemic Radiation of Pelagic Top Predators. Journal of Heredity, 2022, 113, 145-159.	1.0	1
19254	ϕζ Azygosporus gen. nov., a synapomorphic clade in the family Ancylistaceae. MycoKeys, 2021, 85, 161-172.	0.8	4
19255	Whole Genome Sequencing and Phylogenetic Analysis of Rabies Viruses from Bats in Connecticut, USA, 2018–2019. Viruses, 2021, 13, 2500.	1.5	2
19256	Genome Sequence of <i>Chrysotila roscoffensis</i> , a Coccolithophore Contributed to Global Biogeochemical Cycles. Genes, 2022, 13, 40.	1.0	2
19259	An empirical test of the relationship between the bootstrap and likelihood ratio support in maximum likelihood phylogenetic analysis. Cladistics, 2021, . .	1.5	0
19260	Characterization and analysis of complete chloroplast genome of <i>Clausena anisum-olens</i> (Blanco) Merrill. Mitochondrial DNA Part B: Resources, 2022, 7, 89-90.	0.2	0
19261	Genome reorganization during emergence of host-associated <i>Mycobacterium abscessus</i> . Microbial Genomics, 2021, 7, .	1.0	6
19262	First Glimpse at the Diverse Aquaporins of Amphipod Crustaceans. Cells, 2021, 10, 3417.	1.8	3
19263	RAxML Grove: an empirical phylogenetic tree database. Bioinformatics, 2022, 38, 1741-1742.	1.8	11
19264	Looking through the FOG: microbiome characterization and lipolytic bacteria isolation from a fatberg site. Microbiology (United Kingdom), 2021, 167, .	0.7	1
19266	Contemporary Clinical and Molecular Epidemiology of Vancomycin-Resistant Enterococcal Bacteremia: A Prospective Multicenter Cohort Study (VENOUS I). Open Forum Infectious Diseases, 2022, 9, ofab616.	0.4	18
19267	Genome sequencing and transcriptome analyses provide insights into the origin and domestication of water caltrop (<i>Trapa</i> spp., Lythraceae). Plant Biotechnology Journal, 2022, 20, 761-776.	4.1	16
19268	A nationwide genomic study of clinical <i>Klebsiella pneumoniae</i> in Norway 2001–15: introduction and spread of ESBLs facilitated by clonal groups CG15 and CG307. Journal of Antimicrobial Chemotherapy, 2022, 77, 665-674.	1.3	16
19269	CNVs with adaptive potential in <i>Rangifer tarandus</i> : genome architecture and new annotated assembly. Life Science Alliance, 2022, 5, e202101207.	1.3	7
19270	Specific gut microbiome signatures and the associated pro-inflammatory functions are linked to pediatric allergy and acquisition of immune tolerance. Nature Communications, 2021, 12, 5958.	5.8	77

#	ARTICLE	IF	CITATIONS
19272	The Miseno Lake (Central-Western Mediterranean Sea): An Overlooked Reservoir of Non-Indigenous and Cryptogenic Ascidiens in a Marine Reserve. <i>Frontiers in Marine Science</i> , 2022, 9, .	1.2	9
19273	ANALYSIS OF POSITIVE SELECTION PROVIDES INSIGHTS INTO LIFESTYLE- AND LINEAGE-SPECIFIC PATTERNS OF MOLECULAR EVOLUTION IN INSECTS. <i>DÄ¼zce Äœniversitesi Bilim Ve Teknoloji Dergisi</i> , 0, , .	0.2	0
19274	Fine-scale population structure within an Eastern Nearctic snake complex (<i>Pituophis</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf,50 662 Td	0.7	5
19275	A LASSO-based approach to sample sites for phylogenetic tree search. <i>Bioinformatics</i> , 2022, 38, i118-i124.	1.8	1
19276	Fingerprints of climatic changes through the late Cenozoic in southern Asian flora: <i>Magnolia</i> section <i>Michelia</i> (Magnoliaceae). <i>Annals of Botany</i> , 2022, 130, 41-52.	1.4	3
19277	Metagenomic investigation of the equine faecal microbiome reveals extensive taxonomic diversity. <i>PeerJ</i> , 2022, 10, e13084.	0.9	18
19278	A revision of the genus <i>Ecpyrrhorhoe</i> HÄ¼bner, 1825 from China based on morphology and molecular data, with descriptions of five new species (Lepidoptera, Crambidae, Pyraustinae). <i>ZooKeys</i> , 2022, 1090, 1-44.	0.5	1
19279	First report of leaf anthracnose caused by <i>Colletotrichum chrysophilum</i> on a <i>Sa-palm</i> (Euterpe) Tj ETQq1 1 0.784314 rgBT /Overlock 1	0.6	3
19281	The Sea Slug <i>Doriopsilla areolata</i> Bergh, 1880 (Mollusca, Gastropoda) in the Mediterranean Sea: Another Case of Cryptic Diversity. <i>Diversity</i> , 2022, 14, 297.	0.7	4
19282	Genomic insights on the contribution of introgressions from Xian/Indica to the genetic improvement of Geng/Japonica rice cultivars. <i>Plant Communications</i> , 2022, 3, 100325.	3.6	8
19283	Two New Species of <i>Sidera</i> (Hymenochaetales, Basidiomycota) from Southwest China. <i>Journal of Fungi</i> (Basel, Switzerland), 2022, 8, 385.	1.5	2
19284	Host diversity and behavior determine patterns of interspecies transmission and geographic diffusion of avian influenza A subtypes among North American wild reservoir species. <i>PLoS Pathogens</i> , 2022, 18, e1009973.	2.1	9
19285	Widespread interspecific phylogenetic tree incongruence between mosquito-borne and insect-specific flaviviruses at hotspots originally identified in Zika virus. <i>Virus Evolution</i> , 2022, 8, veac027.	2.2	2
19286	Localized Phylogenetic Discordance Among Nuclear Loci Due to Incomplete Lineage Sorting and Introgression in the Family of Cotton and Cacao (Malvaceae). <i>Frontiers in Plant Science</i> , 2022, 13, 850521.	1.7	0
19287	<i>Mycobacterium tuberculosis</i> Lineages Associated with Mutations and Drug Resistance in Isolates from India. <i>Microbiology Spectrum</i> , 2022, 10, e0159421.	1.2	10
19288	Amplicon Sequencing of Single-Copy Protein-Coding Genes Reveals Accurate Diversity for Sequence-Discrete Microbiome Populations. <i>Microbiology Spectrum</i> , 2022, 10, e0210521.	1.2	0
19290	Prevalence of an Insect-Associated Genomic Region in Environmentally Acquired <i>Burkholderiaceae</i> Symbionts. <i>Applied and Environmental Microbiology</i> , 2022, 88, e0250221.	1.4	2
19291	Genomic characterisation of an entomopathogenic strain of <i>Serratia ureilytica</i> in the critically endangered phasmid <i>Dryococelus australis</i> . <i>PLoS ONE</i> , 2022, 17, e0265967.	1.1	0

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19292	Comparative Genomics Provides Insights into Adaptive Evolution in Tactile-Foraging Birds. <i>Genes</i> , 2022, 13, 678.	1.0	1
19293	Genome-based classification of <i>Streptomyces pinistramenti</i> sp. nov., a novel actinomycete isolated from a pine forest soil in Poland with a focus on its biotechnological and ecological properties. <i>Antonie Van Leeuwenhoek</i> , 2022, 115, 783-800.	0.7	3
19294	Insights into the systematics of the family Ophryoscolecidae (Ciliophora, Entodiniomorphida). <i>Journal of Eukaryotic Microbiology</i> , 2022, , e12915.	0.8	1
19295	Molecular analyses reveal a new species of Palmariaceae from Subantarctic Chile: <i>Devaleraea yagan</i> sp. nov. (Palmariales, Rhodophyta). <i>Phycologia</i> , 0, , 1-9.	0.6	1
19296	<i>Pusillimonas faecipullorum</i> sp. nov., isolated from the poultry manure. <i>Archives of Microbiology</i> , 2022, 204, 256.	1.0	9
19297	Differential Modulation of the European Sea Bass Gut Microbiota by Distinct Insect Meals. <i>Frontiers in Microbiology</i> , 2022, 13, 831034.	1.5	17
19298	Population expansion, divergence, and persistence in Western Fence Lizards (<i>Sceloporus occidentalis</i>) at the northern extreme of their distributional range. <i>Scientific Reports</i> , 2022, 12, 6310.	1.6	2
19299	Symbiotic Dinoflagellates of the Giant Clam, <i>Tridacna squamosa</i> , Express Ammonium Transporter 2 at the Plasma Membrane and Increase Its Expression Levels During Illumination. <i>Frontiers in Marine Science</i> , 2022, 9, .	1.2	4
19300	R gene triplication confers European fodder turnip with improved clubroot resistance. <i>Plant Biotechnology Journal</i> , 2022, 20, 1502-1517.	4.1	15
19301	Phylogenetic Analyses of Cyprinid Species from the Rokel River Basin of Sierra Leone, West Africa: Taxonomic, Biogeographic, and Conservation Implications. <i>Diversity</i> , 2022, 14, 299.	0.7	1
19302	Unlocking Andean sigmodontine diversity: five new species of <i>Chilomys</i> (Rodentia: Cricetidae) from the montane forests of Ecuador. <i>PeerJ</i> , 2022, 10, e13211.	0.9	7
19303	The role of climate and islands in species diversification and reproductive-mode evolution of Old World tree frogs. <i>Communications Biology</i> , 2022, 5, 347.	2.0	7
19304	The <i>Cycas</i> genome and the early evolution of seed plants. <i>Nature Plants</i> , 2022, 8, 389-401.	4.7	80
19305	Molecular phylogeny of the genus <i>Chondrina</i> (Gastropoda, Panpulmonata, Chondrinidae) in the Iberian Peninsula. <i>Molecular Phylogenetics and Evolution</i> , 2022, 172, 107480.	1.2	0
19306	Microbial Ecology of Sulfur Biogeochemical Cycling at a Mesothermal Hot Spring Atop Northern Himalayas, India. <i>Frontiers in Microbiology</i> , 2022, 13, 848010.	1.5	6
19307	Mutational meltdown or controlled chain reaction: The dynamics of rapid plastome evolution in the hyperdiversity of Poaceae. <i>Journal of Systematics and Evolution</i> , 2023, 61, 328-344.	1.6	5
19309	Synopsis of Leptosphaeriaceae and Introduction of Three New Taxa and One New Record from China. <i>Journal of Fungi</i> (Basel, Switzerland), 2022, 8, 416.	1.5	4
19310	Two new <i>Clitocella</i> species from North China revealed by phylogenetic analyses and morphological characters. <i>MycoKeys</i> , 2022, 88, 151-170.	0.8	3

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19311	Identification of the original plants of cultivated <i>Bupleuri Radix</i> based on DNA barcoding and chloroplast genome analysis. <i>PeerJ</i> , 2022, 10, e13208.	0.9	5
19313	Morphological and phylogenetic analyses reveal two new species of Sporocadaceae from Hainan, China. <i>MycKeys</i> , 2022, 88, 171-192.	0.8	13
19314	Stripes Matter: Integrative Systematics of <i>Coryphellina rubrolineata</i> Species Complex (Gastropoda: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.7	8
19315	Fluctuating Starvation Conditions Modify Host-Symbiont Relationship Between a Leaf Beetle and Its Newly Identified Gregarine Species. <i>Frontiers in Ecology and Evolution</i> , 2022, 10, .	1.1	0
19316	Genomic Architecture and Evolution of the Cellulose synthase Gene Superfamily as Revealed by Phylogenomic Analysis. <i>Frontiers in Plant Science</i> , 2022, 13, 870818.	1.7	6
19317	pmTR database: population matched (pm) germline allelic variants of T-cell receptor (TR) loci. <i>Genes and Immunity</i> , 2022, 23, 99-110.	2.2	2
19318	Genetic assessment and climate modelling of the Iberian specialist butterfly <i>Euchloe bazae</i> (Lepidoptera: Pieridae). <i>Insect Conservation and Diversity</i> , 2022, 15, 594-605.	1.4	2
19319	Reassessing fish diversity of Penang Island's freshwaters (northwest Peninsular Malaysia) through a molecular approach raises questions on its conservation status. <i>Biodiversity and Conservation</i> , 0, , 1.	1.2	0
19320	Glacial vicariance and oceanic circulation shape population structure of the coastal legume <i>Derris trifoliata</i> in the Indo-West Pacific. <i>American Journal of Botany</i> , 2022, 109, 1016-1034.	0.8	1
19321	Class C β -Lactamases: Molecular Characteristics. <i>Clinical Microbiology Reviews</i> , 2022, 35, e0015021.	5.7	15
19322	The Effects of Predictive Factors on Patient Prognosis in the Administration of Medical and Surgical Treatment in Patients with Acute Pancreatitis. <i>The Journal of Tepecik Education and Research Hospital</i> , 2022, 32, 107-114.	0.2	0
19323	Mitochondrial genomes of the freshwater monogonont rotifer <i>Brachionus fernandoi</i> and of two additional <i>B. calyciflorus</i> sensu stricto lineages from Germany and the USA (Rotifera.) Tj ETQq1 1 0.784014 rgBT /Overlock 1	0.7	14
19324	First report of <i>Nigrospora lacticolonia</i> causing leaf spot of <i>Bougainvillea spectabilis</i> in China. <i>Canadian Journal of Plant Pathology</i> , 2022, 44, 695-701.	0.8	2
19325	<i>Qipengyuania pacifica</i> sp. nov., a Novel Carotenoid-Producing Marine Bacterium of the Family Erythrobacteraceae, Isolated from Sponge (Demospongiae), and Antimicrobial Potential of Its Crude Extract. <i>Diversity</i> , 2022, 14, 295.	0.7	8
19326	Genomic and Chemical Decryption of the Bacteroidetes Phylum for Its Potential to Biosynthesize Natural Products. <i>Microbiology Spectrum</i> , 2022, 10, e0247921.	1.2	11
19327	Phylogenomic analysis does not support a classic but controversial hypothesis of progenitor-derivative origins for the serpentine endemic <i>Clarkia franciscana</i> . <i>Evolution; International Journal of Organic Evolution</i> , 2022, 76, 1246-1259.	1.1	2
19328	Understanding Diversity, Evolution, and Structure of Small Heat Shock Proteins in Annelida Through in Silico Analyses. <i>Frontiers in Physiology</i> , 2022, 13, 817272.	1.3	2
19329	Origin and early evolution of the plant terpene synthase family. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2100361119.	3.3	48

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19330	Microbial Activities and Selection from Surface Ocean to Subseafloor on the Namibian Continental Shelf. Applied and Environmental Microbiology, 2022, 88, e0021622.	1.4	4
19331	A century of stasis: Taxonomy of <i>Ctenomys</i> (Rodentia: Hystricomorpha) populations in northeastern Patagonia limits, Argentina. Zoologischer Anzeiger, 2022, 298, 136-147.	0.4	4
19332	Species delimitation and molecular diagnosis of <i>Cyrtomium yamomotoi</i> (Dryopteridaceae). Plant Systematics and Evolution, 2022, 308, 1.	0.3	0
19333	Loosening the belt: unknown diversity of the strangled stinkhorn genus <i>Staheliomyces</i> (Phallales.) Tj ETQq1 1 0.784314 rgBT /Overlock 0,5 1	0.5	1
19334	Genomic evidence for homoploid hybrid speciation between ancestors of two different genera. Nature Communications, 2022, 13, 1987.	5.8	18
19335	Identification of a KPC Variant Conferring Resistance to Ceftazidime-Avibactam from ST11 Carbapenem-Resistant <i>Klebsiella pneumoniae</i> Strains. Microbiology Spectrum, 2022, 10, e0265521.	1.2	5
19336	DNA Barcoding of Fresh and Historical Collections of Lichen-Forming Basidiomycetes in the Genera <i>Cora</i> and <i>Corella</i> (Agaricales: Hygrophoraceae): A Success Story?. Diversity, 2022, 14, 284.	0.7	3
19337	Transcriptome analysis provides new insights into cold adaptation of corsac fox (<i>Vulpes</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 0,8 5	0.8	5
19338	Plastome structure, phylogenomics and evolution of plastid genes in <i>Swertia</i> (Gentianaceae) in the Qing-Tibetan Plateau. BMC Plant Biology, 2022, 22, 195.	1.6	11
19339	Comparative Analyses of 3,654 Plastid Genomes Unravel Insights Into Evolutionary Dynamics and Phylogenetic Discordance of Green Plants. Frontiers in Plant Science, 2022, 13, 808156.	1.7	8
19340	<i>Glugea</i> sp. infecting <i>Sardinella aurita</i> in Algeria. Journal of Parasitic Diseases, 0, , 1.	0.4	0
19341	A Chromosome-Level Genome of the Camphor Tree and the Underlying Genetic and Climatic Factors for Its Top-Geoherbalism. Frontiers in Plant Science, 2022, 13, 827890.	1.7	9
19343	Using Mitogenomes to Explore the Social and Ecological Contexts of Crocodile Mummification in Ancient Egypt. Bulletin of the Peabody Museum of Natural History, 2022, 63, .	0.6	1
19344	Assessment of ITS2 Region Relevance for Taxa Discrimination and Phylogenetic Inference among Pinaceae. Plants, 2022, 11, 1078.	1.6	4
19345	On the Phylogenetic Position of <i>Raphidocystis pallida</i> with Some Notes on Its Life Cycle. Journal of Eukaryotic Microbiology, 2022, , e12916.	0.8	1
19346	Structures of distant diphtheria toxin homologs reveal functional determinants of an evolutionarily conserved toxin scaffold. Communications Biology, 2022, 5, 375.	2.0	4
19347	<i>Acinetobacter silvestris</i> sp. nov. discovered in forest ecosystems in Czechia. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	7
19348	Global genetic diversity status and trends: towards a suite of Essential Biodiversity Variables (EBVs) for genetic composition. Biological Reviews, 2022, 97, 1511-1538.	4.7	73

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19349	Five new mitogenomes sequences of Calidridine sandpipers (Aves: Charadriiformes) and comparative mitogenomics of genus <i>Calidris</i> . PeerJ, 2022, 10, e13268.	0.9	2
19350	How many single-copy orthologous genes from whole genomes reveal deep gastropod relationships?. PeerJ, 2022, 10, e13285.	0.9	1
19351	Anopheles mosquitoes reveal new principles of 3D genome organization in insects. Nature Communications, 2022, 13, 1960.	5.8	19
19352	Chromosome-level genome assembly for the horned gall aphid provides insights into interactions between gall-making insect and its host plant. Ecology and Evolution, 2022, 12, e8815.	0.8	8
19353	Genome Streamlining, Proteorhodopsin, and Organic Nitrogen Metabolism in Freshwater Nitrifiers. MBio, 2022, 13, e0237921.	1.8	7
19354	Rapid Identification and Source Tracing of a <i>Salmonella</i> Typhimurium Outbreak in China by Metagenomic and Whole-Genome Sequencing. Foodborne Pathogens and Disease, 2022, 19, 259-265.	0.8	1
19355	Phylogenetic Distribution and Evolution of Type VI Secretion System in the Genus <i>Xanthomonas</i> . Frontiers in Microbiology, 2022, 13, 840308.	1.5	5
19356	Distinct mtDNA lineages in free-ranging <i>Ammotragus</i> (aoudad) from the United States indicate multiple introductions from northern Africa. Ecology and Evolution, 2022, 12, e8849.	0.8	3
19357	Dynamic evolutionary history of spiral-specific TALE homeobox genes in mollusks. Development Growth and Differentiation, 2022, 64, 198-209.	0.6	2
19358	Improving the efficiency of Rubisco by resurrecting its ancestors in the family Solanaceae. Science Advances, 2022, 8, eabm6871.	4.7	32
19359	Highly pathogenic avian influenza virus incursions of subtype H5N8, H5N5, H5N1, H5N4, and H5N3 in Germany during 2020-21. Virus Evolution, 2022, 8, veac035.	2.2	19
19360	Characterization of the Entomopathogenic Fungal Species <i>Conoideocrella luteorostrata</i> on the Scale Insect Pest <i>Fiorinia externa</i> Infesting the Christmas Tree <i>Abies fraseri</i> in the USA. Florida Entomologist, 2022, 105, .	0.2	1
19361	A chromosome-level genome of the kuruma shrimp (<i>Marsupenaeus japonicus</i>) provides insights into its evolution and cold-resistance mechanism. Genomics, 2022, 114, 110373.	1.3	8
19362	Genome analysis of five recently described species of the CUG-Ser clade uncovers <i>Candida theae</i> as a new hybrid lineage with pathogenic potential in the <i>Candida parapsilosis</i> species complex. DNA Research, 2022, , .	1.5	4
19363	A novel structure-based approach for identification of vertebrate susceptibility to SARS-CoV-2: Implications for future surveillance programmes. Environmental Research, 2022, 212, 113303.	3.7	6
19364	Epidemiology and Comparative Analyses of the S Gene on Feline Coronavirus in Central China. Pathogens, 2022, 11, 460.	1.2	8
19365	Identification and Tissue Expression Profiles of Odorant Receptor Genes in the Green Peach Aphid <i>Myzus persicae</i> . Insects, 2022, 13, 398.	1.0	2
19366	Genome-scale phylogeography resolves the native population structure of the Asian longhorned beetle, <i>Anoplophora glabripennis</i> (Motschulsky). Evolutionary Applications, 2022, 15, 934-953.	1.5	7

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19367	Prediction of Prophages and Their Host Ranges in Pathogenic and Commensal <i>Neisseria</i> Species. <i>MSystems</i> , 2022, 7, e0008322.	1.7	9
19369	Understanding the Genetic Diversity of <i>Mycobacterium africanum</i> Using Phylogenetics and Population Genomics Approaches. <i>Frontiers in Genetics</i> , 2022, 13, 800083.	1.1	0
19370	Morphology, Morphogenesis and Molecular Phylogeny of a New Soil Ciliate, <i>Holostichides eastensis</i> nov. spec. (Ciliophora, Hypotrichia). <i>Protist</i> , 2022, 173, 125881.	0.6	1
19371	Incomplete lineage sorting and local extinction shaped the complex evolutionary history of the Paleogene relict conifer genus, <i>Chamaecyparis</i> (Cupressaceae). <i>Molecular Phylogenetics and Evolution</i> , 2022, 172, 107485.	1.2	4
19372	Substrate loading and nutrient composition steer caproic acid production and biofilm aggregation in high-rate granular reactors. <i>Journal of Environmental Chemical Engineering</i> , 2022, 10, 107727.	3.3	8
19373	Genome-wide loss of <i>CHH</i> methylation with limited transcriptome changes in <i>Setaria viridis</i> DOMAINS REARRANGED METHYLTRANSFERASE (<i>DRM</i>) mutants. <i>Plant Journal</i> , 2022, 111, 103-116.	2.8	2
19374	Habitats hold an evolutionary signal of past climatic refugia. <i>Biodiversity and Conservation</i> , 0, , 1.	1.2	3
19375	Alternating nuclear DNA content in chrysophytes provides evidence of their isomorphic haploid-diploid life cycle. <i>Algal Research</i> , 2022, 64, 102707.	2.4	1
19376	Isolation and identification of <i>Bacillus vallismortis</i> HSB-2 and its biocontrol potential against apple replant disease. <i>Biological Control</i> , 2022, 170, 104921.	1.4	7
21006	Phylogenomic analyses in Phrymaceae reveal extensive gene tree discordance in relationships among major clades. <i>American Journal of Botany</i> , 2022, 109, 1035-1046.	0.8	6
21007	<i>Plesiochorus irwinorum</i> n. sp. (Trematoda: Gorgoderidae) from the urinary bladder of the hawksbill turtle, <i>Eretmochelys imbricata</i> (Testudines: Cheloniidae), off the east coast of Australia. <i>Systematic Parasitology</i> , 2022, , 1.	0.5	3
21008	Deletion and tandem duplications of biosynthetic genes drive the diversity of triterpenoids in <i>Aralia elata</i> . <i>Nature Communications</i> , 2022, 13, 2224.	5.8	34
21009	New genera, species, and combinations of Boletaceae from Brazil and Guyana. <i>Mycologia</i> , 2022, 114, 607-625.	0.8	9
21011	Dissemination of <i>bla</i> _{NDM-5} in <i>Escherichia coli</i> through the IncX3 Plasmid from Different Regions in China. <i>Microbial Drug Resistance</i> , 2022, 28, 453-460.	0.9	3
21012	First report of cedar-quince rust <i>Gymnosporangium clavipes</i> on fruit of dwarf hawthorn <i>Crataegus uniflora</i> in Florida, USA. <i>Plant Disease</i> , 2022, , .	0.7	0
21013	<i>Companilactobacillus salsicarnum</i> Zheng et al. 2020 is a later heterotypic synonym of <i>Companilactobacillus mishanensis</i> (Wei and Gu 2019) Zheng et al. 2020. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	3
21014	A functional <i>Wood</i> – <i>Ljungdahl</i> pathway devoid of a formate dehydrogenase in the gut acetogens <i>Blautia wexlerae</i> , <i>Blautia luti</i> and beyond. <i>Environmental Microbiology</i> , 2022, 24, 3111-3123.	1.8	14
21015	Taxonomy and phylogeny of the freshwater tintinnid <i>Tintinnopsis tubuformis</i> Chiang, 1956 (Ciliophora, Oligotrichea) and a proposed synonymization of <i>T. longa</i> nom. corr. Chiang, 1956. <i>Journal of Eukaryotic Microbiology</i> , 2022, 69, e12918.	0.8	3

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21016	Chromosome-level genome assembly for takin (<i>Budorcas taxicolor</i>) provides insights into its taxonomic status and genetic diversity. <i>Molecular Ecology</i> , 2023, 32, 1323-1334.	2.0	5
21017	River network rearrangements promote speciation in lowland Amazonian birds. <i>Science Advances</i> , 2022, 8, eabn1099.	4.7	18
21018	<i>Mycobacterium bovis</i> and <i>M. caprae</i> in Bulgaria: insight into transmission and phylogeography gained through whole-genome sequencing. <i>BMC Veterinary Research</i> , 2022, 18, 148.	0.7	4
21019	Genome-wide identification and expression profiling of odorant receptor genes in the malaria vector <i>Anopheles sinensis</i> . <i>Parasites and Vectors</i> , 2022, 15, 143.	1.0	4
21021	Toward a better understanding of phylogenetic relationships within Conringieae (Brassicaceae).. <i>Molecular Biology Research Communications</i> , 2022, 11, 37-54.	0.2	1
21022	Analyzing phylogenetic trees with timed and probabilistic model checking: the lactose persistence case study. <i>Journal of Integrative Bioinformatics</i> , 2014, 11, 248.	1.0	1
21023	Genomic Epidemiology of Global Carbapenemase-Producing <i>Escherichia coli</i> , 2015–2017. <i>Emerging Infectious Diseases</i> , 2022, 28, .	2.0	39
21024	Carbapenemase-Producing Extraintestinal Pathogenic <i>Escherichia coli</i> From Argentina: Clonal Diversity and Predominance of Hyperepidemic Clones CC10 and CC131. <i>Frontiers in Microbiology</i> , 2022, 13, 830209.	1.5	6
21029	Mitogenomics of historical type specimens clarifies the taxonomy of Ethiopian Boulenger, 1917 (<i>Anura</i>). <i>Tj ETQq0 0.0 rgBT /Qverlock 10</i>	0.5	0
21033	Identifying A New Phylogeographic Population of the Blyth's Tragopan (<i>Tragopan blythii</i>) through Multi-locus Analyses.. <i>Zoological Studies</i> , 2021, 60, e40.	0.3	0
21034	Towards Large-Scale Integrative Taxonomy (LIT): Resolving the Data Conundrum for Dark Taxa. <i>Systematic Biology</i> , 2022, 71, 1404-1422.	2.7	23
21035	Cryptic speciation shapes the biogeographic history of a northern distributed moss. <i>Botanical Journal of the Linnean Society</i> , 2023, 201, 114-134.	0.8	2
21036	Discovery of a wild, genetically pure Chinese giant salamander creates new conservation opportunities. <i>Zoological Research</i> , 2022, 43, 469-480.	0.9	14
21037	Multi-locus phylogeny unmask hidden species within the specialised spider-parasitic fungus, <i>Gibellula</i> (<i>Hypocreales</i> , <i>Cordycipitaceae</i>) in Thailand. <i>Studies in Mycology</i> , 2022, 101, 245-286.	4.5	6
21038	Reconstruction of the evolutionary biogeography reveals the origin and diversification of <i>Arisaema</i> (<i>Araceae</i>). <i>Acta Botanica Brasilica</i> , 0, 36, .	0.8	0
21039	Phylogenetic relationships of <i>Origanum</i> taxa (<i>Lamiaceae</i>) from Greece: Initial insights from molecular and morphological data. <i>Botanica Serbica</i> , 2022, 46, 71-83.	0.4	0
21040	Comparative Phylogenetic Analyses of Phoenix Dancong Tea Using Complete Chloroplast Genome Sequences. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
21042	Bacterial Assemblage in Mediterranean Salt Marshes: Disentangling the Relative Importance of Seasonality, Zonation and Halophytes. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0

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21043	Enhanced Cultured Diversity of the Mouse Gut Microbiota Enables Custom-Made Synthetic Communities. SSRN Electronic Journal, 0, , .	0.4	1
21045	<i>Aspicilia nigromaculata</i> sp. nov. (Megasporaceae, Pertusariales, Ascomycota) from Azad Jammu and Kashmir, Pakistan, evidence from morphology and DNA sequencing data. <i>Botanica Serbica</i> , 2022, 46, 105-111.	0.4	2
21046	GNAT toxins evolve toward narrow tRNA target specificities. <i>Nucleic Acids Research</i> , 2022, 50, 5807-5817.	6.5	2
21047	Evolution and functionalization of <i>vitellogenin</i> genes in the termite <i>Reticulitermes speratus</i> . <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2023, 340, 68-80.	0.6	5
21048	Molecular evolution and phylogenetic relationships of <i>Ligusticum</i> (Apiaceae) inferred from the whole plastome sequences. <i>Bmc Ecology and Evolution</i> , 2022, 22, 55.	0.7	7
21049	Dynamics and Impacts of Transposable Element Proliferation in the <i>Drosophila nasuta</i> Species Group Radiation. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	13
21050	<i>Laetitia sardoa</i> gen. & sp. nov., a new member of the Chlorellales (Trebouxiophyceae,) Tj ETQq0 0 0 rgBT /Overlock 10	0.6	3
21051	Phylogenetic inferences using nuclear ribosomal ITS and chloroplast sequences provide insights into the biogeographic origins, diversification timescales and trait evolution of <i>Rubus</i> in the Japanese Archipelago. <i>Plant Systematics and Evolution</i> , 2022, 308, 1.	0.3	5
21052	Two Hidden mtDNA-Clades of Crown-of-Thorns Starfish in the Pacific Ocean. <i>Frontiers in Marine Science</i> , 2022, 9, .	1.2	3
21053	Occurrence of High Levels of Cefiderocol Resistance in Carbapenem-Resistant <i>Escherichia coli</i> before Its Approval in China: a Report from China CRE-Network. <i>Microbiology Spectrum</i> , 2022, 10, e0267021.	1.2	30
21054	Reassessing the systematics of <i>Leptodeira</i> (Serpentes, Dipsadidae) with emphasis in the South American species. <i>Zoologica Scripta</i> , 2022, 51, 415-433.	0.7	8
21055	Amanitaceous fungi of central Western Ghats: taxonomy, phylogeny, and six new reports to Indian mycobiota. <i>Journal of Threatened Taxa</i> , 2022, 14, 20890-20902.	0.1	1
21056	Novel evolutionary insights into nemacheilid cavefish: evidence from comparative analysis of mitochondrial genomes. <i>Journal of Oceanology and Limnology</i> , 0, , 1.	0.6	2
21057	Outline, Divergence Times, and Phylogenetic Analyses of Trechisporales (Agaricomycetes,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	1.5	12
21058	Quantifying dominant bacterial genera detected in metagenomic data from fish eggs and larvae using genus-specific primers. <i>MicrobiologyOpen</i> , 2022, 11, .	1.2	2
21059	Evolution of Reproductive Traits and Implications for Adaptation and Diversification in the Yam Genus <i>Dioscorea</i> L.. <i>Diversity</i> , 2022, 14, 349.	0.7	1
21060	Metagenome-assembled genomes of phytoplankton microbiomes from the Arctic and Atlantic Oceans. <i>Microbiome</i> , 2022, 10, 67.	4.9	17
21061	Mitogenome-wise codon usage pattern from comparative analysis of the first mitogenome of <i>Blepharipa</i> sp. (<i>Muga uzifly</i>) with other Oestroid flies. <i>Scientific Reports</i> , 2022, 12, 7028.	1.6	4

#	ARTICLE	IF	CITATIONS
21062	Disentangling the taxonomic status of <i>Ctenomys</i> (Rodentia: Ctenomyidae) populations inhabiting northern areas of La Rioja Province, Argentina. <i>Mammalia</i> , 2022, 86, 527-538.	0.3	4
21063	Nuclear phylogeography reveals strong impacts of gene flow in big brown bats. <i>Journal of Biogeography</i> , 2022, 49, 1061-1074.	1.4	3
21064	ERK1/2 is an ancestral organising signal in spiral cleavage. <i>Nature Communications</i> , 2022, 13, 2286.	5.8	16
21065	Chloroplast Genome of <i>Salvia</i> Sect. <i>Drymosphace</i> : Comparative and Phylogenetic Analysis. <i>Diversity</i> , 2022, 14, 324.	0.7	5
21066	Coping With Dynamism: Phylogenetics and Phylogeographic Analyses Reveal Cryptic Diversity in <i>Heleobia</i> Snails of Atacama Saltpan, Chile. <i>Frontiers in Ecology and Evolution</i> , 2022, 10, .	1.1	4
21067	Comparative analysis of the complete mitochondrial genomes of four cordyceps fungi. <i>Ecology and Evolution</i> , 2022, 12, e8818.	0.8	3
21069	<i>Gelidium rosulatum</i> (Gelidiales, Rhodophyta), a new species of subtidal marine algae from Korea. <i>Phycologia</i> , 0, , 1-9.	0.6	1
21070	Cryptic Species Exist in <i>Vietnamella sinensis</i> Hsu, 1936 (Insecta: Ephemeroptera) from Studies of Complete Mitochondrial Genomes. <i>Insects</i> , 2022, 13, 412.	1.0	3
21071	Coprinoid Psathyrellaceae species from Cyprus: three new sabulicolous taxa from sand dunes and a four-spored form of the fimicolous species <i>Parasola cuniculorum</i> . <i>Mycological Progress</i> , 2022, 21, .	0.5	2
21072	DEPP: Deep Learning Enables Extending Species Trees using Single Genes. <i>Systematic Biology</i> , 2023, 72, 17-34.	2.7	11
21073	Molecular phylogeny and DNA barcode regions efficacy for identification of the cultivar of <i>Capsicum annuum</i> L. in Thailand. <i>Acta Horticulturae</i> , 2022, , 419-428.	0.1	0
21074	Survival and Genome Diversity of <i>Vibrio parahaemolyticus</i> Isolated from Edible Aquatic Animals. <i>Diversity</i> , 2022, 14, 350.	0.7	7
21075	Characterization of <i>Klebsiella pneumoniae</i> isolated from patients suspected of pulmonary or bubonic plague during the Madagascar epidemic in 2017. <i>Scientific Reports</i> , 2022, 12, 6871.	1.6	2
21076	<i>Marasmius tageticolor</i> and <i>M. tucumanus</i> from the Dominican Republic. <i>Mycotaxon</i> , 2022, 137, 153-169.	0.1	0
21077	<i>Phyllachora</i> species infecting maize and other grass species in the Americas represents a complex of closely related species. <i>Ecology and Evolution</i> , 2022, 12, e8832.	0.8	6
21078	Resurrected Rubisco suggests uniform carbon isotope signatures over geologic time. <i>Cell Reports</i> , 2022, 39, 110726.	2.9	18
21079	Phylogeny and Biogeographic History of <i>Parnassius</i> Butterflies (Papilionidae: Parnassiinae) Reveal Their Origin and Deep Diversification in West China. <i>Insects</i> , 2022, 13, 406.	1.0	7
21080	Discovery of Early-Branching <i>Wolbachia</i> Reveals Functional Enrichment on Horizontally Transferred Genes. <i>Frontiers in Microbiology</i> , 2022, 13, 867392.	1.5	6

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21081	Need for split: integrative taxonomy reveals unnoticed diversity in the subaquatic species of <i>Pseudohygrohypnum</i> (Pylaisiaceae, Bryophyta). PeerJ, 2022, 10, e13260.	0.9	6
21082	Human-mediated eco-evolutionary processes of the herbivorous insect <i>Hyalopterus arundiniformis</i> during the Holocene. Diversity and Distributions, 0, .	1.9	1
21083	<i>Agrilactobacillus fermenti</i> sp. nov. isolated from fermented vegetable residue. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	5
21084	Environmental Monitoring for Enteroviruses in Maputo, Mozambique—2018. Pathogens, 2022, 11, 527.	1.2	1
21085	Recent Zoonotic Spillover and Tropism Shift of a Canine Coronavirus Is Associated with Relaxed Selection and Putative Loss of Function in NTD Subdomain of Spike Protein. Viruses, 2022, 14, 853.	1.5	11
21086	Dysbiosis of the Female Murine Gut Microbiome Exacerbates Neutrophil-Mediated Vascular Allograft Injury by Affecting Immunoregulation by Acetate. Transplantation, 2022, Publish Ahead of Print, .	0.5	1
21087	Two new species in <i>Capillidium</i> (Ancylistaceae, Entomophthorales) from China, with a proposal for a new combination. MycoKeys, 0, 89, 139-153.	0.8	2
21088	Virulence and Host Range of Fungi Associated With the Invasive Plant <i>Ageratina adenophora</i> . Frontiers in Microbiology, 2022, 13, 857796.	1.5	2
21089	The numbers of fungi: contributions from traditional taxonomic studies and challenges of metabarcoding. Fungal Diversity, 2022, 114, 327-386.	4.7	53
21090	Species Diversity and Ecological Habitat of <i>Absidia</i> (Cunninghamellaceae, Mucorales) with Emphasis on Five New Species from Forest and Grassland Soil in China. Journal of Fungi (Basel, Switzerland), 2022, 8, 471.	1.5	4
21091	Taxonomy and phylogeny of the phlegmacioid clade <i>Camptori</i> (<i>Cortinarius</i> s.l., Basidiomycota) in Europe with description of four new species. Mycological Progress, 2022, 21, .	0.5	0
21092	Sequence Analysis of the Complete Mitochondrial Genome of a Medicinal Plant, <i>Vitex rotundifolia</i> Linnaeus f. (Lamiales: Lamiaceae). Genes, 2022, 13, 839.	1.0	11
21093	Draft Genome Sequence of <i>Nereida</i> sp. Strain MMG025, Isolated from Giant Kelp. Microbiology Resource Announcements, 2022, 11, e0012222.	0.3	1
21094	The complete chloroplast genome sequence of <i>Potentilla bifurca</i> L.. Mitochondrial DNA Part B: Resources, 2022, 7, 753-754.	0.2	2
21095	The complete chloroplast genome of <i>Camellia leyeensis</i> (theaceae). Mitochondrial DNA Part B: Resources, 2022, 7, 735-737.	0.2	2
21096	Microbiome Inception: an Intestinal Cestode Shapes a Hierarchy of Microbial Communities Nested within the Host. MBio, 2022, 13, e0067922.	1.8	8
21098	Genomic Sequencing and Analysis of a Novel Human Cowpox Virus With Mosaic Sequences From North America and Old World Orthopoxvirus. Frontiers in Microbiology, 2022, 13, 868887.	1.5	13
21099	Testing the Complete Plastome for Species Discrimination, Cryptic Species Discovery and Phylogenetic Resolution in <i>Cephalotaxus</i> (Cephalotaxaceae). Frontiers in Plant Science, 2022, 13, .	1.7	16

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21100	The complete mitochondrial genome of <i>Zelkova schneideriana</i> Hand-Mazz (Ulmaceae) and phylogenetic analysis. <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 778-779.	0.2	1
21101	Recurrent inversion polymorphisms in humans associate with genetic instability and genomic disorders. <i>Cell</i> , 2022, 185, 1986-2005.e26.	13.5	67
21102	A metagenomic study of the bacteria in snow algae microbiomes. <i>Canadian Journal of Microbiology</i> , 2022, , .	0.8	1
21103	Parental origins of the cultivated tetraploid sour cherry (<sc><i>Prunus cerasus</i></sc> L.). <i>Plants People Planet</i> , 2022, 4, 444-450.	1.6	5
21104	Widespread Occurrence of Two Planktonic Ciliate Species (Urotricha, Prostomatida) Originating from High Mountain Lakes. <i>Diversity</i> , 2022, 14, 362.	0.7	4
21105	Integrative studies on the taxonomy and molecular phylogeny of four new <i>Pleuronema</i> species (Protozoa, Ciliophora, Scuticociliata). <i>Marine Life Science and Technology</i> , 2022, 4, 179-200.	1.8	19
21106	An NGS-Based Phylogeny of Orthotricheae (Orthotrichaceae, Bryophyta) With the Proposal of the New Genus <i>Rehubryum</i> From Zealandia. <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	7
21107	Draft Genome Assembly of an Iconic Arctic Species: Muskox (<i>Ovibos moschatus</i>). <i>Genes</i> , 2022, 13, 809.	1.0	1
21108	<i>Siphoderina hustoni</i> n. sp. (Platyhelminthes: Trematoda: Cryptogonimidae) from the Maori snapper <i>Lutjanus rivulatus</i> (Cuvier) on the Great Barrier Reef. <i>Systematic Parasitology</i> , 2022, 99, 403-417.	0.5	3
21109	Taxonomy and Biogeography of <i>Andinia</i> -Complex (Orchidaceae). <i>Diversity</i> , 2022, 14, 372.	0.7	1
21110	Third Generation Genome Sequencing Reveals That Endobacteria in Nematophagous Fungi <i>Esteya vermicola</i> Contain Multiple Genes Encoding for Nematicidal Proteins. <i>Frontiers in Microbiology</i> , 2022, 13, 842684.	1.5	1
21111	The genome sequencing and comparative analysis of a wild kiwifruit <i>Actinidia eriantha</i> . <i>Molecular Horticulture</i> , 2022, 2, .	2.3	13
21112	Genomic dissection of the microevolution of Australian epidemic <i>Bordetella pertussis</i> . <i>Emerging Microbes and Infections</i> , 2022, 11, 1460-1473.	3.0	4
21113	Fungal phylogeny and plant functional traits structure plantâ€rhizosphere fungi networks in a subtropical forest. <i>Oikos</i> , 2022, 2022, .	1.2	5
21114	Multi-Locus Sequence Analysis Reveals Diversity of the Rice Kernel Smut Populations in the United States. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	4
21115	The complete chloroplast genome of dalmatian pyrethrum (<i>Tanacetum cinerariifolium</i> (Trevir.)) Tj ETQq1 1 0.784314 rgBT /Ove Resources, 2022, 7, 775-777.	0.2	0
21117	Precipitation and temperature shape the biogeography of arbuscular mycorrhizal fungi across the Brazilian Caatinga. <i>Journal of Biogeography</i> , 2022, 49, 1137-1150.	1.4	3
21118	Unveiling an enigma from the Cerrado: taxonomic revision of two sympatric species of <i>Apostolepis</i> Cope, 1862 (Dipsadidae: Xenodontinae: Elapomorhini) from central Brazil. <i>European Journal of Taxonomy</i> , 0, 817, .	0.6	0

#	ARTICLE	IF	CITATIONS
21120	Whole genome sequencing of cyanobacterium <i>Nostoc</i> sp. CCCryo 231-06 using microfluidic single cell technology. <i>IScience</i> , 2022, 25, 104291.	1.9	6
21121	Draft Genome Sequences for Three <i>Ophiostoma</i> Species Acquired during Revisions of Australian Plant Pathogen Reference Collections. <i>Microbiology Resource Announcements</i> , 2022, 11, e0017522.	0.3	2
21122	Gene regulatory networks shape developmental plasticity of root cell types under water extremes in rice. <i>Developmental Cell</i> , 2022, 57, 1177-1192.e6.	3.1	27
21123	Pathways to polar adaptation in fishes revealed by long-read sequencing. <i>Molecular Ecology</i> , 2023, 32, 1381-1397.	2.0	8
21124	The complete chloroplast genome and phylogenetic analysis of <i>Astragalus sinicus</i> Linne 1767. <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 851-853.	0.2	1
21125	Cryptic Genes for Interbacterial Antagonism Distinguish <i>Rickettsia</i> Species Infecting Blacklegged Ticks From Other <i>Rickettsia</i> Pathogens. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 880813.	1.8	8
21126	Rapid diversification of the Variable Seedeater superspecies complex despite widespread gene flow. <i>Molecular Phylogenetics and Evolution</i> , 2022, 173, 107510.	1.2	3
21127	Effects of biological nitrification inhibitor in regulating NH ₃ volatilization and fertilizer nitrogen recovery efficiency in soils under rice cropping. <i>Science of the Total Environment</i> , 2022, 838, 155857.	3.9	9
21128	Genetic assimilation and the evolution of direction of genital asymmetry in anablepid fishes. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2022, 289, 20220266.	1.2	3
21129	Selective Whole-Genome Amplification as a Tool to Enrich Specimens with Low <i>Treponema pallidum</i> Genomic DNA Copies for Whole-Genome Sequencing. <i>MSphere</i> , 2022, 7, e0000922.	1.3	12
21130	Genome analysis of <i>Pseudomonas</i> species reveals that <i>Pseudomonas panacis</i> Park et al. 2005 is a later heterotypic synonym of <i>Pseudomonas marginalis</i> (Brown 1918) Stevens 1925 (Approved Lists 1980). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	6
21131	PhyloM: A Computer Program for Phylogenetic Inference from Measurement or Binary Data, with Bootstrapping. <i>Life</i> , 2022, 12, 719.	1.1	1
21132	Taxonomy and Phylogeny of Meruliaceae with Descriptions of Two New Species from China. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 501.	1.5	2
21133	Recent and local diversification of Central American understory palms. <i>Global Ecology and Biogeography</i> , 2022, 31, 1513-1525.	2.7	3
21135	Free-living Trichomonads are Unexpectedly Diverse. <i>Protist</i> , 2022, 173, 125883.	0.6	5
21136	Genome sequencing and analysis of genomic diversity in the locally transmitted SARS-CoV-2 in Pakistan. <i>Transboundary and Emerging Diseases</i> , 2022, 69, .	1.3	3
21137	Ancient mitochondrial and modern whole genomes unravel massive genetic diversity loss during near extinction of Alpine ibex. <i>Molecular Ecology</i> , 2022, 31, 3548-3565.	2.0	9
21138	A hominoid-specific endogenous retrovirus may have rewired the gene regulatory network shared between primordial germ cells and naïve pluripotent cells. <i>PLoS Genetics</i> , 2022, 18, e1009846.	1.5	12

#	ARTICLE	IF	CITATIONS
21139	The complete plastid genome of <i>Terminalia myriocarpa</i> Vaniot Huerck et Muell.-Arg (Combretaceae), a tropical rainforest indicator species in Southern China. Mitochondrial DNA Part B: Resources, 2022, 7, 834-835.	0.2	0
21140	Phytophythium chamaehyphon causing corm and root rot of uncultivated taro (Colocasia esculenta). European Journal of Plant Pathology, 0, , .	0.8	0
21141	Genome of a giant isopod, Bathynomus jamesi, provides insights into body size evolution and adaptation to deep-sea environment. BMC Biology, 2022, 20, 113.	1.7	5
21142	Virological characteristics of the SARS-CoV-2 Omicron BA.2 spike. Cell, 2022, 185, 2103-2115.e19.	13.5	273
21143	Complex Scenarios of Reticulation, Polyploidization, and Species Diversity within Annual Pansies of Subsect. Bracteolatae (Viola Sect. Melanium, Violaceae) in Italy: Insights from 5S-IGS High-Throughput Sequencing and Plastid DNA Variation. Plants, 2022, 11, 1294.	1.6	2
21144	Gaur genome reveals expansion of sperm odorant receptors in domesticated cattle. BMC Genomics, 2022, 23, 344.	1.2	3
21145	Genomic insights into recent species divergence in <i>Nicotiana benthamiana</i> and natural variation in <i>Rdr1</i> gene controlling viral susceptibility. Plant Journal, 2022, 111, 7-18.	2.8	9
21146	Earliest Photic Zone Niches Probed by Ancestral Microbial Rhodopsins. Molecular Biology and Evolution, 2022, 39, .	3.5	5
21147	The Effects of Foraging Ecology and Allometry on Avian Skull Shape Vary across Levels of Phylogeny. American Naturalist, 2022, 200, E174-E188.	1.0	12
21148	Pangenome analysis of Enterobacteria reveals richness of secondary metabolite gene clusters and their associated gene sets. Synthetic and Systems Biotechnology, 2022, 7, 900-910.	1.8	9
21150	Comparative transcriptomic analysis unveils the deep phylogeny and secondary metabolite evolution of 116 <i>Camellia</i> plants. Plant Journal, 2022, 111, 406-421.	2.8	27
21151	Combining Species Delimitation, Species Trees, and Tests for Gene Flow Clarifies Complex Speciation in Scrub-Jays. Systematic Biology, 2022, 71, 1453-1470.	2.7	14
21152	Emergence of multiple Diaporthe species causing kiwifruit rot and occurrence of resistance to a methyl benzimidazole carbamate fungicide in South Korea. Crop Protection, 2022, 158, 106016.	1.0	3
21153	First two mitochondrial genomes for the order Filobasidiales reveal novel gene rearrangements and intron dynamics of Tremellomycetes. IMA Fungus, 2022, 13, 7.	1.7	6
21154	Whole-genome sequencing of Mycobacterium tuberculosis from Cambodia. Scientific Reports, 2022, 12, 7693.	1.6	3
21155	High-Resolution Metagenomics of Human Gut Microbiota Generated by Nanopore and Illumina Hybrid Metagenome Assembly. Frontiers in Microbiology, 2022, 13, .	1.5	4
21156	Coalescent-based species delimitation in North American pinyon pines using low-copy nuclear genes and plastomes. American Journal of Botany, 2022, 109, 706-726.	0.8	3
21157	Transposable element accumulation drives size differences among polymorphic Y Chromosomes in <i>Drosophila</i> . Genome Research, 2022, 32, 1074-1088.	2.4	8

#	ARTICLE	IF	CITATIONS
21158	Hybrid Sequencing Resolved Inverted Terminal Repeats in the Genome of Megavirus Baoshan. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	3
21159	The complete mitochondrial genome of <i>Dendrophyllia minuscula</i> (Cnidaria: Scleractinia) from the NEOM region of the Northern Red Sea. <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 848-850.	0.2	1
21160	The flying spider-monkey tree fern genome provides insights into fern evolution and arborescence. <i>Nature Plants</i> , 2022, 8, 500-512.	4.7	42
21161	<i>Copranaerobaculum intestinale</i> gen. nov., sp. nov., a novel anaerobic bacterium isolated from human faeces. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	6
21162	<i>Gorgoniapolynoe caeciliae</i> revisited: The discovery of new species and molecular connectivity in deep-sea commensal polynoids from the Central Atlantic. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2022, 185, 103804.	0.6	3
21163	Early stages of speciation with gene flow in the <i>Amazilia</i> Hummingbird (<i>Amazilia amazilia</i>) subspecies complex of Western South America. <i>Ecology and Evolution</i> , 2022, 12, e8895.	0.8	1
21164	Evidence of multiple genome duplication events in <i>Mytilus</i> evolution. <i>BMC Genomics</i> , 2022, 23, 340.	1.2	12
21165	Functional and phylogenetic diversity of sharks in the Northeastern Pacific. <i>Journal of Biogeography</i> , 2022, 49, 1313-1326.	1.4	3
21166	Mobility of antimicrobial resistance across serovars and disease presentations in non-typhoidal <i>Salmonella</i> from animals and humans in Vietnam. <i>Microbial Genomics</i> , 2022, 8, .	1.0	2
21167	Dressing like a pathogen: Comparative analysis of different <i>Pseudomonas</i> genomospecies wearing different features to infect <i>Corylus avellana</i> . <i>Journal of Phytopathology</i> , 2022, 170, 504-516.	0.5	4
21169	Ten <i>Ostreobium</i> (Ulvophyceae) strains from Great Barrier Reef corals as a resource for algal endolith biology and genomics. <i>Phycologia</i> , 2022, 61, 452-458.	0.6	6
21170	Evolutionary Dynamics of Mexican Lineage H5N2 Avian Influenza Viruses. <i>Viruses</i> , 2022, 14, 958.	1.5	2
21171	Cryptic Diversity in <i>Paramecium multimicronucleatum</i> Revealed with a Polyphasic Approach. <i>Microorganisms</i> , 2022, 10, 974.	1.6	7
21172	Elevational Gradients Impose Dispersal Limitation on <i>Streptomyces</i> . <i>Frontiers in Microbiology</i> , 2022, 13, 856263.	1.5	1
21173	The Morphology, Ultrastructure and Molecular Phylogeny of a New Soil-Dwelling Kinetoplastid <i>Avlakibodo gracilis</i> gen. et sp. nov. (Neobodonida; Kinetoplastea). <i>Protist</i> , 2022, , 125885.	0.6	2
21174	Palaeogenomic analysis of black rat (<i>Rattus rattus</i>) reveals multiple European introductions associated with human economic history. <i>Nature Communications</i> , 2022, 13, 2399.	5.8	12
21176	Spatial phylogenetic patterns in the North American moss flora are shaped by history and climate. <i>Journal of Biogeography</i> , 2022, 49, 1327-1338.	1.4	7
21177	Invasions of an obligate asexual daphnid species support the nearly neutral theory. <i>Scientific Reports</i> , 2022, 12, 7305.	1.6	3

#	ARTICLE	IF	CITATIONS
21178	Discovery of <i>Nemophora chrysoprasias</i> Meyrick (Lepidoptera: Adelidae) from China, with notes on its related species. <i>Journal of Asia-Pacific Biodiversity</i> , 2022, , .	0.2	3
21179	Radiocarbon and genomic evidence for the survival of <i>Equus Sussemionus</i> until the late Holocene. <i>ELife</i> , 2022, 11, .	2.8	6
21180	Effect of childhood vaccination and antibiotic use on pneumococcal populations and genome-wide associations with disease among children in Nepal: an observational study. <i>Lancet Microbe</i> , The, 2022, 3, e503-e511.	3.4	2
21181	Whole genome sequencing and phylogenomic analysis show support for the splitting of genus <i>Pythium</i> . <i>Mycologia</i> , 2022, 114, 501-515.	0.8	21
21182	Complex fitness landscape shapes variation in a hyperpolymorphic species. <i>ELife</i> , 2022, 11, .	2.8	5
21183	Investigating the reliability of molecular estimates of evolutionary time when substitution rates and speciation rates vary. <i>Bmc Ecology and Evolution</i> , 2022, 22, 61.	0.7	2
21184	<i>Helicobacter cinaedi</i> is a human-adapted lineage in the <i>Helicobacter cinaedi/canicola</i> – <i>magdeburgensis</i> ™ complex. <i>Microbial Genomics</i> , 2022, 8, .	1.0	4
21185	Genomic characterization of lytic bacteriophages targeting genetically diverse <i>Pseudomonas aeruginosa</i> clinical isolates. <i>IScience</i> , 2022, 25, 104372.	1.9	16
21186	Biogeography of endosymbionts (Symbiodiniaceae) associated with zoantharian species (Hexacorallia): Tj ETQq0 0.0 rgBT /Oyerlock 10	0.9	1
21187	Evolutionary patterns within the New World Clade <i>Polygala</i> sections <i>Clinclinia</i> and <i>Monninopsis</i> (Polygalaceae). <i>Perspectives in Plant Ecology, Evolution and Systematics</i> , 2022, 55, 125673.	1.1	1
21188	An overlooked dispersal route of <i>Cardueae</i> (Asteraceae) from the Mediterranean to East Asia revealed by phylogenomic and biogeographical analyses of <i>Atractylodes</i> . <i>Annals of Botany</i> , 2022, 130, 53-64.	1.4	5
21189	Ancient genome provides insights into the history of Eurasian lynx in Iberia and Western Europe. <i>Quaternary Science Reviews</i> , 2022, 285, 107518.	1.4	3
21190	Differentiation within the <i>Drawida ghilarovi</i> complex (Moniligastridae: Annelida) revealed by multigene transcriptomic dataset analysis. <i>European Journal of Soil Biology</i> , 2022, 111, 103411.	1.4	3
21191	Ultra-conserved elements provide insights to the biogeographic patterns of three benthic macroinvertebrate species in the Baltic Sea. <i>Estuarine, Coastal and Shelf Science</i> , 2022, 271, 107863.	0.9	3
21192	Recombinant expression, purification and characterization of an active bacterial feruloyl-CoA synthase with potential for application in vanillin production. <i>Protein Expression and Purification</i> , 2022, 197, 106109.	0.6	1
21193	Global phylogeny of the Shiitake mushroom and related <i>Lentinula</i> species uncovers novel diversity and suggests an origin in the Neotropics. <i>Molecular Phylogenetics and Evolution</i> , 2022, 173, 107494.	1.2	8
21194	Emergence of blaNDM-1, blaNDM-5, blaKPC-2 and blaIMP-4 carrying plasmids in <i>Raoultella</i> spp. in the environment. <i>Environmental Pollution</i> , 2022, 306, 119437.	3.7	10
21195	On Partial Gene Transfer and Its Impact on Gene Tree Reconstruction. <i>Lecture Notes in Computer Science</i> , 2022, , 168-186.	1.0	1

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21196	Phloem wedges in Malpighiaceae: origin, structure, diversification, and systematic relevance. <i>EvoDevo</i> , 2022, 13, 11.	1.3	7
21197	Antimicrobial susceptibility and genomic analysis of <i>Histophilus somni</i> isolated from cases of bovine respiratory disease in Australian feedlot cattle. <i>Veterinary Microbiology</i> , 2022, 270, 109460.	0.8	3
21198	Phylogenetics and an updated taxonomic status of the Tamarins (Callitrichinae, Cebidae). <i>Molecular Phylogenetics and Evolution</i> , 2022, 173, 107504.	1.2	9
21199	The complete mitochondrial genome of cricket <i>Sclerogryllus punctatus</i> (Orthoptera: Gryllidae) and phylogenetic analysis. <i>Journal of Asia-Pacific Entomology</i> , 2022, 25, 101933.	0.4	2
21200	Phenotypic Variability and Genetic Diversity of the Pathogenic Fungus <i>Macrophomina phaseolina</i> from Several Hosts and Host Specialization in Strawberry. <i>Current Microbiology</i> , 2022, 79, 189.	1.0	4
21201	Chromosome-level genome of <i>Pedinomonas minor</i> (Chlorophyta) unveils adaptations to abiotic stress in a rapidly fluctuating environment. <i>New Phytologist</i> , 2022, , .	3.5	2
21202	Comparative genomics among cyst nematodes reveals distinct evolutionary histories among effector families and an irregular distribution of effector-associated promoter motifs. <i>Molecular Ecology</i> , 2023, 32, 1515-1529.	2.0	7
21203	Species limits and introgression in <i>Pimelodus</i> from the Magdalena-Cauca River basin. <i>Molecular Phylogenetics and Evolution</i> , 2022, 173, 107517.	1.2	3
21204	Benefits of alignment quality control processing steps and an Angiosperms353 phylogenomics pipeline applied to the Celastrales. <i>Cladistics</i> , 2022, 38, 595-611.	1.5	1
21205	<i>Pseudomonas phenolilytica</i> sp. nov., a novel phenol-degrading bacterium. <i>Archives of Microbiology</i> , 2022, 204, 320.	1.0	5
21206	The phylogenetic position of ridley's worm lizard reveals the complex biogeographic history of New World insular amphisbaenids. <i>Molecular Phylogenetics and Evolution</i> , 2022, 173, 107518.	1.2	6
21207	Biogeographical and diversification analyses of Indian pseudoscorpions reveal the Western Ghats as museums of ancient biodiversity. <i>Molecular Phylogenetics and Evolution</i> , 2022, 175, 107495.	1.2	7
21208	Recurrent founder-event speciation across the Mediterranean likely shaped the species diversity and geographic distribution of the freshwater snail genus <i>Mercuria</i> Boeters, 1971 (Caenogastropoda: Tj ETQq0 0 0 rgBTzOverlock 10 Tf 50		
21209	<i>Russula</i> (Russulales, Agaricomycetes) associated with <i>Pinus</i> spp. plantations from northeastern Argentina. <i>Rodriguesia</i> , 0, 73, .	0.9	1
21210	The Hox gene <i>Abdominal-B</i> regulates the appendage development during the embryogenesis of scorpionflies. <i>Insect Molecular Biology</i> , 2022, 31, 609-619.	1.0	3
21211	Phylogeography and evolutionary history of the Panamic Clingfish <i>Gobiesox adustus</i> in the Tropical Eastern Pacific. <i>Molecular Phylogenetics and Evolution</i> , 2022, 173, 107496.	1.2	3
21212	Biogeography and Diversification of the Tropical and Subtropical Asian Genus <i>Gastrochilus</i> (Orchidaceae, Aeridinae). <i>Diversity</i> , 2022, 14, 396.	0.7	4
21213	Taxonomy and SSU rRNA gene-based phylogeny of two new <i>Euplotes</i> species from China: <i>E. chongmingensis</i> n. sp. and <i>E. paramieti</i> n. sp. (Protista, Ciliophora). <i>BMC Microbiology</i> , 2022, 22, 133.	1.3	3

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21214	Temperature and Geographic Location Impact the Distribution and Diversity of Photoautotrophic Gene Variants in Alkaline Yellowstone Hot Springs. <i>Microbiology Spectrum</i> , 2022, 10, e0146521.	1.2	7
21215	Assessment of simple sequence repeats signature in hepatitis E virus (HEV) genomes. <i>Journal of Genetic Engineering and Biotechnology</i> , 2022, 20, 73.	1.5	3
21216	HIV-1 drug resistance genotyping success rates and correlates of Dried-blood spots and plasma specimen genotyping failure in a resource-limited setting. <i>BMC Infectious Diseases</i> , 2022, 22, 474.	1.3	2
21217	The Old Yellow Enzyme OfrA Fosters <i>Staphylococcus aureus</i> Survival via Affecting Thiol-Dependent Redox Homeostasis. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	2
21218	Comparative Genomics Identifies Features Associated with Methicillin-Resistant <i>Staphylococcus aureus</i> (MRSA) Transmission in Hospital Settings. <i>MSphere</i> , 2022, , e0011622.	1.3	1
21219	Diversity of Microbial Eukaryotes Along the West Antarctic Peninsula in Austral Spring. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	2
21220	Parallel decay of vision genes in subterranean water beetles. <i>Molecular Phylogenetics and Evolution</i> , 2022, 173, 107522.	1.2	14
21221	High Prevalence of bla _{CTXM} 1/IncI1- β /ST3 Plasmids in Extended-Spectrum β -Lactamase-Producing <i>Escherichia coli</i> Isolates Collected From Domestic Animals in Guadeloupe (French West Indies). <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	3
21222	Plastid phylogenomic analyses of the <i>Selaginella sanguinolenta</i> group (Selaginellaceae) reveal conflict signatures resulting from sequence types, outlier genes, and pervasive RNA editing. <i>Molecular Phylogenetics and Evolution</i> , 2022, 173, 107507.	1.2	7
21223	SARS-CoV-2 variant trends in Ireland: Wastewater-based epidemiology and clinical surveillance. <i>Science of the Total Environment</i> , 2022, 838, 155828.	3.9	25
21224	Genome-Based Analysis of <i>Aspergillus niger</i> Aggregate Species from China and Their Potential for Fumonisin B2 and Ochratoxin A Production. <i>Current Microbiology</i> , 2022, 79, 193.	1.0	0
21225	Mitogenomics and mitochondrial gene phylogeny decipher the evolution of <i>Saccharomycotina</i> yeasts. <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	8
21226	Metagenomes from 25 Low-Abundance Microbes in a Partial Nitritation Anammox Microbiome. <i>Microbiology Resource Announcements</i> , 2022, 11, e0021222.	0.3	2
21227	Evolutionary history of the Australasian Scirtinae (Scirtidae; Coleoptera) inferred from ultraconserved elements. <i>Invertebrate Systematics</i> , 2022, 36, 291-305.	0.5	7
21228	Prevalence and Characterization of the Cefazolin Inoculum Effect in North American Methicillin-Susceptible <i>Staphylococcus aureus</i> Isolates. <i>Journal of Clinical Microbiology</i> , 2022, 60, e0249521.	1.8	7
21229	High-Quality Genome Assembly of <i>Olea europaea</i> subsp. <i>cuspidata</i> Provides Insights Into Its Resistance to Fungal Diseases in the Summer Rain Belt in East Asia. <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	5
21230	The chloroplast genomes comparative analysis of <i>Taihangia rupestris</i> var. <i>rupestris</i> and <i>Taihangia rupestris</i> var. <i>ciliata</i> , two endangered and endemic cliff plants in Taihang Mountain of China. <i>South African Journal of Botany</i> , 2022, 148, 499-509.	1.2	2
21231	Distinct gene clusters drive formation of ferrosome organelles in bacteria. <i>Nature</i> , 2022, 606, 160-164.	13.7	15

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21232	Hmx gene conservation identifies the origin of vertebrate cranial ganglia. <i>Nature</i> , 2022, 605, 701-705.	13.7	15
21233	ROV observations reveal infection dynamics of gill parasites in midwater cephalopods. <i>Scientific Reports</i> , 2022, 12, 8282.	1.6	2
21234	Genetic variation and structure of complete chloroplast genome in alien monoecious and dioecious <i>Amaranthus</i> weeds. <i>Scientific Reports</i> , 2022, 12, 8255.	1.6	1
21235	Genomic biosurveillance detects a sexual hybrid in the sudden oak death pathogen. <i>Communications Biology</i> , 2022, 5, 477.	2.0	4
21236	Target Enrichment and Extensive Population Sampling Help Untangle the Recent, Rapid Radiation of <i>Oenothera</i> Sect. <i>Calylophus</i> . <i>Systematic Biology</i> , 2023, 72, 249-263.	2.7	6
21238	<i>Vagococcus allomyrinae</i> sp. nov. and <i>Enterococcus larvae</i> sp. nov., isolated from larvae of <i>Allomyrina dichotoma</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	10
21239	<i>Methanococcoides orientis</i> sp. nov., a methylotrophic methanogen isolated from sediment of the East China Sea. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	9
21240	Biochemical and structural characterization of the cyanophage-encoded phosphate-binding protein: implications for enhanced phosphate uptake of infected cyanobacteria. <i>Environmental Microbiology</i> , 2022, 24, 3037-3050.	1.8	7
21241	Epistatic drift causes gradual decay of predictability in protein evolution. <i>Science</i> , 2022, 376, 823-830.	6.0	38
21242	Molecular and genomic investigation of an urban outbreak of dengue virus serotype 2 in Angola, 2017-2019. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010255.	1.3	9
21243	Epidemiologic, Clinical, and Genetic Characteristics of Human Infections with Influenza A(H5N6) Viruses, China. <i>Emerging Infectious Diseases</i> , 2022, 28, 1332-1344.	2.0	27
21244	Species diversity, systematic revision and molecular phylogeny of <i>Ganodermataceae</i> (<i>Polyporales</i> , <i>Basidiomycota</i>) with an emphasis on Chinese collections. <i>Studies in Mycology</i> , 2022, 101, 287-415.	4.5	33
21245	Mitochondrial phylogenomics provides insights into the phylogeny and evolution of spiders (Arthropoda: Araneae). <i>Zoological Research</i> , 2022, 43, 566-584.	0.9	5
21246	Redescription, complete mitochondrial genome and phylogenetic relationships of <i>Hexostoma thynni</i> (Delaroche, 1811) Rafinesque, 1815 (Monogenea, Hexostomatidae). <i>Parasite</i> , 2022, 29, 29.	0.8	5
21257	Invariant transformers of Robinson and Foulds distance matrices for Convolutional Neural Network. <i>Journal of Bioinformatics and Computational Biology</i> , 2022, 20, .	0.3	2
21258	Comparative Analysis of Pseudo-nitzschia Chloroplast Genomes Revealed Extensive Inverted Region Variation and Pseudo-nitzschia Speciation. <i>Frontiers in Marine Science</i> , 2022, 9, .	1.2	6
21260	<i>Aphelidium parallelum</i> , sp. nov., a new aphelid parasitic on selenastracean green algae. <i>Mycologia</i> , 2022, 114, 544-555.	0.8	3
21261	Genome Assembly and Population Resequencing Reveal the Geographical Divergence of Shanmei (<i>Rubus</i>) TJ ETQq1_1.0.784314 rgBT	3.0	3

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21262	Two New Species and One New Genus of Glass Sponges (Hexactinellida: Euplectellidae and Euretidae), From a Transect on a Seamount in the Northwestern Pacific Ocean. <i>Frontiers in Marine Science</i> , 2022, 9, .	1.2	0
21263	A mechanistic study of the influence of nitrogen and energy availability on the NH ₄ ⁺ sensitivity of nitrogen assimilation in <i>Synechococcus</i> . <i>Journal of Experimental Botany</i> , 2022, 73, 5596-5611.	2.4	1
21264	Off-season RSV epidemics in Australia after easing of COVID-19 restrictions. <i>Nature Communications</i> , 2022, 13, .	5.8	135
21265	<i>Paraphysoderma sedebokerense</i> GlnS III Is Essential for the Infection of Its Host <i>Haematococcus lacustris</i> . <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 561.	1.5	0
21266	First Glimpse of Gut Microbiota of Quarantine Insects in China. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 394-404.	3.0	1
21268	Isolation of SARS CoV-2 and evaluation of human-animal cases. <i>Etlik Veteriner Mikrobiyoloji Dergisi</i> , 0, .	0.2	0
21269	Morphology, taxonomy and phylogenetic positions of two <i>Spirogyra</i> species (Zygnematophyceae, Streptophyta) with replicate and semi-replicate transverse walls from Japan. <i>Phycologia</i> , 0, , 1-11.	0.6	0
21272	Is Hyperdermium Congeneric with <i>Ascopolyporus</i> ? Phylogenetic Relationships of <i>Ascopolyporus</i> spp. (Cordycipitaceae, Hypocreales) and a New Genus <i>Neohyperdermium</i> on Scale Insects in Thailand. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 516.	1.5	3
21273	Complete Chloroplast Genomes Provide Insights Into Evolution and Phylogeny of <i>Campylotropis</i> (Fabaceae). <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	6
21274	<i>Streptomyces spinosus</i> sp. nov. and <i>Streptomyces shenzhenensis</i> subsp. <i>oryzicola</i> subsp. nov. endophytic actinobacteria isolated from Jasmine rice and their genome mining for potential as antibiotic producers and plant growth promoters. <i>Antonie Van Leeuwenhoek</i> , 0, , .	0.7	4
21275	Evolutionary Conservation Genomics Reveals Recent Speciation and Local Adaptation in Threatened Takins. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	7
21276	Organization, Phylogenetic Marker Exploitation, and Gene Evolution in the Plastome of <i>Thalictrum</i> (Ranunculaceae). <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	6
21277	Anaerobic Degradation of Naphthalene and Pyrene by Sulfate-Reducing Cultures Enriched from Former Manufactured Gas Plant Soil. <i>Microbial Ecology</i> , 2023, 86, 271-281.	1.4	1
21278	Comparative Analyses of <i>Scylla olivacea</i> Gut Microbiota Composition and Function Suggest the Capacity for Polyunsaturated Fatty Acid Biosynthesis. <i>Microbial Ecology</i> , 2023, 86, 575-588.	1.4	4
21279	The complete chloroplast genome of the newly recorded species <i>Tainia acuminata</i> Averyanov (Orchidaceae) from China. <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 884-885.	0.2	2
21281	Intra-genomic <i>rRNA</i> gene variability of <i>Nassellaria</i> and <i>Spumellaria</i> (Rhizaria, Radiolaria) assessed by Sanger, <i>MiniON</i> and Illumina sequencing. <i>Environmental Microbiology</i> , 2022, 24, 2979-2993.	1.8	7
21282	Evidence for an Independent Hydrogenosome-to-Mitosome Transition in the CL3 Lineage of Fornicates. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	3
21283	Circumscription and typification of sphagnumicolous omphalinoïd species of <i>Arrhenia</i> (Hygrophoraceae) in Newfoundland and Labrador: three obligate and one facultative species. <i>Mycological Progress</i> , 2022, 21, .	0.5	2

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21284	Two new species of Dugesia (Platyhelminthes, Tricladida, Dugesiidae) from the subtropical monsoon region in Southern China, with a discussion on reproductive modalities. BMC Zoology, 2022, 7, .	0.3	2
21285	First multigene phylogeny of Cumacea (crustacea: Peracarida). Zoologica Scripta, 2022, 51, 460-477.	0.7	3
21288	Natronocalculus amylovorans gen. nov., sp. nov., and Natranaeroarchaeum aerophilus sp. nov., dominant culturable amylolytic natronoarchaea from hypersaline soda lakes in southwestern Siberia. Systematic and Applied Microbiology, 2022, 45, 126336.	1.2	4
21289	Comparative genome analysis of the monogonont marine rotifer Brachionus manjavacas Australian strain: Potential application for ecotoxicology and environmental genomics. Marine Pollution Bulletin, 2022, 180, 113752.	2.3	2
21290	Comparative analysis of complete chloroplast genome sequences of five endangered species and new insights into phylogenetic relationships of Paris. Gene, 2022, 833, 146572.	1.0	8
21291	Nitrogen addition altered the plant-arbuscular mycorrhizal fungi network through reducing redundant interactions in an alpine meadow. Soil Biology and Biochemistry, 2022, 171, 108727.	4.2	7
21292	Species diversity, phylogeny, endemism and geography of the truffle genus <i>Tuber</i> in China based on morphological and molecular data. Persoonia: Molecular Phylogeny and Evolution of Fungi, 2022, 48, 175-202.	1.6	8
21294	Limited accumulation of high-frequency somatic mutations in a 1700-year-old <i>Osmanthus fragrans</i> tree. Tree Physiology, 0, , .	1.4	4
21295	Genome Assembly and Evolutionary Analysis of the Mandarin Duck <i>Aix galericulata</i> Reveal Strong Genome Conservation among Ducks. Genome Biology and Evolution, 2022, 14, .	1.1	1
21296	Genome sequences of 24 <i>Aspergillus niger sensu stricto</i> strains to study strain diversity, heterokaryon compatibility, and sexual reproduction. G3: Genes, Genomes, Genetics, 0, , .	0.8	4
21298	Reconstruction of the rRNA Sequences of LUCA, with Bioinformatic Implication of the Local Similarities Shared by Them. Biology, 2022, 11, 837.	1.3	0
21299	<i>Apilactobacillus zhangquensis</i> sp. nov. and <i>Apilactobacillus xinyiensis</i> sp. nov., isolated from the gut of honeybee (<i>Apis mellifera</i>). International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	9
21300	A chromosome-level genome assembly of the pollinating fig wasp <i>Valisia javana</i> . DNA Research, 2022, 29, .	1.5	3
21301	Functional Diversity and Evolution of Bitter Taste Receptors in Egg-Laying Mammals. Molecular Biology and Evolution, 2022, 39, .	3.5	2
21302	ROCKER Models for Reliable Detection and Typing of Short-Read Sequences Carrying β -Lactamase Genes. MSystems, 2022, 7, .	1.7	1
21303	New Contribution to the Diversity of the Anaerobic Genus <i>Metopus</i> (Ciliophora, Armophorea), With Descriptions of Three New Marine Species. Frontiers in Marine Science, 2022, 9, .	1.2	6
21304	The COI haplotype diversity of the pelagic polychaete <i>Tomopteris</i> (Annelida: Tomopteridae) collected from the Pacific coast off Kii Peninsula, central Japan. Plankton and Benthos Research, 2022, 17, 214-220.	0.2	1
21305	PhyloTraVis: A New Approach to Visualization of the Phylogenetic Tree. Programming and Computer Software, 2022, 48, 215-226.	0.5	1

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21306	Taxonomy and molecular phylogeny of <i>Trametopsis</i> (Polyporales, Basidiomycota) with descriptions of two new species. <i>MycKeys</i> , 0, 90, 31-51.	0.8	3
21307	<i>Dendrocorticopsis orientalis</i> gen. et sp. nov. of the Punctulariaceae (Corticiales, Basidiomycota) revealed by molecular data. <i>MycKeys</i> , 0, 90, 19-30.	0.8	0
21308	Molecular Phylogenetic Evidence and Biogeographic History of Indian Endemic <i>Portulaca</i> L. (<i>Portulacaceae</i>) Species. <i>Diversity</i> , 2022, 14, 443.	0.7	1
21310	Two new species of <i>Fulvifomes</i> (<i>Basidiomycota</i>) (<i>Basidiomycota</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 627 <i>Mycoscience</i> , 2022, 63, 131-141.	0.3	5
21311	The complete mitochondrial genomes of the flapper skate <i>Dipturus intermedius</i> and the longnose skate <i>Dipturus oxyrinchus</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 897-899.	0.2	1
21312	Characterization of <i>Pseudomonas viridiflava</i> isolates associated with a new leaf spot disease in <i>Cichorium</i> species. , 2022, 104, 1061-1070.		2
21314	Phylogeography and Population Genetics of <i>Rosa chinensis</i> var. <i>spontanea</i> and <i>R. lucidissima</i> Complex, the Important Ancestor of Modern Roses. <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	3
21315	<i>Bifidobacterium mizhiense</i> sp. nov., isolated from the gut of honeybee (<i>Apis mellifera</i>). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	6
21316	Novel Gene Rearrangements in the Mitochondrial Genomes of Cynipoid Wasps (Hymenoptera:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 42 1.0		4
21317	<i>Pachygenium laureense</i> (<i>Orchidaceae</i> , <i>Spiranthinae</i>), a new orchid species from Argentina—morphological evidence and phylogenetic reconstruction. <i>PeerJ</i> , 0, 10, e13433.	0.9	1
21318	Mitochondrial genome recombination in somatic hybrids of <i>Solanum commersonii</i> and <i>S. tuberosum</i> . <i>Scientific Reports</i> , 2022, 12, .	1.6	5
21319	Population Structure, Genetic Diversity, and Conservation Strategies of a Commercially Important Sleeper Fish, <i>Odontobutis potamophilus</i> (Gobiiformes: <i>Odontobutidae</i>) Based on Gene-Capture Data. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1
21320	Characterization of the Largest Secretory Protein Family, Ricin B Lectin-like Protein, in <i>Nosema bombycis</i> : Insights into Microsporidian Adaptation to Host. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 551.	1.5	3
21321	The First Mitochondrial Genomes of the Family Haplodiplatyidae (Insecta: <i>Dermaptera</i>) Reveal Intraspecific Variation and Extensive Gene Rearrangement. <i>Biology</i> , 2022, 11, 807.	1.3	5
21325	Identification and Pathogenicity of <i>Paramyrothecium</i> Species Associated with Leaf Spot Disease in Northern Thailand. <i>Plants</i> , 2022, 11, 1445.	1.6	4
21326	Evidence of Selection in the Ectodysplasin Pathway among Endangered Aquatic Mammals. <i>Integrative Organismal Biology</i> , 2022, 4, .	0.9	2
21328	Putative Novel Avian Paramyxovirus (AMPV) and Reidentification of APMV-2 and APMV-6 to the Species Level Based on Wild Bird Surveillance (United States, 2016–2018). <i>Applied and Environmental Microbiology</i> , 2022, 88, .	1.4	5
21329	The Genomic Evolution and the Transmission Dynamics of H6N2 Avian Influenza A Viruses in Southern China. <i>Viruses</i> , 2022, 14, 1154.	1.5	4

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21330	Structural Plastome Evolution in Holoparasitic Hydnoraceae with Special Focus on Inverted and Direct Repeats. <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	8
21331	Three dispersal routes out of Africa: A puzzling biogeographical history in freshwater planarians. <i>Journal of Biogeography</i> , 2022, 49, 1219-1233.	1.4	10
21333	Sequencing-Based Genotyping of Pakistani Burkholderia mallei Strains: A Useful Way for Investigating Glanders Outbreaks. <i>Pathogens</i> , 2022, 11, 614.	1.2	5
21334	Mitochondrial DNA and Population Genomics Reveal Additional Cryptic Diversity in the Green Salamander (Subgenus Castaneides) Species Complex. <i>Frontiers in Conservation Science</i> , 2022, 3, .	0.9	0
21336	Phylogeography and Population History of Eleutharrhena macrocarpa (Tiliacoreae, Menispermaceae) in Southeast Asia's Most Northerly Rainforests. <i>Diversity</i> , 2022, 14, 437.	0.7	0
21337	PhyloFunDB: A Pipeline to Create and Update Functional Gene Taxonomic Databases. <i>Microorganisms</i> , 2022, 10, 1093.	1.6	1
21338	Phylogenetic Evidence for the Cyphocharax saladensis Clade with Description of a New Species of Cyphocharax Endemic to the Upper Rio Paraguai Basin (Teleostei: Curimatidae). <i>Ichthyology and Herpetology</i> , 2022, 110, .	0.3	1
21339	Metagenomic Analysis Using Phylogenetic Placement—A Review of the First Decade. <i>Frontiers in Bioinformatics</i> , 2022, 2, .	1.0	17
21340	Inter-Specific Genetic Exchange Despite Strong Divergence in Deep-Sea Hydrothermal Vent Gastropods of the Genus Alviniconcha. <i>Genes</i> , 2022, 13, 985.	1.0	5
21341	Hidden in the tropics: Retiperidiolia gen. nov., a new genus of bird's nest fungi (Nidulariaceae), and a systematic study of the genus Mycocalia. <i>Mycological Progress</i> , 2022, 21, .	0.5	3
21343	Huntsman spider phylogeny informs evolution of life history, egg sacs, and morphology. <i>Molecular Phylogenetics and Evolution</i> , 2022, 174, 107530.	1.2	6
21346	Postglacial range expansion of high-elevation plants is restricted by dispersal ability and habitat specialization. <i>Journal of Biogeography</i> , 2022, 49, 1739-1752.	1.4	4
21348	Worldwide phylogeography of rough-toothed dolphins (<i>Steno bredanensis</i>) provides evidence for subspecies delimitation. <i>Marine Mammal Science</i> , 2022, 38, 1371-1397.	0.9	5
21349	Amanita Section Phalloideae Species in the Mediterranean Basin: Destroying Angels Reviewed. <i>Biology</i> , 2022, 11, 770.	1.3	5
21350	Chromosome-Level Genome Assembly of Acanthogobius ommaturus Provides Insights Into Evolution and Lipid Metabolism. <i>Frontiers in Marine Science</i> , 2022, 9, .	1.2	3
21352	Three New Species of Microdochium (Sordariomycetes, Amphisphaeriales) on Miscanthus sinensis and Phragmites australis from Hainan, China. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 577.	1.5	7
21353	Taxonomy of Dianthus (Caryophyllaceae) — overall phylogenetic relationships and assessment of species diversity based on a first comprehensive checklist of the genus. <i>PhytoKeys</i> , 0, 196, 91-214.	0.4	9
21354	Ottowia testudinis sp. nov., isolated from the cloaca of a giant Asian pond turtle (Heosemys grandis). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	5

#	ARTICLE	IF	CITATIONS
21356	<i>Tragopogon dubius</i> : Multiple introductions to North America and the formation of the New World tetraploids. <i>Taxon</i> , 2022, 71, 1287-1298.	0.4	5
21357	Human-to-human transmission of <i>Chlamydia psittaci</i> in China, 2020: an epidemiological and aetiological investigation. <i>Lancet Microbe</i> , The, 2022, 3, e512-e520.	3.4	40
21359	Microsatellite Signature of Reference Genome Sequence of SARS-CoV-2 and 32 Species of Coronaviridae Family. <i>International Journal of Infection</i> , 2022, 9, .	0.4	3
21360	Integrative taxonomy supports two new species of <i>Chimarra</i> Stephens, 1829 from Brazil (Trichoptera: Tj ETQq1 1 0.784314 rgBT /Over	5.5	1
21361	Origin, Phylogeny, and Transmission of the Epidemic Clone ST208 of Carbapenem-Resistant <i>Acinetobacter baumannii</i> on a Global Scale. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	3
21362	Two new species of <i>Sistotrema</i> s.l. (<i>Cantharellales</i>) from Japan with descriptions of their ectomycorrhizae. <i>Mycoscience</i> , 2022, 63, 102-117.	0.3	3
21363	Genomic insights into evolution and control of <i>Wohlfahrtia magnifica</i> , a widely distributed myiasis-causing fly of warm-blooded vertebrates. <i>Molecular Ecology Resources</i> , 2022, 22, 2744-2757.	2.2	4
21364	Genome of a novel <i>Sediminibacterium</i> discovered in association with two species of freshwater cyanobacteria from streams in Southern California. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	2
21365	Genomic Surveillance of Clinical <i>Pseudomonas aeruginosa</i> Isolates Reveals an Additive Effect of Carbapenemase Production on Carbapenem Resistance. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	4
21366	Mineralogical and Genomic Constraints on the Origin of Microbial Mn Oxide Formation in Complexed Microbial Community at the Terrestrial Hot Spring. <i>Life</i> , 2022, 12, 816.	1.1	1
21367	Multigene Phylogenetic Support for Novel <i>Rhytidhysterion</i> Speg. Species (<i>Hysteriaceae</i>) from Sichuan Province, China. <i>Cryptogamie, Mycologie</i> , 2022, 43, .	0.2	1
21368	First record of <i>Bulaceros porcellanus</i> Newman & Cannon, 1996 (Platyhelminthes,) morphology and molecular phylogeny. <i>Plankton and Benthos Research</i> , 2022, 17, 147-155.	0.2	0
21369	Characterization of carbapenem-resistant <i>Acinetobacter baumannii</i> ST540 and <i>Klebsiella pneumoniae</i> ST2237 isolates in a pneumonia case from China. <i>Journal of Applied Microbiology</i> , 2022, 133, 1434-1445.	1.4	1
21370	Detection of Genus and Three Important Species of <i>Cronobacter</i> Using Novel Genus- and Species-Specific Genes Identified by Large-Scale Comparative Genomic Analysis. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	1
21371	A new species of deep-sea grunt, <i>Rhonciscus pauc</i> (Lutjaniformes: Haemulidae), from Puerto Rico. <i>PeerJ</i> , 0, 10, e13502.	0.9	1
21372	Intron losses and gains in the nematodes. <i>Biology Direct</i> , 2022, 17, .	1.9	4
21373	Comparative analysis of 343 plastid genomes of <i>Solanum</i> section <i>Petota</i> : Insights into potato diversity, phylogeny, and species discrimination. <i>Journal of Systematics and Evolution</i> , 2023, 61, 599-612.	1.6	7
21374	High-quality chromosome-level genome assembly of <i>Litsea coreana</i> L. provides insights into Magnoliids evolution and flavonoid biosynthesis. <i>Genomics</i> , 2022, 114, 110394.	1.3	2

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21375	Analysis of the pathogenicity and phylogeny of <i>Colletotrichum</i> species associated with brown blight of tea (<i>Camellia sinensis</i>) in Taiwan. <i>Plant Disease</i> , 0, , .	0.7	4
21376	High-throughput, single-microbe genomics with strain resolution, applied to a human gut microbiome. <i>Science</i> , 2022, 376, .	6.0	100
21377	A Survey of <i>Helicobacter pylori</i> Antibiotic-Resistant Genotypes and Strain Lineages by Whole-Genome Sequencing in China. <i>Antimicrobial Agents and Chemotherapy</i> , 2022, 66, .	1.4	8
21378	The complete mitochondrial genome of <i>Porodaedalea mongolica</i> (Hymenochaetaceae,) Tj ETQq1 1 0.784314 rgBT /Overlock 100.2	0.2	2
21379	Intradiol ring cleavage dioxygenases from herbivorous spider mites as a new detoxification enzyme family in animals. <i>BMC Biology</i> , 2022, 20, .	1.7	14
21380	Discovery and genome sequencing of a new virus related to members of the family Tymoviridae, isolated from mosquitoes of the genus <i>Mansonia</i> in Brazil. <i>Archives of Virology</i> , 2022, 167, 1889-1892.	0.9	6
21381	The Maternal Donor of Chrysanthemum Cultivars Revealed by Comparative Analysis of the Chloroplast Genome. <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	8
21382	Genome Sequencing of <i>Amomum tsao-ko</i> Provides Novel Insight Into Its Volatile Component Biosynthesis. <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	1
21383	The Visayan Warty Pig (<i>Sus cebifrons</i>) Genome Provides Insight Into Chromosome Evolution and Sensory Adaptation in Pigs. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	3
21385	Microsporidia: a new taxonomic, evolutionary, and ecological synthesis. <i>Trends in Parasitology</i> , 2022, 38, 642-659.	1.5	51
21387	Genome, genetic evolution, and environmental adaptation mechanisms of <i>Schizophyllum commune</i> in deep subseafloor coal-bearing sediments. <i>IScience</i> , 2022, 25, 104417.	1.9	8
21388	Divergent Viruses Discovered in Swine Alter the Understanding of Evolutionary History and Genetic Diversity of the <i>Respirovirus</i> Genus and Related Porcine Parainfluenza Viruses. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	3
21389	PhyloHerb: A high-throughput phylogenomic pipeline for processing genome skimming data. Applications in Plant Sciences, 2022, 10, .	0.8	14
21390	Genetic Diversity and Population Differentiation of Chinese Lizard Gudgeon (<i>Saurogobio dabryi</i>) in the Upper Yangtze River. <i>Frontiers in Ecology and Evolution</i> , 0, 10, .	1.1	1
21391	Genomic insights into the recent chromosome reduction of autopolyploid sugarcane <i>Saccharum spontaneum</i> . <i>Nature Genetics</i> , 2022, 54, 885-896.	9.4	33
21392	<i>Aquirufa lenticrescens</i> sp. nov. and <i>Aquirufa aurantiipilula</i> sp. nov.: two new species of a lineage of widespread freshwater bacteria. <i>Archives of Microbiology</i> , 2022, 204, .	1.0	9
21393	Genome sequencing and evolutionary analysis of a new endophytic <i>Trichoderma</i> species isolated from orchid roots with reduced repertoire of protein-coding genes. <i>Mycological Progress</i> , 2022, 21, .	0.5	0
21394	<i>Digenea nana</i> sp. nov. (Rhodomelaceae, Rhodophyta), a new turf-forming, coral reef species from the Western Tropical Atlantic. <i>Phycologia</i> , 2022, 61, 444-451.	0.6	3

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21396	Ancient DNA refines taxonomic classification of Roman equids north of the Alps, elaborated with osteomorphology and geometric morphometrics. <i>Journal of Archaeological Science</i> , 2022, 143, 105624.	1.2	4
21404	Soil Collected in the Great Smoky Mountains National Park Yielded a Novel <i>Listeria sensu stricto</i> Species, <i>L. swaminathanii</i> . <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	9
21406	Genomic and Evolutionary Study from SARS-CoV-2 Virus Isolates from Bangladesh During the Early Stage of Pandemic Strongly Correlate with European Origin and Not with China. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
21407	Chromosome-level genome assembly of the black widow spider <i>Latrodectus elegans</i> illuminates composition and evolution of venom and silk proteins. <i>GigaScience</i> , 2022, 11, .	3.3	9
21409	Chromosomal-Level Reference Genome of the Moth <i>Heortia vitessoides</i> (Lepidoptera: Crambidae), A Major Pest of Agarwood-Producing Trees. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
21410	Textile Industry Wastewater Microbiome: Recovery of Metagenome Assembled Genomes (Mags) Using Shotgun Sequencing Approach from Jetpur, Gujarat, India. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
21411	Re-evaluation of Symptoventuriaceae. <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2022, , .	1.6	2
21412	<i>Lecithaster</i> (Lecithasteridae, Digenea) in the White Sea: an unnoticed guest from the Pacific?. <i>Journal of Helminthology</i> , 2022, 96, .	0.4	5
21413	From Argentinian Abyssal Plain to Farmed Turbot in Spain: A Ubiquitous Amoeba Species <i>Vannella robusta</i> Sp. Nov. (Amoebozoa, Vannellida). <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
21414	Deep Insights Into the Plastome Evolution and Phylogenetic Relationships of the Tribe Urticeae (Family) <i>Tj ETQq1 1 0.784314 rgBT /Overl</i>	1.7	11
21415	Linked-Read Sequencing of Eight Falcons Reveals a Unique Genomic Architecture in Flux. <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	3
21416	Rediscovery and phylogenetic analysis of the Shelta Cave Crayfish (<i>Orconectes sheltae</i> Cooper) Alabama, USA. <i>Subterranean Biology</i> , 0, 43, 11-31.	5.0	1
21417	Integrative Taxonomy Reveals a New Species of the Genus <i>Lejeunea</i> (Marchantiophyta: Lejeuneaceae) from Peninsular Malaysia. <i>Plants</i> , 2022, 11, 1642.	1.6	4
21418	Old genes in new places: A taxon-rich analysis of interdomain lateral gene transfer events. <i>PLoS Genetics</i> , 2022, 18, e1010239.	1.5	6
21419	Phylogenomics and evolutionary history of Oreocnide (Urticaceae) shed light on recent geological and climatic events in SE Asia. <i>Molecular Phylogenetics and Evolution</i> , 2022, 175, 107555.	1.2	4
21420	A chromosome-level <i>Populus qiongdaoensis</i> genome assembly provides insights into tropical adaptation and a cryptic turnover of sex determination. <i>Molecular Ecology</i> , 2023, 32, 1366-1380.	2.0	10
21421	Characterization of the Complete Chloroplast Genome Sequence of the Socotra Dragon's Blood Tree (<i>Dracaena cinnabari</i> Balf.). <i>Forests</i> , 2022, 13, 932.	0.9	3
21422	Using molecular phylogenetic and stable isotopic analysis to identify species, geographical origin and production method of mullet roes. <i>Food Control</i> , 2022, 141, 109206.	2.8	4

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21423	A chromosome-level genome assembly for the rabbit tapeworm <i>Taenia pisiformis</i> . <i>Gene</i> , 2022, 834, 146650.	1.0	2
21424	Evolution, Transmission, and Pathogenicity of High Pathogenicity Avian Influenza Virus A (H5N8) Clade 2.3.4.4, South Korea, 2014–2016. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	2
21425	Four new members of the family Cytophagaceae: <i>Chryseosolibacter histidini</i> gen. nov., sp. nov., <i>Chryseosolibacter indicus</i> gen. nov., sp. nov., <i>Dawidia cretensis</i> , gen. nov., sp. nov., and <i>Dawidia soli</i> , gen. nov., sp. nov. isolated from diverse habitat. <i>Antonie Van Leeuwenhoek</i> , 2022, 115, 1059-1072.	0.7	1
21426	Molecular Structure and Phylogenetic Analyses of the Complete Chloroplast Genomes of Three Medicinal Plants <i>Conioselinum vaginatum</i> , <i>Ligusticum sinense</i> , and <i>Ligusticum jeholense</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	4
21427	Evolutionary History of DMSP Lyase-Like Genes in Animals and Their Possible Involvement in Evolution of the Scleractinian Coral Genus, <i>Acropora</i> . <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	4
21428	Genomic Diversity of Hospital-Acquired Infections Revealed through Prospective Whole-Genome Sequencing-Based Surveillance. <i>MSystems</i> , 2022, 7, .	1.7	10
21429	Back from the deaf: integrative taxonomy revalidates an earless and mute species, <i>Hylodes grandoculis</i> van Lidth de Jeude, 1904, and confirms a new species of <i>Pristimantis jimenez de la Espada</i> , 1870 (Anura: Tj ETQq0,0 0 rgBTj /Overlock 0,7 9	0.7	9
21430	<i>Photobacterium arenosum</i> WH24, Isolated from the Gill of Pacific Oyster <i>Crassostrea gigas</i> from the North Sea of Germany: Co-cultivation and Prediction of Virulence. <i>Current Microbiology</i> , 2022, 79, .	1.0	2
21431	<i>Chromobacterium alticapitis</i> sp. nov. and <i>Chromobacterium sinusclupearum</i> sp. nov. isolated from wild cranberry bogs in the Cape Cod National Seashore, USA. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	8
21432	Sulfated glycan recognition by carbohydrate sulfatases of the human gut microbiota. <i>Nature Chemical Biology</i> , 2022, 18, 841-849.	3.9	16
21433	High sorbic acid resistance of <i>Penicillium roqueforti</i> is mediated by the SORBUS gene cluster. <i>PLoS Genetics</i> , 2022, 18, e1010086.	1.5	4
21434	<i>Cordyceps mexicana</i> sp. nov., parasitizing <i>Paradirphia</i> sp. moths: A new sister species of the <i>Cordyceps militaris</i> complex, distributed in central Mexican <i>Quercus-Pinus</i> mixed forests. <i>Mycologia</i> , 0, , 1-16.	0.8	1
21435	Isolation of <i>Listeria ivanovii</i> from Bulk-Tank Milk of Sheep and Goat Farms—From Clinical Work to Bioinformatics Studies: Prevalence, Association with Milk Quality, Antibiotic Susceptibility, Predictors, Whole Genome Sequence and Phylogenetic Relationships. <i>Biology</i> , 2022, 11, 871.	1.3	3
21436	Taxonomy, comparative genomics and evolutionary insights of <i>Penicillium ucsense</i> : a novel species in series <i>Oxalica</i> . <i>Antonie Van Leeuwenhoek</i> , 2022, 115, 1009-1029.	0.7	5
21437	A high-quality de novo genome assembly based on nanopore sequencing of a wild-caught coconut rhinoceros beetle (<i>Oryctes rhinoceros</i>). <i>BMC Genomics</i> , 2022, 23, .	1.2	6
21438	Genetic diversity and population structure of <i>Caryopteris mongholica</i> revealed by reduced representation sequencing. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	3
21439	Characterization of inositol lipid metabolism in gut-associated Bacteroidetes. <i>Nature Microbiology</i> , 2022, 7, 986-1000.	5.9	19
21440	The first complete mitochondrial genome of <i>Hexagenia rigida</i> Mc Dunnough, 1924 (Ephemeroptera: Ephemeridae) and its phylogeny. <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 1093-1095.	0.2	0

#	ARTICLE	IF	CITATIONS
21441	Global Taxonomy and Phylogeny of Irpicaceae (Polyporales, Basidiomycota) With Descriptions of Seven New Species and Proposals of Two New Combinations. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	5
21442	Chromosome-level and haplotype-resolved genome provides insight into the tetraploid hybrid origin of patchouli. <i>Nature Communications</i> , 2022, 13, .	5.8	20
21443	GR13-type plasmids in <i>Acinetobacter</i> potentiate the accumulation and horizontal transfer of diverse accessory genes. <i>Microbial Genomics</i> , 2022, 8, .	1.0	8
21444	From Western Asia to the Mediterranean Basin: Diversification of the Widespread <i>Euphorbia nicaeensis</i> Alliance (Euphorbiaceae). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3
21445	<i>Blastococcus tunisiensis</i> sp. nov., isolated from limestone collected in Tunisia. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	5
21446	Accounting for Errors in Data Improves Divergence Time Estimates in Single-cell Cancer Evolution. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	5
21447	The complete chloroplast genome sequence of <i>Begonia arachnoidea</i> (Begoniaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 1106-1108.	0.2	1
21448	Genome Sequence and Characterization of a Xanthorhodopsin-Containing, Aerobic Anoxygenic Phototrophic Rhodobacter Species, Isolated from Mesophilic Conditions at Yellowstone National Park. <i>Microorganisms</i> , 2022, 10, 1169.	1.6	3
21449	Plastome characteristics and species identification of Chinese medicinal wintergreens (<i>Gaultheria</i>). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50</i>	1.8	4
21451	<i>Retiboletus atrofuscus</i> (Boletaceae, Boletales), a new species from China. <i>Archives of Microbiology</i> , 2022, 204, .	1.0	3
21452	The genome of a mangrove plant, <i>Avicennia marina</i> , provides insights into adaptation to coastal intertidal habitats. <i>Planta</i> , 2022, 256, .	1.6	5
21453	Phylogeny and historical biogeography of the Panama hat family (Cyclanthaceae, Pandanales). <i>Taxon</i> , 2022, 71, 963-980.	0.4	3
21454	Beyond Nuclear Ribosomal DNA Sequences: Evolution, Taxonomy, and Closest Known Saprobiic Relatives of Powdery Mildew Fungi (Erysiphaceae) Inferred From Their First Comprehensive Genome-Scale Phylogenetic Analyses. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	7
21455	Taxonomic and Phylogenetic Insights into Novel Ascomycota from Forest Woody Litter. <i>Biology</i> , 2022, 11, 889.	1.3	4
21456	The complete mitochondrial genome of <i>Semblis atrata</i> (Trichoptera: Phryganeidae). <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 956-958.	0.2	2
21457	Association mapping of colour variation in a butterfly provides evidence that a supergene locks together a cluster of adaptive loci. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2022, 377, .	1.8	22
21458	Sequence Characteristics and Phylogenetic Analysis of the <i>Artemisia argyi</i> Chloroplast Genome. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	8
21459	The complete genome sequence of <i>Melia azedarach</i> Linn. (Meliaceae): a multi-purpose pesticide species. <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 1103-1105.	0.2	2

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21460	Candida auris: outbreak fungal pathogen in COVID-19 pandemic: a systematic review and meta-analysis. Iranian Journal of Microbiology, 0, , .	0.8	0
21461	Four New Pale-Spored Species of Xylaria (Xylariaceae, Xylariales) with a Key to Worldwide Species on Fallen Fruits and Seeds. Biology, 2022, 11, 885.	1.3	2
21462	Phylogeny, molecular evolution, and dating of divergences in Lagerstroemia using plastome sequences. Horticultural Plant Journal, 2022, , .	2.3	6
21463	Isolation and Whole-Genome Sequencing of Four Antibiotic-Producing Pseudomonas Strains. Microbiology Resource Announcements, 0, , .	0.3	0
21464	On the verge of extinction – revision of a highly endangered Swiss alpine snail with description of a new genus, Raeticella gen. nov. (Gastropoda, Eupulmonata, Hygromiidae). ZooKeys, 0, 1104, 69-91.	0.5	0
21465	The Microbiological Drivers of Temporally Dynamic Dimethylsulfoniopropionate Cycling Processes in Australian Coastal Shelf Waters. Frontiers in Microbiology, 0, 13, .	1.5	5
21466	Sedimentimonas flavescens gen. nov., sp. nov., isolated from sediment of Clam Island, Liaoning Province. Antonie Van Leeuwenhoek, 0, , .	0.7	0
21467	Complete chloroplast genome of Lilium ledebourii (Baker) Boiss and its comparative analysis: lights into selective pressure and adaptive evolution. Scientific Reports, 2022, 12, .	1.6	14
21468	Nuclear and Mitochondrial Phylogenomics of the Sifakas Reveal Cryptic Variation in the Diademed Sifaka. Genes, 2022, 13, 1026.	1.0	0
21469	Genetic diversity and demography of <i>Bufo japonicus</i> and <i>B. torrenticola</i> (Amphibia): Tj ETQq1 1 0.784314 rgBT ₅ Overl	0.9	5
21470	Hidden in plain sight: novel molecular data reveal unexpected genetic diversity among paramphistome parasites (Digenea: Paramphistomoidea) of European water frogs. Parasitology, 2022, 149, 1425-1438.	0.7	4
21471	Phylotranscriptomic analyses reveal multiple whole-genome duplication events, the history of diversification and adaptations in the Araceae. Annals of Botany, 2023, 131, 199-214.	1.4	7
21473	Biogeography, autecology, and phylogeny of Percolomonads based on newly described species. Journal of Eukaryotic Microbiology, 2023, 70, .	0.8	2
21474	Halomonas jincaotanensis sp. nov., isolated from the Pamir Plateau degrading polycyclic aromatic hydrocarbon. Archives of Microbiology, 2022, 204, .	1.0	4
21475	To kill or to be killed: pangenome analysis of Escherichia coli strains reveals a tailocin specific for pandemic ST131. BMC Biology, 2022, 20, .	1.7	10
21476	First Report of Chromosome-Level Genome Assembly for Flathead Grey Mullet, Mugil cephalus (Linnaeus, 1758). Frontiers in Genetics, 0, 13, .	1.1	0
21477	Detection of Ancient Viruses and Long-Term Viral Evolution. Viruses, 2022, 14, 1336.	1.5	8
21478	Dimorphic life cycle through transverse division in burrowing hard coral Deltocyathoides orientalis. Scientific Reports, 2022, 12, .	1.6	1

#	ARTICLE	IF	CITATIONS
21479	Genome sequence of <i>Gossypium anomalum</i> facilitates interspecific introgression breeding. <i>Plant Communications</i> , 2022, 3, 100350.	3.6	14
21480	<i>Chlorophytum delicatulum</i> (Asparagaceae), a newly described species from Zambia. <i>Kew Bulletin</i> , 0, , .	0.4	0
21481	Whole-genome sequencing analysis and protocol for RNA interference of the endoparasitoid wasp <i>Asobara japonica</i> . <i>DNA Research</i> , 2022, 29, .	1.5	1
21482	<i>Gomphocantharellus</i> , a new genus of Gomphales. <i>Mycologia</i> , 2022, 114, 748-756.	0.8	2
21483	The Complete Mitochondrial Genome of a Neglected Breed, the Peruvian Creole Cattle (<i>Bos taurus</i>), and Its Phylogenetic Analysis. <i>Data</i> , 2022, 7, 76.	1.2	3
21484	Rediscovery, redescription and identity of <i>Pristimantis nebulosus</i> (Henle, 1992), and description of a new terrestrial-breeding frog from montane rainforests of central Peru (Anura, Strabomantidae). <i>Zoosystematics and Evolution</i> , 2022, 98, 213-232.	0.4	5
21485	Occurrence and diversity of black-foot pathogens on asymptomatic nursery-produced grapevines in Türkiye. <i>European Journal of Plant Pathology</i> , 2022, 164, 21-32.	0.8	1
21486	Updates on <i>Geastrum</i> sect. <i>Exareolata</i> , with a description of a striking new species from the Neotropics. <i>Plant Systematics and Evolution</i> , 2022, 308, .	0.3	2
21487	New insights into intergeneric relationships of <i>Hickeliinae</i> (Poaceae: Bambusoideae) revealed by complete plastid genomes. <i>Plant Diversity</i> , 2023, 45, 125-132.	1.8	1
21489	Invasive <i>Coptodon</i> (Perciformes: Cichlidae) in southwest Turkey: Species identification using sequence data. <i>Su Akademi Dergisi</i> , 2022, 39, 135-144.	0.1	0
21490	<i>Thesium muasyae</i> (Santalaceae), a new species from the limestone fynbos of the Overberg, South Africa. <i>PhytoKeys</i> , 0, 201, 1-14.	0.4	3
21491	A comparative genomic analysis of lichen-forming fungi reveals new insights into fungal lifestyles. <i>Scientific Reports</i> , 2022, 12, .	1.6	6
21492	<i>Pluteus insidiosus</i> Complex, Four New Species Described and <i>Pluteus reisneri</i> Resurrected. <i>Journal of Fungi</i> (Basel, Switzerland), 2022, 8, 623.	1.5	1
21493	The first complete chloroplast genome of <i>Briggsia chienii</i> W. Y. Chun and its phylogenetic position within Gesneriaceae. <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 1120-1122.	0.2	2
21494	Composition of a chemical signalling trait varies with phylogeny and precipitation across an Australian lizard radiation. <i>Journal of Evolutionary Biology</i> , 2022, 35, 919-933.	0.8	2
21495	<i>Pseudomonas petroselini</i> sp. nov., a pathogen causing bacterial rot of parsley in Japan. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	5
21496	<i>Enenterum kyphosi</i> Yamaguti, 1970 and <i>Enenterum petrae</i> n. sp. (Digenea: Enenteridae) from kyphosid fishes (Centrarchiformes: Kyphosidae) collected in marine waters off eastern Australia. <i>Zootaxa</i> , 2022, 5154, 271-288.	0.2	3
21497	The complete chloroplast genome sequence of <i>Clerodendrum cyrtophyllum</i> from Guangzhou, China. <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 1117-1119.	0.2	1

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21498	Complete genome sequence and phylogenetic analysis of medicinal plant <i>Abrus cantoniensis</i> for evolutionary research and germplasm utilization. <i>Plant Genome</i> , 0, , .	1.6	2
21500	Genomic and Evolutionary Analysis of <i>Salmonella enterica</i> Serovar Kentucky Sequence Type 198 Isolated From Livestock In East Africa. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	5
21501	Fourteen new <i>Polynucleobacter</i> species: <i>P. brandtiae</i> sp. nov., <i>P. kasalickyi</i> sp. nov., <i>P. antarcticus</i> sp. nov., <i>P. arcticus</i> sp. nov., <i>P. tropicus</i> sp. nov., <i>P. bastaniensis</i> sp. nov., <i>P. corsicus</i> sp. nov., <i>P. finlandensis</i> sp. nov., <i>P. ibericus</i> sp. nov., <i>P. hallstattensis</i> sp. nov., <i>P. alcilacus</i> sp. nov., <i>P. nymphae</i> sp. nov., <i>P. paludilacus</i> sp. nov. and <i>P. parvulilacunae</i> sp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	47
21503	High levels of inbreeding with spatial and host-associated structure in lice of an endangered freshwater seal. <i>Molecular Ecology</i> , 2022, 31, 4593-4606.	2.0	10
21504	Novel Mitochondrial Gene Rearrangement and Intergenic Regions Exist in the Mitochondrial Genomes from Four Newly Established Families of Praying Mantises (Insecta: Mantodea). <i>Insects</i> , 2022, 13, 564.	1.0	5
21505	Comparative genomic analysis reveals contraction of gene families with putative roles in pathogenesis in the fungal boxwood pathogens <i>Calonectria henricotiae</i> and <i>C. pseudonaviculata</i> . <i>Bmc Ecology and Evolution</i> , 2022, 22, .	0.7	2
21506	Rapid adaptation of a complex trait during experimental evolution of <i>Mycobacterium tuberculosis</i> . <i>ELife</i> , 0, 11, .	2.8	9
21507	Whole-genome sequencing analysis of Shiga toxin-producing <i>Escherichia coli</i> O22:H8 isolated from cattle prediction pathogenesis and colonization factors and position in STEC universe phylogeny. <i>Journal of Microbiology</i> , 0, , .	1.3	4
21508	The international and intercontinental spread and expansion of antimicrobial-resistant <i>Salmonella</i> Typhi: a genomic epidemiology study. <i>Lancet Microbe</i> , The, 2022, 3, e567-e577.	3.4	38
21509	Bacterial Enoyl-Reductases: The Ever-Growing List of Fabs, Their Mechanisms and Inhibition. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
21510	Characterization of antibiotic-resistant, coagulase-negative staphylococci from fresh produce and description of <i>Staphylococcus shinii</i> sp. nov. isolated from chives. <i>Journal of Microbiology</i> , 0, , .	1.3	2
21511	<i>Frankia</i> diversity in sympatrically occurring red alder (<i>Alnus rubra</i>) and Sitka alder (<i>Alnus viridis</i>) trees in an early successional environment. <i>Trees - Structure and Function</i> , 2022, 36, 1665-1675.	0.9	4
21512	Stepwise evolution of a butterfly supergene via duplication and inversion. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2022, 377, .	1.8	24
21513	Morphological and Phylogenetic Analyses Reveal Five New Species in <i>Chaetosphaeriaceae</i> . <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 643.	1.5	3
21514	Prevalence and Genomic Diversity of <i>Salmonella enterica</i> Recovered from River Water in a Major Agricultural Region in Northwestern Mexico. <i>Microorganisms</i> , 2022, 10, 1214.	1.6	4
21515	Characterization of the complete chloroplast genome of <i>Cycas ferruginea</i> , a vulnerable species. <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 1048-1049.	0.2	2
21516	A polar bear paleogenome reveals extensive ancient gene flow from polar bears into brown bears. <i>Nature Ecology and Evolution</i> , 2022, 6, 936-944.	3.4	10
21517	Molecular epidemiology and genotype-specific disease severity of hepatitis E virus infections in Germany, 2010–2019. <i>Emerging Microbes and Infections</i> , 2022, 11, 1754-1763.	3.0	13

#	ARTICLE	IF	CITATIONS
21518	New phylogenetic insights on some species of Unionidae from Switzerland (Bivalvia.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 742 Td (Palaeo)	1.0	1
21519	Phylogenomic Analysis Reconstructed the Order Matoniales from Paleopolyploidy Veil. Plants, 2022, 11, 1529.	1.6	3
21520	Mating pair stabilization mediates bacterial conjugation species specificity. Nature Microbiology, 2022, 7, 1016-1027.	5.9	43
21521	Genome Sequence Analysis and Characterization of Shiga Toxin 2 Production by Escherichia coli O157:H7 Strains Associated With a Laboratory Infection. Frontiers in Cellular and Infection Microbiology, 0, 12, .	1.8	3
21522	Physiologic, Genomic, and Electrochemical Characterization of Two Heterotrophic Marine Sediment Microbes from the Idiomarina Genus. Microorganisms, 2022, 10, 1219.	1.6	0
21523	Moraxella tetraodonis sp. nov., isolated from freshwater pufferfish (Tetraodon cutcutia) skin. Archives of Microbiology, 2022, 204, .	1.0	2
21524	Unravelling the species diversity, phylogeny and biogeography of the mycoheterotrophic Voyriaceae (Gentianaceae) and the description of a new species. Taxon, 0, , .	0.4	0
21525	Uncovering haplotype diversity in cultivated Mexican vanilla species. American Journal of Botany, 0, , .	0.8	5
21526	Maintenance and dissemination of avian-origin influenza A virus within the northern Atlantic Flyway of North America. PLoS Pathogens, 2022, 18, e1010605.	2.1	9
21527	The complete chloroplast genome sequence of <i>Habenaria dentata</i> (Orchidaceae). Mitochondrial DNA Part B: Resources, 2022, 7, 969-970.	0.2	0
21528	Clustered Regularly Interspaced Short Palindromic Repeats Genotyping of Multidrug-Resistant Salmonella Heidelberg Strains Isolated From the Poultry Production Chain Across Brazil. Frontiers in Microbiology, 0, 13, .	1.5	4
21529	Comparison of buckwheat genomes reveals the genetic basis of metabolomic divergence and ecotype differentiation. New Phytologist, 2022, 235, 1927-1943.	3.5	18
21531	A phylogenetic overview of <i>Squamanita</i> , with descriptions of nine new species and four new combinations. Mycologia, 2022, 114, 769-797.	0.8	1
21532	Translational Frameshifting in the chlD Gene Gives a Clue to the Coevolution of the Chlorophyll and Cobalamin Biosyntheses. Microorganisms, 2022, 10, 1200.	1.6	2
21533	Microbial isolates with Anti-Pseudogymnoascus destructans activities from Western Canadian bat wings. Scientific Reports, 2022, 12, .	1.6	6
21534	The First High-quality Reference Genome of Sika Deer Provides Insights into High-tannin Adaptation. Genomics, Proteomics and Bioinformatics, 2023, 21, 203-215.	3.0	9
21535	The population genetics of the causative agent of snake fungal disease indicate recent introductions to the USA. PLoS Biology, 2022, 20, e3001676.	2.6	23
21536	The source of the Black Death in fourteenth-century central Eurasia. Nature, 2022, 606, 718-724.	13.7	58

#	ARTICLE	IF	CITATIONS
21538	African mitochondrial haplogroup L7: a 100,000-year-old maternal human lineage discovered through reassessment and new sequencing. <i>Scientific Reports</i> , 2022, 12, .	1.6	4
21539	Replacement of <i>Leishmania (Leishmania) infantum</i> Populations in an Endemic Focus of Visceral Leishmaniasis in Brazil. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	0
21540	Tuberculosis caused by <i>Mycobacterium orygis</i> in wild ungulates in Chennai, South India. <i>Transboundary and Emerging Diseases</i> , 2022, 69, .	1.3	6
21541	<i>Mojavia aguilerae</i> and <i>M. dolomitestrus</i> two new Nostocaceae (Cyanobacteria) species from the Americas. <i>Journal of Phycology</i> , 2022, 58, 502-516.	1.0	12
21542	Phylogenetic Analysis Reveals Four New Species of Otidea from China. <i>Biology</i> , 2022, 11, 866.	1.3	0
21543	The complete mitochondrial genome of <i>Leptomantella tonkinae</i> (Hebard, 1920) (Mantodea: Tj ETQq1 1 0.784314 rgBT /Overlock 0.2	0.2	0
21544	Complete chloroplast genome of <i>Nyctocalos pinnatum</i> : chloroplast features and phylogenetic relationships within Bignoniaceae. <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 1035-1037.	0.2	0
21545	The Chromosome-Scale Assembly of the <i>Curcuma alismatifolia</i> Genome Provides Insight Into Anthocyanin and Terpenoid Biosynthesis. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	4
21546	Turtle ants harbor metabolically versatile microbiomes with conserved functions across development and phylogeny. <i>FEMS Microbiology Ecology</i> , 2022, 98, .	1.3	3
21547	Novel Insights Into the Phylogeny and Biotechnological Potential of <i>Weissella</i> Species. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	9
21548	Detection of Prokaryotes on the Astomatous Ciliated Protist <i>Kentrophoros flavus</i> (Ciliophora, Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 347 Science, 0, 9, .	1.2	2
21549	Testing alternative hypotheses on the origin and speciation of Hawaiian katydids. <i>Bmc Ecology and Evolution</i> , 2022, 22, .	0.7	1
21550	Evolutionarily conserved odorant-binding proteins participate in establishing tritrophic interactions. <i>IScience</i> , 2022, 25, 104664.	1.9	5
21551	<i>Corallococcus soli</i> sp. Nov., a Soil Myxobacterium Isolated from Subtropical Climate, Chalus County, Iran, and Its Potential to Produce Secondary Metabolites. <i>Microorganisms</i> , 2022, 10, 1262.	1.6	7
21552	Comparative analysis of two Korean irises (<i>Iris ruthenica</i> and <i>I. uniflora</i> , Iridaceae) based on plastome sequencing and micromorphology. <i>Scientific Reports</i> , 2022, 12, .	1.6	7
21553	Highly Specialized Carbohydrate Metabolism Capability in <i>Bifidobacterium</i> Strains Associated with Intestinal Barrier Maturation in Early Preterm Infants. <i>MBio</i> , 2022, 13, .	1.8	10
21554	Identification of Abietane-Type Diterpenoids and Phenolic Acids Biosynthesis Genes in <i>Salvia apiana</i> Jepson Through Full-Length Transcriptomic and Metabolomic Profiling. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3
21555	Identification of <i>nosZ</i> -expressing microorganisms consuming trace N ₂ O in microaerobic chemostat consortia dominated by an uncultured <i>Burkholderiales</i> . <i>ISME Journal</i> , 2022, 16, 2087-2098.	4.4	12

#	ARTICLE	IF	CITATIONS
21556	Phylogenetic Characterization and Genome Sequence Analysis of Burkholderia glumae Strains Isolated in Thailand as the Causal Agent of Rice Bacterial Panicle Blight. Pathogens, 2022, 11, 676.	1.2	3
21557	Primula xinningensis (Primulaceae), a new species from karst caves in Hunan, China. PhytoKeys, 0, 199, 155-166.	0.4	0
21558	A target capture approach for phylogenomic analyses at multiple evolutionary timescales in rosewoods (<i>Dalbergia</i> spp.) and the legume family (Fabaceae). Molecular Ecology Resources, 2022, 22, 3087-3105.	2.2	5
21559	Full-genome sequencing and mutation analysis of SARS-CoV-2 isolated from Makassar, South Sulawesi, Indonesia. PeerJ, 0, 10, e13522.	0.9	3
21560	The chromosome-scale assembly of endive (Cichorium endivia) genome provides insights into the sesquiterpenoid biosynthesis. Genomics, 2022, 114, 110400.	1.3	6
21562	The taxonomic position of brooding limpets of the genera Erginus and Rhodopetala (Patellogastropoda). Zoologischer Anzeiger, 2022, 299, 200-206.	0.4	1
21563	Discovery of the parasite Marteilia cocosarum sp. nov. In common cockle (Cerastoderma edule) fisheries in Wales, UK and its comparison with Marteilia cochillia. Journal of Invertebrate Pathology, 2022, 192, 107786.	1.5	3
21564	Quantification of members of the Mycobacterium chelonae-abscessus complex in lesions of the endangered houston toad (Anaxyrus houstonensis). Systematic and Applied Microbiology, 2022, 45, 126342.	1.2	1
21565	Diversity and Phylogenetic Position of Bothrostoma Stokes, 1887 (Ciliophora: Metopida), with Description of Four New Species. Protist, 2022, 173, 125887.	0.6	6
21566	Genomic data reveal local endemism in Southern California Rubber Boas (Serpentes: Boidae, Charina) and the critical need for enhanced conservation actions. Molecular Phylogenetics and Evolution, 2022, 174, 107542.	1.2	2
21567	Molecular phylogenetics of the avian feather louse Philopterus-complex (Phthiraptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 342 Td (Ph	1.2	2
21568	A phylotranscriptome study using silica gel-dried leaf tissues produces an updated robust phylogeny of Ranunculaceae. Molecular Phylogenetics and Evolution, 2022, 174, 107545.	1.2	10
21569	Interpreting phylogenetic conflict: Hybridization in the most speciose genus of lichen-forming fungi. Molecular Phylogenetics and Evolution, 2022, 174, 107543.	1.2	2
21570	Plastid and mitochondrial phylogenomics reveal correlated substitution rate variation in Koenigia (Polygonaceae) and a reduced plastome for Koenigia delicatula including loss of all ndh genes. Molecular Phylogenetics and Evolution, 2022, 174, 107544.	1.2	5
21571	Taxon-rich transcriptomics supports higher-level phylogeny and major evolutionary trends in Foraminifera. Molecular Phylogenetics and Evolution, 2022, 174, 107546.	1.2	6
21572	Categorical edge-based analyses of phylogenomic data reveal conflicting signals for difficult relationships in the avian tree. Molecular Phylogenetics and Evolution, 2022, 174, 107550.	1.2	1
21573	Fertilizing-induced changes in the nitrifying microbiota associated with soil nitrification and crop yield. Science of the Total Environment, 2022, 841, 156752.	3.9	12
21574	Comparative plastome analyses and genomic resource development in wild rice (Zizania spp., Poaceae) using genome skimming data. Industrial Crops and Products, 2022, 186, 115244.	2.5	12

#	ARTICLE	IF	CITATIONS
21575	Genomic insights to facilitate the construction of a high-xylose-utilization <i>Enterococcus faecalis</i> OPS2 for 2,3-BDO production. <i>Chemical Engineering Journal</i> , 2022, 448, 137617.	6.6	5
21576	Co-dispersal of symbionts in the lichen <i>Cladonia stellaris</i> inferred from genomic data. <i>Fungal Ecology</i> , 2022, 60, 101165.	0.7	2
21577	The Manchurian Walnut Genome: Insights into Juglone and Lipid Biosynthesis. <i>GigaScience</i> , 2022, 11, .	3.3	13
21578	A Viral Metagenomic Protocol for Nanopore Sequencing of Group a Rotavirus. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
21579	Lignin-Oxidizing <i>Vibrios</i> Involved in the Mineralization of Plant Detritus in the Continental Slope. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0

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#	ARTICLE	IF	CITATIONS
21595	Seasonality of parasitic and saprotrophic zoosporic fungi: linking sequence data to ecological traits. ISME Journal, 2022, 16, 2242-2254.	4.4	19
21596	Sequencing and characterization of the chloroplast genome of <i>Aconitum forrestii</i> Stapf provide insights into phylogenetics in <i>Aconitum</i> . Mitochondrial DNA Part B: Resources, 2022, 7, 1165-1167.	0.2	1
21597	Phylogeny and Taxonomic Synopsis of the Genus <i>Bougainvillea</i> (Nyctaginaceae). Plants, 2022, 11, 1700.	1.6	5
21599	The structure of EXTL3 helps to explain the different roles of bi-domain exostosins in heparan sulfate synthesis. Nature Communications, 2022, 13, .	5.8	14
21600	Unprecedented frequency of mitochondrial introns in colonial bilaterians. Scientific Reports, 2022, 12, .	1.6	1
21601	Divergent gut microbiota in two closely related house mouse subspecies under common garden conditions. FEMS Microbiology Ecology, 2022, 98, .	1.3	5
21602	Endophytic Fungi Associated with Coffee Leaves in China Exhibited In Vitro Antagonism against Fungal and Bacterial Pathogens. Journal of Fungi (Basel, Switzerland), 2022, 8, 698.	1.5	8
21603	The Impact of Fast Radiation on the Phylogeny of <i>Bactrocera</i> Fruit Flies as Revealed by Multiple Evolutionary Models and Mutation Rate-Calibrated Clock. Insects, 2022, 13, 603.	1.0	4
21604	Mitochondrial genome of the critically Endangered silver boa (<i>Chilabothrus argenteum</i>); Tj ETQq0 0 0 rgBT /Overlock 1Q Tf 50 422	0.2	1
21605	Plastid Phylogenomics and Plastome Evolution of Nandinoideae (Berberidaceae). Frontiers in Plant Science, 0, 13, .	1.7	2
21606	Umbilicaria phaea var. coccinea: conservation status, variety rank, and secondary chemistry. Bryologist, 2022, 125, .	0.1	0
21608	Re-evaluating the Systematics of <i>Dendrolycopodium</i> Using Restriction-Site Associated DNA-Sequencing. Frontiers in Plant Science, 0, 13, .	1.7	1
21609	Species Tree Estimation and the Impact of Gene Loss Following Whole-Genome Duplication. Systematic Biology, 2022, 71, 1348-1361.	2.7	10
21610	The complete mitochondrial genome of <i>Megalurothrips usitatus</i> (Bagnall 1913) (Thysanoptera:); Tj ETQq1 1 0.784314 rgBT /Overlock 1 0.784314	0.2	1
21611	Evolutionary Relationships and Range Evolution of Greenhood Orchids (Subtribe Pterostylidinae): Insights From Plastid Phylogenomics. Frontiers in Plant Science, 0, 13, .	1.7	3
21613	“New” species are not always new: a case study of <i>Ephedra sumlingensis</i> and <i>E. khurikensis</i> (Ephedraceae). Plant Systematics and Evolution, 2022, 308, .	0.3	3
21614	Phylogeny, Classification, and Character Evolution of <i>Acalypha</i> (Euphorbiaceae: Acalyphoideae). Systematic Botany, 2022, 47, 477-497.	0.2	2
21615	<i>Agaricus macrochlamys</i> , a New Species from the (Sub)tropical Cloud Forests of North America and the Caribbean, and <i>Agaricus fiardii</i> , a New Synonym of <i>Agaricus subrufescens</i> . Journal of Fungi (Basel, Switzerland), Tj ETQq1 1 0.784314 rgBT /Overlock 1 0.784314	0.2	1

#	ARTICLE	IF	CITATIONS
21616	Climate dictates microbial community composition and diversity in Australian biological soil crusts (biocrusts). <i>Environmental Microbiology</i> , 2022, 24, 5467-5482.	1.8	6
21617	The Kinetoplastid-Specific Protein TcCAL1 Plays Different Roles During In Vitro Differentiation and Host-Cell Invasion in <i>Trypanosoma cruzi</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	0
21618	Gllac7 Is Induced by Agricultural and Forestry Residues and Exhibits Allelic Expression Bias in <i>Ganoderma lucidum</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
21619	Chromosomal Assembly of the <i>Hexagrammos agrammus</i> Genome via Third-Generation DNA Sequencing and Hi-C Technology. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	0
21620	Comparative Mitogenome Analyses of Subgenera and Species Groups in <i>Epeorus</i> (Ephemeroptera): Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.0	3
21621	Characteristics of the complete plastid genome sequence of <i>Lindera angustifolia</i> (Lauraceae) in the geographically separated northern edge. <i>Korean Journal of Plant Taxonomy</i> , 2022, 52, 114-117.	0.3	0
21622	A chromosome-level genome of <i>Brachymystax tsinlingensis</i> provides resources and insights into salmonids evolution. <i>G3: Genes, Genomes, Genetics</i> , 0, , .	0.8	0
21623	Dehalogenation of Chlorinated Ethenes to Ethene by a Novel Isolate, <i>Candidatus</i> <i>Dehalogenimonas etheniformans</i> . <i>Applied and Environmental Microbiology</i> , 2022, 88, .	1.4	14
21624	Phylogenomic Analyses and Molecular Signatures Elucidating the Evolutionary Relationships amongst the Chlorobia and Ignavibacteria Species: Robust Demarcation of Two Family-Level Clades within the Order Chlorobiales and Proposal for the Family Chloroherpetonaceae fam. nov. <i>Microorganisms</i> , 2022, 10, 1312.	1.6	5
21625	A critical evaluation of <i>Mycobacterium bovis</i> pangenomics, with reference to its utility in outbreak investigation. <i>Microbial Genomics</i> , 2022, 8, .	1.0	7
21626	Genomic and phenotypic divergence with gene flow across an ecological and elevational gradient in a neotropical bird. <i>Journal of Biogeography</i> , 2022, 49, 1535-1548.	1.4	1
21627	<i>Acinetobacter baumannii</i> Sampled from Cattle and Pigs Represent Novel Clones. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	9
21628	Chloroplast genome structure and phylogenetic analysis of <i>Glycosmis parviflora</i> (Sims) Little 1948, a folk medicinal plant featured in Lingnan Region, China. <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 1160-1162.	0.2	0
21629	The complete chloroplast genome of <i>Mimusops elengi</i> (Sapotaceae: Sapoteae). <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 1146-1147.	0.2	0
21630	The complete chloroplast genome sequence of <i>Rubus peltatus</i> Maxim. (Rosaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 1056-1057.	0.2	1
21631	Complete chloroplast genome of <i>Euphorbia micractina</i> Boiss (Euphorbiaceae: Euphorbia). <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 1129-1130.	0.2	1
21632	Telomere-to-Telomere Genome Sequences across a Single Genus Reveal Highly Variable Chromosome Rearrangement Rates but Absolute Stasis of Chromosome Number. <i>Journal of Fungi (Basel)</i> , Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 97 Td	1.0	3
21633	A chromosome-level genome assembly of the orange wheat blossom midge, <i>Sitodiplosis mosellana</i> GÄ©hin (Diptera: Cecidomyiidae) provides insights into the evolution of a detoxification system. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	1

#	ARTICLE	IF	CITATIONS
21634	Diversity and Molecular Barcoding of Stink Bugs (Hemiptera: Pentatomidae) Associated with Macadamia in South Africa. <i>Insects</i> , 2022, 13, 601.	1.0	2
21635	Taxonomic Identification of Two Poorly Known Lantern Shark Species Based on Mitochondrial DNA From Wet-Collection Paratypes. <i>Frontiers in Ecology and Evolution</i> , 0, 10, .	1.1	6
21636	Conservation genomics of urban populations of Streamside Salamander (<i>Ambystoma barbouri</i>). <i>PLoS ONE</i> , 2022, 17, e0260178.	1.1	2
21638	Gill monogeneans of neotropical cichlid fish: diversity, phylogenetic relationships, and host-parasite cophylogenetic associations. <i>International Journal for Parasitology</i> , 2022, 52, 603-615.	1.3	4
21639	Molecular Systematics, Species Concepts, and Myrmecophytism in <i>Cecropia</i> (Cecropieae). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50</i>	0.2	0
21640	The Tracking of Moist Habitats Allowed Aiphanes (Arecaceae) to Cover the Elevation Gradient of the Northern Andes. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3
21641	Stable antibiotic resistance and rapid human adaptation in livestock-associated MRSA. <i>ELife</i> , 0, 11, .	2.8	28
21642	The Galapagos giant tortoise <i>Chelonoidis phantasticus</i> is not extinct. <i>Communications Biology</i> , 2022, 5, .	2.0	3
21643	<i>Liobagrus brevispina</i> , a new species of torrent catfish (Siluriformes). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 422 Td</i>	0.7	1
21644	<i>Aeromicrobium stalagmiti</i> sp. nov., isolated from a lava cave. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	4
21645	Evolution of Chromosome Number in Wild Onions (<i>Allium</i> , Amaryllidaceae). <i>Systematic Botany</i> , 2022, 47, 335-346.	0.2	0
21646	Morphological and Molecular Evidence Support Elevating <i>Erythroxyllum macrophyllum</i> var. <i>savannarum</i> (Erythroxylaceae) to Specific Status. <i>Systematic Botany</i> , 2022, 47, 467-476.	0.2	1
21647	N-linked glycosylation enhances hemagglutinin stability in avian H5N6 influenza virus to promote adaptation in mammals. , 2022, 1, .		6
21650	GTSF1 accelerates target RNA cleavage by PIWI-clade Argonaute proteins. <i>Nature</i> , 2022, 608, 618-625.	13.7	24
21651	Chromosome-level genome assembly of the aquatic plant <i>Nymphoides indica</i> reveals transposable element bursts and NBS-LRR gene family expansion shedding light on its invasiveness. <i>DNA Research</i> , 2022, 29, .	1.5	4
21652	Lichen speciation is sparked by a substrate requirement shift and reproduction mode differentiation. <i>Scientific Reports</i> , 2022, 12, .	1.6	1
21653	The complete chloroplast genome and phylogenetic position of <i>Thamnocalamus unispiculatus</i> (Poaceae: Bambusoideae: Arundinarieae). <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 1168-1170.	0.2	0
21654	Multilocus Data Analysis Reveal the Diversity of Cryptic Species in the <i>Tillandsia ionantha</i> (Bromeliaceae: Tillandsioideae) Complex. <i>Plants</i> , 2022, 11, 1706.	1.6	3

#	ARTICLE	IF	CITATIONS
21655	Lagenaâ€™an overlooked oomycete genus with a wide range of hosts. Mycological Progress, 2022, 21, .	0.5	3
21656	Analysis of Childrenâ€™s Sports Heuristic Teaching Based on Deep Learning. Scientific Programming, 2022, 2022, 1-8.	0.5	0
21659	Plastome evolution of Aeonium and Monanthes (Crassulaceae): insights into the variation of plastomic tRNAs, and the patterns of codon usage and aversion. Planta, 2022, 256, .	1.6	9
21660	Impact of host demography and evolutionary history on endosymbiont molecular evolution: A test in carpenter ants (genus <i>Camponotus</i>) and their <i>Blochmannia</i> endosymbionts. Ecology and Evolution, 2022, 12, .	0.8	7
21661	Incomplete denitrification phenotypes in diverse <i>Thermus</i> species from diverse geothermal spring sediments and adjacent soils in southwest China. Extremophiles, 2022, 26, .	0.9	4
21662	HIVâ€™1 Subtype Shift in the Philippines is Associated With High Transmitted Drug Resistance, High Viral Loads, and Fast Immunologic Decline. International Journal of Infectious Diseases, 2022, 122, 936-943.	1.5	3
21663	Historical genetic diversity and population structure of wild red pandas (<i>Ailurus fulgens</i>) in Nepal. Mammalian Biology, 0, , .	0.8	0
21664	Different phylogenomic methods support monophyly of enigmatic â€™Mesozoaâ€™ (Dicyemida +) Tj ETQq1 1 0.784314 rgBT /Overlock 1.2 7	1.2	7
21665	Phylotranscriptomics Illuminates the Placement of Whole Genome Duplications and Gene Retention in Ferns. Frontiers in Plant Science, 0, 13, .	1.7	10
21666	Deep structure, longâ€™distance migration and admixture in the colour polymorphic land snail <i>Cepaea nemoralis</i> . Journal of Evolutionary Biology, 2022, 35, 1110-1125.	0.8	1
21667	Novel Microorganisms Contribute to Biosulfidogenesis in the Deep Layer of an Acidic Pit Lake. Frontiers in Bioengineering and Biotechnology, 0, 10, .	2.0	3
21668	Subtyping Evaluation of <i>Salmonella</i> Enteritidis Using Single Nucleotide Polymorphism and Core Genome Multilocus Sequence Typing with Nanopore Reads. Applied and Environmental Microbiology, 2022, 88, .	1.4	2
21669	The complete mitochondrial genome of <i>Tuberolachnus salignus</i> (Gmelin, 1790) (Hemiptera:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 0.2	0.2	10
21670	Reâ€™assessing the phylogenetic status and evolutionary relationship of Forest Owlet (<i>Athene</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 1.0 0	1.0	0
21671	Species discrimination in <i>Schima</i> (Theaceae): Nextâ€™generation superâ€™barcodes meet evolutionary complexity. Molecular Ecology Resources, 2022, 22, 3161-3175.	2.2	10
21672	Genome-Wide Study of Drug Resistant <i>Mycobacterium tuberculosis</i> and Its Intra-Host Evolution during Treatment. Microorganisms, 2022, 10, 1440.	1.6	5
21673	Reference genome assemblies reveal the origin and evolution of allohexaploid oat. Nature Genetics, 2022, 54, 1248-1258.	9.4	45
21674	The complete mitochondrial genome of the edible mushroom <i>Pleurotus giganteus</i> (Agaricales,) Tj ETQq1 1 0.784314 rgBT /Overlock 0.2 2	0.2	2

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21675	Transcriptomic comparison sheds new light on regulatory networks for dimorphic flower development in response to photoperiod in <i>Viola prionantha</i> . <i>BMC Plant Biology</i> , 2022, 22, .	1.6	3
21677	Planktonic diatom communities in temperate South-Central Chilean lakes with a focus on <i>Asterionella formosa</i> and the genus <i>Aulacoseira</i> . <i>Journal of Paleolimnology</i> , 2022, 68, 279-296.	0.8	2
21678	Plastome comparison and phylogenomics of <i>Fagopyrum</i> (Polygonaceae): insights into sequence differences between <i>Fagopyrum</i> and its related taxa. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	7
21679	Phylogenomics of arboreal alligator lizards shed light on the geographical diversification of cloud forest-adapted biotas. <i>Journal of Biogeography</i> , 2022, 49, 1862-1876.	1.4	3
21680	A de novo assembled high-quality chromosome-scale <i>Trifolium pratense</i> genome and fine-scale phylogenetic analysis. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	6
21682	Lilac (<i>Syringa oblata</i>) genome provides insights into its evolution and molecular mechanism of petal color change. <i>Communications Biology</i> , 2022, 5, .	2.0	13
21683	Interspecies Transmission of CMY-2-Producing <i>Escherichia coli</i> Sequence Type 963 Isolates between Humans and Gulls in Australia. <i>MSphere</i> , 2022, 7, .	1.3	6
21684	Dioecy and chromosomal sex determination are maintained through allopolyploid speciation in the plant genus <i>Mercurialis</i> . <i>PLoS Genetics</i> , 2022, 18, e1010226.	1.5	4
21685	Revised Species Delimitation in the Giant Water Lily Genus <i>Victoria</i> (Nymphaeaceae) Confirms a New Species and Has Implications for Its Conservation. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	9
21686	Complete chloroplast genome sequence of <i>Kosteletzkya pentacarpos</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 1232-1233.	0.2	0
21687	The complete chloroplast genome of <i>Tulipa gesneriana</i> (Liliaceae) and its phylogenetic analysis. <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 1255-1256.	0.2	1
21688	Adaptation to a new environment with pre-adaptive genomic features " Evidence from woody plants colonizing the land-sea interface. <i>Plant Journal</i> , 2022, 111, 1411-1424.	2.8	4
21689	Intracellular development and impact of a marine eukaryotic parasite on its zombified microalgal host. <i>ISME Journal</i> , 2022, 16, 2348-2359.	4.4	10
21690	Use of Whole-Genome Sequencing to Unravel the Genetic Diversity of a Prevalent <i>Mycobacterium bovis</i> Spoligotype in a Multi-Host Scenario in Spain. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
21691	An enhancer of <i>Agouti</i> contributes to parallel evolution of cryptically colored beach mice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	9
21693	<i>Xylella fastidiosa</i> Outbreak in Israel: Population Genetics, Host Range, and Temporal and Spatial Distribution Analysis. <i>Phytopathology</i> , 2022, 112, 2296-2309.	1.1	6
21694	New insights into the phylogeny of the complex thalloid liverworts (Marchantiopsida) based on chloroplast genomes. <i>Cladistics</i> , 2022, 38, 649-662.	1.5	9
21695	Genome-wide identification and comparative evolutionary analysis of sorbitol metabolism pathway genes in four Rosaceae species and three model plants. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	5

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21696	Genome of <i>Lindera glauca</i> provides insights into the evolution of biosynthesis genes for aromatic compounds. <i>IScience</i> , 2022, 25, 104761.	1.9	2
21697	The complete chloroplast genome of the genus <i>Azadirachta</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 1267-1269.	0.2	0
21698	Comparative genomic analysis of <i>Babesia duncani</i> responsible for human babesiosis. <i>BMC Biology</i> , 2022, 20, .	1.7	11
21699	Molecular phylogenetics reveals the evolutionary history of marine fishes (Actinopterygii) endemic to the subtropical islands of the Southwest Pacific. <i>Molecular Phylogenetics and Evolution</i> , 2022, , 107584.	1.2	1
21700	Genome-Wide Identification, Characterization, and Comparative Analysis of NLR Resistance Genes in <i>Coffea</i> spp.. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
21701	Genomic Characteristics and Comparative Genomics Analysis of <i>Parafenestella ontariensis</i> sp. nov.. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 732.	1.5	4
21702	Spatial and biological oceanographic insights into the massive fish-killing bloom of the haptophyte <i>Chrysochromulina leadbeateri</i> in northern Norway. <i>Harmful Algae</i> , 2022, 118, 102287.	2.2	16
21703	High-quality ice plant reference genome analysis provides insights into genome evolution and allows exploration of genes involved in the transition from C3 to CAM pathways. <i>Plant Biotechnology Journal</i> , 2022, 20, 2107-2122.	4.1	17
21705	Genetic variability and the ecology of geographic range: A test of the central-marginal hypothesis in Australian scincid lizards. <i>Molecular Ecology</i> , 2022, 31, 4242-4253.	2.0	5
21706	Evolutionary relationships of poorly known Aegean endemic monotypic genus <i>Microsciadium</i> (Apiaceae). <i>Plant Biosystems</i> , 0, , 1-14.	0.8	0
21707	Activity of Drug Combinations against <i>Mycobacterium abscessus</i> Grown in Aerobic and Hypoxic Conditions. <i>Microorganisms</i> , 2022, 10, 1421.	1.6	4
21708	Complete chloroplast genome sequences of <i>Sinosenecio baojingensis</i> Ying Liu & Q.E. Yang (Asteraceae). <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 1280-1281.	0.2	1
21710	Multigene phylogenetic analysis reveals non-monophyly of <i>Anisakis</i> s.l. and <i>Pseudoterranova</i> (Nematoda: Anisakidae). <i>Parasitology International</i> , 2022, 91, 102631.	0.6	7
21711	Hierarchical phylogenetic community assembly of soil protists in a temperate agricultural field. <i>Environmental Microbiology</i> , 2022, 24, 5498-5508.	1.8	5
21712	Characterization of the complete chloroplast genome of <i>Elaeagnus pungens</i> (elaegnaceae) and phylogeny within elaeagnaceae. <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 1213-1215.	0.2	4
21713	Evolution of the North American Lineage H7 Avian Influenza Viruses in Association with H7 Virus™s Introduction to Poultry. <i>Journal of Virology</i> , 2022, 96, .	1.5	6
21715	Multiple compensatory mutations contribute to the de-domestication of Iberian weedy rice. <i>Plants People Planet</i> , 2022, 4, 499-510.	1.6	4
21716	The complete chloroplast genome sequence of <i>Lithocarpus longinux</i> (Fagaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 1229-1231.	0.2	4

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21717	Haplotype-resolved genome assembly of <i>Bletilla striata</i> (Thunb.) Reichb.f. to elucidate medicinal value. <i>Plant Journal</i> , 2022, 111, 1340-1353.	2.8	22
21719	The MAP3Ks DLK and LZK Direct Diverse Responses to Axon Damage in Zebrafish Peripheral Neurons. <i>Journal of Neuroscience</i> , 2022, 42, 6195-6210.	1.7	6
21720	Hidden Species Diversity was Explored in Two Genera of Catapyrenioid Lichens (Verrucariaceae.) <i>Tj ETQq0 0 0 rgBT /Qverlock_10 Tf 50 6</i>	1.5	3
21721	Comparative Genomics and Pan-Genome Driven Prediction of a Reduced Genome of <i>Akkermansia muciniphila</i> . <i>Microorganisms</i> , 2022, 10, 1350.	1.6	5
21722	Genome Size Variation and Evolution Driven by Transposable Elements in the Genus <i>Oryza</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	10
21723	Bacterial Microbiome in the Phyllo-Endosphere of Highly Specialized Rock Spleenwort. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
21724	Chromosome-Level Genome Assembly and Transcriptome Comparison Analysis of <i>Cephalopholis sonnerati</i> and Its Related Grouper Species. <i>Biology</i> , 2022, 11, 1053.	1.3	4
21725	High clustering rate and genotypic drug-susceptibility screening for the newly recommended anti-tuberculosis drugs among global extensively drug-resistant <i>Mycobacterium tuberculosis</i> isolates. <i>Emerging Microbes and Infections</i> , 2022, 11, 1857-1866.	3.0	6
21726	Uncovering the enigmatic evolution of bears in greater depth: The hybrid origin of the Asiatic black bear. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	13
21727	Whole-genome single nucleotide polymorphism analysis for typing the pandemic pathogen <i>Fusarium graminearum sensu stricto</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
21728	Replicated radiation of a plant clade along a cloud forest archipelago. <i>Nature Ecology and Evolution</i> , 2022, 6, 1318-1329.	3.4	11
21729	Widespread emergence of OmpK36 loop 3 insertions among multidrug-resistant clones of <i>Klebsiella pneumoniae</i> . <i>PLoS Pathogens</i> , 2022, 18, e1010334.	2.1	16
21730	Phylogenomics of the world's otters. <i>Current Biology</i> , 2022, 32, 3650-3658.e4.	1.8	14
21731	Characterization of Cultivable Diversity and Carbon Substrate Utilization in the Sediments of Lake Tuz. <i>Eurasian Soil Science</i> , 0, , .	0.5	0
21732	Substrate-restricted methanogenesis and limited volatile organic compound degradation in highly diverse and heterogeneous municipal landfill microbial communities. <i>ISME Communications</i> , 2022, 2, .	1.7	8
21733	The minnow <i>Phoxinus phoxinus</i> (Leuciscidae) shifts the Adriatic-Black Sea basin divide in the northwestern Dinaric Karst region. <i>Ecohydrology</i> , 2022, 15, .	1.1	2
21734	Genome-Wide Analysis of the TCP Gene Family and Their Expression Pattern Analysis in Tea Plant (<i>Camellia sinensis</i>). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	8
21735	Prosthecate aerobic anoxygenic phototrophs <i>Photocaulis sulfatitolerans</i> gen. nov. sp. nov. and <i>Photocaulis rubescens</i> sp. nov. isolated from alpine meromictic lakes in British Columbia, Canada. <i>Archives of Microbiology</i> , 2022, 204, .	1.0	3

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21736	Genomic and Immunological Characterization of Hypermucoviscous Carbapenem-Resistant <i>Klebsiella pneumoniae</i> ST25 Isolates from Northwest Argentina. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7361.	1.8	7
21737	<i>Ganoderma ovisporum</i> sp. nov. (Polyporales, Polyporaceae) from Southwest China. <i>Biodiversity Data Journal</i> , 0, 10, .	0.4	3
21740	The complete chloroplast genome of <i>Hydrocotyle pseudoconferta</i> Masamune 1932 (Araliaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 1199-1200.	0.2	1
21741	Genetic characterization of <i>Salmonella Infantis</i> from South Africa, 2004–2016. <i>Access Microbiology</i> , 2022, 4, .	0.2	1
21743	Small mammal diversity of a poorly known and threatened Amazon region, the Tapaj�s Area of Endemism. <i>Biodiversity and Conservation</i> , 2022, 31, 2683-2697.	1.2	1
21744	<i>Trachymyrmex septentrionalis</i> Ant Microbiome Assembly Is Unique to Individual Colonies and Castes. <i>MSphere</i> , 2022, 7, .	1.3	4
21745	Microbial genomic trait evolution is dominated by frequent and rare pulsed evolution. <i>Science Advances</i> , 2022, 8, .	4.7	7
21746	The durability of natural infection and vaccine-induced immunity against future infection by SARS-CoV-2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	47
21747	Biogeographic history of a large clade of ectomycorrhizal fungi, the Russulaceae, in the Neotropics and adjacent regions. <i>New Phytologist</i> , 2022, 236, 698-713.	3.5	12
21748	Identification and Characterization of <i>Calonectria</i> Species Associated with Plant Diseases in Southern China. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 719.	1.5	8
21749	Caryophylliids (Anthozoa, Scleractinia) and mitochondrial gene order: Insights from mitochondrial and nuclear phylogenomics. <i>Molecular Phylogenetics and Evolution</i> , 2022, 175, 107565.	1.2	9
21750	Phylogeny and pathogenicity of <i>Colletotrichum lindemuthianum</i> causing anthracnose of <i>Phaseolus vulgaris</i> cv. Bhaderwah-Rajmash from northern Himalayas, India. <i>3 Biotech</i> , 2022, 12, .	1.1	1
21751	Marine gregarine genomes reveal the breadth of apicomplexan diversity with a partially conserved glideosome machinery. <i>BMC Genomics</i> , 2022, 23, .	1.2	7
21752	Resistance to Extreme Stresses by a Newly Discovered Japanese Tardigrade Species, <i>Macrobiotus kyoukenus</i> (Eutardigrada, Macrobiotidae). <i>Insects</i> , 2022, 13, 634.	1.0	6
21753	Resolving species-level diversity of <i>Beringiana</i> and <i>Sinanodonta</i> mussels (Bivalvia: Unionidae) in the Japanese archipelago using genome-wide data. <i>Molecular Phylogenetics and Evolution</i> , 2022, 175, 107563.	1.2	10
21755	Diversity of <i>Colletotrichum</i> Species Causing Apple Bitter Rot and <i>Glomerella</i> Leaf Spot in China. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 740.	1.5	15
21756	Wide distribution of the <i>sad</i> gene cluster for subterminal oxidation in alkane utilizers. <i>Environmental Microbiology</i> , 2022, 24, 6307-6319.	1.8	6
21758	The Evolution of a Specialized, Highly Virulent Fish Pathogen through Gene Loss and Acquisition of Host-Specific Survival Mechanisms. <i>Applied and Environmental Microbiology</i> , 2022, 88, .	1.4	2

#	ARTICLE	IF	CITATIONS
21759	From East Asia to Beringia: reconstructed range dynamics of <i>Geranium erianthum</i> (Geraniaceae) during the last glacial period in the northern Pacific region. <i>Plant Systematics and Evolution</i> , 2022, 308, .	0.3	2
21761	Convergence of MCR-8.2 and Chromosome-Mediated Resistance to Colistin and Tigecycline in an NDM-5-Producing ST656 <i>Klebsiella pneumoniae</i> Isolate From a Lung Transplant Patient in China. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	7
21763	Molecular phylogenetics of the Clupeiformes based on exon-capture data and a new classification of the order. <i>Molecular Phylogenetics and Evolution</i> , 2022, 175, 107590.	1.2	9
21765	The evolutionary history of cribellate orb-weaver capture thread spiders. <i>Bmc Ecology and Evolution</i> , 2022, 22, .	0.7	6
21766	The stepwise Indianâ€Eurasian collision and uplift of the Himalayanâ€Tibetan plateau drove the diversification of high-elevation <i>Scytodes</i> spiders. <i>Cladistics</i> , 2022, 38, 582-594.	1.5	6
21768	Extended disordered regions of ribosome-associated NAC proteins paralogs belong only to the germline in <i>Drosophila melanogaster</i> . <i>Scientific Reports</i> , 2022, 12, .	1.6	1
21769	Two New Records of Genus <i>Lepiota</i> (Agaricaceae) from Pakistan. <i>Biology Bulletin</i> , 2022, 49, 458-465.	0.1	2
21770	Polyzoa is back: The effect of complete gene sets on the placement of Ectoprocta and Entoprocta. <i>Science Advances</i> , 2022, 8, .	4.7	12
21771	Molecular footprint of parasite co-introduction with Nile tilapia in the Congo Basin. <i>Organisms Diversity and Evolution</i> , 2022, 22, 1003-1019.	0.7	8
21772	The complete plastid genome of <i>Amphicarpaea ferruginea</i> Bentham (Leguminosae), a grass species with development and utilization prospect. <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 1221-1223.	0.2	1
21773	Software Choice and Sequencing Coverage Can Impact Plastid Genome Assemblyâ€A Case Study in the Narrow Endemic <i>Calligonum bakuense</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
21774	Phylogenomic Analysis of <i>Salmonella enterica</i> Serovar Indiana ST17, an Emerging Multidrug-Resistant Clone in China. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	5
21775	The complete mitogenome of the potentially invasive flatworm <i>Australopacifica atrata</i> (Platyhelminthes, Geoplanidae) displays unusual features common to other Rhynchodeminae. <i>ZooKeys</i> , 0, 1110, 121-133.	0.5	3
21776	Conserved and lineage-specific hypothetical proteins may have played a central role in the rise and diversification of major archaeal groups. <i>BMC Biology</i> , 2022, 20, .	1.7	4
21777	Phylogeny, Divergence Time Estimation and Biogeography of the Genus <i>Onnia</i> (Basidiomycota). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 18</i>	1.5	8
21779	Phylogenetic relationships in Indian <i>Daphne</i> (Thymelaeaceae) based on nuclear ITS and cpDNA data. , 2022, 77, 3071-3086.		2
21780	Morphological and phylogenetic analyses reveal two new species and a new record of <i>Phyllosticta</i> (Botryosphaerales, Phyllostictaceae) from Hainan, China. <i>MycKeys</i> , 0, 91, 1-23.	0.8	5
21782	<i>Alloexidiopsis</i> gen. nov., A Revision of Generic Delimitation in Auriculariales (Basidiomycota). <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2

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21783	Genome Analysis of <i>Enterobacter asburiae</i> and <i>Lelliottia</i> spp. Proliferating in Oligotrophic Drinking Water Reservoirs and Lakes. <i>Applied and Environmental Microbiology</i> , 2022, 88, .	1.4	8
21784	<i>Longitalea arenae</i> gen. nov., sp. nov. and <i>Longitalea luteola</i> sp. nov., two new members of the family Chitinophagaceae isolated from desert soil. <i>Archives of Microbiology</i> , 2022, 204, .	1.0	4
21785	Description of a new species of <i>Hypaeus</i> (Araneae: Salticidae: Salticinae: Amycini) based on integrative taxonomy. <i>Studies on Neotropical Fauna and Environment</i> , 0, , 1-9.	0.5	0
21786	Stirring the Deep, Disentangling the Complexity: Report on the Third Species of <i>Thermochiton</i> (Mollusca: Polyplacophora) From Haima Cold Seeps. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	1
21787	<i>Candolleomyces asiaticus</i> sp. nov. (Psathyrellaceae, Agaricales), a novel species from Punjab, Pakistan. <i>European Journal of Taxonomy</i> , 0, 826, .	0.6	4
21788	Insight into the evolutionary history of <i>Indoplanorbis exustus</i> (Bulinidae: Gastropoda) at the scale of population and species. <i>Biological Journal of the Linnean Society</i> , 2022, 137, 68-84.	0.7	2
21789	A conserved odorant receptor identified from antennal transcriptome of <i>Megoura crassicauda</i> that specifically responds to cis-jasmone. <i>Journal of Integrative Agriculture</i> , 2022, 21, 2042-2054.	1.7	3
21790	The complete chloroplast genome of <i>Rubus rosifolius</i> (Rosaceae), an ornamental and medicinal plant. <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 1296-1298.	0.2	0
21791	Evolution of woody plants to the land-sea interface – The atypical genomic features of mangroves with atypical phenotypic adaptation. <i>Molecular Ecology</i> , 2023, 32, 1351-1365.	2.0	8
21792	A Chromosome Level Genome Assembly of a Winter Turnip Rape (<i>Brassica rapa</i> L.) to Explore the Genetic Basis of Cold Tolerance. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	4
21793	<i>Pseudocryphonectria elaeocarpicola</i> gen. et sp. nov. (Cryphonectriaceae, Diaporthales) causing stem blight of <i>Elaeocarpus</i> spp. in China. <i>MycoKeys</i> , 0, 91, 67-84.	0.8	3
21794	The complete chloroplast genome sequence of <i>Cyathula officinalis</i> and comparative analysis with four related species. <i>Gene</i> , 2022, 839, 146728.	1.0	2
21795	<i>Winogradskyella luteola</i> sp. nov., <i>Erythrobacter ani</i> sp. nov., and <i>Erythrobacter crassostrea</i> sp. nov., isolated from the hemolymph of the Pacific Oyster <i>Crassostrea gigas</i> . <i>Archives of Microbiology</i> , 2022, 204, .	1.0	13
21796	Distinct <i>Streptococcus pneumoniae</i> cause invasive disease in Papua New Guinea. <i>Microbial Genomics</i> , 2022, 8, .	1.0	0
21797	Comparative genome anatomy reveals evolutionary insights into a unique amphitriploid fish. <i>Nature Ecology and Evolution</i> , 2022, 6, 1354-1366.	3.4	29
21799	Genome sequencing reveals chromosome fusion and extensive expansion of genes related to secondary metabolism in <i>Artemisia argyi</i> . <i>Plant Biotechnology Journal</i> , 2022, 20, 1902-1915.	4.1	25
21800	Utilizing paralogues for phylogenetic reconstruction has the potential to increase species tree support and reduce gene tree discordance in target enrichment data. <i>Molecular Ecology Resources</i> , 2022, 22, 3018-3034.	2.2	8
21801	International Spread of Tet(X4)-Producing <i>Escherichia coli</i> Isolates. <i>Foods</i> , 2022, 11, 2010.	1.9	6

#	ARTICLE	IF	CITATIONS
21802	Oxidative stress-mediated synergistic deleterious effects of nano- and microplastics in the hypoxia-conditioned marine rotifer <i>Brachionus plicatilis</i> . <i>Marine Pollution Bulletin</i> , 2022, 181, 113933.	2.3	7
21803	Taxonomy and molecular phylogeny of two new <i>Blepharisma</i> species (Ciliophora, Heterotrichea) from northeastern China. <i>European Journal of Protistology</i> , 2022, 85, 125908.	0.5	2
21804	Genome-centric metagenomics analysis revealed the metabolic function of abundant microbial communities in thermal hydrolysis-assisted thermophilic anaerobic digesters under propionate stress. <i>Bioresource Technology</i> , 2022, 360, 127574.	4.8	12
21805	Comparative transcriptome analysis on the mangrove <i>Acanthus ilicifolius</i> and its two terrestrial relatives provides insights into adaptation to intertidal habitats. <i>Gene</i> , 2022, 839, 146730.	1.0	3
21806	Endemicity and radiation in waterfalls of the Western Ghats: The genus <i>Cremnoconchus</i> (Gastropoda: Tj ETQq0 0 0 rgBT /Overlock 10 T	1.2	2
21807	Taxonomic evaluation of the "schidlovskii" species complex (Rodentia: Cricetidae) in the Middle East: a morphological and genetic combination. <i>Zoologischer Anzeiger</i> , 2022, 300, 1-11.	0.4	2
21808	Comparison of S gene mutations in patients with occult and chronic hepatitis B virus infection. <i>Virus Research</i> , 2022, 318, 198855.	1.1	1
21809	Old specimens for old branches: Assessing effects of sample age in resolving a rapid Neotropical radiation of squirrels. <i>Molecular Phylogenetics and Evolution</i> , 2022, 175, 107576.	1.2	6
21810	Out of chaos: Phylogenomics of Asian Sonerileae. <i>Molecular Phylogenetics and Evolution</i> , 2022, 175, 107581.	1.2	5
21811	Systematics of the New World bats <i>Eptesicus</i> and <i>Histiotus</i> suggest trans-marine dispersal followed by Neotropical cryptic diversification. <i>Molecular Phylogenetics and Evolution</i> , 2022, 175, 107582.	1.2	4
21812	Reemergence of an atypical bluetongue virus strain in goats, Sardinia, Italy. <i>Research in Veterinary Science</i> , 2022, 151, 36-41.	0.9	5
21813	Molecular Phylogeny of the Genus <i>Nipponnemertes</i> (Nemertea: Monostilifera: Cratenemertidae) and Descriptions of 10 New Species, With Notes on Small Body Size in a Newly Discovered Clade. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	5
21814	Re-evaluation of the genus <i>Englerodendron</i> (Leguminosae "Detarioideae), including <i>Isomacrobium</i> and <i>Pseudomacrobium</i> . <i>Australian Systematic Botany</i> , 2019, 32, 564-571.	0.3	8
21815	Characterization of the complete plastome of <i>Thalictrum aquilegifolium</i> var. <i>sibiricum</i> (Ranunculaceae), an annual herb. <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 1347-1349.	0.2	0
21816	Phylogenomic analysis of the genus <i>Leuconostoc</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	6
21817	Climatic niche pre-adaptation facilitated island colonization followed by budding speciation in the Madeiran ivy (<i>Hedera maderensis</i> , Araliaceae). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	4
21818	Comparative Analysis of the Complete Chloroplast Genomes in <i>Allium</i> Section <i>Bromatorrhiza</i> Species (Amaryllidaceae): Phylogenetic Relationship and Adaptive Evolution. <i>Genes</i> , 2022, 13, 1279.	1.0	5
21819	Finding a needle in a haystack: larval stages of Didymozoidae (Trematoda: Digenea) parasitizing marine zooplankton. <i>Parasitology Research</i> , 2022, 121, 2661-2672.	0.6	4

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21820	A chromosomal inversion contributes to divergence in multiple traits between deer mouse ecotypes. <i>Science</i> , 2022, 377, 399-405.	6.0	47
21821	Time Series Genomics of <i>Pseudomonas aeruginosa</i> Reveals the Emergence of a Hypermutator Phenotype and Within-Host Evolution in Clinical Inpatients. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	2
21822	Species diversity and systematics of the <i>Leptodactylus melanonotus</i> group (Anura). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 667 Td (Systematics and Biodiversity</i> , 2022, 20, 1-31.	0.5	3
21823	Landscape scale ecology of <i>Tetracladium</i> spp. fungal root endophytes. <i>Environmental Microbiomes</i> , 2022, 17, .	2.2	6
21824	Comprehensive treatise of <i>Hevansia</i> and three new genera <i>Jenniferia</i> , <i>Parahevansia</i> and <i>Polystromomyces</i> on spiders in Cordycipitaceae from Thailand. <i>Mycology</i> , 2022, 91, 113-149.	0.8	6
21825	New contributions to the Ciliophora ciliates (Protista, Ciliophora): Establishment of new taxa and phylogenetic analyses using two ribosomal genes. <i>Journal of Eukaryotic Microbiology</i> , 2023, 70, .	0.8	5
21826	Evolution of mitochondrial rRNA editing in extant gymnosperms. <i>Plant Journal</i> , 2022, 111, 1676-1687.	2.8	4
21827	Differential survival of potentially pathogenic, septicemia- and meningitis-causing <i>E. coli</i> across the wastewater treatment train. <i>Npj Clean Water</i> , 2022, 5, .	3.1	1
21828	Efficient management of the nitrification-anammox microbiome through intermittent aeration: absence of the NOB guild and expansion and diversity of the NOx reducing guild suggests a highly reticulated nitrogen cycle. <i>Environmental Microbiomes</i> , 2022, 17, .	2.2	1
21829	Phylogeography and population genetics of a widespread cold-adapted ant, <i>Prenolepis imparis</i> . <i>Molecular Ecology</i> , 2022, 31, 4884-4899.	2.0	0
21831	The Draft Genome of Chinese Endemic Species <i>Phascolosoma esculenta</i> (Sipuncula). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 342 Td (Phascolosoma</i>	1.1	1
21832	<i>Iqbalia kashmirensis</i> gen. et sp. nov. from Pakistan (Teloschistaceae, lichenized ascomycetes) based on multigene phylogeny. <i>Mycological Progress</i> , 2022, 21, .	0.5	1
21833	Tracking Asian tiger mosquito introductions in the Netherlands using Nextstrain. <i>Journal of the European Mosquito Control Association</i> , 2022, 40, 11-21.	0.5	1
21834	<i>Actinospica acidithermotolerans</i> sp. nov., a novel actinomycete isolated from sediment from an Indonesian hot spring. <i>Archives of Microbiology</i> , 2022, 204, .	1.0	3
21835	Arbuscular Mycorrhizal Fungi Taxa Show Variable Patterns of Micro-Scale Dispersal in Prairie Restorations. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	2
21836	Core Genome Multilocus Sequence Typing Scheme for Improved Characterization and Epidemiological Surveillance of Pathogenic <i>Brucella</i> . <i>Journal of Clinical Microbiology</i> , 2022, 60, .	1.8	15
21837	<i>Bahiana</i> , a new Euphorbiaceae (Acalyphoideae) genus from seasonally dry forest in northeastern Brazil, corroborated by molecular and morphological evidence. <i>Taxon</i> , 2022, 71, .	0.4	1
21838	Morphology and DNA barcodes of two sympatric species of <i>Filchneria</i> (Plecoptera: Perlodidae): intraspecific variation and underestimated biodiversity of the genus. <i>Aquatic Insects</i> , 2023, 44, 87-105.	0.6	2

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21839	Exon-based Phylogenomics and the Relationships of African Cichlid Fishes: Tackling the Challenges of Reconstructing Phylogenies with Repeated Rapid Radiations. <i>Systematic Biology</i> , 2023, 72, 134-149.	2.7	7
21840	The analysis of genetic structure and characteristics of the chloroplast genome in different Japanese apricot germplasm populations. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	5
21842	Divergent evolution of extreme production of variant plant monounsaturated fatty acids. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	3
21843	Analysis and characterization of the chloroplast genome of <i>Stephania cepharantha</i> Hayata. <i>Biotechnology and Biotechnological Equipment</i> , 2022, 36, 496-505.	0.5	1
21844	Cypress canker: An important disease discovered for the first time on a native South African tree. <i>Plant Pathology</i> , 0, , .	1.2	1
21845	The complete chloroplast genome of <i>Nageia fleuryi</i> (Hickel) de Laub. (Podocarpaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 1294-1295.	0.2	0
21846	Holarctic Species in the <i>Pluteus romellii</i> Clade. Five New Species Described and Old Names Reassessed. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 773.	1.5	2
21847	Species delineation and systematics of a hemiclinal hybrid complex in Australian freshwaters (Gobiiformes: Gobioidae: Eleotridae: <i>Hypseleotris</i>). <i>Royal Society Open Science</i> , 2022, 9, .	1.1	4
21848	Phylogenomic Analyses of 2,786 Genes in 158 Lineages Support a Root of the Eukaryotic Tree of Life between Opisthokonts and All Other Lineages. <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	8
21849	Phylogeny, character evolution and biogeography of the genus <i>Sclerophylax</i> (Solanaceae). <i>Taxon</i> , 0, , .	0.4	0
21850	Community structure of coral microbiomes is dependent on host morphology. <i>Microbiome</i> , 2022, 10, .	4.9	11
21851	Genetic and Structural Variation in the O-Antigen of <i>Salmonella enterica</i> Serovar Typhimurium Isolates Causing Bloodstream Infections in the Democratic Republic of the Congo. <i>MBio</i> , 2022, 13, .	1.8	4
21852	Phylogenetic Analysis of Wild Species and the Maternal Origin of Cultivars in the Genus <i>Lilium</i> Using 114 Plastid Genomes. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3
21853	The genome of <i>Dioscorea zingiberensis</i> sheds light on the biosynthesis, origin and evolution of the medicinally important diosgenin saponins. <i>Horticulture Research</i> , 2022, 9, .	2.9	14
21854	The Complete Mitochondrial Genome of <i>Plectorhinchus Chaetodonoides</i> (Perciformes: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 182	0.2	0
21855	Maintenance of divergent lineages of the Rice Blast Fungus <i>Pyricularia oryzae</i> through niche separation, loss of sex and post-mating genetic incompatibilities. <i>PLoS Pathogens</i> , 2022, 18, e1010687.	2.1	23
21856	Integrative taxonomy confirms the presence of the enigmatic <i>Lysmata olavoi</i> Fransen, 1991 (Decapoda: Lysmatidae) in the Mediterranean Sea. <i>Journal of the Marine Biological Association of the United Kingdom</i> , 0, , 1-6.	0.4	2
21857	Toward finally unraveling the phylogenetic relationships of Juncaceae with respect to another cyperid family, Cyperaceae. <i>Molecular Phylogenetics and Evolution</i> , 2022, 177, 107588.	1.2	4

#	ARTICLE	IF	CITATIONS
21858	Draft-genome analysis provides insights into the virulence properties and genome plasticity of <i>Vibrio fluvialis</i> organisms isolated from shrimp farms and Turag river in Bangladesh. Archives of Microbiology, 2022, 204, .	1.0	0
21859	The hole is deeper: description of two new species within the <i>Parastacus brasiliensis</i> (von Martens.) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T	0.2	2
21860	First records of the non-indigenous green algal species <i>Siphonocladus tropicus</i> (Cladophorales, Chlorophyta) and <i>Caulerpa integerrima</i> (Bryopsidales, Chlorophyta) in the Mediterranean Sea. European Journal of Phycology, 0, , 1-13.	0.9	0
21861	Highly contiguous genome assemblies of the Guinea paper wasp (<i>Polistes exclamans</i>) and <i>Mischocyttarus mexicanus</i> . Genome Biology and Evolution, 0, , .	1.1	4
21863	Bacterial assemblage in Mediterranean salt marshes: Disentangling the relative importance of seasonality, zonation and halophytes. Science of the Total Environment, 2022, 846, 157514.	3.9	2
21864	Two Hypotrachs (Ciliophora, Hypotracha) from China: Morphology and Ssu Rdna Sequence of <i>Holosticha Aestuarina</i> Nov. Spec. And <i>H. Muuiensis</i> . SSRN Electronic Journal, 0, , .	0.4	0
21865	Detection of Equus Caballus Papillomavirus Type-2 in Asymptomatic Italian Horses. Viruses, 2022, 14, 1696.	1.5	4
21866	Genome Sequencing of up to 6,000-Year-Old <i>Citrullus</i> Seeds Reveals Use of a Bitter-Fleshed Species Prior to Watermelon Domestication. Molecular Biology and Evolution, 2022, 39, .	3.5	4
21867	<i>Formica picea</i> and <i>F. candida</i> (Hymenoptera: Formicidae): Synonyms or Two Species?. Diversity, 2022, 14, 613.	0.7	2
21868	New <i>Microviridae</i> isolated from <i>Sulfitobacter</i> reveals two cosmopolitan subfamilies of single-stranded DNA phages infecting marine and terrestrial Alphaproteobacteria. Virus Evolution, 2022, 8, .	2.2	5
21869	Phylogenomics Supports the Monophyly of Aphelids and Fungi and Identifies New Molecular Synapomorphies. Systematic Biology, 2023, 72, 505-515.	2.7	15
21870	Phylogenomics of the Caribbean melocacti: Cryptic species and multiple invasions. Taxon, 2022, 71, 993-1012.	0.4	9
21871	Assessment of phylogenetic approaches to study the timing of recombination cessation on sex chromosomes. Journal of Evolutionary Biology, 2022, 35, 1721-1733.	0.8	3
21872	Illuminating protist diversity in pitcher plants and bromeliad tanks. PLoS ONE, 2022, 17, e0270913.	1.1	1
21873	Assessing taxonomic, functional and phylogenetic diversity of giant clams across the Indo-Pacific for conservation prioritization. Diversity and Distributions, 2022, 28, 2124-2138.	1.9	5
21874	The complete chloroplast genome of <i>Diarthron tianschanicum</i> (Thymelaeaceae). Mitochondrial DNA Part B: Resources, 2022, 7, 1326-1328.	0.2	0
21875	Travel-associated extensively drug-resistant typhoid fever: a case series to inform management in non-endemic regions. Journal of Travel Medicine, 2023, 30, .	1.4	4
21876	Endophytic <i>Diaporthe</i> Associated with <i>Morinda officinalis</i> in China. Journal of Fungi (Basel,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T	1.5	5

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21877	Morphological and Phylogenetic Analyses Reveal Four New Species of <i>Gnomoniopsis</i> (Gnomoniaceae.) <i>Tj ETQq0 0 0 rgBT /Overlock 10 T</i>	1.5	0
21878	Genomic characterization of polyextremotolerant black yeasts isolated from food and food production environments. <i>Frontiers in Fungal Biology</i> , 0, 3, .	0.9	0
21879	Genomic variation in the Black-throated Green Warbler (<i>Setophaga virens</i>) suggests divergence in a disjunct Atlantic Coastal Plain population (<i>S. v. waynei</i>). <i>Auk</i> , 0, , .	0.7	2
21880	A Review of the Fungi That Degrade Plastic. <i>Journal of Fungi</i> (Basel, Switzerland), 2022, 8, 772.	1.5	25
21881	Taxonomy and phylogeny of <i>Smaragdinisetia musae</i> sp. nov. and <i>Albifimbria verrucaria</i> (Hypocreales.) <i>Tj ETQq0 0 0 rgBT /Overlock 10 T</i>	0.4	0
21882	Comparative Genomic Analysis of Seven <i>Vibrio alginolyticus</i> Strains Isolated From Shrimp Larviculture Water With Emphasis on Chitin Utilization. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
21883	Analysis of the earliest complete mtDNA genome of a Caribbean colonial horse (<i>Equus caballus</i>) from 16th-century Haiti. <i>PLoS ONE</i> , 2022, 17, e0270600.	1.1	1
21885	High genetic stability of co-circulating human adenovirus type 31 lineages over 59 years. <i>Virus Evolution</i> , 2022, 8, .	2.2	5
21886	Chromosomal-level reference genome of the moth <i>Heortia vitessoides</i> (Lepidoptera: Crambidae), a major pest of agarwood-producing trees. <i>Genomics</i> , 2022, 114, 110440.	1.3	2
21887	Testing candidate genes linked to corolla shape variation of a pollinator shift in <i>Rhytidophyllum</i> (Gesneriaceae). <i>PLoS ONE</i> , 2022, 17, e0267540.	1.1	1
21888	Diversification rates in Tardigrada indicate a decreasing tempo of lineage splitting regardless of reproductive mode. <i>Organisms Diversity and Evolution</i> , 0, , .	0.7	1
21889	Divergent Host-Microbe Interaction and Pathogenesis Proteins Detected in Recently Identified <i>Liberibacter</i> Species. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	3
21890	Human Coronavirus Spike Protein Based Multi-Epitope Vaccine against COVID-19 and Potential Future Zoonotic Coronaviruses by Using Immunoinformatic Approaches. <i>Vaccines</i> , 2022, 10, 1150.	2.1	1
21891	Genetic markers in Andean <i>Puya</i> species (Bromeliaceae) with implications on plastome evolution and phylogeny. <i>Ecology and Evolution</i> , 2022, 12, .	0.8	3
21892	The complete chloroplast genome and phylogenetic analysis of <i>Salvia karwinskii</i> (Lamiaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 1384-1386.	0.2	0
21893	Complete chloroplast genome of <i>Zanthoxylum avicennae</i> (Lam.) DC (Rutaceae: <i>Zanthoxylum</i>). <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 1329-1331.	0.2	1
21894	Global Spread of MCR-Producing <i>Salmonella enterica</i> Isolates. <i>Antibiotics</i> , 2022, 11, 998.	1.5	6
21896	TRIM7 Restricts Coxsackievirus and Norovirus Infection by Detecting the C-Terminal Glutamine Generated by 3C Protease Processing. <i>Viruses</i> , 2022, 14, 1610.	1.5	3

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21897	First Report of Leaf blight Caused by <i>Stagonosporopsis citrulli</i> on Garden Geranium in China. <i>Plant Disease</i> , 0, , .	0.7	0
21899	Comparative Genomic Analysis of Antarctic <i>Pseudomonas</i> Isolates with 2,4,6-Trinitrotoluene Transformation Capabilities Reveals Their Unique Features for Xenobiotics Degradation. <i>Genes</i> , 2022, 13, 1354.	1.0	12
21900	Phylogenomic analysis and metabolic role reconstruction of mutualistic <i>Rhizobiales</i> hindgut symbionts of <i>Acromyrmex</i> leaf-cutting ants. <i>FEMS Microbiology Ecology</i> , 2022, 98, .	1.3	1
21901	Comparative Mitogenomic Analysis Reveals Intraspecific, Interspecific Variations and Genetic Diversity of Medical Fungus <i>Ganoderma</i> . <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 781.	1.5	6
21902	Application of chloroplast genome in the identification of Traditional Chinese Medicine <i>Viola philippica</i> . <i>BMC Genomics</i> , 2022, 23, .	1.2	12
21903	A new species of <i>Gibsmithia</i> (<i>Dumontiaceae</i> , <i>Rhodophyta</i>) from mesophotic depths of the Papahānaumokuākea Marine National Monument, Hawai'i, USA. <i>Phycologia</i> , 2022, 61, 558-569.	0.6	3
21904	Comparative genomics reveals the molecular mechanism of salt adaptation for zoysiagrasses. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	5
21905	<i>Coronamoeba villafranca</i> gen. nov. sp. nov. (Amoebozoa, Dermamoebida) challenges the correlation of morphology and phylogeny in Amoebozoa. <i>Scientific Reports</i> , 2022, 12, .	1.6	2
21906	Description of <i>Alvania wangi</i> Xu, Qi & Kong, sp. nov. (Mollusca, Gastropoda, Littorinimorpha). <i>Tj ETQq0 0 0 rgBT /Overlock 10 T</i>	0.5	1
21907	Genome characteristics of clinical <i>Salmonella enterica</i> population from a state public health laboratory, New Hampshire, USA, 2017–2020. <i>BMC Genomics</i> , 2022, 23, .	1.2	5
21908	Fine-scale population genetic structure and barriers to gene flow in a widespread seabird (<i>Ardenna</i>). <i>Tj ETQq0 0 0 rgBT /Overlock 10 T</i>	0.7	5
21909	Phylogeographic inference of Sumatran ranids bearing gastromyzophorous tadpoles with regard to the Pleistocene drainage systems of Sundaland. <i>Scientific Reports</i> , 2022, 12, .	1.6	0
21910	Two new species of <i>Craterellus</i> (<i>Cantharellales</i> , <i>Hydnaceae</i>) with veined hymenophore from north-eastern China. <i>MycKeys</i> , 0, 91, 97-111.	0.8	1
21911	A New Insight Into <i>Amicula</i> , a Genus of Tiny Marine Benthic Diatoms With the Description of Two New Tropical Species and the Largest Mitogenome Known for a Stramenopile. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	1
21912	The genome of the rice planthopper egg parasitoid wasps <i>Anagrus nilaparvatae</i> casts light on the chemo- and mechanosensation in parasitism. <i>BMC Genomics</i> , 2022, 23, .	1.2	5
21913	Population-based sequencing of <i>Mycobacterium tuberculosis</i> reveals how current population dynamics are shaped by past epidemics. <i>ELife</i> , 0, 11, .	2.8	8
21914	Fungal diversity in Sahara dust: <i>Aspergillus sydowii</i> and other opportunistic pathogens. <i>Aerobiologia</i> , 2022, 38, 367-378.	0.7	3
21915	The complete chloroplast genome and phylogenetic analysis of <i>Salvia oxyphora</i> Briq. 1896 (<i>Nepetoideae</i> , <i>Lamiaceae</i>). <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 1342-1344.	0.2	0

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21916	The complete mitochondrial genome of <i>Crematogaster matsumurai</i> (Forel 1901) (Hymenoptera: Tj ETQq0 0,2 rgBT /Overlock 10	0.2	0
21917	Diversity of <i>Parengyodontium</i> spp. strains isolated from the cultural heritage environment: Phylogenetic diversity, phenotypical diversity, and occurrence. <i>Mycologia</i> , 0, , 1-16.	0.8	0
21918	The complete chloroplast genome of <i>Gynura japonica</i> and its phylogenetic implications. <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 1392-1394.	0.2	0
21919	Hybridization and genome duplication for early evolutionary success in the Asian Palmate group of Araliaceae. <i>Journal of Systematics and Evolution</i> , 2022, 60, 1303-1318.	1.6	5
21920	Adaptive Bird-like Genome Miniaturization During the Evolution of Scallop Swimming Lifestyle. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 1066-1077.	3.0	1
21921	Molecular Mechanisms of the Convergent Adaptation of Bathypelagic and Abyssopelagic Fishes. <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	5
21922	Mitogenomics supports the monophyly of Mysidacea and Peracarida (Malacostraca). <i>Zoologica Scripta</i> , 2022, 51, 603-613.	0.7	6
21923	Multi-omics profiling of the cold tolerant <i>Monoraphidium minutum</i> 26B-AM in response to abiotic stress. <i>Algal Research</i> , 2022, 66, 102794.	2.4	3
21924	<i>Lasiodiplodia fici</i> sp. nov., Causing Leaf Spot on <i>Ficus altissima</i> in China. <i>Pathogens</i> , 2022, 11, 840.	1.2	6
21925	Multiplex Polymerase Chain Reaction Method with Species-specific Primers for Differentiation of Two Closely Related Fish Species, <i>Beryx splendens</i> and <i>B. mollis</i> (Actinopterygii: Beryciformes). <i>Japan Agricultural Research Quarterly</i> , 2022, 56, 283-294.	0.1	0
21926	Comprehensive Phylogenomics of <i>Methylobacterium</i> Reveals Four Evolutionary Distinct Groups and Underappreciated Phyllosphere Diversity. <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	8
21927	Whole genome-based taxonomy of <i>Shewanella</i> and <i>Parashewanella</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	11
21928	Phylogeny of <i>Agaricus</i> subgenus <i>Pseudochitonina</i> with the description of a new section and a new species from Oman. <i>Mycological Progress</i> , 2022, 21, .	0.5	2
21929	Complete mitochondrial genome sequence of <i>Acer miaotaiense</i> (Aceraceae). <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 1389-1391.	0.2	1
21930	Multi-Gene Phylogenetic Approach for Identification and Diversity Analysis of <i>Bipolaris maydis</i> and <i>Curvularia lunata</i> Isolates Causing Foliar Blight of <i>Zea mays</i> . <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 802.	1.5	22
21933	Comparative chloroplast genome and transcriptome analysis on the ancient genus <i>Isoetes</i> from China. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	0
21934	ï¿¿New segregates from the Neotropical genus <i>Stryphnodendron</i> (Leguminosae, Caesalpinoideae,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.4	6
21935	Multi-omics Analyses Provide Insight into the Biosynthesis Pathways of Fucoxanthin in <i>Isochrysis galbana</i> . <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 1138-1153.	3.0	9

#	ARTICLE	IF	CITATIONS
21936	Chromosome-level assembly of <i>Bactericera cockerelli</i> reveals rampant gene family expansions impacting genome structure, function and insect-microbe-plant interactions. <i>Molecular Ecology Resources</i> , 2023, 23, 233-252.	2.2	5
21937	Constraints on the evolution of toxin-resistant Na,K-ATPases have limited dependence on sequence divergence. <i>PLoS Genetics</i> , 2022, 18, e1010323.	1.5	8
21938	Revision of the freshwater crabs of the genus <i>Tehuana</i> Rodríguez & Smalley in Smalley 1970 (Decapoda, Pseudothelphusidae), with the descriptions of two new species. <i>ZooKeys</i> , 0, 1117, 1-35.	0.5	2
21939	The complete chloroplast genome of <i>Abies ernestii</i> Rehder (Pinaceae) and its phylogenetic implications. <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 1497-1503.	0.2	2
21940	Filling a gap in the taxonomy of phyllachoroid fungi: Proposition of <i>Neopolystigma</i> , gen. nov., and the new family Neopolystigmataceae. <i>Mycologia</i> , 0, , 1-14.	0.8	0
21941	Chromosome-level Genome Assembly of the High-altitude Leopard (<i>Panthera pardus</i>) Sheds Light on Its Environmental Adaptation. <i>Genome Biology and Evolution</i> , 0, , .	1.1	1
21942	New insights into the formation of biodiversity hotspots of the Kenyan flora. <i>Diversity and Distributions</i> , 2022, 28, 2696-2711.	1.9	5
21943	Phylogenetic and Multiple-Locus Variable number tandem repeat analysis of <i>Mycobacterium avium</i> subsp. paratuberculosis isolates from Argentina. <i>Veterinary Research Communications</i> , 2022, 46, 1121-1129.	0.6	2
21944	New Piper species from the eastern slopes of the Andes in northern South America. <i>PhytoKeys</i> , 0, 206, 25-48.	0.4	3
21945	Genome assembly of <i>Luehdorfia taibai</i> , an endangered butterfly endemic to Qinling Mountains in China with extremely small populations. <i>Frontiers in Ecology and Evolution</i> , 0, 10, .	1.1	2
21946	Fungi associated with dead branches of <i>Magnolia grandiflora</i> : A case study from Qujing, China. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
21947	Comparative and Phylogenetic Analysis of Complete Chloroplast Genomes in <i>Leymus</i> (Triticodae), Tj ETQq1 1 0.784314 rgBT ₂ Overload	1.0	0
21948	The complete chloroplast genome of <i>Pterobryopsis orientalis</i> (Pterobryaceae, Hypnales) and its phylogenetic implications. <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 1484-1485.	0.2	0
21949	The complete chloroplast sequence of <i>phalaenopsis malipoensis</i> , a rare orchidaceae species in China. <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 1489-1491.	0.2	1
21950	Effectors from a Bacterial Vector-Borne Pathogen Exhibit Diverse Subcellular Localization, Expression Profiles, and Manipulation of Plant Defense. <i>Molecular Plant-Microbe Interactions</i> , 2022, 35, 1067-1080.	1.4	3
21952	Chromosome-scale genome assemblies and annotations for Poales species <i>Carex cristatella</i> , <i>Carex scoparia</i> , <i>Juncus effusus</i> , and <i>Juncus inflexus</i> . <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	9
21953	Complete gammaproteobacterial endosymbiont genome assembly from a seep tubeworm <i>Lamellibrachia satsuma</i> . <i>Journal of Microbiology</i> , 2022, 60, 916-927.	1.3	1
21955	A scalable analytical approach from bacterial genomes to epidemiology. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2022, 377, .	1.8	14

#	ARTICLE	IF	CITATIONS
21956	A new species of Bathypathes (Cnidaria, Anthozoa, Antipatharia, Schizopathidae) from the Red Sea and its phylogenetic position. ZooKeys, 0, 1116, 1-22.	0.5	4
21957	Global patterns and rates of habitat transitions across the eukaryotic tree of life. Nature Ecology and Evolution, 2022, 6, 1458-1470.	3.4	19
21958	Morphology, Palynology and Molecular Phylogeny of Barleria cristata L. (Acanthaceae) Morphotypes from India. Diversity, 2022, 14, 677.	0.7	0
21959	Two Novel Genera, Neostemphylium and Scleromyces (Pleosporaceae) from Freshwater Sediments and Their Global Biogeography. Journal of Fungi (Basel, Switzerland), 2022, 8, 868.	1.5	6
21960	Genetic Diversity of Virulent Polymyxin-Resistant Klebsiella aerogenes Isolated from Intensive Care Units. Antibiotics, 2022, 11, 1127.	1.5	4
21963	A New Cryptic Lineage in Parmeliaceae (Ascomycota) with Pharmacological Properties. Journal of Fungi (Basel, Switzerland), 2022, 8, 826.	1.5	1
21964	Türkiye'nin Batı Akdeniz bölgesinden yeni bir kayış, Melanoleuca tristis (Bazidiyomikota, Agaricales). Anatolian Journal of Botany, 0, , .	0.5	0
21965	Insertions and deletions as phylogenetic signal in an alignment-free context. PLoS Computational Biology, 2022, 18, e1010303.	1.5	1
21966	The diversity of microfungi associated with grasses in the Sporobolus indicus complex in Queensland, Australia. Frontiers in Fungal Biology, 0, 3, .	0.9	1
21967	Bioinformatics and its role in the study of the evolution and probiotic potential of lactic acid bacteria. Food Science and Biotechnology, 2023, 32, 389-412.	1.2	4
21968	A mutant allele of the flowering promoting factor 1 gene at the tomato BRACHYTIC locus reduces plant height with high quality fruit. Plant Direct, 2022, 6, .	0.8	6
21969	Reinstatement and phylogenetic allocation of the palm rust genus Cerradoa in the Pucciniaceae, and establishment of Pseudocerradoa, gen. nov.. Mycologia, 2022, 114, 868-886.	0.8	5
21970	Cryptic diversity in the genus Croisettea (Kallymeniaceae, Rhodophyta) from Hawaiian mesophotic reefs. Phycologia, 2022, 61, 572-583.	0.6	5
21971	Thecochaos is not a myth: study of the genus Thecochaos (Amoebozoa, Discosea) – a rediscovered group of lobose amoeba, with short SSU gene. Organisms Diversity and Evolution, 2023, 23, 7-24.	0.7	2
21972	Spatiotemporal characteristics of the pharyngeal teeth in interspecific distant hybrids of cyprinid fish: Phylogeny and expression of the initiation marker genes. Frontiers in Genetics, 0, 13, .	1.1	0
21973	Emergence and Molecular Epidemiology of Campylobacter jejuni ST-2993 Associated with a Large Outbreak of Guillain-Barré Syndrome in Peru. Microbiology Spectrum, 2022, 10, .	1.2	4
21974	Comparative Genomics of Mortierellaceae Provides Insights into Lipid Metabolism: Two Novel Types of Fatty Acid Synthase. Journal of Fungi (Basel, Switzerland), 2022, 8, 891.	1.5	4
21976	Studies in Gyromitra II: cryptic speciation in the Gyromitra gigas species complex; rediscovery of G. ussuriensis and G. americanigigas sp. nov.. Mycological Progress, 2022, 21, .	0.5	2

#	ARTICLE	IF	CITATIONS
21977	Genome-Scale Metabolic Modeling Combined with Transcriptome Profiling Provides Mechanistic Understanding of <i>Streptococcus thermophilus</i> CH8 Metabolism. <i>Applied and Environmental Microbiology</i> , 2022, 88, .	1.4	6
21978	Genomic surveillance of <i>Salmonella</i> spp. in the Philippines during 2013–2014. <i>Transactions of the Royal Society of Tropical Medicine and Hygiene</i> , 2022, 116, 1202-1213.	0.7	3
21979	Hypervariable-Locus Melting Typing: a Novel Approach for More Effective High-Resolution Melting-Based Typing, Suitable for Large Microbiological Surveillance Programs. <i>Microbiology Spectrum</i> , 0, , .	1.2	1
21980	A remarkable new genus and species of Euryproctini (Hymenoptera: Ichneumonidae, Ctenopelmatinae) from Thailand. <i>European Journal of Taxonomy</i> , 0, 834, .	0.6	1
21981	Phototrophy and carbon fixation in Chlorobi postdate the rise of oxygen. <i>PLoS ONE</i> , 2022, 17, e0270187.	1.1	2
21982	New plastome structural rearrangements discovered in core Tillandsioideae (Bromeliaceae) support recently adopted taxonomy. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3
21983	The high-quality genome of pummelo provides insights into the tissue-specific regulation of citric acid and anthocyanin during domestication. <i>Horticulture Research</i> , 2022, 9, .	2.9	5
21984	Reinstatement of <i>Ticanto</i> (Leguminosae-Caesalpinioideae) – the final piece in the <i>Caesalpinia</i> group puzzle. <i>PhytoKeys</i> , 0, 205, 59-98.	0.4	2
21985	Simultaneously collecting coding and non-coding phylogenomic data using homemade full-length cDNA probes, tested by resolving the high-level relationships of Colubridae. <i>Frontiers in Ecology and Evolution</i> , 0, 10, .	1.1	1
21986	Genetic characterization and evolution of H6N6 subtype avian influenza viruses. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
21987	Viral informatics: bioinformatics-based solution for managing viral infections. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	10
21988	Repeated genetic adaptation to altitude in two tropical butterflies. <i>Nature Communications</i> , 2022, 13, .	5.8	17
21989	Phylogenomic Analysis of the Parrots of the World Distinguishes Artifactual from Biological Sources of Gene Tree Discordance. <i>Systematic Biology</i> , 2023, 72, 228-241.	2.7	17
21990	The mitochondrial genome and phylogenetic analysis of <i>Rhacophorus rhodopus</i> . <i>Scientific Reports</i> , 2022, 12, .	1.6	1
21991	Genetic determinants of antimicrobial resistance in three multi-drug resistant strains of <i>Cutibacterium acnes</i> isolated from patients with acne: a predictive in silico study. <i>Access Microbiology</i> , 2022, 4, .	0.2	3
21992	Dispersals from the West Tethys as the source of the Indo-West Pacific diversity hotspot in comatulid crinoids. <i>Paleobiology</i> , 0, , 1-14.	1.3	1
21993	Phylogenomic analysis of 997 nuclear genes reveals the need for extensive generic re-delimitation in <i>Caesalpinioideae</i> (Leguminosae). <i>PhytoKeys</i> , 0, 205, 3-58.	0.4	29
21994	Recent progress on methods for estimating and updating large phylogenies. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2022, 377, .	1.8	5

#	ARTICLE	IF	CITATIONS
21995	Dysfunction of Ras-GAP protein AfgapA contributes to hypoxia fitness in <i>Aspergillus fumigatus</i> . <i>Current Genetics</i> , 0, .	0.8	1
21997	Morphology and molecular phylogeny of two new <i>Aspidisca</i> species (Ciliophora, Spirotrichea). <i>Tj ETQq1 1 0.784314 1.27 /Overlock 10</i>	1.2	1
21998	Host taxonomy determines the composition, structure, and diversity of the earthworm cast microbiome under homogenous feeding conditions. <i>FEMS Microbiology Ecology</i> , 2022, 98, .	1.3	7
21999	Geographic isolation drives speciation in Nearctic aphids. <i>Communications Biology</i> , 2022, 5, .	2.0	2
22000	From Argentine Abyssal Plain to farmed turbot in Spain: A ubiquitous amoeba species <i>Vannella robusta</i> sp. nov. (Amoebozoa, Vannellida). <i>European Journal of Protistology</i> , 2022, 85, 125912.	0.5	0
22001	<i>Cellulomonas palmilyticum</i> sp. nov., from earthworm soil biofertilizer with the potential to degrade oil palm empty fruit bunch. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	1
22002	TreeKnit: Inferring ancestral reassortment graphs of influenza viruses. <i>PLoS Computational Biology</i> , 2022, 18, e1010394.	1.5	7
22003	Chromosome-level genome assembly and population genomic analyses provide insights into adaptive evolution of the red turpentine beetle, <i>Dendroctonus valens</i> . <i>BMC Biology</i> , 2022, 20, .	1.7	5
22004	A novel Zn ²⁺ -Cys ⁶ transcription factor <i>clcA</i> contributes to copper homeostasis in <i>Aspergillus fumigatus</i> . <i>Current Genetics</i> , 2022, 68, 605-617.	0.8	2
22005	Sexual Signals Persist over Deep Time: Ancient Co-option of Bioluminescence for Courtship Displays in Cypridinid Ostracods. <i>Systematic Biology</i> , 2023, 72, 264-274.	2.7	7
22006	Phylogenetically and catabolically diverse diazotrophs reside in deep-sea cold seep sediments. <i>Nature Communications</i> , 2022, 13, .	5.8	29
22007	Complete mitochondrial genome of <i>Pectocera</i> sp. (Elateridae: Dendrometrinae: Oxynopterini) and its phylogenetic implications. <i>Archives of Insect Biochemistry and Physiology</i> , 2022, 111, .	0.6	5
22008	Identification and Functional Characterization of Sex Pheromone Receptors in the Oriental Fruit Moth, <i>Grapholita molesta</i> (Lepidoptera: Tortricidae). <i>Journal of Agricultural and Food Chemistry</i> , 2022, 70, 9845-9855.	2.4	0
22009	A new genus of Pseudospirobolellidae (Diplopoda, Spirobolida) from limestone karst areas in Thailand, with descriptions of three new species. <i>Zoosystematics and Evolution</i> , 2022, 98, 313-326.	0.4	2
22010	A chromosome-level genome assembly of the Walking goby (<i>Scartelaos histophorus</i>). <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	2
22011	Taxonomic Characterization, Antiviral Activity and Induction of Three New Kenalactams in <i>Nocardiosis</i> sp. CG3. <i>Current Microbiology</i> , 2022, 79, .	1.0	1
22012	Legume NCRs and nodule-specific defensins of actinorhizal plants – Do they share a common origin?. <i>PLoS ONE</i> , 2022, 17, e0268683.	1.1	2
22013	Comparative Genome and Evolution Analyses of an Endangered Stony Coral Species <i>Dendrophyllia cribrosa</i> Near Dokdo Islands in the East Sea. <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	1

#	ARTICLE	IF	CITATIONS
22014	Underestimated Neotropical diversity: Integrative taxonomy reveals two unrelated look-alike species in a suboscine bird (<i>Pachyramphus albobrissus</i>). <i>Auk</i> , 2023, 140, .	0.7	4
22015	Genome-wide analysis resolves the radiation of New Zealand's freshwater <i>Galaxias vulgaris</i> complex and reveals a candidate species obscured by mitochondrial capture. <i>Diversity and Distributions</i> , 2022, 28, 2255-2267.	1.9	6
22016	Morphology, Phenotype, and Molecular Identification of Clinical and Environmental <i>Fusarium solani</i> Species Complex Isolates from Malaysia. <i>Journal of Fungi</i> (Basel, Switzerland), 2022, 8, 845.	1.5	5
22017	Comparative Chloroplast Genomics and Phylogenetic Analysis of <i>Persicaria amphibia</i> (Polygonaceae). <i>Diversity</i> , 2022, 14, 641.	0.7	4
22018	The final piece of the Triangle of U: Evolution of the tetraploid <i>Brassica carinata</i> genome. <i>Plant Cell</i> , 2022, 34, 4143-4172.	3.1	18
22019	Genomic architecture of adaptive radiation and hybridization in Alpine whitefish. <i>Nature Communications</i> , 2022, 13, .	5.8	25
22020	Colony self-shading facilitates Symbiodiniaceae cohabitation in a South Pacific coral community. <i>Coral Reefs</i> , 0, , .	0.9	2
22021	Metabolic Strategies Shared by Basement Residents of the Lost City Hydrothermal Field. <i>Applied and Environmental Microbiology</i> , 2022, 88, .	1.4	14
22022	The evolutionary network of whiptail lizards reveals predictable outcomes of hybridization. <i>Science</i> , 2022, 377, 773-777.	6.0	12
22024	Human Y chromosome sequences from Q Haplogroup reveal a South American settlement pre-18,000 years ago and a profound genomic impact during the Younger Dryas. <i>PLoS ONE</i> , 2022, 17, e0271971.	1.1	6
22025	Notes on the distribution of <i>Dalmanella simonae</i> (Gastropoda: Hydrobiidae) in Croatia and the utility of barcoding in its determination. <i>Folia Malacologica</i> , 2022, 30, 128-134.	0.1	0
22026	Evidence for a conserved queen-worker genetic toolkit across slave-making ants and their ant hosts. <i>Molecular Ecology</i> , 2022, 31, 4991-5004.	2.0	4
22028	The chromosome-scale genome sequence of <i>Triadica sebifera</i> provides insight into fatty acids and anthocyanin biosynthesis. <i>Communications Biology</i> , 2022, 5, .	2.0	6
22029	Phylotranscriptomic and Evolutionary Analyses of the Green Algal Order Chaetophorales (Chlorophyceae, Chlorophyta). <i>Genes</i> , 2022, 13, 1389.	1.0	1
22030	Behavioral innovation and genomic novelty are associated with the exploitation of a challenging dietary opportunity by an avivorous bat. <i>IScience</i> , 2022, 25, 104973.	1.9	7
22031	Two new species of <i>Alainites</i> (Ephemeroptera, Baetidae) from the Mediterranean biodiversity hotspot. <i>ZooKeys</i> , 0, 1118, 73-95.	0.5	5
22032	A new species of the long-tailed wasp genus <i>Eurobracon</i> Ashmead (Hymenoptera, Braconidae.) <i>Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50</i>	0.5	2
22033	Seven Unrecorded Indigenous Fungi from Mudeungsan National Park in Korea. <i>Mycobiology</i> , 0, , 1-10.	0.6	0

#	ARTICLE	IF	CITATIONS
22034	Species complexes and life cycles of digenetic trematodes from the family Derogenidae. <i>Parasitology</i> , 2022, 149, 1590-1606.	0.7	4
22035	Sequencing and comparative analysis of chloroplast genomes of three medicinal plants: <i>Gentiana manshurica</i> , <i>G. scabra</i> and <i>G. triflora</i> . <i>Physiology and Molecular Biology of Plants</i> , 0, , .	1.4	3
22036	Differences in the Characteristics and Pathogenicity of <i>Pyrenophora</i> Species Associated with Seeds of Italian Ryegrass (<i>Lolium multiflorum</i> Lam.). <i>Plant Disease</i> , 0, , .	0.7	0
22037	Diverge and Conquer: Phylogenomics of southern Wallacean forest skinks (Genus: <i>Sphenomorphus</i>) and their colonization of the Lesser Sunda Archipelago. <i>Evolution; International Journal of Organic Evolution</i> , 2022, 76, 2281-2301.	1.1	6
22038	Molecular phylogenetics and tribal classification of Japanese Pyraustinae and Spilomelinae (Lepidoptera: Crambidae). <i>Insect Systematics and Evolution</i> , 2022, 54, 77-106.	0.2	7
22039	The <i>Umbelopsis ramanniana</i> Sensu Lato Consists of Five Cryptic Species. <i>Journal of Fungi (Basel)</i> Tj ETQq1 1 0.784314 rgBT /Overlock 1.5 2	1.5	2
22041	<i>Acrocalymma chuxiongense</i> sp. nov., a new species of Acrocalymmaeae (Pleosporales) on leaves of <i>Quercus</i> . <i>Biodiversity Data Journal</i> , 0, 10, .	0.4	1
22042	An outbreak of a novel recombinant Coxsackievirus A4 in a kindergarten, Shandong province, China, 2021. <i>Emerging Microbes and Infections</i> , 2022, 11, 2207-2210.	3.0	3
22043	ESBL plasmids in <i>Klebsiella pneumoniae</i> : diversity, transmission and contribution to infection burden in the hospital setting. <i>Genome Medicine</i> , 2022, 14, .	3.6	23
22044	Integrative species delimitation of <i>Selaginella labordei</i> and closely related species: Uncovering the mysterious identity of <i>S. Âjugorum</i> and <i>S. Âtibetica</i> , and description of a new species. <i>Taxon</i> , 2022, 71, 1155-1169.	0.4	3
22045	<i>Boliviadendron</i> , a new segregate genus of mimosoid legume (Leguminosae, Caesalpinioideae, mimosoid) Tj ETQq0 0 0 rgBT /Overlock 0.4 2	0.4	2
22046	The complete chloroplast genome sequence of <i>Ficus pandurata</i> Hance var. <i>angustifolia</i> W.C. Cheng (Moraceae). <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 1522-1524.	0.2	0
22047	Enhancing the Thermal and Kinetic Stability of Ketol-Acid Reductoisomerase, a Central Catalyst of a Cell-Free Enzyme Cascade for the Manufacture of Platform Chemicals. , 2022, 1, 163-178.		0
22048	A new generic circumscription of <i>Hydrochorea</i> (Leguminosae, Caesalpinioideae, mimosoid clade) with an amphi-Atlantic distribution. <i>PhytoKeys</i> , 0, 205, 401-437.	0.4	5
22050	The microbiome of a bacterivorous marine choanoflagellate contains a resource-demanding obligate bacterial associate. <i>Nature Microbiology</i> , 2022, 7, 1466-1479.	5.9	5
22051	Transcriptome Analysis of <i>Podoscypha petalodes</i> Strain GGF6 Reveals the Diversity of Proteins Involved in Lignocellulose Degradation and Lignolytic Function. <i>Indian Journal of Microbiology</i> , 2022, 62, 569-582.	1.5	3
22052	Molecular phylogenetic assessment of the genus <i>Scutellinia</i> (Pezizales: Pyronemataceae). <i>Plant Biosystems</i> , 0, , 1-11.	0.8	0
22053	New Insights Into the Backbone Phylogeny and Character Evolution of <i>Corydalis</i> (Papaveraceae) Based on Plastome Data. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	4

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22074	The Complete Mitochondrial Genomes of Three Sphenomorphinae Species (Squamata: Scincidae) and the Selective Pressure Analysis on Mitochondrial Genomes of Limbless <i>Isopachys gyldenstolpei</i> . <i>Animals</i> , 2022, 12, 2015.	1.0	2
22075	A new species of <i>Phymatolithon</i> Foslie, <i>P. abuqirensis</i> (Hapalidiaceae, Hapalidiales), from Mediterranean Egypt. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	1
22076	Whole genome sequencing of mesorhizobia isolated from northern Canada. <i>Canadian Journal of Microbiology</i> , 2022, 68, 661-673.	0.8	2
22077	Molecular Epidemiology of <i>Mycobacterium abscessus</i> Isolates Recovered from German Cystic Fibrosis Patients. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	8
22078	Evolution of the Noncoding Features of Sea Snake Mitochondrial Genomes within Elapidae. <i>Genes</i> , 2022, 13, 1470.	1.0	1
22079	Connect to Protect: Dynamics and Genetic Connections of Highly Pathogenic Avian Influenza Outbreaks in Poultry from 2016 to 2021 in Germany. <i>Viruses</i> , 2022, 14, 1849.	1.5	5
22080	First integrative study of the diversity and specificity of metacercariae of <i>Posthodiplostomum</i> Dubois, 1936 from native and introduced fishes in the Caribbean. <i>Parasitology</i> , 2022, 149, 1894-1909.	0.7	3
22081	Genomics reveals the history of a complex plant invasion and improves the management of a biological invasion from the South African–Australian biotic exchange. <i>Ecology and Evolution</i> , 2022, 12, .	0.8	4
22082	Allopolyploid origin and niche expansion of <i>Rhodiola integrifolia</i> (Crassulaceae). <i>Plant Diversity</i> , 2023, 45, 36-44.	1.8	3
22083	<i>The Dasya baillouviana</i> and <i>D. cryptica</i> complexes (Delesseriaceae, Rhodophyta) in Bermuda with three additional new species from the archipelago. <i>Journal of Phycology</i> , 2022, 58, 731-745.	1.0	4
22084	A new species of lotic breeding salamander (Amphibia, Caudata, Hynobiidae) from Shikoku, Japan. <i>PeerJ</i> , 0, 10, e13891.	0.9	1
22085	Structural mutations of small single copy (SSC) region in the plastid genomes of five <i>Cistanche</i> species and inter-species identification. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	5
22087	Genetic drift drives rapid speciation of an Arctic insular endemic shrew (<i>Sorex pribilofensis</i>). <i>Molecular Ecology</i> , 2022, 31, 5231-5248.	2.0	4
22089	Genomic insights into the phylogeny and biomass-degrading enzymes of rumen ciliates. <i>ISME Journal</i> , 2022, 16, 2775-2787.	4.4	32
22090	Co-Occurrence of β -Lactam and Aminoglycoside Resistance Determinants among Clinical and Environmental Isolates of <i>Klebsiella pneumoniae</i> and <i>Escherichia coli</i> : A Genomic Approach. <i>Pharmaceuticals</i> , 2022, 15, 1011.	1.7	6
22091	Phylogenetic analysis based on single-copy orthologous proteins in highly variable chloroplast genomes of <i>Corydalis</i> . <i>Scientific Reports</i> , 2022, 12, .	1.6	1
22094	Novel Freshwater Ascomycetes from Spain. <i>Journal of Fungi</i> (Basel, Switzerland), 2022, 8, 849.	1.5	1
22095	The nearly complete assembly of the <i>Cercis chinensis</i> genome and Fabaceae phylogenomic studies provide insights into new gene evolution. <i>Plant Communications</i> , 2023, 4, 100422.	3.6	4

#	ARTICLE	IF	CITATIONS
22096	High Nucleotide Substitution Rates Associated with Retrotransposon Proliferation Drive Dynamic Secretome Evolution in Smut Pathogens. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	3
22098	Taxonomy of Cryptic Isoetes Species from the Brazilian Semi-Arid Region, with a Note about the Putative Maternal Origin of Polyploids. <i>American Fern Journal</i> , 2022, 112, .	0.2	0
22099	A reference-grade genome assembly for <i>Gossypium bickii</i> and insights into its genome evolution and formation of pigment glands and gossypol. <i>Plant Communications</i> , 2023, 4, 100421.	3.6	10
22100	The complete chloroplast genome of <i>Prunus campanulata</i> (Rosaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 1534-1535.	0.2	0
22101	A new species of <i>Quercus</i> genus (Fagaceae) from Son Tra Peninsula, Central Vietnam. <i>PhytoKeys</i> , 0, 206, 61-73.	0.4	1
22102	Comprehensive characterization of Cysteine-rich protein-coding genes of <i>Giardia lamblia</i> and their role during antigenic variation. <i>Genomics</i> , 2022, 114, 110462.	1.3	6
22103	Structural insights into partner selection for MYB and bHLH transcription factor complexes. <i>Nature Plants</i> , 2022, 8, 1108-1117.	4.7	19
22104	Genomic Analysis Reveals Adaptation of <i>Vibrio campbellii</i> to the Hadal Ocean. <i>Applied and Environmental Microbiology</i> , 2022, 88, .	1.4	5
22106	Evolution of zygomycete secretomes and the origins of terrestrial fungal ecologies. <i>IScience</i> , 2022, 25, 104840.	1.9	13
22107	Contrasting long-term dynamics of antimicrobial resistance and virulence plasmids in <i>Salmonella Typhimurium</i> from animals. <i>Microbial Genomics</i> , 2022, 8, .	1.0	1
22108	Chromosome-level and graphic genomes provide insights into metabolism of bioactive metabolites and cold-adaption of <i>Pueraria lobata</i> var. <i>montana</i> . <i>DNA Research</i> , 2022, 29, .	1.5	7
22109	The complete mitochondrial genome of <i>Simulium jisigouense</i> (Diptera: Simuliidae) and phylogenetic analysis of Simuliidae. <i>Frontiers in Ecology and Evolution</i> , 0, 10, .	1.1	1
22110	Hexabothriidae and Monocotylidae (Monogenoidea) from the gills of neonate hammerhead sharks (Sphyrnidae) <i>Sphyrna gilberti</i> , <i>Sphyrna lewini</i> and their hybrids from the western North Atlantic Ocean. <i>Parasitology</i> , 2022, 149, 1910-1927.	0.7	2
22111	<i>Croceicoccus hydrothermalis</i> sp. nov., isolated from shallow-sea hydrothermal system off Kueishantao Island. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	1
22112	Draft Metagenome-Assembled Genome Sequences of Three Novel Ammonia-Oxidizing <i>Nitrososphaera</i> Strains Recovered from Agricultural Soils in Western Colorado. <i>Microbiology Resource Announcements</i> , 0, , .	0.3	0
22113	Extensive genome introgression between domestic ferret and European polecat during population recovery in Great Britain. <i>Journal of Heredity</i> , 2022, 113, 500-515.	1.0	2
22114	Alien Travel Companies: The Case of Two Sea Slugs and One Bryozoan in the Mediterranean Sea. <i>Diversity</i> , 2022, 14, 687.	0.7	2
22115	Elucidating the <i>Colletotrichum</i> spp. diversity responsible for papaya anthracnose in Brazil. <i>Fungal Biology</i> , 2022, 126, 623-630.	1.1	4

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22116	<sc>eQTLs</sc> play critical roles in regulating gene expression and identifying key regulators in rice. <i>Plant Biotechnology Journal</i> , 2022, 20, 2357-2371.	4.1	9
22117	Timing and characteristics of nuclear events during conjugation and genomic exclusion in <i>Paramecium multimicronucleatum</i> . <i>Marine Life Science and Technology</i> , 2022, 4, 317-328.	1.8	15
22119	Molecular tools for resolving <i>Merodon ruficornis</i> group (Diptera, Syrphidae) taxonomy. <i>Organisms Diversity and Evolution</i> , 0, , .	0.7	0
22120	Dilemmas in generic delimitation of <i>Senegalia</i> and allies (Caesalpinoideae, mimosoid clade): how to reconcile phylogenomic evidence with morphology and taxonomy?. <i>PhytoKeys</i> , 0, 205, 261-278.	0.4	7
22121	Paleogene emergence and evolutionary history of the Amazonian fossorial fish genus <i>Tarumania</i> (Teleostei: Tarumaniidae). <i>Frontiers in Ecology and Evolution</i> , 0, 10, .	1.1	0
22122	Morphological and Phylogenetic Analyses Reveal Four New Species of <i>Acrodictys</i> (Acrodictyceae) in China. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 853.	1.5	2
22123	ï»¿A new <i>Arthrinium</i> -like genus of <i>Amphisphaeriales</i> in China. <i>MycKeys</i> , 0, 92, 27-43.	0.8	13
22124	ï»¿Diversity of fungi associated with <i>Monochamus alternatus</i> larval habitats in <i>Bursaphelenchus xylophilus</i> -infected <i>Pinus massoniana</i> and identification of two new ophiostomatalean species (Ascomycota, Ophiostomatales). <i>MycKeys</i> , 0, 92, 1-25.	0.8	0
22125	Phage Resistance Accompanies Reduced Fitness of Uropathogenic <i>Escherichia coli</i> in the Urinary Environment. <i>MSphere</i> , 2022, 7, .	1.3	12
22126	Molecular phylogeny of Japanese marine <i>Tanytarsini</i> chironomids (Chironomidae: Chironominae). <i>Genetica</i> , 0, , .	0.5	0
22127	Metagenomic data from cerebrospinal fluid permits tracing the origin and spread of <i>Neisseria meningitidis</i> CC4821 in China. <i>Communications Biology</i> , 2022, 5, .	2.0	1
22128	Biotic colonization of subtropical East Asian caves through time. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	5
22129	Range-wide population genetics of the tapertail anchovy <i>Coilia nasus</i> based on exon-capture data. <i>Marine Biodiversity</i> , 2022, 52, .	0.3	1
22130	A chromosome-level genome of the helmet catfish (<i>Cranoglanis boudierus</i>). <i>Frontiers in Genetics</i> , 0, 13, .	1.1	2
22131	Detection and molecular characterization of Avipoxvirus in <i>Culex</i> spp. (Culicidae) captured in domestic areas in Rio de Janeiro, Brazil. <i>Scientific Reports</i> , 2022, 12, .	1.6	2
22132	Whole Genome Sequencing Suggests that "Nonpathogenicity on Banana (NPB)" is the Ancestral State of the <i>Ralstonia solanacearum</i> IIB-4 Lineage. <i>PhytoFrontiers</i> , 2023, 3, 262-267.	0.8	3
22133	Learning Hyperbolic Embedding for Phylogenetic Tree Placement and Updates. <i>Biology</i> , 2022, 11, 1256.	1.3	5
22134	An integrative bioinformatics pipeline shows that honeybee-associated microbiomes are driven primarily by pollen composition. <i>Insect Science</i> , 0, , .	1.5	0

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22135	Genomic Insights into Genetic Diploidization in the Homosporous Fern <i>Adiantum nelumboides</i> . <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	7
22136	The Ligule in Poaceae: a Historical and Evolutionary Review. <i>Botanical Review</i> , The, 0, , .	1.7	0
22137	Distribution and Genomic Variation of Thermophilic Cyanobacteria in Diverse Microbial Mats at the Upper Temperature Limits of Photosynthesis. <i>MSystems</i> , 2022, 7, .	1.7	9
22138	The large-sample asymptotic behaviour of quartet-based summary methods for species tree inference. <i>Journal of Mathematical Biology</i> , 2022, 85, .	0.8	3
22140	Skimming for barcodes: rapid production of mitochondrial genome and nuclear ribosomal repeat reference markers through shallow shotgun sequencing. <i>PeerJ</i> , 0, 10, e13790.	0.9	13
22142	The yeast lichenosphere: high diversity of basidiomycetes from the lichens <i>Tephromela atra</i> and <i>Rhizoplaca melanophthalma</i> . <i>Fungal Biology</i> , 2022, 126, 587-608.	1.1	10
22143	Chromosomal polymorphism of the <i>Ceratocystis fimbriata</i> species complex in Brazil. <i>Fungal Genetics and Biology</i> , 2022, 162, 103728.	0.9	2
22144	Phylogenomics AND biogeography of <i>Castanea</i> (chestnut) and <i>Hamamelis</i> (witch-hazel) – Choosing between RAD-seq and Hyb-Seq approaches. <i>Molecular Phylogenetics and Evolution</i> , 2022, 176, 107592.	1.2	7
22145	DNA Barcoding of genus <i>Culicoides</i> biting midges (Diptera: Ceratopogonidae) in the Brazilian Amazon. <i>Acta Tropica</i> , 2022, 235, 106619.	0.9	4
22146	Evidence for the involvement of branchial Vacuolar-type H ⁺ -ATPase in the acidification of the external medium by the West African lungfish, <i>Protopterus annectens</i> , exposed to ammonia-loading conditions. <i>Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology</i> , 2022, 273, 111297.	0.8	3
22147	Revision of the Cretaceous shark <i>Protosynodus</i> (Chondrichthyes, Squaliformes) and early evolution of somniosid sharks. <i>Cretaceous Research</i> , 2022, 140, 105331.	0.6	3
22148	Phylogeny and evolution of Cupressaceae: Updates on intergeneric relationships and new insights on ancient intergeneric hybridization. <i>Molecular Phylogenetics and Evolution</i> , 2022, 177, 107606.	1.2	4
22149	Impact of abiotic factors and husbandry on saprolegniosis in salmonid farms. <i>Aquaculture</i> , 2022, 561, 738679.	1.7	2
22150	Characterization of the complete mitogenome of <i>Trachylophus sinensis</i> (Coleoptera: Cerambycidae: Tj ETQq1 1 0.784314 rgBT /Overlo Asia-Pacific Entomology, 2022, 25, 101977.	0.4	4
22151	Large-scale genomic analysis reveals the pESI-like megaplasmid presence in <i>Salmonella Agona</i> , Muenchen, Schwarzengrund, and Senftenberg. <i>Food Microbiology</i> , 2022, 108, 104112.	2.1	11
22152	<i>Canoparmelia texana</i> (<i>Parmeliaceae</i> , <i>Ascomycota</i>) consists of two independent lineages. <i>Lichenologist</i> , 2022, 54, 245-251.	0.5	1
22154	Global phylogeography of hyperdiverse lanternfishes indicates sympatric speciation in the deep sea. <i>Global Ecology and Biogeography</i> , 2022, 31, 2353-2367.	2.7	3
22155	Massive expansion of P-selectin genes in two <i>Venerida</i> species, <i>Sinonovacula constricta</i> and <i>Mercenaria mercenaria</i> : evidence from comparative genomics of <i>Bivalvia</i> . <i>BMC Genomics</i> , 2022, 23, .	1.2	0

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22156	<i>Melanoleuca subgriseoflava</i> and <i>M. substridula</i> —two new <i>Melanoleuca</i> species (Agaricales, Basidiomycota) described from China. PeerJ, 0, 10, e13807.	0.9	0
22157	Immunomodulatory Effect of Polysaccharides from the Mushroom-Forming Basidiomycete <i>Gymnopilus imperialis</i> (Agaricomycetes, Basidiomycota). Pharmaceuticals, 2022, 15, 1179.	1.7	1
22158	Functional genomics analysis reveals the evolutionary adaptation and demographic history of pygmy lorises. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	5
22159	Massive-scale genomic analysis reveals SARS-CoV-2 mutation characteristics and evolutionary trends. , 0, , .		2
22160	Plastome structure, phylogenomics, and divergence times of tribe Cinnamomeae (Lauraceae). BMC Genomics, 2022, 23, .	1.2	7
22161	<i>Zwartia hollandica</i> gen. nov., sp. nov., <i>Jezberella montanilacus</i> gen. nov., sp. nov. and <i>Sheuella amnicola</i> gen. nov., comb. nov., representing the environmental GKS98 (betIII) cluster. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	3
22162	Characterization of the complete chloroplast genome of <i>Hevea pauciflora</i> (Euphorbiaceae), an important wild relative of the rubber tree. Mitochondrial DNA Part B: Resources, 2022, 7, 1589-1593.	0.2	0
22164	SP and KLF Transcription Factors in Cancer Metabolism. International Journal of Molecular Sciences, 2022, 23, 9956.	1.8	12
22165	Analysis of complete chloroplast genome sequences and insight into the phylogenetic relationships of <i>Ferula</i> L.. BMC Genomics, 2022, 23, .	1.2	11
22166	Is phenotypic evolution affected by spiders™ construction behaviors?. Systematic Biology, 0, , .	2.7	2
22167	Microbiome composition is shaped by geography and population structure in the parasitic wasp <i>Asobara japonica</i> , but not in the presence of the endosymbiont <i>Wolbachia</i> . Molecular Ecology, 2023, 32, 6644-6658.	2.0	3
22168	ï»¿New species of <i>Sticta</i> (lichenised Ascomycota, lobarioid Peltigeraceae) from Bolivia suggest a high level of endemism in the Central Andes. MycoKeys, 0, 92, 131-160.	0.8	6
22170	Discovery of the first PD-1 ligand encoded by a pathogen. Frontiers in Immunology, 0, 13, .	2.2	1
22171	Genome-centric metagenomics insights into functional divergence and horizontal gene transfer of denitrifying bacteria in anammox consortia. Water Research, 2022, 224, 119062.	5.3	10
22172	Molecular phylogeny of <i>Chonotrichia</i> (Ciliophora, Phyllopharyngea) inferred from SSU rDNA sequences. European Journal of Protistology, 2022, 86, 125920.	0.5	1
22173	Resilience of organohalide-detoxifying microbial community to oxygen stress in sewage sludge. Water Research, 2022, 224, 119055.	5.3	12
22174	Ultrastructure and phylogeny of <i>Parvodinium cunningtonii</i> comb. nov. (syn. <i>Peridiniopsis</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 107 Td (0.5	2
22175	Genome sequencing and comparative analysis of <i>Ficus benghalensis</i> and <i>Ficus religiosa</i> species reveal evolutionary mechanisms of longevity. IScience, 2022, 25, 105100.	1.9	12

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22176	Autochthonous transmission of the Indomalayan parasite, <i>Transversotrema patialense</i> , in the Caribbean: Molecular, morphological, and experimental evidence. <i>Experimental Parasitology</i> , 2022, 242, 108368.	0.5	4
22177	Butanol production from Thai traditional beverage (Sato) factory wastewater using newly isolated <i>Clostridium beijerinckii</i> CUEA02. <i>Biochemical Engineering Journal</i> , 2022, 187, 108648.	1.8	1
22178	Comprehensive taxon sampling and vetted fossils help clarify the time tree of shorebirds (Aves). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 60</i>	1.2	20
22179	Evidence of flow and low genetic structure between populations of the Gulf of Mexico and the Mexican Pacific of white mullet, <i>Mugil curema</i> (Pisces) inferred from single nucleotide polymorphisms. <i>Fisheries Research</i> , 2022, 256, 106484.	0.9	2
22180	<i>Colletotrichum siamense</i> causing anthracnose on <i>Etlingera elatior</i> . <i>Crop Protection</i> , 2022, 162, 106092.	1.0	1
22181	<i>Curvularia verruculosa</i> as new causal pathogen of common bean leaf spot disease in China. <i>Crop Protection</i> , 2022, 162, 106091.	1.0	5
22182	Floral synomone components of fruit fly-attracting orchids, <i>Bulbophyllum sinapis</i> and <i>B. hahlianum</i> , in Papua New Guinea. <i>Biochemical Systematics and Ecology</i> , 2022, 105, 104481.	0.6	3
22183	<i>Clostridium perfringens</i> associated with dairy farm systems show diverse genotypes. <i>International Journal of Food Microbiology</i> , 2022, 382, 109933.	2.1	5
22184	First report of <i>Pseudopithomyces maydicus</i> causing leaf spots in strawberry. <i>Crop Protection</i> , 2022, 162, 106081.	1.0	1
22185	Insights into the phylogeny of the family Deviatidae (Protozoa, Ciliophora, Hypotrichia) based on multi-gene, morphological and ontogenetic information, with the establishment of a new species <i>Deviatea multilineae</i> n. sp.. <i>Molecular Phylogenetics and Evolution</i> , 2022, 177, 107623.	1.2	4
22186	Chromosome-level genome assembly of <i>Monochamus saltuarius</i> reveals its adaptation and interaction mechanism with pine wood nematode. <i>International Journal of Biological Macromolecules</i> , 2022, 222, 325-336.	3.6	2
22187	Assessing the utility of mitochondrial gene markers in the family Suessiaceae (Dinophyta) with phylogenomic validation. <i>Molecular Phylogenetics and Evolution</i> , 2022, 177, 107625.	1.2	1
22188	Evolution of nacre- and prisms-related shell matrix proteins in the pen shell, <i>Atrina pectinata</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2022, 44, 101025.	0.4	4
22189	Compartment niche and bamboo variety influence the diversity, composition, network and potential keystone taxa functions of rhizobacterial communities. <i>Rhizosphere</i> , 2022, 24, 100593.	1.4	4
22190	Water-energy relationships shape the phylogenetic diversity of terricolous lichen communities in Mediterranean mountains: Implications for conservation in a climate change scenario. <i>Fungal Ecology</i> , 2022, 60, 101189.	0.7	0
22191	Lignin-oxidizing and xylan-hydrolyzing <i>Vibrio</i> involved in the mineralization of plant detritus in the continental slope. <i>Science of the Total Environment</i> , 2023, 854, 158714.	3.9	2
22192	Lichens as material for Lepidoptera's housing: A molecular approach to a widespread and highly selective interaction. <i>Fungal Ecology</i> , 2023, 61, 101195.	0.7	2
22193	Genomics and morphometrics reveal the adaptive evolution of pikas. <i>Zoological Research</i> , 2022, 43, 813-826.	0.9	5

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22194	Molecular phylogeny and taxonomy of four <i>Remanella</i> species (Protozoa, Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 747 To Zoological Research, 2022, 43, 827-842.	0.9	4
22195	Testing Phylogenetic Stability with Variable Taxon Sampling. <i>Methods in Molecular Biology</i> , 2022, , 167-188.	0.4	1
22196	Assembling a Reference Phylogenomic Tree of Bacteria and Archaea by Summarizing Many Gene Phylogenies. <i>Methods in Molecular Biology</i> , 2022, , 137-165.	0.4	1
22197	A New Melastomataceae Classification Informed by Molecular Phylogenetics and Morphology. , 2022, , 109-165.		9
22198	Genetic Structure of Helianthemum Populations with a Disjunctive Distribution in Central Asia and Northwestern China and the Implications for Conservation. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
22199	Estimating the Divergence Times of Alphaproteobacteria Based on Mitochondrial Endosymbiosis and Eukaryotic Fossils. <i>Methods in Molecular Biology</i> , 2022, , 95-116.	0.4	0
22200	Ethanol-Lactate Transition of Lachancea Thermotolerans Linked to Nitrogen Metabolism. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
22201	Reconstruction of Archaeal Genomes from Short-Read Metagenomes. <i>Methods in Molecular Biology</i> , 2022, , 487-527.	0.4	0
22202	Metagenomic Approaches for the Discovery of Pollutant-Remediating Enzymes: Recent Trends and Challenges. , 2022, , 571-604.		0
22203	<i>Lentinus squarrosulus</i> ; an edible macro-fungus reported from Pakistan. <i>Studies in Fungi</i> , 2022, 7, 1-3.	0.5	0
22204	Reconstructing Gene Gains and Losses with BadiRate. <i>Methods in Molecular Biology</i> , 2022, , 213-232.	0.4	1
22205	Metagonia spiders of Galapagos: blind cave-dwellers and their epigeal relatives (Araneae, Pholcidae). <i>Invertebrate Systematics</i> , 2022, 36, 647.	0.5	4
22206	Proposal of a New Genus, Doorochen (Digenea: Lepocreadioidae), for Reef-Inhabiting Members of the Genus Postlepidapedon Zdzitowiecki, 1993. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
22207	Ultrastructure and Phylogeny of Parvodinium Cunningtonii Comb. Nov. And Description of P. Cunningtonii VAR. Inerme VAR. Nov. (Peridiniopsidaceae, Dinophyceae). <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
22208	Evolutionary genomics of structural variation in the tea plant, <i>Camellia sinensis</i> . , 2022, 1, 1-11.		3
22209	Morphology, Morphogenesis, and Molecular Characterization of Castula Specialis Sp. Nov. (Ciliophora, Armophorea, Metopida). <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
22210	Limited Role of Recombination in the Global Diversification of Begomovirus DNA-B Proteins. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
22211	Diversity and biogeography of planktonic diatoms in Svalbard fjords: The role of dispersal and Arctic endemism in phytoplankton community structuring. <i>Elementa</i> , 2022, 10, .	1.1	8

#	ARTICLE	IF	CITATIONS
22212	Investigations into the ancestry of the Grape-eye Seabass (<i>Hemilutjanus macrophthalmos</i>) reveal novel limits and relationships for the Acropomatiformes (Teleostei: Percomorpha). <i>Neotropical Ichthyology</i> , 2022, 20, .	0.5	4
22213	Phylogeny of the <i>Rhinocylapus</i> complex (Heteroptera, Miridae, Cylapinae, Fulviini). <i>Invertebrate Systematics</i> , 2022, 36, 751.	0.5	4
22214	Chloroplast Genome of <i>Diospyros</i> Species. <i>Compendium of Plant Genomes</i> , 2022, , 85-96.	0.3	0
22215	Integrative taxonomy reveals a new species of <i>Cyphocharax</i> (Characiformes: Curimatidae) from the Upper Para�ba do Sul River basin, Brazil. <i>Neotropical Ichthyology</i> , 2022, 20, .	0.5	1
22216	An Integrated Method to Reconstruct Ancient Proteins. <i>Methods in Molecular Biology</i> , 2022, , 267-281.	0.4	0
22217	Three highly variable genome regions of the four dengue virus serotypes can accurately recapitulate the CDS phylogeny. <i>MethodsX</i> , 2022, 9, 101859.	0.7	1
22218	A new species of <i>Lecidella</i> (Lecanorales, Ascomycota) from Azad Jammu and Kashmir, Pakistan. <i>Acta Botanica Brasilica</i> , 0, 36, .	0.8	1
22219	Complete Mitogenome of <i>Cruznema tripartitum</i> Confirms Highly Conserved Gene Arrangement within Family Rhabditidae. <i>Journal of Nematology</i> , 2022, 54, 1-10.	0.4	4
22220	Seagrass Colonization Alters Diversity, Abundance, Taxonomic, and Functional Community Structure of Benthic Microbial Eukaryotes. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
22221	Phylogeography and taxonomy of <i>Coleonyx elegans</i> Gray 1845 (Squamata: Eublepharidae) in Mesoamerica: The Isthmus of Tehuantepec as an environmental barrier. <i>Molecular Phylogenetics and Evolution</i> , 2023, 178, 107632.	1.2	6
22222	Pre-Treatment With Polysaccharide Depolymerase Enhances the Infective Performance of <i>Klebsiella</i> Phage KP1079. , 2022, , .		0
22223	A Novel <i>Acinetobacter</i> Phage Cato: Lytic Myovirus Containing Tailspike Depolymerase. , 2022, , .		1
22224	Comparative analysis of genome-encoded viral sequences reveals the evolutionary history of flavivirids (family <i>Flaviviridae</i>). <i>Virus Evolution</i> , 2022, 8, .	2.2	13
22225	Re-Identification on Korean <i>Penicillium</i> Sequences in GenBank Collected by Software GenMine. <i>Mycobiology</i> , 2022, 50, 231-237.	0.6	1
22226	Chromosome-Level Genome Assembly of a Fragrant Japonica Rice Cultivar ‘‘Changxianggeng 1813’’ Provides Insights into Genomic Variations between Fragrant and Non-Fragrant Japonica Rice. <i>International Journal of Molecular Sciences</i> , 2022, 23, 9705.	1.8	5
22227	The complete mitochondrial genome of the jumping plant bug <i>Halticus minutus</i> Reuter, 1885 (Hemiptera: Miridae). <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 1568-1570.	0.2	0
22228	WGS-Based Lineage and Antimicrobial Resistance Pattern of <i>Salmonella</i> Typhimurium Isolated during 2000–2017 in Peru. <i>Antibiotics</i> , 2022, 11, 1170.	1.5	7
22229	Comparative Analysis of Complete Chloroplast Genome and Phenotypic Characteristics of Japanese Apricot Accessions. <i>Horticulturae</i> , 2022, 8, 794.	1.2	3

#	ARTICLE	IF	CITATIONS
22230	A new large tortoise from the early Oligocene (Arikareean NALMA) of Oaxaca, southern Mexico and its phylogenetic position within <i>Pan-Testudinidae</i> . <i>Historical Biology</i> , 0, , 1-14.	0.7	1
22232	Chromosome-level Genomes Reveal the Genetic Basis of Descending Dysploidy and Sex Determination in <i>Morus</i> Plants. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 1119-1137.	3.0	6
22234	Genomic Variations in the Tea Leafhopper Reveal the Basis of Its Adaptive Evolution. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 1092-1105.	3.0	5
22235	<i>Neopestalotiopsis longiappendiculata</i> as the agent of grey blight disease of <i>Camellia</i> spp.. <i>Journal of Phytopathology</i> , 2022, 170, 770-777.	0.5	2
22236	The complete mitochondrial genome of <i>Periphyllus diacerivorus</i> Zhang, 1982 (Hemiptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 417	0.2	0
22237	Diversity of Ascomycota in Jilin: Introducing Novel Woody Litter Taxa in Cucurbitariaceae. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 905.	1.5	5
22238	Two newly recorded species of the genera, <i>Chamaemyces</i> and <i>Hodophilus</i> , from Turkey. <i>Nordic Journal of Botany</i> , 0, , .	0.2	0
22239	Oneâ€™s trash is someone elseâ€™s treasure: sequence read archives from Lepidoptera genomes provide material for genome reconstruction of their endosymbionts. <i>BMC Microbiology</i> , 2022, 22, .	1.3	6
22241	Fungal Species from <i>Rhododendron</i> sp.: <i>Discosia rhododendricola</i> sp.nov, <i>Neopestalotiopsis rhododendricola</i> sp.nov and <i>Diaporthe nobilis</i> as a New Host Record.. <i>Journal of Fungi (Basel)</i> , Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 417	0.2	0
22242	Genomic diversity and biosynthetic capabilities of sponge-associated chlamydiae. <i>ISME Journal</i> , 2022, 16, 2725-2740.	4.4	8
22243	Unraveling usnic acid: a comparison of biosynthetic gene clusters between two reindeer lichen (<i>Cladonia rangiferina</i> and <i>C. Auncialis</i>). <i>Fungal Biology</i> , 2022, 126, 697-706.	1.1	5
22244	<i>Nanobdella aerobiophila</i> gen. nov., sp. nov., a thermoacidophilic, obligate ectosymbiotic archaeon, and proposal of <i>Nanobdellaceae</i> fam. nov., <i>Nanobdellales</i> ord. nov. and <i>Nanobdellia</i> class. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	14
22245	Species delimitation in the <i>Trichocentrum cepula</i> (<i>Oncidiinae</i> , <i>Orchidaceae</i>) complex: a multidisciplinary approach. <i>Systematics and Biodiversity</i> , 2022, 20, 1-18.	0.5	3
22246	Deep evaluation of the evolutionary history of the Heat Shock Factor (HSF) gene family and its expansion pattern in seed plants. <i>PeerJ</i> , 0, 10, e13603.	0.9	3
22247	Characterization of 15 Earthworm Mitogenomes from Northeast China and Its Phylogenetic Implication (<i>Oligochaeta</i> : <i>Lumbricidae</i> , <i>Moniligastridae</i>). <i>Diversity</i> , 2022, 14, 714.	0.7	5
22248	Detection of human pathogenic bacteria in rectal DNA samples from <i>Zalophus californianus</i> in the Gulf of California, Mexico. <i>Scientific Reports</i> , 2022, 12, .	1.6	0
22249	Evolution of a chordate-specific mechanism for myoblast fusion. <i>Science Advances</i> , 2022, 8, .	4.7	8
22250	A chromosome-scale genome assembly of <i>Quercus gilva</i> : Insights into the evolution of <i>Quercus</i> section <i>Cyclobalanopsis</i> (<i>Fagaceae</i>). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	8

#	ARTICLE	IF	CITATIONS
22252	Identification and expression of functionally conserved circadian clock genes in lichen-forming fungi. <i>Scientific Reports</i> , 2022, 12, .	1.6	1
22253	Recovery of chloroplast genomes from medieval millet grains excavated from the Areni-1 cave in southern Armenia. <i>Scientific Reports</i> , 2022, 12, .	1.6	1
22254	The complete chloroplast genome of <i>Rubus pacificus</i> (Rosaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 1622-1623.	0.2	0
22255	Complete chloroplast genome and evolutionary analysis of <i>Acer paihengii</i> (Sapindales:Aceraceae). <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 1630-1632.	0.2	0
22256	Systematic Analysis of Copy Number Variations in the Pathogenic Yeast <i>Candida parapsilosis</i> Identifies a Gene Amplification in <i>RTA3</i> That is Associated with Drug Resistance. <i>MBio</i> , 2022, 13, .	1.8	13
22257	Differences in pseudogene evolution contributed to the contrasting flavors of turnip and Chiifu, two <i>Brassica rapa</i> subspecies. <i>Plant Communications</i> , 2023, 4, 100427.	3.6	5
22258	Taxonomic and Phylogenetic Reassessment of <i>Pyrgidium</i> (Mycocaliciales) and Investigation of Ascospore Morphology. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 966.	1.5	3
22259	Home and hub: pet trade and traditional medicine impact reptile populations in source locations and destinations. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2022, 289, .	1.2	3
22260	Comparative and Phylogenetic Analyses of Complete Chloroplast Genomes of <i>Scrophularia incisa</i> Complex (Scrophulariaceae). <i>Genes</i> , 2022, 13, 1691.	1.0	6
22261	<i>Colletotrichum chinense</i> sp. nov. from <i>Yucca gloriosa</i> and <i>C. quercicola</i> sp. nov. from <i>Quercus variabilis</i> in China. <i>MycologyKeys</i> , 0, 93, 1-21.	0.8	4
22262	The <i>cnf1</i> gene is associated with an expanding <i>Escherichia coli</i> ST131 <i>H</i> 30Rx/C2 subclade and confers a competitive advantage for gut colonization. <i>Gut Microbes</i> , 2022, 14, .	4.3	2
22264	Splitting blades: why genera need to be more carefully defined; the case for <i>Pyropia</i> (Bangiales, Rhodophyta). <i>Algae</i> , 2022, 37, 205-211.	0.9	14
22265	Evolutionary analysis of the <i>LORELEI</i> gene family in plants reveals regulatory subfunctionalization. <i>Plant Physiology</i> , 2022, 190, 2539-2556.	2.3	5
22266	Monsoon boosted radiation of the endemic East Asian carps. <i>Science China Life Sciences</i> , 2023, 66, 563-578.	2.3	4
22267	Plant speciation in the Namib Desert: potential origin of a widespread derivative species from a narrow endemic. <i>Plant Ecology and Diversity</i> , 2022, 15, 329-353.	1.0	2
22268	Hidden species behind <i>Ophiocordyceps</i> (Ophiocordycipitaceae, Hypocreales) on termites: four new species from Thailand. <i>Mycological Progress</i> , 2022, 21, .	0.5	5
22269	Genomic Sequencing and Phylogenomics of Cowpox Virus. <i>Viruses</i> , 2022, 14, 2134.	1.5	8
22270	<i>Littoraria flava</i> (Gastropoda: Littorinidae) mitogenome: phylogenetic considerations within the Caenogastropoda and evidence of microscale local adaptation. <i>Marine Biology</i> , 2022, 169, .	0.7	0

#	ARTICLE	IF	CITATIONS
22271	VanA-Enterococcus faecalis in Poland: hospital population clonal structure and vanA mobilome. European Journal of Clinical Microbiology and Infectious Diseases, 2022, 41, 1245-1261.	1.3	5
22272	Molecular genetics and epidemiological characteristics of HIV-1 epidemic strains in various sexual risk behaviour groups in developed Eastern China, 2017–2020. Emerging Microbes and Infections, 2022, 11, 2326-2339.	3.0	5
22273	The systematics of Tachymenini (Serpentes, Dipsadidae): An updated classification based on molecular and morphological evidence. Zoologica Scripta, 2022, 51, 643-663.	0.7	5
22274	Limited Transmission of Klebsiella pneumoniae among Humans, Animals, and the Environment in a Caribbean Island, Guadeloupe (French West Indies). Microbiology Spectrum, 2022, 10, .	1.2	7
22275	Persistence of Rare Salmonella Typhi Genotypes Susceptible to First-Line Antibiotics in the Remote Islands of Samoa. MBio, 2022, 13, .	1.8	6
22277	A new symbiotic relationship between a polyclad flatworm and a mantis shrimp: description of a new species of Emprostopharynx (Polycladida: Acotylea) associated with Lysiosquilla maculata (Crustacea: Stomatopoda). Marine Biodiversity, 2022, 52, .	0.3	0
22278	Plastomes of Bletilla (Orchidaceae) and Phylogenetic Implications. International Journal of Molecular Sciences, 2022, 23, 10151.	1.8	9
22280	Equus caballus Papillomavirus Type-9 (EcPV9): First Detection in Asymptomatic Italian Horses. Viruses, 2022, 14, 2050.	1.5	3
22281	Cryptic species diversity in a widespread neotropical tree genus: the case of <i>Cedrela odorata</i> . American Journal of Botany, 0, , .	0.8	3
22283	Tropical and Temperate Lineages of <i>Rhipicephalus sanguineus</i> s.l. Ticks (Acari: Ixodidae) Host Different Strains of <i>Coxiella</i> -like Endosymbionts. Journal of Medical Entomology, 0, , .	0.9	0
22284	Genomic Profiling of Non-O157 Shiga Toxigenic <i>Escherichia coli</i> -Infecting Bacteriophages from South Africa. Phage, 2022, 3, 221-230.	0.8	1
22285	Two hypotrichs (Ciliophora, Hypotricha) from China: morphology and SSU rDNA sequence of <i>Holosticha aestuarina</i> nov. spec. and <i>H. muiensis</i> Kim et al., 2017. European Journal of Protistology, 2022, 86, 125931.	0.5	3
22288	Functional Divergence in a Multi-gene Family Is a Key Evolutionary Innovation for Anaerobic Growth in <i>Saccharomyces cerevisiae</i> . Molecular Biology and Evolution, 2022, 39, .	3.5	3
22289	Convergence without divergence in North American red-flowering <i>Silene</i> . Frontiers in Plant Science, 0, 13, .	1.7	2
22290	Intraspecific differentiation of <i>Allium canadense</i> var. <i>canadense</i> (Amaryllidaceae) across the North American Coastal Plain. Plant Species Biology, 0, , .	0.6	0
22291	Improving environmental monitoring of Vibrionaceae in coastal ecosystems through 16S rRNA gene amplicon sequencing. Environmental Science and Pollution Research, 2022, 29, 67466-67482.	2.7	5
22292	Plastome sequences fail to resolve shallow level relationships within the rapidly radiated genus <i>Isodon</i> (Lamiaceae). Frontiers in Plant Science, 0, 13, .	1.7	2
22293	Plastomes Provide Insights into Differences between Morphology and Molecular Phylogeny: <i>Ostericum</i> and <i>Angelica</i> (Apiaceae) as an Example. Diversity, 2022, 14, 776.	0.7	3

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22294	Multiomics provides new insights into the domestication and improvement of dark jute (<i>T. tetragynum</i>). <i>Frontiers in Plant Science</i> , 2022, 13, 742111.	2.8	1
22295	Characterization of <i>Colletotrichum</i> Isolates from Strawberry and Other Hosts with Reference to Cross-Inoculation Potential. <i>Plants</i> , 2022, 11, 2373.	1.6	1
22296	Genome sequencing and comparative analysis of <i>Wolbachia</i> strain wAlbA reveals <i>Wolbachia</i> -associated plasmids are common. <i>PLoS Genetics</i> , 2022, 18, e1010406.	1.5	8
22297	Large-scale and small-scale population genetic structure of the medically important gastropod species <i>Bulinus truncatus</i> (Gastropoda, Heterobranchia). <i>Parasites and Vectors</i> , 2022, 15, .	1.0	3
22298	Phylogenomics and evolutionary diversification of the subfamily Polygonoideae. <i>Journal of Systematics and Evolution</i> , 0, , .	1.6	2
22299	Evidence for Assimilatory Nitrate Reduction as a Previously Overlooked Pathway of Reactive Nitrogen Transformation in Estuarine Suspended Particulate Matter. <i>Environmental Science & Technology</i> , 2022, 56, 14852-14866.	4.6	16
22300	Placoid scales in bioluminescent sharks: Scaling their evolution using morphology and elemental composition. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	2
22303	Temporo-spatial variations in resistance determinants and clonality of <i>Acinetobacter baumannii</i> and <i>Pseudomonas aeruginosa</i> strains from Romanian hospitals and wastewaters. <i>Antimicrobial Resistance and Infection Control</i> , 2022, 11, .	1.5	9
22306	Band 3-mediated <i>Plasmodium vivax</i> invasion is associated with transcriptional variation in PvTRAg genes. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	8
22307	New Insights into Lichenization in Agaricomycetes Based on an Unusual New Basidiolichen Species of <i>Omphalina</i> s. str.. <i>Journal of Fungi</i> (Basel, Switzerland), 2022, 8, 1033.	1.5	2
22308	Convergent evolution of a genotoxic stress response in a parasite-specific p53 homolog. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	7
22309	Characterization and fungicide sensitivity of <i>Colletotrichum godetiae</i> causing sweet cherry fruit anthracnose in Guizhou, China. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
22310	Type 1 vomeronasal receptors expressed in the olfactory organs of two African lungfish, <i>Protopterus annectens</i> and <i>Protopterus amphibius</i> . <i>Journal of Comparative Neurology</i> , 2023, 531, 116-131.	0.9	4
22311	Inventario de Amphipoda (Peracarida: Senticaudata y Amphilochidea) del Río Miño Internacional, Península Ibérica. <i>Graellsia</i> , 2022, 78, e175.	0.1	1
22312	A Parasitoid Puzzle: Phylogenomics, Total-evidence Dating, and the Role of Gondwanan Vicariance in the Diversification of Labeninae (Hymenoptera, Ichneumonidae). <i>Insect Systematics and Diversity</i> , 2022, 6, .	0.7	2
22313	First report of <i>Porcine respirovirus 1</i> in South Korea. <i>Transboundary and Emerging Diseases</i> , 2022, 69, 4041-4047.	1.3	6
22314	Finding a home for the ram's horn squid: phylogenomic analyses support <i>Spirula spirula</i> (Cephalopoda: Decapodiformes) as a close relative of Oegopsida. <i>Organisms Diversity and Evolution</i> , 2023, 23, 91-101.	0.7	4
22316	Aneuploidy promotes intraspecific diversification of the endemic East Asian herb <i>Lycoris aurea</i> complex. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	0

#	ARTICLE	IF	CITATIONS
22317	Taxonomy and control of <i>Trichoderma hymenopellicola</i> sp. nov. responsible for the first green mold disease on <i>Hymenopellis raphanipes</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	5
22318	The complete chloroplast genome of <i>Miliusa glochidioides</i> (Annonaceae) and phylogenetic analysis. <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 1604-1605.	0.2	0
22319	Prospects for genomic surveillance for selection in schistosome parasites. , 0, 2, .		0
22321	Chromosome-level genome assembly of <i>Amomum tsao-ko</i> provides insights into the biosynthesis of flavor compounds. <i>Horticulture Research</i> , 2022, 9, .	2.9	5
22323	Critical assessment of pan-genomic analysis of metagenome-assembled genomes. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	6
22324	Genomes From Historic DNA Unveil Massive Hidden Extinction and Terminal Endangerment in a Tropical Asian Songbird Radiation. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	5
22325	virDTL: Viral Recombination Analysis Through Phylogenetic Reconciliation and Its Application to Sarbecoviruses and SARS-CoV-2. <i>Journal of Computational Biology</i> , 2023, 30, 3-20.	0.8	0
22328	Convergent evolution of barnacles and molluscs sheds lights in origin and diversification of calcareous shell and sessile lifestyle. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2022, 289, .	1.2	4
22330	In Depth Viral Diversity Analysis in Atypical Neurological and Neonatal Chikungunya Infections in Rio de Janeiro, Brazil. <i>Viruses</i> , 2022, 14, 2006.	1.5	2
22331	Comparative mitogenomic analyses provide evolutionary insights into the retrolateral tibial apophysis clade (Araneae: Entelegynae). <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1
22332	Comparative Genome Analysis Reveals the Genomic Basis of Semi-Aquatic Adaptation in American Mink (<i>Neovison vison</i>). <i>Animals</i> , 2022, 12, 2385.	1.0	2
22333	Transcriptome analysis provides insight into adaptive mechanisms of scallops under environmental stress. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	7
22334	Divergence Dating and Biogeography of Xenosauridae Including Fossils as Terminal Taxa. <i>Journal of Herpetology</i> , 2022, 56, .	0.2	0
22335	Using Genomes and Evolutionary Analyses to Screen for Host-Specificity and Positive Selection in the Plant Pathogen <i>Xylella fastidiosa</i> . <i>Applied and Environmental Microbiology</i> , 2022, 88, .	1.4	6
22336	Analysis of Cyp51 protein sequences shows 4 major Cyp51 gene family groups across fungi. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	3
22337	Not the same: phylogenetic relationships and ecological niche comparisons between two different forms of <i>Aglaoctenus lagotis</i> from Argentina and Uruguay. <i>Organisms Diversity and Evolution</i> , 0, , .	0.7	0
22338	A novel function of the key nitrogen-fixation activator NifA in beta-rhizobia: Repression of bacterial auxin synthesis during symbiosis. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	6
22339	Additions to <i>Neopestalotiopsis</i> (Amphisphaeriales, Sporocadaceae) fungi: two new species and one new host record from China. <i>Biodiversity Data Journal</i> , 0, 10, .	0.4	2

#	ARTICLE	IF	CITATIONS
22340	Revision of the <i>Diploderma fasciatum</i> (Mertens, 1926) Complex (Reptilia: Agamidae: Draconinae). <i>Ichthyology and Herpetology</i> , 2022, 110, .	0.3	2
22341	Draft genome assemblies of four manakins. <i>Scientific Data</i> , 2022, 9, .	2.4	2
22342	Comparative Mitogenomics of Two Sympatric Catfishes of <i>Exostoma</i> (Siluriformes: Sisoridae) from the Lower Yarlung Tsangpo River and Its Application for Phylogenetic Consideration. <i>Genes</i> , 2022, 13, 1615.	1.0	1
22343	Genetic-morphological uncoupling and crypsis in <i>Ectinogonia</i> (Coleoptera: Buprestidae) suggest a complex evolutionary history in these polymorphic jewel beetles from Chile. <i>Biological Journal of the Linnean Society</i> , 0, , .	0.7	0
22344	<i>Shingomonas baiyangensis</i> sp. nov., isolated from water in Baiyang Lake. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	0
22345	A high-quality chromosome-level genome assembly of the bivalve mollusk <i>Mactra veneriformis</i> . <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	3
22346	Metagenomic and metatranscriptomic insights into sulfate-reducing bacteria in a revegetated acidic mine wasteland. <i>Npj Biofilms and Microbiomes</i> , 2022, 8, .	2.9	2
22347	Comparative chloroplast genome and phylogenetic analyses of Chinese <i>Polyspora</i> . <i>Scientific Reports</i> , 2022, 12, .	1.6	5
22348	The genetic mechanisms underlying the convergent evolution of pollination syndromes in the Neotropical radiation of <i>Costus</i> L.. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3
22349	Newly reported chloroplast genome of <i>Sinosenecio albonervius</i> Y. Liu & Q. E. Yang and comparative analyses with other <i>Sinosenecio</i> species. <i>BMC Genomics</i> , 2022, 23, .	1.2	13
22350	Functional and Structural Characterization of OXA-935, a Novel OXA-10-Family β -Lactamase from <i>Pseudomonas aeruginosa</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2022, 66, .	1.4	3
22353	Phylotranscriptomics reveal the spatio-temporal distribution and morphological evolution of <i>Macrozamia</i> , an Australian endemic genus of Cycadales. <i>Annals of Botany</i> , 2022, 130, 671-685.	1.4	5
22354	Systematic classification and phylogenetic relationships of the brown-rot fungi within the Polyporales. <i>Fungal Diversity</i> , 2023, 118, 1-94.	4.7	17
22355	An Evolutionary Framework of Acanthaceae Based on Transcriptomes and Genome Skims. <i>Systematic Botany</i> , 2022, 47, 716-728.	0.2	0
22356	Biogeography of <i>Zehneria</i> (Cucurbitaceae) and a New Species from India. <i>Systematic Botany</i> , 2022, 47, 738-747.	0.2	0
22357	A New Species of <i>Lithocarpus</i> (Fagaceae) from Ca Dam Mountain of Quang Ngai Province, Vietnam. <i>Systematic Botany</i> , 2022, 47, 729-737.	0.2	0
22358	Pollen DNA metabarcoding reveals cryptic diversity and high spatial turnover in alpine plant-pollinator networks. <i>Molecular Ecology</i> , 2023, 32, 6377-6393.	2.0	11
22359	Phylogenomic analysis of the hemp family (Cannabaceae) reveals deep cyto-nuclear discordance and provides new insights into generic relationships. <i>Journal of Systematics and Evolution</i> , 2023, 61, 806-826.	1.6	4

#	ARTICLE	IF	CITATIONS
22360	The complete chloroplast genome of <i>Zanthoxylum stenophyllum</i> Hemsl. (Rutaceae), a traditional Chinese medicinal plant. Mitochondrial DNA Part B: Resources, 2022, 7, 1642-1644.	0.2	1
22362	Phylogeny and systematics of the tribe Sonerileae (Melastomataceae) in Africa: A revised taxonomic classification. Journal of Systematics and Evolution, 2023, 61, 657-681.	1.6	2
22363	Bacterial composition in Swedish raw drinking water reveals three major interacting ubiquitous metacommunities. MicrobiologyOpen, 2022, 11, .	1.2	0
22364	The complete mitochondrial genome of <i>Priotyranus closteroides</i> Thomson, 1877 (Coleoptera: Tj ETQq1 1 0.784314 gBT /Over	0.2	0
22365	Dynamic genome evolution in a model fern. Nature Plants, 2022, 8, 1038-1051.	4.7	56
22367	The complete paternally inherited mitochondrial genomes of three clam species in genus <i>Macridiscus</i> (Bivalvia: Veneridae): A TDRL model of dimer-mitogenome rearrangement of doubly uniparental inheritance. Frontiers in Marine Science, 0, 9, .	1.2	1
22368	Microbial succession in a marine sediment: Inferring interspecific microbial interactions with marine cable bacteria. Environmental Microbiology, 2022, 24, 6348-6364.	1.8	11
22370	Composition Diversity and Expression Specificity of the TPS Gene Family among 24 <i>Ficus</i> Species. Diversity, 2022, 14, 721.	0.7	1
22371	Reconstitution of monoterpene indole alkaloid biosynthesis in genome engineered <i>Nicotiana benthamiana</i> . Communications Biology, 2022, 5, .	2.0	27
22372	Genetic origin of donkeys in Brazil. Tropical Animal Health and Production, 2022, 54, .	0.5	0
22375	<i>GNL3</i> is an evolutionarily conserved stem cell gene influencing cell proliferation, animal growth and regeneration in the hydrozoan <i>Hydractinia</i> . Open Biology, 2022, 12, .	1.5	5
22376	Assembly and comparative analysis of the complete mitochondrial genome of <i>Bupleurum chinense</i> DC. BMC Genomics, 2022, 23, .	1.2	17
22377	Genomic evidence refutes the hypothesis that the Bornean banteng is a distinct species. BMC Ecology and Evolution, 2022, 22, .	0.7	0
22378	Revision of Ardissonaceae (Bacillariophyta, Mediophyceae) from Micronesian populations, with descriptions of two new genera, <i>Ardissonopsis</i> and <i>Grunowago</i> , and new species in <i>Ardissona</i> , <i>Synedrosphenia</i> and <i>Climacosphenia</i> . PhytoKeys, 0, 208, 103-184.	0.4	2
22379	Using average nucleotide identity (ANI) to evaluate microsporidia species boundaries based on their genetic relatedness. Journal of Eukaryotic Microbiology, 2023, 70, .	0.8	5
22380	NDR1/HIN1-Like Protein 13 Interacts with Symbiotic Receptor Kinases and Regulates Nodulation in <i>Lotus japonicus</i> . Molecular Plant-Microbe Interactions, 2022, 35, 845-856.	1.4	2
22381	Using phylogenomics to untangle the taxonomic incongruence of yellow-flowered <i>Camellia</i> species (Theaceae) in China. Journal of Systematics and Evolution, 2023, 61, 748-763.	1.6	2
22382	Characterization and genome analysis of a psychrophilic methanotroph representing a ubiquitous <i>Methylobacter</i> spp. cluster in boreal lake ecosystems. ISME Communications, 2022, 2, .	1.7	6

#	ARTICLE	IF	CITATIONS
22384	Purifying selection enduringly acts on the sequence evolution of highly expressed proteins in <i>Escherichia coli</i> . <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	1
22385	Heterogeneous Evolution of Sex Chromosomes in the Torrent Frog Genus <i>Amolops</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 11146.	1.8	3
22387	<i>De novo</i> assembly of a wild swan goose (<i>Anser cygnoides</i>) genome. <i>Animal Genetics</i> , 2022, 53, 878-880.	0.6	2
22388	Phylogenomic characterization and pangenomic insights into the surfactin-producing bacteria <i>Bacillus subtilis</i> strain RI4914. <i>Brazilian Journal of Microbiology</i> , 2022, 53, 2051-2063.	0.8	1
22389	Comparative phylogenetic analysis of complete plastid genomes of <i>Renanthera</i> (Orchidaceae). <i>Frontiers in Genetics</i> , 0, 13, .	1.1	8
22390	Phylogenetic analysis and structural prediction reveal the potential functional diversity between green algae SWEET transporters. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	0
22391	Genomic and geographic diversification of a "great-speciator" (<i>Rhipidura rufifrons</i>). <i>Auk</i> , 0, , .	0.7	9
22392	Infectious Bronchitis Virus: A Comprehensive Multilocus Genomic Analysis to Compare DMV/1639 and QX Strains. <i>Viruses</i> , 2022, 14, 1998.	1.5	1
22393	Functional characterization of the pUceS8.3 promoter and its potential use for ectopic gene overexpression. <i>Planta</i> , 2022, 256, .	1.6	3
22394	<i>Rocella ramitimidula</i> (Roccellaceae), a new species from the tropical dry forest of Mexico. <i>Bryologist</i> , 2022, 125, .	0.1	0
22395	Memory persistence and differentiation into antibody-secreting cells accompanied by positive selection in longitudinal BCR repertoires. <i>ELife</i> , 0, 11, .	2.8	5
22396	Transmission of Carbapenem-Resistant <i>Klebsiella pneumoniae</i> in US Hospitals. <i>Clinical Infectious Diseases</i> , 2023, 76, 229-237.	2.9	7
22397	Widespread occurrence of endogenous cellulase production and glycosyl hydrolase in grapsoid crabs along the land-sea transition indicates high potential for mineralisation of mangrove production. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	1
22398	Does IR-loss promote plastome structural variation and sequence evolution?. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
22400	Taxon-specific ultraconserved element probe design for phylogenetic analyses of scale insects (Hemiptera: Sternorrhyncha: Coccoidea). <i>Frontiers in Ecology and Evolution</i> , 0, 10, .	1.1	5
22401	Genomic insights into rapid speciation within the world's largest tree genus <i>Syzygium</i> . <i>Nature Communications</i> , 2022, 13, .	5.8	13
22402	Characterization of the complete chloroplast genome sequence of <i>Isodon japonicus</i> (N.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 100	0.2	2
22403	Estimating the relative proportions of SARS-CoV-2 haplotypes from wastewater samples. <i>Cell Reports Methods</i> , 2022, , 100313.	1.4	1

#	ARTICLE	IF	CITATIONS
22404	The complete chloroplast genome sequence of <i>Durio oxleyanus</i> (Malvaceae) and its phylogenetic position. Mitochondrial DNA Part B: Resources, 2022, 7, 1709-1712.	0.2	0
22405	Cultivating epizoic diatoms provides insights into the evolution and ecology of both epibionts and hosts. Scientific Reports, 2022, 12, .	1.6	3
22406	Characterization of the complete chloroplast genome of the <i>Helleborus atrorubens</i> Waldst. & Kit. (Ranunculaceae). Mitochondrial DNA Part B: Resources, 2022, 7, 1633-1635.	0.2	0
22407	Vegetative and Trichome Morphology Distinguish the <i>Monardella ovata</i> Species Complex from the <i>Monardella odoratissima</i> Species Complex: Taxonomic Studies in <i>Monardella</i> (Lamiaceae) VII. Systematic Botany, 2022, 47, 697-715.	0.2	0
22408	Additions to the Knowledge of the Genus <i>Pezicula</i> (Dermateaceae, Helotiales, Ascomycota) in China. Biology, 2022, 11, 1386.	1.3	0
22409	Systematics of the Sri Lankan Water Snakes of the Genus <i>Fowlea</i> Theobald 1868 (Reptilia: Natricidae). Herpetologica, 2022, 78, .	0.2	2
22411	Plastomes of limestone karst gesneriad genera <i>Petrocodon</i> and <i>Primulina</i> , and the comparative plastid phylogenomics of Gesneriaceae. Scientific Reports, 2022, 12, .	1.6	4
22412	Rapid phylogenetic analysis using open reading frame content patterns acquired by Oxford nanopore sequencing. Journal of Applied Microbiology, 0, , .	1.4	0
22413	Integrated data lead to correct identification: the case of yam insect pest, <i>Digitivalva hemiglypha</i> (Lepidoptera: Glyphipterigidae: Acrolepiinae). Journal of Asia-Pacific Biodiversity, 2022, , .	0.2	0
22414	<i>Sinosenecio yangii</i> (Asteraceae), a new species from Guizhou, China. PhytoKeys, 0, 210, 1-13.	0.4	2
22415	The first two mitochondrial genomes for the genus <i>Ramaria</i> reveal mitochondrial genome evolution of <i>Ramaria</i> and phylogeny of Basidiomycota. IMA Fungus, 2022, 13, .	1.7	4
22416	Comparative Analyses of Complete Chloroplast Genomes and Karyotypes of Allotetraploid <i>Iris koreana</i> and Its Putative Diploid Parental Species (<i>Iris</i> Series <i>Chinenses</i> , Iridaceae). International Journal of Molecular Sciences, 2022, 23, 10929.	1.8	6
22417	Genome-Wide Diversity Analysis of African Swine Fever Virus Based on a Curated Dataset. Animals, 2022, 12, 2446.	1.0	8
22418	Two new forest pathogens in <i>Phaeolus</i> (Polyporales, Basidiomycota) on Chinese coniferous trees were confirmed by molecular phylogeny. Frontiers in Microbiology, 0, 13, .	1.5	9
22419	Comparative analysis of two genomes of <i>Chlamydia pecorum</i> isolates from an Alpine chamois and a water buffalo. BMC Genomics, 2022, 23, .	1.2	0
22420	Green diatom mutants reveal an intricate biosynthetic pathway of fucoxanthin. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	30
22421	Transmission of anelloviruses to HIV-1 infected children. Frontiers in Microbiology, 0, 13, .	1.5	0
22423	In silico approach to identify microsatellite candidate biomarkers to differentiate the biovar of <i>Corynebacterium pseudotuberculosis</i> genomes. Frontiers in Bioinformatics, 0, 2, .	1.0	2

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22425	Revealing the Complete Chloroplast Genome of an Andean Horticultural Crop, Sweet Cucumber (<i>Solanum muricatum</i>), and Its Comparison with Other Solanaceae Species. <i>Data</i> , 2022, 7, 123.	1.2	0
22426	Large-scale phylogenetic analysis provides insights into the diversification and evolution of sessilid peritrich ciliates (Protista: Ciliophora). <i>Journal of Eukaryotic Microbiology</i> , 2023, 70, .	0.8	2
22427	Identification of region of difference and H37Rv-related deletion in <i>Mycobacterium tuberculosis</i> complex by structural variant detection and genome assembly. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	5
22428	A revision of the <i>Inocybe grammata</i> group in North America including four new taxa. <i>Brittonia</i> , 2022, 74, 436-464.	0.8	1
22430	Coevolution of Metabolic Pathways in Blattodea and Their <i>Blattabacterium</i> Endosymbionts, and Comparisons with Other Insect-Bacteria Symbioses. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	2
22431	DNA barcodes reveal population-dependent cryptic diversity and various cases of sympatry of Korean leptonetid spiders (Araneae: Leptonetidae). <i>Scientific Reports</i> , 2022, 12, .	1.6	4
22434	<i>Vibrio tarrae</i> sp. nov., a novel member of the Cholerae clade. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	5
22435	Dinoflagellate hosts determine the community structure of marine Chytridiomycota: Demonstration of their prominent interactions. <i>Environmental Microbiology</i> , 2022, 24, 5951-5965.	1.8	5
22436	Comparative mitogenomic analyses and gene rearrangements reject the alleged polyphyly of a bivalve genus. <i>PeerJ</i> , 0, 10, e13953.	0.9	1
22437	Differential transcriptomic responses to heat stress in surface and subterranean diving beetles. <i>Scientific Reports</i> , 2022, 12, .	1.6	6
22438	Deep-branching ANME-1c archaea grow at the upper temperature limit of anaerobic oxidation of methane. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	12
22439	Rapid structural evolution of <i>Dendrobium</i> mitogenomes and mito-nuclear phylogeny discordances in <i>Dendrobium</i> (Orchidaceae). <i>Journal of Systematics and Evolution</i> , 2023, 61, 790-805.	1.6	4
22441	Taxonomic revision of the free-living marine nematode genus <i>Deontostoma</i> (Enoplida: Leptosomatidae) and inclusion of a new species from the Southern Ocean. <i>Nematology</i> , 2022, 24, 1031-1047.	0.2	0
22442	The complete plastid genome of <i>Vincetoxicum junzifengense</i> B.J. Ye and S.P. Chen (Apocynaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 1645-1647.	0.2	1
22443	Genomic analyses of rice bean landraces reveal adaptation and yield related loci to accelerate breeding. <i>Nature Communications</i> , 2022, 13, .	5.8	13
22444	Comparative analysis of the chloroplast genomes of eight <i>Piper</i> species and insights into the utilization of structural variation in phylogenetic analysis. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	2
22445	Genomic basis of insularity and ecological divergence in barn owls (<i>Tyto alba</i>) of the Canary Islands. <i>Heredity</i> , 2022, 129, 281-294.	1.2	3
22446	Omics data unveil early molecular response underlying limb regeneration in the Chinese mitten crab, <i>Eriocheir sinensis</i> . <i>Science Advances</i> , 2022, 8, .	4.7	9

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22448	First Record of <i>Alternaria pogostemonis</i> : A Novel Species Causing Leaf Spots in <i>Pogostemon cablin</i> . <i>Pathogens</i> , 2022, 11, 1105.	1.2	2
22449	A novel alkane monooxygenase (<i>alkB</i>) clade revealed by massive genomic survey and its dissemination association with IS elements. <i>PeerJ</i> , 0, 10, e14147.	0.9	4
22450	Molecular concordance of methicillin-resistant <i>Staphylococcus aureus</i> isolates from healthcare workers and patients. <i>Infection Control and Hospital Epidemiology</i> , 0, , 1-11.	1.0	0
22452	Repeated turnovers keep sex chromosomes young in willows. <i>Genome Biology</i> , 2022, 23, .	3.8	14
22453	Virological characteristics of the SARS-CoV-2 Omicron BA.2 subvariants, including BA.4 and BA.5. <i>Cell</i> , 2022, 185, 3992-4007.e16.	13.5	167
22454	Characterization of the complete chloroplast genome of <i>Zanthoxylum esquirolii</i> (Rutaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 1719-1721.	0.2	0
22455	Characterization of the complete chloroplast genome of <i>Pellionia scabra</i> (Urticaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 1732-1733.	0.2	0
22456	Key features of pneumococcal isolates recovered in Central and Northwestern Russia in 2011–2018 determined through whole-genome sequencing. <i>Microbial Genomics</i> , 2022, 8, .	1.0	3
22458	Morphology and Molecular Phylogeny of Genus <i>Oedogonium</i> (Oedogoniales, Chlorophyta) from China. <i>Plants</i> , 2022, 11, 2422.	1.6	1
22460	Assembly dynamics of East Asian subtropical evergreen broadleaved forests: New insights from the dominant Fagaceae trees. <i>Journal of Integrative Plant Biology</i> , 2022, 64, 2126-2134.	4.1	12
22461	New findings on the fungal species <i>Tricholoma matsutake</i> from Ukraine, and revision of its taxonomy and biogeography based on multilocus phylogenetic analyses. <i>Mycoscience</i> , 2022, 63, 197-214.	0.3	7
22462	Genome assembly of the Brassicaceae diploid <i>Orychophragmus violaceus</i> reveals complex whole-genome duplication and evolution of Δ hydroxy fatty acid metabolism. <i>Plant Communications</i> , 2023, 4, 100432.	3.6	7
22463	The Natural Product Domain Seeker version 2 (NaPDoS2) webtool relates ketosynthase phylogeny to biosynthetic function. <i>Journal of Biological Chemistry</i> , 2022, 298, 102480.	1.6	27
22464	Genetic differentiation pattern and evidence of an early speciation process in the genus <i>Reithrodon</i> (Rodentia: Sigmodontinae). <i>Mammalian Biology</i> , 2023, 103, 161-171.	0.8	1
22465	Pan-genome evolution and its association with divergence of metabolic functions in <i>Bifidobacterium</i> genus. <i>World Journal of Microbiology and Biotechnology</i> , 2022, 38, .	1.7	1
22466	A Unique Set of Auxiliary Metabolic Genes Found in an Isolated Cyanophage Sheds New Light on Marine Phage-Host Interactions. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	6
22467	Integrative Studies on Three Epibiotic <i>Epistylis</i> Species (Protozoa, Ciliophora, Peritrichia) in Lake Weishan Wetland, Northern China, Including the Establishment of a New Species. <i>Protist</i> , 2022, 173, 125909.	0.6	8
22468	The draft genome sequence and characterization of <i>Exserohilum rostratum</i> , a new causal agent of maize leaf spot disease in Chinese Mainland. <i>European Journal of Plant Pathology</i> , 0, , .	0.8	1

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22469	A new species of land planarian split off from <i>Luteostriata ernesti</i> (Leal-Zanchet & Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 747 1-15.	0.5	0
22471	The genomic and bulked segregant analysis of <i>Curcuma alismatifolia</i> revealed its diverse bract pigmentation. <i>ABIOTECH</i> , 2022, 3, 178-196.	1.8	10
22472	Closing the gap: a new phylogeny and classification of the chemosymbiotic bivalve family Lucinidae with molecular evidence for 73% of living genera. <i>Journal of Molluscan Studies</i> , 2022, 88, .	0.4	2
22473	New TNT routines for parallel computing with MPI. <i>Molecular Phylogenetics and Evolution</i> , 2023, 178, 107643.	1.2	4
22474	Morphological and molecular reinvestigation of acanthoecid species II. "Pseudostephanoea paucicostata (Tong et al., 1998) gen. et comb. nov. (= <i>Stephanoea diplocostata</i> var. <i>paucicostata</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 3 Stephanoea ellisfiordensis sp. nov.. <i>European Journal of Protistology</i> , 2022, 86, 125919.	0.5	3
22475	A novel lineage of the <i>Capra</i> genus discovered in the Taurus Mountains of Turkey using ancient genomics. <i>ELife</i> , 0, 11, .	2.8	1
22476	Novel genome sequence of Chinese cavefish (<i>Triplophysa rosa</i>) reveals pervasive relaxation of natural selection in cavefish genomes. <i>Molecular Ecology</i> , 2022, 31, 5831-5845.	2.0	12
22477	Lactic Acid Resistance and Population Structure of <i>Escherichia coli</i> from Meat Processing Environment. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	1
22478	Limited role of recombination in the global diversification of begomovirus DNA-B proteins. <i>Virus Research</i> , 2023, 323, 198959.	1.1	0
22481	Morphology of ctenostome bryozoans: 6. <i>Amphibiobeania epiphylla</i> . <i>Journal of Morphology</i> , 2022, 283, 1505-1516.	0.6	2
22483	Population genomics of emerging <i>Elizabethkingia anophelis</i> pathogens reveals potential outbreak and rapid global dissemination. <i>Emerging Microbes and Infections</i> , 2022, 11, 2590-2599.	3.0	5
22484	Genomic Epidemiology and Phylodynamic Analysis of Enterovirus A71 Reveal Its Transmission Dynamics in Asia. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	2
22486	Enhanced cultured diversity of the mouse gut microbiota enables custom-made synthetic communities. <i>Cell Host and Microbe</i> , 2022, 30, 1630-1645.e25.	5.1	26
22487	Multigene phylogeny of the Indo-West Pacific genus <i>Enosteoides</i> (Crustacea, Decapoda,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 98, 387-397.	0.4	1
22488	Genomic analysis reveals strong population structure in the Giant Sydney Crayfish (<i>Euastacus spinifer</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 1.2 1	1.2	1
22490	Phylogenomic and morphological evidence reveal a new species of spider lily, <i>Lycoris longifolia</i> (Amaryllidaceae) from China. <i>PhytoKeys</i> , 0, 210, 79-92.	0.4	3
22492	Museomics and the holotype of a critically endangered cricetid rodent provide key evidence of an undescribed genus. <i>Frontiers in Ecology and Evolution</i> , 0, 10, .	1.1	6
22493	The complete chloroplast genome of <i>Sonneratia griffithii</i> Kurz (Lythraceae). <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 1761-1763.	0.2	0

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22495	Molecular phylogenetic and taxonomic status of the large-eared desert shrew <i>Notiosorex evotis</i> (Eulipotyphla: Soricidae). <i>Journal of Mammalogy</i> , 0, , .	0.6	0
22496	Revealing the uncharacterised diversity of amphibian and reptile viruses. <i>ISME Communications</i> , 2022, 2, .	1.7	15
22497	Two New Tardigrade Genera from New Zealand's Southern Alp Glaciers Display Morphological Stasis and Parallel Evolution. <i>Molecular Phylogenetics and Evolution</i> , 2022, , 107634.	1.2	2
22498	Slow and steady wins the race: Diversification rate is independent from body size and lifestyle in Malagasy skinks (Squamata: Scincidae: Scincinae). <i>Molecular Phylogenetics and Evolution</i> , 2022, , 107635.	1.2	0
22499	Plastome phylogenomics and biogeography of the subfam. Polygonoideae (Polygonaceae). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
22500	Systematics of <i>Thraupis</i> (Aves, Passeriformes) reveals an extensive hybrid zone between <i>T. episcopus</i> (Blue-gray Tanager) and <i>T. sayaca</i> (Sayaca Tanager). <i>PLoS ONE</i> , 2022, 17, e0270892.	1.1	0
22502	<i>Cortinarius</i> subgenus <i>Leprocybe</i> (Agaricales) in New Zealand. <i>New Zealand Journal of Botany</i> , 0, , 1-22.	0.8	1
22504	Genomes of Two Flying Squid Species Provide Novel Insights into Adaptations of Cephalopods to Pelagic Life. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 1053-1065.	3.0	0
22505	Haplotype assignment of longitudinal viral deep sequencing data using covariation of variant frequencies. <i>Virus Evolution</i> , 2022, 8, .	2.2	4
22506	Whole genome population structure of North Atlantic kelp confirms high-latitude glacial refugia. <i>Molecular Ecology</i> , 2022, 31, 6473-6488.	2.0	5
22507	Meiotic drive is associated with sexual incompatibility in <i>Neurospora</i> . <i>Evolution; International Journal of Organic Evolution</i> , 2022, 76, 2687-2696.	1.1	0
22508	Genomic characterization of <i>Bacillus cereus</i> sensu stricto 3A ES isolated from eye shadow cosmetic products. <i>BMC Microbiology</i> , 2022, 22, .	1.3	2
22509	Oral and Rectal Colonization by Antimicrobial-Resistant Gram-Negative Bacteria and Their Association with Death among Residents of Long-Term Care Facilities: A Prospective, Multicenter, Observational, Cohort Study. <i>Gerontology</i> , 2023, 69, 261-272.	1.4	5
22511	A highly contiguous, scaffold-level nuclear genome assembly for the fever tree (<i>Cinchona pubescens</i>) Tj ETQq1 1 0.784314 rgBT /Overlo 0.0	0.0	1
22512	A European nudibranch new to the Gulf of Maine: <i>Doris pseudoargus</i> Rapp, 1827. <i>Biological Invasions</i> , 2023, 25, 339-350.	1.2	1
22513	Description of five novel thermophilic species of the genus <i>Thermus</i> : <i>Thermus hydrothermalis</i> sp. nov., <i>Thermus neutrinimicus</i> sp. nov., <i>Thermus thalophilus</i> sp. nov., <i>Thermus albus</i> sp. nov., and <i>Thermus altitudinis</i> sp. nov., isolated from hot spring sediments. <i>Systematic and Applied Microbiology</i> , 2022, 45, 126361.	1.2	2
22514	Genomic and evolutionary study from SARS-CoV-2 virus isolates from Bangladesh during the early stage of pandemic strongly correlate with European origin and not with China. <i>Genomics</i> , 2022, 114, 110497.	1.3	0
22515	Chloroplast genome structure and phylogeny of <i>Geoffroea decorticans</i> , a native tree from Atacama Desert. <i>Electronic Journal of Biotechnology</i> , 2022, 60, 19-25.	1.2	2

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22516	Genome analysis of Psilogamma increta granulovirus and its intrapopulation diversity. <i>Virus Research</i> , 2022, 322, 198946.	1.1	0
22517	Shrimps of the genus <i>Thor</i> Kingsley, 1878 (Caridea, Thoridae): description of a new species using integrative data, remarks on <i>Thor manningi</i> Chace, 1972, and a world identification key. <i>Nauplius</i> , 0, 30, .	0.3	1
22518	The first report of a parasitic â€˜turbellarianâ€™™ from a cephalopod mollusc, with description of <i>Octopoxenus antarcticus</i> gen. nov., sp. nov. (Platyhelminthes: Fecampiida: Notenteridae). <i>Journal of Helminthology</i> , 2022, 96, .	0.4	0
22519	A phylogenetic investigation of the taxonomically problematic <i>Eucalyptus odorata</i> complex (E. section) Tj ETQq1 1 0.784314 rgBT /Over evolution. <i>Australian Systematic Botany</i> , 2022, 35, 403.	0.3	3
22520	Phylogeny, taxonomy, and character evolution in <i>Entoloma</i> subgenus <i>Nolanea</i> . <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2022, , .	1.6	1
22521	Multigene phylogeny of reef lobsters of the family <i>Enoplometopidae</i> (Decapoda: Crustacea). <i>Invertebrate Systematics</i> , 2022, 36, 973.	0.5	0
22522	Brazilian Atlantic Forest and Pampa Biomes in the spotlight: an overview of <i>Aspergillus</i> , <i>Penicillium</i> , and <i>Talaromyces</i> (Eurotiales) species and the description of <i>Penicillium nordestinense</i> sp. nov.. <i>Acta Botanica Brasilica</i> , 0, 36, .	0.8	3
22524	Two New Species of <i>Backusella</i> (Mucorales, Mucoromycota) from Soil in an Upland Forest in Northeastern Brazil with an Identification Key of <i>Backusella</i> from the Americas. <i>Journal of Fungi</i> (Basel, Switzerland), 2022, 8, 1038.	1.5	2
22525	ï»¿ <i>Sinosenecio yangii</i> (Asteraceae), a new species from Guizhou, China. <i>PhytoKeys</i> , 0, 210, 1-13.	0.4	1
22526	One clone to rule them all: Culture-independent genomics of <i>Chlamydia psittaci</i> from equine and avian hosts in Australia. <i>Microbial Genomics</i> , 2022, 8, .	1.0	5
22527	A novel species of lactic acid bacteria, <i>Ligilactobacillus pabuli</i> sp. nov., isolated from alfalfa silage. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	3
22528	Fidelity varies in the symbiosis between a gutless marine worm and its microbial consortium. <i>Microbiome</i> , 2022, 10, .	4.9	6
22529	Phylogenetic relationships, hybridization events, and drivers of diversification of East Asian wild grapes as revealed by phylogenomic analyses. <i>Journal of Systematics and Evolution</i> , 2023, 61, 273-283.	1.6	6
22531	Breeding system and geospatial variation shape the population genetics of <i>Triodanis perfoliata</i> . <i>Ecology and Evolution</i> , 2022, 12, .	0.8	1
22532	Syndinean dinoflagellates of the genus <i>Euduboscquella</i> are paraphyletic. <i>Journal of Eukaryotic Microbiology</i> , 2023, 70, .	0.8	2
22533	Relationship between genome-wide and MHC class I and II genetic diversity and complementarity in a nonhuman primate. <i>Ecology and Evolution</i> , 2022, 12, .	0.8	1
22534	Evolution and codon usage bias of mitochondrial and nuclear genomes in <i>Aspergillus</i> section <i>Flavi</i> . <i>G3: Genes, Genomes, Genetics</i> , 2023, 13, .	0.8	5
22535	Two New Species and Two New Records of the Lichen-Forming Fungal Genus <i>Peltula</i> (Ascomycota:) Tj ETQq1 1 0.784314 rgBT /Overl	1.3	0

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22536	The silkworm gustatory receptor BmGr63 is dedicated to the detection of isoquercetin in mulberry. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2022, 289, .	1.2	1
22538	Genomic Signatures of Mitonuclear Coevolution in Mammals. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	8
22539	Cross-species transmission of an ancient endogenous retrovirus and convergent co-option of its envelope gene in two mammalian orders. <i>PLoS Genetics</i> , 2022, 18, e1010458.	1.5	4
22540	Biochemical and Molecular Profiling of Wild Edible Mushrooms from Huila, Angola. <i>Foods</i> , 2022, 11, 3240.	1.9	7
22541	Bloom of <i>Prorocentrum cordatum</i> in Paracas Bay, Peru. <i>Diversity</i> , 2022, 14, 844.	0.7	3
22542	Detecting signals of adaptive evolution in grape plastomes with a focus on the Cretaceous–Palaeogene (K/Pg) transition. <i>Annals of Botany</i> , 2022, 130, 965-980.	1.4	1
22543	Additions to the List of Teloschistaceae (Teloschistales, Ascomycota) in Pakistan. <i>Biology Bulletin</i> , 0, , .	0.1	0
22545	Complex origins indicate a potential bridgehead introduction of an emerging amphibian invader (<i>Eleutherodactylus planirostris</i>) in China. <i>NeoBiota</i> , 0, 77, 23-37.	1.0	1
22546	Traits of soil bacteria predict plant responses to soil moisture. <i>Ecology</i> , 0, , .	1.5	2
22547	The chromosome-level genome of female ginseng (<i>Angelica sinensis</i>) provides insights into molecular mechanisms and evolution of coumarin biosynthesis. <i>Plant Journal</i> , 2022, 112, 1224-1237.	2.8	19
22548	Morphology, morphogenesis and phylogeny of a new soil ciliate, <i>Bistichella sinensis</i> n. sp., and morphology of two oxytrichids (Ciliophora, Hypotrichia). <i>European Journal of Protistology</i> , 2022, 86, 125934.	0.5	2
22549	Remarkably low host specificity in the bat fly <i>Penicillidia fulvida</i> (Diptera: Nycteribiidae) as assessed by mitochondrial COI and nuclear 28S sequence data. <i>Parasites and Vectors</i> , 2022, 15, .	1.0	2
22550	Population analysis of heavy metal and biocide resistance genes in <i>Salmonella enterica</i> from human clinical cases in New Hampshire, United States. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	5
22551	Conservation priorities for global marine biodiversity across multiple dimensions. <i>National Science Review</i> , 2023, 10, .	4.6	9
22552	Characterization of the complete chloroplast genome of <i>Carallia diplopetala</i> (Rhizophoraceae). <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 1870-1872.	0.2	0
22553	The complete chloroplast genome sequence of <i>Zygophyllum kansuense</i> Y. X. Liou (Zygophyllaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 1864-1866.	0.2	1
22554	<i>Lithocarpus encleisocarpus</i> (Korth.) A. Camus - A newly recorded from Vietnam and its phylogenetic relationship based on genome-wide SNPs. <i>Can Tho University Journal of Science</i> , 2022, 14, 17-24.	0.1	0
22555	High-resolution phylogenetic and population genetic analysis of microbial communities with RoC-ITS. <i>ISME Communications</i> , 2022, 2, .	1.7	0

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22556	The pangenome of the wheat pathogen <i>Pyrenophora tritici-repentis</i> reveals novel transposons associated with necrotrophic effectors ToxA and ToxB. <i>BMC Biology</i> , 2022, 20, .	1.7	15
22558	The evolution and polymorphism of mono-amino acid repeats in androgen receptor and their regulatory role in health and disease. <i>Frontiers in Medicine</i> , 0, 9, .	1.2	2
22559	Comparative mitogenomes provide new insights into phylogeny and taxonomy of the subfamily Xenocyprinae (Cypriniformes: Cyprinidae). <i>Frontiers in Genetics</i> , 0, 13, .	1.1	0
22560	Molecular, morphometric, and spatial data analyses provide new insights into the evolutionary history of the <i>Peromyscus boylii</i> species complex (Rodentia: Cricetidae) in the mountains of Mexico. <i>Systematics and Biodiversity</i> , 2022, 20, 1-19.	0.5	0
22561	Genomic and Phylogenetic Characterization of <i>Rhodopseudomonas infernalis</i> sp. nov., Isolated from the Hell Creek Watershed (Nebraska). <i>Microorganisms</i> , 2022, 10, 2024.	1.6	0
22562	Phylogenomic Analysis of the Plastid Genome of the Peruvian Purple Maize <i>Zea mays</i> subsp. <i>mays</i> cv. 'INIA 601'. <i>Plants</i> , 2022, 11, 2727.	1.6	2
22563	Molecular phylogeny and taxonomy of the genus <i>Nectogale</i> (Mammalia: Eulipotyphla: Tj ETQq0 0 0 rgBT / Overlock 10 Tf 50 502	0.8	1
22565	<i>Akhania</i> , a new genus for <i>Salsola daghestanica</i> , <i>Caroxylon canescens</i> and <i>C. carpathum</i> (Salsoloideae). Tj ETQq1 1 0.784314 rgBT / Ov	0.4	0
22566	Population genomics of an icefish reveals mechanisms of glacier-driven adaptive radiation in Antarctic notothenioids. <i>BMC Biology</i> , 2022, 20, .	1.7	5
22567	UFCG: database of universal fungal core genes and pipeline for genome-wide phylogenetic analysis of fungi. <i>Nucleic Acids Research</i> , 2023, 51, D777-D784.	6.5	7
22568	Chromatin remodeling is required for sRNA-guided DNA elimination in <i>Paramecium</i> . <i>EMBO Journal</i> , 2022, 41, .	3.5	8
22569	<i>Niabella agricola</i> sp. nov., isolated from paddy soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	0
22570	The resistomes of <i>Mycobacteroides abscessus</i> complex and their possible acquisition from horizontal gene transfer. <i>BMC Genomics</i> , 2022, 23, .	1.2	3
22572	Increasing taxon sampling suggests a complete taxonomic rearrangement in Echinantherini (Serpentes: Dipsadidae). <i>Frontiers in Ecology and Evolution</i> , 0, 10, .	1.1	1
22573	Species Diversity of <i>Gelidium</i> from Southern Madagascar Evaluated by an Integrative Taxonomic Approach. <i>Diversity</i> , 2022, 14, 826.	0.7	5
22574	<i>Pseudognaphalium</i> (Asteraceae, Gnaphalieae) diversity in New Zealand revealed by DNA sequences with notes on the phylogenetic relationships of Hawaiian Islands plants referred to <i>Pseudognaphalium sandwicense</i> . <i>New Zealand Journal of Botany</i> , 2023, 61, 304-331.	0.8	2
22575	A new arboreal Pseudoeurycea (Caudata: Plethodontidae) from the Sierra de Zongolica, Veracruz, Mexico. <i>Vertebrate Zoology</i> , 0, 72, 937-950.	2.0	0
22576	Ticket to ride: fungi from bat ectoparasites in a tropical cave and the description of two new species. <i>Brazilian Journal of Microbiology</i> , 2022, 53, 2077-2091.	0.8	7

#	ARTICLE	IF	CITATIONS
22577	Favolus rugulosus en Colombia: producción de micelio y basidiomas en diferentes condiciones nutricionales. Lilloa, 0, , 427-444.	0.1	0
22578	Ancient homomorphy of molluscan sex chromosomes sustained by reversible sex-biased genes and sex determiner translocation. Nature Ecology and Evolution, 2022, 6, 1891-1906.	3.4	23
22580	Characterization and Whole Genome Sequencing of Chromobacterium violaceum Ouat_2017: A Zoonotic Pathogen Found Fatal to a Wild Asiatic Elephant. Indian Journal of Microbiology, 0, , .	1.5	1
22581	The emergence of a cryptic lineage and cytonuclear discordance through past hybridization in the Japanese fire-bellied newt, <i>Cynops pyrrhogaster</i> (Amphibia: Urodela). Biological Journal of the Linnean Society, 0, , .	0.7	0
22582	Phylogenetic analyses of Phaseolinae (Leguminosae) reveal a new genus endemic to limestone outcrops in Seasonally Dry Forests of Bahia, Brazil. Taxon, 0, , .	0.4	1
22585	Morphology, morphogenesis and molecular phylogeny of Lamtostyla granulifera sinensis subsp. nov. (Ciliophora, Hypotrichia) from a wetland in China. European Journal of Protistology, 2023, 87, 125938.	0.5	2
22586	<i>Kyonemichthys rumengani</i> (Teleostei: Syngnathidae) is Sister Taxon to the Pipefish Genus <i>Urocampus</i> : Genetic and Morphological Evidence. Species Diversity, 2022, 27, 293-299.	0.1	0
22587	Phylogenomics reveals the evolution, biogeography, and diversification history of voles in the Hengduan Mountains. Communications Biology, 2022, 5, .	2.0	3
22588	Chromosomal inversion polymorphisms shape the genomic landscape of deer mice. Nature Ecology and Evolution, 2022, 6, 1965-1979.	3.4	22
22589	A new study of Nagraomyces: with two new species proposed and taxonomic status inferred by phylogenetic methods. MycoKeys, 0, 93, 131-148.	0.8	0
22590	Characterization of the Asian Citrus Psyllid-â€˜Candidatus Liberibacter Asiaticusâ€™ Pathosystem in Saudi Arabia Reveals Two Predominant CLas Lineages and One Asian Citrus Psyllid Vector Haplotype. Microorganisms, 2022, 10, 1991.	1.6	0
22591	Modular, multi-â€˜barcode amplicon sequencing for improved species-level detection of fungal phytopathogens: A case study of pipeline establishment targeting the <i>Ophiostomatales</i> . Environmental DNA, 2024, 6, .	3.1	5
22593	West Side Story: A molecular and morphological study of Caridina longicarpus Roux, 1926 (Decapoda.) Tj ETQq0 0,0 rgBT /Oyerlock 10 0,2		0
22594	The genome of single-petal jasmine (Jasminum sambac) provides insights into heat stress tolerance and aroma compound biosynthesis. Frontiers in Plant Science, 0, 13, .	1.7	2
22597	Subspecies at crossroads: the evolutionary significance of genomic and phenotypic variation in a wide-ranging Australian lizard (<i>Ctenotus pantherinus</i>). Zoological Journal of the Linnean Society, 2023, 197, 768-786.	1.0	3
22598	Coevolution of tandemly repeated <i>hlips</i> and RpaB-like transcriptional factor confers desiccation tolerance to subaerial <i>Nostoc</i> species. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	3
22599	Discovery of a New Species Provides a Deeper Insight into Taxonomic Grouping of the Deep-Sea Genus Acanthephyra (Crustacea: Decapoda). Diversity, 2022, 14, 907.	0.7	4
22600	A deep learning approach to real-time HIV outbreak detection using genetic data. PLoS Computational Biology, 2022, 18, e1010598.	1.5	3

#	ARTICLE	IF	CITATIONS
22602	Ethanol-lactate transition of Lachancea thermotolerans is linked to nitrogen metabolism. Food Microbiology, 2023, 110, 104167.	2.1	8
22604	Demographic history and conservation genomics of caribou (<i>Rangifer tarandus</i>) in Québec. Evolutionary Applications, 2022, 15, 2043-2053.	1.5	4
22605	H1N1 G4 swine influenza T cell epitope analysis in swine and human vaccines and circulating strains uncovers potential risk to swine and humans. Influenza and Other Respiratory Viruses, 2023, 17, .	1.5	0
22607	DNA Barcoding and Species Classification of Morchella. Genes, 2022, 13, 1806.	1.0	4
22611	Complete chloroplast genome sequences of Phlomis fruticosa and Phlomoides strigosa and comparative analysis of the genus Phlomis sensu lato (Lamiaceae). Frontiers in Plant Science, 0, 13, .	1.7	1
22612	The complete chloroplast genome of <i>Salix matsudana</i> f. <i>tortuosa</i> . Mitochondrial DNA Part B: Resources, 2022, 7, 1794-1796.	0.2	0
22613	Complete chloroplast genome of <i>Leptopus chinensis</i> (Bunge) Pojark (Euphorbiaceae), a traditional Chinese herbal medicine. Mitochondrial DNA Part B: Resources, 2022, 7, 1817-1819.	0.2	0
22614	Contrasting sea ice conditions shape microbial food webs in Hudson Bay (Canadian Arctic). ISME Communications, 2022, 2, .	1.7	4
22615	<i>Brucella ceti</i> and <i>Brucella pinnipedialis</i> genome characterization unveils genetic features that highlight their zoonotic potential. MicrobiologyOpen, 2022, 11, .	1.2	2
22616	Evasion of cGAS and TRIM5 defines pandemic HIV. Nature Microbiology, 2022, 7, 1762-1776.	5.9	18
22617	The effect of the Messinian salinity crisis on the early diversification of the <i>Tettigettna</i> cicadas. Zoologica Scripta, 2023, 52, 100-116.	0.7	2
22618	<i>Dongia deserti</i> sp. nov., Isolated from the Gurbantunggut Desert Soil. Current Microbiology, 2022, 79, .	1.0	3
22619	OrthoSNAP: A tree splitting and pruning algorithm for retrieving single-copy orthologs from gene family trees. PLoS Biology, 2022, 20, e3001827.	2.6	10
22620	The complete mitochondrial genome of the woodwasp <i>Euxiphidria potanini</i> (Hymenoptera, Tj ETQq1 1 0.784314 ggBT /Overlock 10	1.6	1
22621	Genomic insights into the physiology of <i>Quinella</i> , an iconic uncultured rumen bacterium. Nature Communications, 2022, 13, .	5.8	10
22622	<i>Fontivita pretiosa</i> gen. nov., sp. nov., a thermophilic planctomycete of the order Tepidisphaerales from a hot spring of Baikal lake region. Systematic and Applied Microbiology, 2022, , 126375.	1.2	3
22624	A high-quality genome assembly of the Laotian shad (<i>Tenualosa thibaudeaui</i>), an endemic species of the Mekong River Basin. Journal of Heredity, 0, , .	1.0	0
22625	Genomic and Epidemiological Features of Two Dominant Methicillin-Susceptible <i>Staphylococcus aureus</i> Clones from a Neonatal Intensive Care Unit Surveillance Effort. MSphere, 2022, 7, .	1.3	1

#	ARTICLE	IF	CITATIONS
22626	Leaf Mycobiome and Mycotoxin Profile of Warm-Season Grasses Structured by Plant Species, Geography, and Apparent Black-Stroma Fungal Structure. <i>Applied and Environmental Microbiology</i> , 2022, 88, .	1.4	1
22627	What are the <i>Laetiporus</i> species present in southern South America?. <i>Lilloa</i> , 0, , 193-218.	0.1	0
22628	Metabolic genes on conjugative plasmids are highly prevalent in <i>Escherichia coli</i> and can protect against antibiotic treatment. <i>ISME Journal</i> , 2023, 17, 151-162.	4.4	16
22629	Circadian regulation of the transcriptome in a complex polyploid crop. <i>PLoS Biology</i> , 2022, 20, e3001802.	2.6	11
22630	Origin of scarlet gynogenetic triploid <i>Carassius</i> fish: Implications for conservation of the sexual-gynogenetic complex. <i>PLoS ONE</i> , 2022, 17, e0276390.	1.1	0
22631	Draft genome of the bluefin tuna blood fluke, <i>Cardicola forsteri</i> . <i>PLoS ONE</i> , 2022, 17, e0276287.	1.1	0
22633	Natural selection drives the evolution of mitogenomes in <i>Acrossocheilus</i> . <i>PLoS ONE</i> , 2022, 17, e0276056.	1.1	6
22635	Species diversity of <i>Ganoderma</i> (Ganodermataceae, Polyporales) with three new species and a key to <i>Ganoderma</i> in Yunnan Province, China. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	7
22637	Integrated Omic Approaches Reveal Molecular Mechanisms of Tolerance during Soybean and <i>Meloidogyne incognita</i> Interactions. <i>Plants</i> , 2022, 11, 2744.	1.6	4
22639	Biogeography and Systematics of the Genus <i>Axyris</i> (Amaranthaceae s.l.). <i>Plants</i> , 2022, 11, 2873.	1.6	2
22640	Integrated phylogenomic analyses unveil reticulate evolution in <i>Parthenocissus</i> (Vitaceae), highlighting speciation dynamics in the Himalayan-Hengduan Mountains. <i>New Phytologist</i> , 2023, 238, 888-903.	3.5	4
22641	Tumour microbiomes and <i>Fusobacterium</i> genomics in Vietnamese colorectal cancer patients. <i>Npj Biofilms and Microbiomes</i> , 2022, 8, .	2.9	9
22642	First Genome-Based Characterisation and Staphylococcal Enterotoxin Production Ability of Methicillin-Susceptible and Methicillin-Resistant <i>Staphylococcus aureus</i> Strains Isolated from Ready-to-Eat Foods in Algiers (Algeria). <i>Toxins</i> , 2022, 14, 731.	1.5	2
22643	Cutting the ribbon: bathyal Nemertea from seeps along the Costa Rica margin, with descriptions of 2 new genera and 9 new species. <i>European Journal of Taxonomy</i> , 0, 845, .	0.6	1
22644	Whole-Genome Sequencing-Based Characterization of <i>Listeria</i> Isolates from Produce Packinghouses and Fresh-Cut Facilities Suggests Both Persistence and Reintroduction of Fully Virulent <i>L. monocytogenes</i> . <i>Applied and Environmental Microbiology</i> , 2022, 88, .	1.4	11
22645	Diversity of the Bamusicolous Fungus <i>Apiospora</i> in Korea: Discovery of New <i>Apiospora</i> Species. <i>Mycobiology</i> , 2022, 50, 302-316.	0.6	1
22646	Variation among the Complete Chloroplast Genomes of the Sumac Species <i>Rhus chinensis</i> : Reannotation and Comparative Analysis. <i>Genes</i> , 2022, 13, 1936.	1.0	2
22647	Two new stipitate species of <i>Phylloporia</i> (Basidiomycota, Hymenochaetaceae) from Chamela Biology Station, U.N.A.M. in Jalisco, Mexico. <i>Lilloa</i> , 0, , 359-375.	0.1	1

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22648	The Genetic Diversity and the Divergence Time in Extant Primitive Mayfly, <i>Siphuriscus chinensis</i> Ulmer, 1920 Using the Mitochondrial Genome. <i>Genes</i> , 2022, 13, 1780.	1.0	2
22649	Engineering indel and substitution variants of diverse and ancient enzymes using Graphical Representation of Ancestral Sequence Predictions (GRASP). <i>PLoS Computational Biology</i> , 2022, 18, e1010633.	1.5	16
22650	Quantifying the uncertainty of assembly-free genome-wide distance estimates and phylogenetic relationships using subsampling. <i>Cell Systems</i> , 2022, 13, 817-829.e3.	2.9	3
22651	The mitochondrial genomes of <i>Crispatotrochus rubescens</i> and <i>Crispatotrochus rugosus</i> (Hexacorallia; Scleractinia): new insights on the phylogeny of the family Caryophylliidae. <i>Molecular Biology Reports</i> , 0, , .	1.0	1
22652	Spatially explicit phylogeographical reconstruction sheds light on the history of the forest cover in the Congo Basin. <i>Journal of Biogeography</i> , 0, , .	1.4	1
22653	<scp>DNA</scp> barcoding of <i>Cymbidium</i> by genome skimming: Call for nextâ€ generation nuclear barcodes. <i>Molecular Ecology Resources</i> , 2023, 23, 424-439.	2.2	13
22654	A Comparative Genomics Approach for Analysis of Complete Mitogenomes of Five Actinidiaceae Plants. <i>Genes</i> , 2022, 13, 1827.	1.0	3
22655	Phylogenomics and classification of <i>Notropis</i> and related shiners (Cypriniformes: Leuciscidae) and the utility of exon capture on lower taxonomic groups. <i>PeerJ</i> , 0, 10, e14072.	0.9	2
22656	SOPHIE: Viral outbreak investigation and transmission history reconstruction in a joint phylogenetic and network theory framework. <i>Cell Systems</i> , 2022, 13, 844-856.e4.	2.9	2
22659	Thermal Endurance by a Hot-Spring-Dwelling Phylogenetic Relative of the Mesophilic <i>Paracoccus</i>. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	2
22662	<i>Acinetobacter amyesii</i> sp. nov., widespread in the soil and water environment and animals. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	3
22663	Phenol and Polyaromatic Hydrocarbons Are Stronger Drivers Than Host Plant Species in Shaping the Arbuscular Mycorrhizal Fungal Component of the Mycorrhizosphere. <i>International Journal of Molecular Sciences</i> , 2022, 23, 12585.	1.8	2
22664	Endemic erythromycin resistant <i>Corynebacterium diphtheriae</i> in Vietnam in the 1990s. <i>Microbial Genomics</i> , 2022, 8, .	1.0	1
22665	Molecular phylogeny of human adenovirus type 41 lineages. <i>Virus Evolution</i> , 2022, 8, .	2.2	9
22666	Comparative analysis of the complete chloroplast genomes of six threatened subgenus <i>Gynopodium</i> (<i>Magnolia</i>) species. <i>BMC Genomics</i> , 2022, 23, .	1.2	1
22668	Reclassification of <i>Clostridium aurantibutyricum</i> Hellinger 1944 and <i>Clostridium roseum</i> (ex McCoy) Tj ETQq1 1 0.784314 rgBT /Overbo. <i>Microbiology</i> , 2022, 72, .	0.8	1
22669	Identification of PKS Gene Clusters from Metagenomic Libraries Using a Next-Generation Sequencing Approach. <i>Methods in Molecular Biology</i> , 2023, , 73-90.	0.4	0
22670	Phylogeography and genetic variation in Western Jacob's ladder (<i>Polemonium occidentale</i>) provide insights into the origin and conservation of rare species in the Great Lakes region. <i>Molecular Ecology</i> , 2023, 32, 79-94.	2.0	0

#	ARTICLE	IF	CITATIONS
22671	A chromosome-level genome of <i>Semiothisa cinerearia</i> provides insights into its genome evolution and control. <i>BMC Genomics</i> , 2022, 23, .	1.2	1
22672	Diversification linked to larval host plant in the butterfly <i>Eumedonia eumedon</i> . <i>Molecular Ecology</i> , 2023, 32, 182-197.	2.0	4
22673	A highly polymorphic effector protein promotes fungal virulence through suppression of plant-associated Actinobacteria. <i>New Phytologist</i> , 2023, 237, 944-958.	3.5	10
22674	Complex statistical modelling for phylogenetic inference. <i>Canadian Journal of Statistics</i> , 2022, 50, 1339-1354.	0.6	0
22675	Long-term ecological monitoring of reefs on Hawai'i Island (2003-2020): Characterization of a common cryptic crust, <i>Ramicrusta hawaiiensis</i> (Peyssonneliales, Rhodophyta). <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	2
22676	The complete chloroplast genome sequences of three <i>Broussonetia</i> species and comparative analysis within the Moraceae. <i>PeerJ</i> , 0, 10, e14293.	0.9	5
22677	Exploring morphological evolution in relation to habitat moisture in the moss genus <i>Fissidens</i> using molecular data generated from herbarium specimens. <i>Journal of Systematics and Evolution</i> , 2023, 61, 868-889.	1.6	2
22678	Serological and Molecular Evidence of the Circulation of the Venezuelan Equine Encephalitis Virus Subtype IIIA in Humans, Wild Vertebrates and Mosquitos in the Brazilian Amazon. <i>Viruses</i> , 2022, 14, 2391.	1.5	1
22679	Evidence that a lineage of teleost-infecting blood flukes (Aporocotylidae) infects bivalves as intermediate hosts. <i>International Journal for Parasitology</i> , 2023, 53, 13-25.	1.3	3
22680	Evolution of increased complexity and specificity at the dawn of form I Rubiscos. <i>Science</i> , 2022, 378, 155-160.	6.0	32
22682	Next Generation Sequencing and Comparative Genomic Analysis Reveal Extreme Plasticity of Two <i>Burkholderia glumae</i> Strains HN1 and HN2. <i>Pathogens</i> , 2022, 11, 1265.	1.2	0
22683	Complete chloroplast genomes of <i>Sorbus sensu stricto</i> (Rosaceae): comparative analyses and phylogenetic relationships. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	11
22684	Spatial-temporal and phylogenetic analyses of epidemiologic data to help understand the modes of transmission of endemic typhoid fever in Samoa. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010348.	1.3	2
22685	Additions to The Knowledge of Tubakia (Tubakiaceae, Diaporthales) in China. <i>Journal of Fungi (Basel)</i> , Tj ETQq1 1 0.784314 rgBT /Over	1.5	2
22686	Molecular mechanisms leading to ceftolozane/tazobactam resistance in clinical isolates of <i>Pseudomonas aeruginosa</i> from five Latin American countries. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
22687	A High-Quality Genome Assembly of the Mitochondrial Genome of the Oil-Tea Tree <i>Camellia gigantocarpa</i> (Theaceae). <i>Diversity</i> , 2022, 14, 850.	0.7	6
22688	H6N8 avian influenza virus in Antarctic seabirds demonstrates connectivity between South America and Antarctica. <i>Transboundary and Emerging Diseases</i> , 0, , .	1.3	2
22689	Insights into the phylogeny of the ciliate of class Colpodea based on multigene data. <i>Ecology and Evolution</i> , 2022, 12, .	0.8	3

#	ARTICLE	IF	CITATIONS
22690	Taming the selection of optimal substitution models in Phylogenomics by site subsampling and upsampling. <i>Molecular Biology and Evolution</i> , 0, , .	3.5	0
22691	Comparative Genomic Analysis of 31 <i>Phytophthora</i> Genomes Reveals Genome Plasticity and Horizontal Gene Transfer. <i>Molecular Plant-Microbe Interactions</i> , 2023, 36, 26-46.	1.4	6
22692	Draft Genome Sequence of <i>Candidatus</i> <i>Nardonella dryophthoridicola</i> Strain NARMHE1, Endosymbiont of <i>Metamasius hemipterus</i> (Coleoptera, Curculionidae, Dryophthorinae). <i>Microbiology Resource Announcements</i> , 2022, 11, .	0.3	1
22693	The wild allotetraploid sesame genome provides novel insights into evolution and lignan biosynthesis. <i>Journal of Advanced Research</i> , 2023, 50, 13-24.	4.4	8
22695	<i>Morchella nipponensis</i> , sp. nov. (Ascomycota, Pezizales): a paleoendemic species of section <i>Morchella</i> discovered in Japan. <i>Mycoscience</i> , 2022, , .	0.3	0
22696	Diversity of Haemogregarine Parasites Infecting Brazilian Anurans, with a Description of New Species of <i>Dactylosoma</i> (Apicomplexa: Adeleorina: Dactylosomatidae). <i>Acta Parasitologica</i> , 2022, 67, 1740-1755.	0.4	2
22697	<i>Hydrangea marunoi</i> (Hydrangeaceae), a new species from Osumi Peninsula, southern Japan. <i>PhytoKeys</i> , 0, 211, 33-44.	0.4	0
22699	Comparative Genomic Analysis of <i>Fusobacterium necrophorum</i> Provides Insights into Conserved Virulence Genes. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	6
22700	The complete chloroplast genome sequence of <i>Intsia bijuga</i> (Colebr.) Kuntze (Fabaceae: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 42	0.2	1
22701	Virological characteristics of the SARS-CoV-2 Omicron BA.2.75 variant. <i>Cell Host and Microbe</i> , 2022, 30, 1540-1555.e15.	5.1	96
22702	Phylogenetic Inference of the 2022 Highly Pathogenic H7N3 Avian Influenza Outbreak in Northern Mexico. <i>Pathogens</i> , 2022, 11, 1284.	1.2	4
22703	Species delimitation and phylogenetic relationships of <i>Silene villosa</i> s.l. (Caryophyllaceae, sect. <i>Silene</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 42	0.3	6
22704	Evolution of the CBL and CIPK gene families in <i>Medicago</i> : genome-wide characterization, pervasive duplication, and expression pattern under salt and drought stress. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	3
22705	<i>Pseudomonas californiensis</i> sp. nov. and <i>Pseudomonas quasicaspiana</i> sp. nov., isolated from ornamental crops in California. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	0
22708	Genetic, biological and epidemiological study on a cluster of H9N2 avian influenza virus infections among chickens, a pet cat, and humans at a backyard farm in Guangxi, China. <i>Emerging Microbes and Infections</i> , 2023, 12, .	3.0	6
22709	A new oerstediid discovered from wood falls in the Sea of Kumano, Japan: Description of <i>Rhombonemertes rublinea</i> gen. et sp. nov. (Nemertea: Eumonostilifera). <i>Zoologischer Anzeiger</i> , 2022, 301, 154-162.	0.4	0
22710	Complete chloroplast genome sequence of a bulbous flowering plant, <i>Allium triquetrum</i> Linnaeus, 1753 (Amaryllidaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 1907-1909.	0.2	0
22711	Next-Generation Sequencing of Four Mitochondrial Genomes of <i>Dolichovespula</i> (Hymenoptera: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 42	1.0	3

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22712	In silico genomic analysis of the potential probiotic <i>Lactiplantibacillus pentosus</i> CF2-10N reveals promising beneficial effects with health promoting properties. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	6
22714	Comparative Genomics of <i>Streptococcus oralis</i> Identifies Large Scale Homologous Recombination and a Genetic Variant Associated with Infection. <i>MSphere</i> , 2022, 7, .	1.3	3
22715	Genetic associations with resistance to <i>Meloidogyne enterolobii</i> in guava (<i>Psidium</i> sp.) using cross-genera SNPs and comparative genomics to <i>Eucalyptus</i> highlight evolutionary conservation across the Myrtaceae. <i>PLoS ONE</i> , 2022, 17, e0273959.	1.1	0
22716	Plastid phylogenomics and morphological character evolution of Chloridoideae (Poaceae). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
22717	Phylogeography and evolutionary lineage diversity in the small-eared greater galago, <i>Otolemur garnettii</i> (Primates: Galagidae). <i>Zoological Journal of the Linnean Society</i> , 0, , .	1.0	1
22718	A new species of <i>Sturisoma</i> Swainson, 1838 (Loricariidae: Loricariinae), from the Madeira River basin, with a discussion of historical biogeography of western Amazonas and Paraguay River basins. <i>Journal of Fish Biology</i> , 2023, 102, 188-203.	0.7	2
22719	Blue Turns to Gray: Paleogenomic Insights into the Evolutionary History and Extinction of the Blue Antelope (<i>Hippotragus leucophaeus</i>). <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	5
22720	Impact of host age on viral and bacterial communities in a waterbird population. <i>ISME Journal</i> , 2023, 17, 215-226.	4.4	6
22721	<i>Paraphlomis hsiwenii</i> (Lamiaceae), a new species from the limestone area of Guangxi, China. <i>PhytoKeys</i> , 0, 212, 85-96.	0.4	2
22723	Whole genome resequencing and comparative genome analysis of three <i>Puccinia striiformis</i> sp. <i>tritici</i> pathotypes prevalent in India. <i>PLoS ONE</i> , 2022, 17, e0261697.	1.1	1
22724	Structure and formation of the perforated theca defining the Pelagophyceae (Heterokonta), and three new genera that substantiate the diverse nature of the class. <i>Journal of Phycology</i> , 0, , .	1.0	0
22725	Influences of carbon sources on N ₂ O production during denitrification in freshwaters: Activity, isotopes and functional microbes. <i>Water Research</i> , 2022, 226, 119315.	5.3	14
22726	Mountain- and brown hare genetic polymorphisms to survey local adaptations and conservation status of the heath hare (<i>Lepus timidus sylvaticus</i> , Nilsson 1831). <i>Scientific Data</i> , 2022, 9, .	2.4	2
22727	Dynamic evolution of transient receptor potential vanilloid (TRPV) ion channel family with numerous gene duplications and losses. <i>Frontiers in Endocrinology</i> , 0, 13, .	1.5	2
22728	Selective sweeps on different pigmentation genes mediate convergent evolution of island melanism in two incipient bird species. <i>PLoS Genetics</i> , 2022, 18, e1010474.	1.5	9
22729	Evaluation of hydrogen fermentation by a newly isolated alkaline tolerant <i>Clostridium felsineum</i> strain CUEA03. <i>International Journal of Hydrogen Energy</i> , 2023, 48, 2130-2144.	3.8	1
22730	Genomic and Phenotypic Comparisons Reveal Distinct Variants of <i>Wolbachia</i> Strain <i>w</i> AlbB. <i>Applied and Environmental Microbiology</i> , 2022, 88, .	1.4	2
22731	Seventy-eight entire mitochondrial genomes and nuclear rRNA genes provide insight into the phylogeny of the hard ticks, particularly the <i>Haemaphysalis</i> species, <i>Africaniella transversale</i> and <i>Robertsicus elaphensis</i> . <i>Ticks and Tick-borne Diseases</i> , 2023, 14, 102070.	1.1	13

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22732	Comparative analysis of chloroplast genomes of <i>Sanguisorba</i> species and insights into phylogenetic implications and molecular dating. <i>Nordic Journal of Botany</i> , 2022, 2022, .	0.2	1
22733	Antimicrobial resistance and genomic characterization of <i>Salmonella enterica</i> serovar Senftenberg isolates in production animals from the United States. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
22734	The complete chloroplast genome of two <i>Firmiana</i> species and comparative analysis with other related species. <i>Genetica</i> , 2022, 150, 395-405.	0.5	2
22735	Methanotrophy by a <i>Mycobacterium</i> species that dominates a cave microbial ecosystem. <i>Nature Microbiology</i> , 2022, 7, 2089-2100.	5.9	22
22736	Lichen phycobiomes as source of biodiversity for microalgae of the <i>Stichococcus</i> -like genera. , 2023, 78, 389-397.		3
22737	A western representative of an eastern clade: Phylogeographic history of the gypsum-associated plant <i>Nepeta hispanica</i> . <i>Perspectives in Plant Ecology, Evolution and Systematics</i> , 2022, 57, 125699.	1.1	1
22738	Invasive fish disrupt host-pathogen dynamics leading to amphibian declines. <i>Biological Conservation</i> , 2022, 276, 109785.	1.9	6
22739	Short-length Homologous Region exhaustive Search algorithm (SHRS): A primer design algorithm for differentiating bacteria at the species, subspecies, or strain level based on a whole genome sequence. <i>Journal of Microbiological Methods</i> , 2022, 203, 106605.	0.7	0
22740	Draft genome sequence data of a psychrophilic tundra soil methanotroph, <i>Methylobacter psychrophilus</i> Z-0021 (DSM 9914). <i>Data in Brief</i> , 2022, 45, 108689.	0.5	1
22741	Phylogenetic group and virulence profile classification in <i>Escherichia coli</i> from distinct isolation sources in Mexico. <i>Infection, Genetics and Evolution</i> , 2022, 106, 105380.	1.0	4
22742	The chromosome-level <i>Melaleuca alternifolia</i> genome provides insights into the molecular mechanisms underlying terpenoids biosynthesis. <i>Industrial Crops and Products</i> , 2022, 189, 115819.	2.5	4
22743	In support of morphology: Molecular analysis successfully delineates the Afrotropical genus <i>Atylotus</i> (Diptera: Tabanidae) into species. <i>Acta Tropica</i> , 2023, 237, 106725.	0.9	0
22744	Dissecting the genome, secretome, and effectome repertoires of <i>Monilinia</i> spp.: The causal agent of brown rot disease: A comparative analysis. <i>Postharvest Biology and Technology</i> , 2023, 195, 112120.	2.9	8
22745	Phylogenetic relationships and species delimitation in <i>Haemopis</i> (Annelida: Hirudinea: Haemopidae). <i>Molecular Phylogenetics and Evolution</i> , 2023, 178, 107648.	1.2	2
22746	Masters of the manipulator: two new hypocrealean genera, <i>Niveomyces</i> (<i>Cordycipitaceae</i>) and <i>Torrubiellomyces</i> (<i>Ophiocordycipitaceae</i>), parasitic on the zombie ant fungus <i>Ophiocordyceps camponoti-floridani</i> . <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2022, 49, 171-194.	1.6	7
22747	<i>Flammulina yunnanensis</i> (Agaricales), a new record from Darjeeling Hills, India. <i>Studies in Fungi</i> , 2022, 7, 1-4.	0.5	0
22748	Identification of sex-linked marker and candidate sex determination gene in ornamental fish, African scat (<i>Scatophagus tetracanthus</i>). <i>Aquaculture</i> , 2023, 563, 739023.	1.7	1
22749	New <i>Botrylloides</i> , <i>Botryllus</i> , and <i>Symplegma</i> (Ascidiacea: Styelidae) in Coral Reefs of the Southern Gulf of Mexico and Mexican Caribbean Sea. <i>Diversity</i> , 2022, 14, 977.	0.7	6

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22750	ï»¿A new species of <i>Encelia</i> (Compositae, Heliantheae, Enceliinae) from the southern Baja California Peninsula. <i>PhytoKeys</i> , 0, 212, 97-109.	0.4	0
22751	Endophytic Fungi Associated with <i>Aquilaria sinensis</i> (Agarwood) from China Show Antagonism against Bacterial and Fungal Pathogens. <i>Journal of Fungi</i> (Basel, Switzerland), 2022, 8, 1197.	1.5	4
22752	Teaching Computational Genomics and Bioinformatics on a High Performance Computing Cluster - A Primer. <i>Biology Methods and Protocols</i> , 0, , .	1.0	0
22753	ï»¿Four new <i>Phragmidium</i> (Phragmidiaceae, Pucciniomycetes) species from Rosaceae plants in Guizhou Province of China. <i>MycKeys</i> , 0, 93, 193-213.	0.8	1
22754	Environmental DNA from archived leaves reveals widespread temporal turnover and biotic homogenization in forest arthropod communities. <i>ELife</i> , 0, 11, .	2.8	8
22755	First complete mitochondrial genome of the Saharan striped polecat (<i>Ictonyx libycus</i>). <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 1957-1960.	0.2	2
22756	Complete chloroplast genome of <i>Isoetes japonica</i> (Isoetaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 1983-1984.	0.2	1
22757	Tissue-specific regulation of lipid polyester synthesis genes controlling oxygen permeation into <i>Lotus japonicus</i> nodules. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	3
22758	The complete chloroplast genome sequence of <i>Michelia macclurei</i> (Dandy, 1928) (Magnoliaceae), an important fire-resistant tree species. <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 1933-1935.	0.2	1
22759	Genomic insight into <i>Chryseobacterium turcicum</i> sp. nov. and <i>Chryseobacterium muglaense</i> sp. nov. isolated from farmed rainbow trout in Turkey. <i>Systematic and Applied Microbiology</i> , 2022, , 126385.	1.2	2
22760	Genome-partitioning strategy, plastid and nuclear phylogenomic discordance, and its evolutionary implications of <i>Clematis</i> (Ranunculaceae). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
22761	De novo genome assembly and analysis of <i>Zalaria</i> sp. Him3, a novel fructooligosaccharides producing yeast. <i>BMC Genomic Data</i> , 2022, 23, .	0.7	0
22762	Historical biogeography highlights the role of Miocene landscape changes on the diversification of a clade of Amazonian tree frogs. <i>Organisms Diversity and Evolution</i> , 2023, 23, 395-414.	0.7	7
22763	Characterization of <i>Colletotrichum</i> isolates causing anthracnose on <i>Artocarpus heterophyllus</i> in Brazil. , 2023, 105, 299-305.		1
22764	Muscle5: High-accuracy alignment ensembles enable unbiased assessments of sequence homology and phylogeny. <i>Nature Communications</i> , 2022, 13, .	5.8	122
22765	ï»¿Genome-wide survey reveals the phylogenomic relationships of <i>Chirolophis japonicus</i> Herzenstein, 1890 (Stichaeidae, Perciformes). <i>ZooKeys</i> , 0, 1129, 55-72.	0.5	2
22767	Formation of secondary allo-bile acids by novel enzymes from gut Firmicutes. <i>Gut Microbes</i> , 2022, 14, .	4.3	11
22768	New insights on <i>Flaviporus</i> (Polyporales) in the neotropics. <i>Mycological Progress</i> , 2022, 21, .	0.5	1

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22769	Comparative Analyses of Plastomes of Four Anubias (Araceae) Taxa, Tropical Aquatic Plants Endemic to Africa. <i>Genes</i> , 2022, 13, 2043.	1.0	1
22770	Longitudinal analysis of the Five Sisters hot springs in Yellowstone National Park reveals a dynamic thermoalkaline environment. <i>Scientific Reports</i> , 2022, 12, .	1.6	4
22771	Taxonomic changes in the Lomentariaceae (Rhodymeniales, Rhodophyta): <i>Yendoa</i> gen. nov. and <i>Ceratodictyon sanctae-crucis</i> sp. nov. <i>Phycologia</i> , 2023, 62, 19-28.	0.6	1
22772	Phylogenomics and genome size evolution in <i>Amomum</i> s. s. (Zingiberaceae): Comparison of traditional and modern sequencing methods. <i>Molecular Phylogenetics and Evolution</i> , 2023, 178, 107666.	1.2	1
22773	The taxonomic revision of <i>Melanogaster</i> (Paxillaceae, Boletales) in China based on molecular and morphological evidence. <i>Mycological Progress</i> , 2022, 21, .	0.5	1
22774	Taxogenomic status of phylogenetically distant <i>Frankia</i> clusters warrants their elevation to the rank of genus: A description of <i>Protofrankia</i> gen. nov., <i>Parafrankia</i> gen. nov., and <i>Pseudofrankia</i> gen. nov. as three novel genera within the family Frankiaceae. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	7
22775	The spread of <i>Carpophilus truncatus</i> is on the razor's edge between an outbreak and a pest invasion. <i>Scientific Reports</i> , 2022, 12, .	1.6	5
22777	Building a foundation for gene family analysis in Rosaceae genomes with a novel workflow: A case study in <i>Pyrus</i> architecture genes. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	6
22778	Defensive spines are associated with large geographic range but not diversification in spiny ants (Hymenoptera: Formicidae: <i>Polyrhachis</i>). <i>Systematic Entomology</i> , 0, , .	1.7	1
22779	A high-quality chromosome-level genome assembly of <i>Pelteobagrus vachelli</i> provides insights into its environmental adaptation and population history. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	0
22780	Squash bees host high diversity and prevalence of parasites in the northeastern United States. <i>Journal of Invertebrate Pathology</i> , 2022, 195, 107848.	1.5	5
22781	South American morels in the <i>Elata</i> group: mitosporic states, distributions, and commentary. <i>Mycological Progress</i> , 2022, 21, .	0.5	1
22782	Comparative genomics of Lactobacillaceae from the gut of honey bees, <i>Apis mellifera</i> , from the Eastern United States. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	3
22783	The first high-quality chromosome-level genome assembly of Phyllanthaceae (<i>Phyllanthus</i>) Tj ETQq1 1 0.784314 rgBT/Overlock 10 Tf 50	1.6	2
22785	Comparative Analysis of Whole Chloroplast Genomes of Three Common Species of <i>Echinochloa</i> (Gramineae) in Paddy Fields. <i>International Journal of Molecular Sciences</i> , 2022, 23, 13864.	1.8	2
22786	Two new millipede species of the genus <i>Coxobolellus</i> Pimvichai, Enghoff, Panha & Backeljau, 2020 (Diplopoda, Spirobolida, Pseudospirobolellidae). <i>ZooKeys</i> , 0, 1128, 171-190.	0.5	0
22787	Gut transcriptome analysis of P450 genes and cytochrome P450 reductase in three moth species feeding on gymnosperms or angiosperms. <i>Frontiers in Ecology and Evolution</i> , 0, 10, .	1.1	0
22788	Taxonomic Novelties of Woody Litter Fungi (Didymosphaeriaceae, Pleosporales) from the Greater Mekong Subregion. <i>Biology</i> , 2022, 11, 1660.	1.3	4

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22791	Characterization and selection of endophytic actinobacteria for growth and disease management of Tea (<i>Camellia sinensis</i> L.). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3
22793	Gene flow and introgression are pervasive forces shaping the evolution of bacterial species. <i>Genome Biology</i> , 2022, 23, .	3.8	8
22794	Nematocyst sequestration within the family Fionidae (Gastropoda: Nudibranchia) considering ecological properties and evolution. <i>Frontiers in Zoology</i> , 2022, 19, .	0.9	1
22795	Ecological speciation of Japanese hedgehog mushroom: <i>Hydnum subalpinum</i> sp. nov. is distinguished from its sister species <i>H. repando-orientale</i> by means of integrative taxonomy. <i>Mycological Progress</i> , 2022, 21, .	0.5	2
22796	Genotyping-by-sequencing for biogeography. <i>Journal of Biogeography</i> , 2023, 50, 262-281.	1.4	5
22797	Taxonomic update of species closely related to <i>Fulvifomes robiniae</i> in America. <i>Mycological Progress</i> , 2022, 21, .	0.5	2
22798	Investigation of the halophilic <i>PET</i> hydrolase <i>PET6</i> from <i>Vibrio gazogenes</i> . <i>Protein Science</i> , 2022, 31, .	3.1	8
22799	Postharvest stem-end browning (SEB) disease in ripe mango (<i>Mangifera indica</i> L.) cultivar TomEJC. <i>European Journal of Plant Pathology</i> , 2023, 165, 447-464.	0.8	3
22800	An ancestral mycobacterial effector promotes dissemination of infection. <i>Cell</i> , 2022, 185, 4507-4525.e18.	13.5	16
22801	<i>Stenamoeba aeronauta</i> n. sp., a new case of sibling species in the order Thecamoebida (Amoebozoa). <i>Tj ETQq1 1 0.784314 rgBT /Overlo</i>	0.5	1
22802	Improved assembly and annotation of the sesame genome. <i>DNA Research</i> , 2022, 29, .	1.5	11
22803	Morphological, ecological, and molecular phylogenetic approaches reveal species boundaries and evolutionary history of <i>Goodyera crassifolia</i> (Orchidaceae, Orchidoideae) and its closely related taxa. <i>PhytoKeys</i> , 0, 212, 111-134.	0.4	0
22804	Pervasive Introgression During Rapid Diversification of the European Mountain Genus <i>Soldanella</i> (L.) (Primulaceae). <i>Systematic Biology</i> , 2023, 72, 491-504.	2.7	5
22805	Novel Alligator Cathelicidin As-CATH8 Demonstrates Anti-Infective Activity against Clinically Relevant and Crocodylian Bacterial Pathogens. <i>Antibiotics</i> , 2022, 11, 1603.	1.5	3
22806	Complete mitochondrial genome and phylogenetic analysis of black-fin stream jewel goby <i>Stiphodon percnopterygionus</i> (Gobiiformes: Gobiidae) from Taiwan. <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 1968-1970.	0.2	1
22807	Complete mitochondrial genome of little ringed plover <i>Charadrius dubius</i> (Charadriiformes). <i>Tj ETQq1 1 0.784314 rgBT /Overlo</i>	0.2	1
22809	Mitochondrial DNA variation of the caracal (<i>Caracal caracal</i>) in Iran and range-wide phylogeographic comparisons. <i>Mammalian Biology</i> , 0, , .	0.8	0
22810	Mitogenome recovered from a 19th Century holotype by shotgun sequencing supplies a generic name for an orphaned clade of African weakly electric fishes (Osteoglossomorpha, Mormyridae). <i>ZooKeys</i> , 0, 1129, 163-196.	0.5	3

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22811	Next-generation sequencing data show rapid radiation and several long-distance dispersal events in early Costaceae. <i>Molecular Phylogenetics and Evolution</i> , 2023, 179, 107664.	1.2	3
22812	A Metabolomics-Based Toolbox to Assess and Compare the Metabolic Potential of Unexplored, Difficult-to-Grow Bacteria. <i>Marine Drugs</i> , 2022, 20, 713.	2.2	0
22814	<i>Fusarium</i> isolates from Belgium causing wilt in lettuce show genetic and pathogenic diversity. <i>Plant Pathology</i> , 0, .	1.2	3
22815	Multi-Gene Phylogenetic Analyses Revealed Five New Species and Two New Records of Distoseptisporales from China. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 1202.	1.5	7
22816	<i>Lacrimispora defluvii</i> PI-S10-B5AT sp. nov., an Obligate Anaerobe, Isolated from an Industrial Waste and Reclassification of <i>Hungatella xylanolytica</i> as <i>Lacrimispora xylanolytica</i> and <i>Clostridium indicum</i> as <i>Lacrimispora indica</i> Comb. nov.. <i>Current Microbiology</i> , 2022, 79, .	1.0	0
22817	The phylogeny of <i>Seseli</i> (Apiaceae, Apioideae): insights from molecular and morphological data. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	4
22818	Isolation of a New Infectious Pancreatic Necrosis Virus (IPNV) Variant from Genetically Resistant Farmed Atlantic Salmon (<i>Salmo salar</i>) during 2021–2022. <i>Pathogens</i> , 2022, 11, 1368.	1.2	3
22820	Two bloom-forming species of <i>Ulva</i> (Chlorophyta) show different responses to seawater temperature and no antagonistic interaction. <i>Journal of Phycology</i> , 2023, 59, 167-178.	1.0	2
22821	Anaerobic mercury methylators inhabit sinking particles of oxic water columns. <i>Water Research</i> , 2023, 229, 119368.	5.3	5
22822	Phylogenomic analysis and development of molecular markers for the determination of twelve plum cultivars (<i>Prunus</i> , Rosaceae). <i>BMC Genomics</i> , 2022, 23, .	1.2	3
22823	Tracing Foodborne Botulism Events Caused by <i>Clostridium botulinum</i> in Xinjiang Province, China, Using a Core Genome Sequence Typing Scheme. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	3
22824	Morphology and Phylogeny of <i>Pestalotiopsis</i> (<i>Sporocadaceae</i> , <i>Amphisphaerales</i>) from <i>Fagaceae</i> Leaves in China. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	17
22825	Morphological trends and genetic divergence in anacondas, genus <i>Eunectes</i> Wagler, 1830 (Serpentes: Tj ETQq0 0,0 rgBT /Oyerlock 10 0,1		1
22826	Exploring clade differentiation of the <i>Faecalibacterium prausnitzii</i> complex. <i>IScience</i> , 2022, 25, 105533.	1.9	0
22827	Evolutionary gain and loss of a plant pattern-recognition receptor for HAMP recognition. <i>ELife</i> , 0, 11, .	2.8	10
22829	First report of a cyst nematode, <i>Heterodera daverti</i> , from Australia. <i>Australasian Plant Disease Notes</i> , 2022, 17, .	0.4	1
22830	Phylogeny, biogeography, and character evolution in the genus <i>Scilla</i> and its close relatives <i>Chionodoxa</i> , <i>Gemicia</i> , <i>Puschkinia</i> , and <i>Prospero</i> (Asparagaceae). <i>Plant Systematics and Evolution</i> , 2022, 308, .	0.3	3
22831	<i>Escherichia coli</i> ST155 as a production-host of three different polyvalent phages and their characterisation with a prospect for wastewater disinfection. <i>Scientific Reports</i> , 2022, 12, .	1.6	2

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22832	Increased phage resistance through lysogenic conversion accompanying emergence of monophasic <i>Salmonella</i> Typhimurium ST34 pandemic strain. <i>Microbial Genomics</i> , 2022, 8, .	1.0	0
22833	The discovery of a key prenyltransferase gene assisted by a chromosome-level <i>Epimedium pubescens</i> genome. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	5
22834	<i>Hansenia trifoliolata</i> , a new species (Apiaceae) from Shaanxi, China. <i>PhytoKeys</i> , 0, 213, 79-93.	0.4	1
22836	Near-shore island lizard fauna shaped by a combination of human-mediated and natural dispersal. <i>Journal of Biogeography</i> , 2023, 50, 116-129.	1.4	5
22838	First record of sponge-associated deep-sea polychaete (Polynoidae: Bathymoorea) on the ultraslow-spreading Southwest Indian Ridge. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2022, , 103923.	0.6	1
22839	Analysis of the chloroplast genome and phylogenetic evolution of three species of <i>Syringa</i> . <i>Molecular Biology Reports</i> , 0, , .	1.0	3
22840	Characterization of the Evolutionary Pressure on <i>Anisodus tanguticus</i> Maxim. with Complete Chloroplast Genome Sequence. <i>Genes</i> , 2022, 13, 2125.	1.0	3
22841	<i>Helicobacter colisuis</i> sp. nov., isolated from caecal contents of domestic pigs (<i>Sus scrofa</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 0.8 4	0.8	4
22843	AvP: A software package for automatic phylogenetic detection of candidate horizontal gene transfers. <i>PLoS Computational Biology</i> , 2022, 18, e1010686.	1.5	5
22844	Plastid phylogenomic insights into relationships, divergence, and evolution of Apiales. <i>Planta</i> , 2022, 256, .	1.6	2
22845	Resolving tricky nodes in the tree of life through amino acid recoding. <i>IScience</i> , 2022, 25, 105594.	1.9	13
22846	The Mitogenome of <i>Sedum plumbizincicola</i> (Crassulaceae): Insights into RNA Editing, Lateral Gene Transfer, and Phylogenetic Implications. <i>Biology</i> , 2022, 11, 1661.	1.3	1
22847	Chromosome-level genome assembly of the Muscovy duck provides insight into fatty liver susceptibility. <i>Genomics</i> , 2022, 114, 110518.	1.3	2
22848	Comparative Analysis of the Chloroplast Genome of <i>Cardamine hupingshanensis</i> and Phylogenetic Study of <i>Cardamine</i> . <i>Genes</i> , 2022, 13, 2116.	1.0	2
22850	<i>Oreocharis qianyuensis</i> , a new species of Gesneriaceae from Southwest, China based on morphological and molecular evidence. <i>PhytoKeys</i> , 0, 213, 119-130.	0.4	2
22851	Revealing the cryptic diversity of the widespread and poorly known South American blind snake genus <i>Amerotyphlops</i> (Typhlopidae: Scolecophidia) through integrative taxonomy. <i>Zoological Journal of the Linnean Society</i> , 2023, 197, 719-751.	1.0	2
22852	Plastome sequencing of South American <i>Podocarpus</i> species reveals low rearrangement rates despite ancient gondwanan disjunctions. <i>Molecular Biology Reports</i> , 2023, 50, 309-318.	1.0	2
22854	<i>Pseudomonas aegrilactucaae</i> sp. nov. and <i>Pseudomonas morbosilactucaae</i> sp. nov., pathogens causing bacterial rot of lettuce in Japan. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	1

#	ARTICLE	IF	CITATIONS
22855	Monogeneans and chubs: Ancient host-parasite system under the looking glass. <i>Molecular Phylogenetics and Evolution</i> , 2023, 179, 107667.	1.2	4
22856	A new species of <i>Megalaria</i> (Ramalinaceae, Ascomycota) from Thailand, and recognition of subgenus <i>Catillochroma</i> . <i>MycKeys</i> , 0, 93, 149-163.	0.8	0
22857	<i>Rahnella sikkimica</i> sp. nov., a novel cold-tolerant bacterium isolated from the glacier of Sikkim Himalaya with plant growth-promoting properties. <i>Extremophiles</i> , 2022, 26, .	0.9	1
22858	Evolutionary Trajectories of Avian Avulaviruses and Vaccines Compatibilities in Poultry. <i>Vaccines</i> , 2022, 10, 1862.	2.1	3
22859	Specificity of a $\hat{2}$ -porphyranase produced by the carrageenophyte red alga <i>Chondrus crispus</i> and implications of this unexpected activity on red algal biology. <i>Journal of Biological Chemistry</i> , 2022, 298, 102707.	1.6	3
22860	Phylogenomic and comparative genomic studies robustly demarcate two distinct clades of <i>Pseudomonas aeruginosa</i> strains: proposal to transfer the strains from an outlier clade to a novel species <i>Pseudomonas paraeruginosa</i> sp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	11
22861	Characterization of <i>Escherichia coli</i> and other bacteria isolated from condemned broilers at a Danish abattoir. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
22862	Genomic Variation across a Clinical <i>Cryptococcus</i> Population Linked to Disease Outcome. <i>MBio</i> , 2022, 13, .	1.8	11
22863	Draft genome of six Cuban <i>Anolis</i> lizards and insights into genetic changes during their diversification. <i>Bmc Ecology and Evolution</i> , 2022, 22, .	0.7	3
22864	Chromosome-level genome and population genomics reveal evolutionary characteristics and conservation status of Chinese indigenous geese. <i>Communications Biology</i> , 2022, 5, .	2.0	3
22866	Geographic Location, Management Strategy, and Huanglongbing Disease Affect Arbuscular Mycorrhizal Fungal Communities Across U.S. Citrus Orchards. <i>Phytobiomes Journal</i> , 2022, 6, 342-353.	1.4	2
22867	Morphological and molecular evidence gives insight into the taxonomic position of <i>Peucedanum pubescens</i> (Apiaceae, Selineae). <i>PhytoKeys</i> , 0, 213, 19-33.	0.4	0
22868	Introducing the Bacterial and Viral Bioinformatics Resource Center (BV-BRC): a resource combining PATRIC, IRD and ViPR. <i>Nucleic Acids Research</i> , 2023, 51, D678-D689.	6.5	229
22869	Taxonomy and phylogeny of <i>Pseudovorticella</i> ciliates (Ciliophora, Peritrichia): Two new and one rare species from the coastal waters of China. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	0
22870	Genomic remnants of ancestral methanogenesis and hydrogenotrophy in Archaea drive anaerobic carbon cycling. <i>Science Advances</i> , 2022, 8, .	4.7	17
22871	Characterization of the plastid genome of <i>Cratoxylum</i> species (Hypericaceae) and new insights into phylogenetic relationships. <i>Scientific Reports</i> , 2022, 12, .	1.6	2
22872	Antarctic <i>Sphingomonas</i> sp. So64.6b showed evolutive divergence within its genus, including new biosynthetic gene clusters. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
22873	Provenance of rhizobial symbionts is similar for invasive and non-invasive acacias introduced to California. <i>FEMS Microbiology Ecology</i> , 0, , .	1.3	2

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22874	De Novo Hybrid Assembly of the <i>Salvia miltiorrhiza</i> Mitochondrial Genome Provides the First Evidence of the Multi-Chromosomal Mitochondrial DNA Structure of <i>Salvia</i> Species. <i>International Journal of Molecular Sciences</i> , 2022, 23, 14267.	1.8	10
22875	Detection and phylogenetic assessment of PRV-1 via sampling of biological materials released from salmon farms in British Columbia. <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 0, , .	0.7	1
22876	Structure and Phylogeny of Chloroplast and Mitochondrial Genomes of a Chlorophycean Algae <i>Pectinodesmus pectinatus</i> (Scenedesmaceae, Sphaeropleales). <i>Life</i> , 2022, 12, 1912.	1.1	0
22877	A curated DNA barcode reference library for parasitoids of northern European cyclically outbreaking geometrid moths. <i>Ecology and Evolution</i> , 2022, 12, .	0.8	1
22878	Evidence for Widespread Class II Microcins in <i>Enterobacterales</i> Genomes. <i>Applied and Environmental Microbiology</i> , 2022, 88, .	1.4	5
22879	From Easy to Hopeless—Predicting the Difficulty of Phylogenetic Analyses. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	13
22880	Seasonal abundance of capitulum-boring insects considered for the biological control of fireweed (<i>Senecio madagascariensis</i>), including molecular phylogenetic analyses to reveal the field host range of lepidopteran candidate agents. <i>Biological Control</i> , 2023, 177, 105119.	1.4	2
22884	A box on the river: The phylogenetics and phylogeography of <i>Eucalyptus baueriana</i> (<i>Eucalyptus</i> sect.) Tj ETQq1 1 0.784314 rgBT /Over	1.1	0
22885	Parallel evolution of amphioxus and vertebrate small-scale gene duplications. <i>Genome Biology</i> , 2022, 23, .	3.8	14
22886	The first complete genome of the simian malaria parasite <i>Plasmodium brasilianum</i> . <i>Scientific Reports</i> , 2022, 12, .	1.6	5
22887	Diversity of <i>Siphonaria</i> Sowerby I, 1823 (Gastropoda, Siphonariidae) in the Seychelles Bank and beyond. <i>Zoologica Scripta</i> , 0, , .	0.7	0
22888	Characterization of the Chloroplast Genome Structure of <i>Gueldenstaedtia verna</i> (Papilionoideae) and Comparative Analyses among IRLC Species. <i>Forests</i> , 2022, 13, 1942.	0.9	2
22889	A comprehensive update to the <i>Mycobacterium tuberculosis</i> H37Rv reference genome. <i>Nature Communications</i> , 2022, 13, .	5.8	8
22891	Genomes of <i>Vibrio metoecus</i> co-isolated with <i>Vibrio cholerae</i> extend our understanding of differences between these closely related species. <i>Gut Pathogens</i> , 2022, 14, .	1.6	0
22893	Antifungal susceptibility profiles and drug resistance mechanisms of clinical <i>Candida duobushaemulonii</i> isolates from China. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
22894	Total evidence phylogeny of platyrrhine primates and a comparison of undated and tip-dating approaches. <i>Journal of Human Evolution</i> , 2023, 174, 103293.	1.3	5
22895	Morphology and multigene phylogeny revealed <i>Peroneutypa aquilariae</i> sp. nov. (Diatrypaceae, Xylariales) from <i>Aquilaria sinensis</i> in Yunnan Province, China. <i>Studies in Fungi</i> , 2022, 7, 1-11.	0.5	0
22896	The entire chloroplast genome sequence of <i>Asparagus setaceus</i> (Kunth) Jessop: Genome structure, gene composition, and phylogenetic analysis in Asparagaceae. <i>Open Life Sciences</i> , 2022, 17, 1541-1554.	0.6	2

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22897	An integrative study of <i>Pannaria hookeri</i> (Ascomycota lichenized) from Argentina and the update of the taxon circumscription based on specimens from the Northern and Southern Hemispheres. <i>Acta Botanica Brasiliica</i> , 0, 36, .	0.8	0
22898	Dispersion Routes of the Main Vectors of Human Malaria in the Americas: Genetic Evidence from the Mitochondrial COI Gene. <i>Journal of Vector Borne Diseases</i> , 2022, .	0.1	0
22899	<i>Lepiota brunneogranulosa</i> (Agaricaceae): a new species from Punjab, Pakistan, based on integrated taxonomy. <i>Acta Botanica Brasiliica</i> , 0, 36, .	0.8	2
22900	Visualization of the Evolutionary Trajectory: Application of Reduced Amino Acid Alphabets and Word2Vec Embedding. , 2022, , .		0
22901	A Chromosome-level assembly of the Japanese eel genome, insights into gene duplication and chromosomal reorganization. <i>GigaScience</i> , 2022, 11, .	3.3	4
22902	Molecular and morphological analysis of <i>Biddulphia sensu lato</i> : a new diagnosis of <i>Biddulphia</i> , with a description of the new genera <i>Biddulphiella</i> and <i>Neobrightwellia</i> . <i>Marine Micropaleontology</i> , 2023, 178, 102186.	0.5	0
22903	Metabarcoding reveals high genetic diversity of harmful algae in the coastal waters of Texas, Gulf of Mexico. <i>Harmful Algae</i> , 2023, 121, 102368.	2.2	3
22904	Two Outbreaks of Foodborne Gastrointestinal Infection Linked to Consumption of Imported Melons, United Kingdom, March to August 2021. <i>Journal of Food Protection</i> , 2023, 86, 100027.	0.8	6
22905	Taxonomic proposal for a deep branching bacterial phylogenetic lineage: transfer of the family <i>Thermodesulfobiaceae</i> to <i>Thermodesulfobiales</i> ord. nov., <i>Thermodesulfobiiia</i> classis nov. and <i>Thermodesulfobiota</i> phyl. nov. <i>Systematic and Applied Microbiology</i> , 2023, 46, 126388.	1.2	6
22906	Integrating morphology, molecular phylogeny and chemotaxonomy for the most effective authentication in Chinese <i>Rubia</i> with insights into origin and distribution of characteristic <i>Rubiaceae</i> -type cyclopeptides. <i>Industrial Crops and Products</i> , 2023, 191, 115775.	2.5	0
22907	Species delimitation using genomic data to resolve taxonomic uncertainties in a speciation continuum of pelagic seabirds. <i>Molecular Phylogenetics and Evolution</i> , 2023, 179, 107671.	1.2	7
22908	Transcriptomic data recover a new superfamily-level phylogeny of Cucujiformia (Coleoptera,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 ff		
22909	Ancient and modern mitogenomes of red deer reveal its evolutionary history in northern China. <i>Quaternary Science Reviews</i> , 2023, 301, 107924.	1.4	2
22910	Bioactivity of bacteria associated with Red Sea nudibranchs and whole genome sequence of <i>Nocardiopsis dassonvillei</i> RACA-4. <i>Marine Genomics</i> , 2023, 67, 101004.	0.4	2
22911	The origin and loss of interferon regulatory factor 10 (IRF10) in different lineages of vertebrates. <i>Gene</i> , 2023, 854, 147083.	1.0	1
22912	A viral metagenomic protocol for nanopore sequencing of group A rotavirus. <i>Journal of Virological Methods</i> , 2023, 312, 114664.	1.0	4
22913	A comparative analysis employing a gene- and genome-centric metagenomic approach reveals changes in composition, function, and activity in waterworks with different treatment processes and source water in Finland. <i>Water Research</i> , 2023, 229, 119495.	5.3	7
22914	Textile industry wastewater microbiome: Recovery of metagenome assembled genomes (MAGs) using shotgun sequencing approach from Jetpur, Gujarat, India. <i>Ecological Genetics and Genomics</i> , 2023, 26, 100155.	0.3	1

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22915	Habitat matters: The role of spore bank fungi in early seedling establishment of Florida slash pines. <i>Fungal Ecology</i> , 2023, 62, 101210.	0.7	0
22916	Proposal of a new genus, <i>Doorochen</i> (Digenea: Lepocreadioidea), for reef-inhabiting members of the genus <i>Postlepidapedon</i> Zdzitowiecki, 1993. <i>Parasitology International</i> , 2023, 93, 102710.	0.6	2
22917	DNA barcode of tilapia fish fillet from the Brazilian market and a standardized COI haplotyping for molecular identification of <i>Oreochromis</i> spp. (Actinopterygii, Cichlidae). <i>Forensic Science International Animals and Environments</i> , 2023, 3, 100059.	0.3	1
22918	Comparative genomic analysis provides insight into the phylogeny and potential mechanisms of adaptive evolution of <i>Sphingobacterium</i> sp. CZ-2. <i>Gene</i> , 2023, 855, 147118.	1.0	0
22919	<i>Penicillium gercinae</i> and <i>Penicillium stangiae</i> (Eurotiomycetes, Ascomycota), two new species from soil in Brazil. <i>Acta Botanica Brasilica</i> , 0, 36, .	0.8	0
22920	Fungal Planet description sheets: 1436–1477. <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2022, 49, 261-350.	1.6	14
22921	Consolidation of <i>Chloridium</i> : new classification into eight sections with 37 species and reinstatement of the genera <i>Gongromeriza</i> and <i>Psilobotrys</i> . <i>Studies in Mycology</i> , 2022, , .	4.5	1
22922	Reducing the number of accepted species in <i>Aspergillus</i> series <i>Nigri</i> . <i>Studies in Mycology</i> , 2022, 102, 95-132.	4.5	11
22923	Identification of European isolates of the lager yeast parent <i>Saccharomyces eubayanus</i> . <i>FEMS Yeast Research</i> , 2022, 22, .	1.1	13
22924	Phylogeny Trees as a Tool to Compare Inference Algorithms of Orthologs. <i>Lecture Notes in Computer Science</i> , 2022, , 128-139.	1.0	0
22925	Molecular characterisation of <i>Giardia duodenalis</i> from human and companion animal sources in the United Kingdom using an improved triosephosphate isomerase molecular marker. <i>Current Research in Parasitology and Vector-borne Diseases</i> , 2022, 2, 100105.	0.7	2
22926	Description of <i>Pseudogemmobacter faecipullorum</i> sp. nov., isolated from poultry manure. <i>FEMS Microbiology Letters</i> , 2022, 369, .	0.7	1
22927	Evidence that host ecology drives first intermediate host use in the Didymozoidae (Trematoda: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 26	0.4	1
22928	High-resolution Microbiome Analyses of Nine Psyllid Species of the Family Trioziidae Identified Previously Unrecognized but Major Bacterial Populations, including <i>Liberibacter</i> and <i>Wolbachia</i> of Supergroup O. <i>Microbes and Environments</i> , 2022, 37, n/a.	0.7	6
22929	Notes on the genus <i>Usnea</i> Adans. (lichenized <i>Ascomycota</i> , <i>Parmeliaceae</i>) from the islands of São Tomé and Príncipe in tropical West Africa. <i>Lichenologist</i> , 2022, 54, 271-289.	0.5	1
22930	Molecular, morphological and chemical variation of the <i>Usnea pectinata</i> aggregate from Tanzania, São Tomé and Príncipe. <i>Lichenologist</i> , 2022, 54, 291-298.	0.5	1
22931	Genetic Diversity and Evolutionary Potential of Rare Plant Species: <i>Mentzelia mollis</i> and <i>M. packardiae</i> (Loasaceae). <i>Western North American Naturalist</i> , 2022, 82, .	0.2	0
22932	Taxonomy and Phylogeny of Cystostereaceae (Agaricales, Basidiomycota): A New Genus, Five New Species, and Three New Combinations. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 1229.	1.5	5

#	ARTICLE	IF	CITATIONS
22933	A new synonym of <i>Enkianthus perulatus</i> (Ericaceae) in East Asia, based on morphological and molecular evidence. <i>PhytoKeys</i> , 0, 214, 61-74.	0.4	1
22934	Ancestral area analyses reveal Pleistocene-influenced evolution in a clade of coastal plain endemic plants. <i>Journal of Biogeography</i> , 2023, 50, 393-405.	1.4	5
22936	A gut microbial metabolite of dietary polyphenols reverses obesity-driven hepatic steatosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	11
22937	Selective isolation of Arctic marine actinobacteria and a down-scaled fermentation and extraction strategy for identifying bioactive compounds. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	0
22938	NOVEL AVIBACTERIUM SPECIES ASSOCIATED WITH SINUSITIS AND CONJUNCTIVITIS IN A MERRIAM'S WILD TURKEY (MELEAGRIS GALLOPAVO MERRIAMII) FLOCK IN COLORADO, USA. <i>Journal of Wildlife Diseases</i> , 2022, 58, .	0.3	0
22940	Taxonomic and Biochemical Characterization of Microalga <i>Graesiella emersonii</i> GEGS21 for Its Potential to Become Feedstock for Biofuels and Bioproducts. <i>Energies</i> , 2022, 15, 8725.	1.6	6
22941	<i>Monotropastrum kirishimense</i> (Ericaceae), a new mycoheterotrophic plant from Japan based on multifaceted evidence. <i>Journal of Plant Research</i> , 2023, 136, 3-18.	1.2	4
22942	Chromosome-Level Genome Assembly and Multi-Omics Dataset Provide Insights into Isoflavone and Puerarin Biosynthesis in <i>Pueraria lobata</i> (Wild.) Ohwi. <i>Biomolecules</i> , 2022, 12, 1731.	1.8	0
22944	Assessment of the phylogenetic relationships within the spondylidine branch of Spondylidinae (Coleoptera, Cerambycidae). <i>Insect Systematics and Evolution</i> , 2022, 54, 281-311.	0.2	4
22945	Taxonomy and Phylogeny of Fungi Associated with <i>Mangifera indica</i> from Yunnan, China. <i>Journal of Fungi</i> (Basel, Switzerland), 2022, 8, 1249.	1.5	4
22947	Climate Relicts: Asian Scorpion Family Pseudochactidae Survived Miocene Aridification in Caves of the Annamite Mountains. <i>Insect Systematics and Diversity</i> , 2022, 6, .	0.7	2
22948	Phylogeny and biogeography of Indochinese freshwater mussels in the genus <i>Pilsbryconcha</i> Simpson, 1900 (Bivalvia: Unionidae) with descriptions of four new species. <i>Scientific Reports</i> , 2022, 12, .	1.6	3
22949	Detritus-hosted methanogenesis sustains the methane paradox in an alpine lake. <i>Limnology and Oceanography</i> , 2023, 68, 248-264.	1.6	5
22950	Has long-distance flight ability been maintained by pigeons in highly insular habitats?. <i>Journal of Biogeography</i> , 2023, 50, 235-246.	1.4	1
22952	Genomic basis of the giga-chromosomes and giga-genome of tree peony <i>Paeonia ostii</i> . <i>Nature Communications</i> , 2022, 13, .	5.8	16
22953	The description of a new brackish water ciliate species from China, <i>Trachelostyla aestuarina</i> n. sp., with a species key and biogeographic investigation for <i>Trachelostyla</i> (Ciliophora, Sporadotrichida). <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	1
22954	Comparative Genomics Reveal the Utilization Ability of Variable Carbohydrates as Key Genetic Features of <i>Listeria</i> Pathogens in Their Pathogenic Lifestyles. <i>Pathogens</i> , 2022, 11, 1430.	1.2	1
22955	Comparative analysis reveals the long-term coevolutionary history of parvoviruses and vertebrates. <i>PLoS Biology</i> , 2022, 20, e3001867.	2.6	3

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22956	An updated classification of cyanobacterial orders and families based on phylogenomic and polyphasic analysis. <i>Journal of Phycology</i> , 2023, 59, 12-51.	1.0	62
22957	A new <i>Parakneria</i> Poll 1965 (Gonorhynchiformes: Kneriidae), "Mikinkidi"™ from the Upper Lufira Basin (Upper Congo: <sc>DRC</sc>): Evidence from a morphologic and <sc>DNA</sc> barcoding integrative approach. <i>Journal of Fish Biology</i> , 2023, 102, 4-26.	0.7	2
22958	The compact genome of <i>Caenorhabditis niphades</i> n. sp., isolated from a wood-boring weevil, <i>Niphades variegatus</i> . <i>BMC Genomics</i> , 2022, 23, .	1.2	1
22961	Evidence from Phylogenomics and Morphology Provide Insights into the Phylogeny, Plastome Evolution, and Taxonomy of <i>Kitagawia</i> . <i>Plants</i> , 2022, 11, 3275.	1.6	4
22962	<i>Salmonella enterica</i> serovar Cerro displays a phylogenetic structure and genomic features consistent with virulence attenuation and adaptation to cattle. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
22965	<i>Phaeophyscia kashmirensis</i> sp. nov. (Lecanorales, Physciaceae) from Azad Jammu and Kashmir, Pakistan. <i>Lichenologist</i> , 2022, 54, 355-361.	0.5	0
22967	First report of chemical composition and cytotoxicity evaluation of <i>Foraminispora rugosa</i> basidiomata from Brazil. , 2022, 63, .		0
22968	Four new species and three new records of helicosporous hyphomycetes from China and their multi-gene phylogenies. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	5
22969	Integrative studies on three new freshwater <i>Amphileptus</i> species (Ciliophora, Pleurostomatida) discovered in northern China. <i>Marine Life Science and Technology</i> , 2022, 4, 452-470.	1.8	5
22970	African Suid Genomes Provide Insights into the Local Adaptation to Diverse African Environments. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	9
22971	Gene transcriptional profiles in gonads of <i>Bacillus</i> taxa (Phasmida) with different cytological mechanisms of automictic parthenogenesis. <i>Zoological Letters</i> , 2022, 8, .	0.7	0
22972	New Records of <i>Sphaerius acaroides</i> (Coleoptera, Sphaeriusidae) from Russia Extend the Known Distribution of <i>Myxophaga</i> to Siberia. <i>Inland Water Biology</i> , 0, , .	0.2	0
22973	Three New <i>Plectolyngbya</i> Species (Leptolyngbyaceae, Cyanobacteria) Isolated from Rocks and Saltern of the Republic of Korea. <i>Diversity</i> , 2022, 14, 1013.	0.7	1
22974	Substrate Affinity Versus Catalytic Efficiency: Ancestral Sequence Reconstruction of tRNA Nucleotidyltransferases Solves an Enzyme Puzzle. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	1
22975	Target-enrichment sequencing reveals for the first time a well-resolved phylogeny of the core Bromelioideae (family Bromeliaceae). <i>Taxon</i> , 2023, 72, 47-63.	0.4	2
22977	Easternmost distribution of <i>Bufo bufo</i> (Linnaeus, 1758) in Türkiye: implications for the putative contact zone between <i>B. bufo</i> and <i>B. verrucosissimus</i> . <i>Genetica</i> , 0, , .	0.5	0
22978	Genomic signatures of recent convergent transitions to social life in spiders. <i>Nature Communications</i> , 2022, 13, .	5.8	7
22979	Soil-borne <i>Calonectria</i> (Hypocreales, Nectriaceae) associated with Eucalyptus plantations in Colombia. <i>MycKeys</i> , 0, 94, 17-35.	0.8	2

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22980	Phylogeny of the anaerobic ciliate genus <i>Sonderia</i> (Protista: Ciliophora: Plagiopylea), including the description of three novel species and a brief revision of the genus. <i>Marine Life Science and Technology</i> , 2022, 4, 493-512.	1.8	8
22982	Chromosome Evolution of the <i>Liolaemus monticola</i> (Liolaemidae) Complex: Chromosomal and Molecular Aspects. <i>Animals</i> , 2022, 12, 3372.	1.0	1
22984	Ancient oral microbiomes support gradual Neolithic dietary shifts towards agriculture. <i>Nature Communications</i> , 2022, 13, .	5.8	13
22985	Selective enrichment on a wide polysaccharide spectrum allowed isolation of novel metabolic and taxonomic groups of haloarchaea from hypersaline lakes. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
22986	Reversible shifts between interstitial and epibenthic habitats in evolutionary history: Molecular phylogeny of the marine flatworm family Boniniidae (Platyhelminthes: Polycladida: Cotylea) with descriptions of two new species. <i>PLoS ONE</i> , 2022, 17, e0276847.	1.1	3
22987	Untying the Gordian knot of plastid phylogenomic conflict: A case from ferns. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	0
22988	<i>Pseudomonas</i> cultivated from <i>Andropogon gerardii</i> rhizosphere show functional potential for promoting plant host growth and drought resilience. <i>BMC Genomics</i> , 2022, 23, .	1.2	3
22989	Complete Chloroplast Genome Sequences of Four Species in the <i>Caladium</i> Genus: Comparative and Phylogenetic Analyses. <i>Genes</i> , 2022, 13, 2180.	1.0	1
22990	Phylogenetic relationships and divergence times of the poorly known genus <i>Spalerosophis</i> (Serpentes: Tj ETQq0 0.0rgBT /Overlock 10	0.7	1
22991	A Comprehensive Account of the Rust Genus <i>Skierka</i> (Skierkaceae). <i>Journal of Fungi (Basel)</i> , Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tj	1.5	0
22992	Community phylogeny and spatial scale affect phylogenetic diversity metrics in a species-rich rainforest in Borneo. <i>Ecology and Evolution</i> , 2022, 12, .	0.8	1
22993	Phylogenetic position of <i>Ptychaphelenchus eucalypticola</i> Hodda, 2009 within the Aphelenchoidoidea Skarbilovich, 1947 (Siddiqi, 1980) inferred from partial 18S and 28S rDNA gene sequences. <i>Nematology</i> , 2022, 25, 59-76.	0.2	2
22994	The evolution of plant proton pump regulation via the R domain may have facilitated plant terrestrialization. <i>Communications Biology</i> , 2022, 5, .	2.0	5
22995	Bacilli in the International Space Station. <i>Microorganisms</i> , 2022, 10, 2309.	1.6	2
22996	A taxonomic assessment of novel and remarkable fungal species in Didymosphaeriaceae (Pleosporales), Tj ETQq0 0.0rgBT /Overlock 10	1.5	1
22997	Characterization of the Complete Chloroplast Genome of <i>Gaultheria nummularioides</i> D.Don 1825 (Ericaceae). <i>F1000Research</i> , 0, 11, 1358.	0.8	0
22999	The rapid evolution of flagellar ion selectivity in experimental populations of <i>E. coli</i> . <i>Science Advances</i> , 2022, 8, .	4.7	5
23000	Strategy of micro-environmental adaptation to cold seep among different brittle stars™ colonization. <i>Frontiers in Ecology and Evolution</i> , 0, 10, .	1.1	2

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23001	Polyenic Antibiotics and Other Antifungal Compounds Produced by Hemolytic Streptomyces Species. International Journal of Molecular Sciences, 2022, 23, 15045.	1.8	1
23002	IMA genome of IMA Fungus, 2022, 13, .	1.7	11
23003	Two new root endophyte and nematode cyst parasite species of the widely distributed genus Laburnicola. Mycological Progress, 2022, 21, .	0.5	1
23004	A draft genome of the medicinal plant Cremastra appendiculata (D. Don) provides insights into the colchicine biosynthetic pathway. Communications Biology, 2022, 5, .	2.0	4
23005	Acinetobacter sedimenti sp. nov., isolated from beach sediment. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	0
23007	Genetic diversity and structure of Bipolaris oryzae and Exserohilum rostratum populations causing brown spot of rice in Burkina Faso based on genotyping-by-sequencing. Frontiers in Plant Science, 0, 13, .	1.7	5
23008	Genomic analysis of emmer wheat shows a complex history with two distinct domestic groups and evidence of differential hybridization with wild emmer from the western Fertile Crescent. Vegetation History and Archaeobotany, 0, , .	1.0	2
23009	Piper section Muldera (Piperaceae) of the Malay Peninsula: variation and species limits. Botanical Journal of the Linnean Society, 0, , .	0.8	0
23010	Pandemic Vibrio cholerae acquired competitive traits from an environmental Vibrio species. Life Science Alliance, 2023, 6, e202201437.	1.3	3
23011	Lack of host phylogenetic structure in the gut bacterial communities of New Zealand cicadas and their interspecific hybrids. Scientific Reports, 2022, 12, .	1.6	4
23012	A large-scale genomic snapshot of Klebsiella spp. isolates in Northern Italy reveals limited transmission between clinical and non-clinical settings. Nature Microbiology, 2022, 7, 2054-2067.	5.9	34
23013	Genomic profiling of Nitrospira species reveals ecological success of comammox Nitrospira. Microbiome, 2022, 10, .	4.9	13
23015	Multilocus molecular phylogenetic-led discovery and formal recognition of four novel root-colonizing Fusarium species from northern Kazakhstan and the phylogenetically divergent Fusarium steppicola lineage. Mycologia, 2023, 115, 16-31.	0.8	3
23017	Genetic diversity and pathogenicity of Fusarium fujikuroi species complex (FFSC) causing sugarcane pokkah boeng disease in China. Plant Disease, 0, , .	0.7	2
23018	Pathogenicity and virulence of bacterial strains associated with summer mortality in marine mussels (Perna canaliculus). FEMS Microbiology Ecology, 2022, 98, .	1.3	5
23019	CONTRIBUTIONS TO MOLECULAR PHYLOGENY OF LICHENS 4. New names in the Teloschistaceae. Acta Botanica Hungarica, 2022, 64, 313-336.	0.1	0
23020	Reviving and characterizing three species of dinoflagellate cysts dormant for about 70 years in the East China Sea: Biecheleria brevisulcata, Biecheleriopsis adriatica, and Scrippsiella donghaiensis. Journal of Oceanology and Limnology, 2022, 40, 2292-2311.	0.6	2
23021	Phylogenomic inference and demographic model selection suggest peripatric separation of the cryptic steppe ant species Plagiolepis pyrenaica stat. rev.. Molecular Ecology, 0, , .	2.0	0

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23022	The Genomic Landscape Resource of <i>Pseudomonas syringae</i> pv. <i>syringae</i> Strains Isolated from Mango Trees. <i>Molecular Plant-Microbe Interactions</i> , 2022, 35, 1109-1114.	1.4	0
23025	Two New Species and a New Record of <i>Microdochium</i> from Grasses in Yunnan Province, South-West China. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 1297.	1.5	2
23026	Co-infection of Peruvian horse sickness virus and West Nile virus associated with neurological diseases in horses from Brazil. <i>Heliyon</i> , 2022, 8, e12097.	1.4	0
23027	Two new species of <i>Fistulina</i> (Agaricales, Basidiomycota) from the Northern Hemisphere. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
23028	SPLACE: A tool to automatically SPLit, Align, and Concatenate genes for phylogenomic inference of several organisms. <i>Frontiers in Bioinformatics</i> , 0, 2, .	1.0	0
23029	Pathogen genomics study of an early medieval community in Germany reveals extensive co-infections. <i>Genome Biology</i> , 2022, 23, .	3.8	6
23030	Dismantling and reorganizing <i>Pseudomonas marginalis</i> sensu lato. <i>Plant Pathology</i> , 2023, 72, 654-666.	1.2	1
23031	Comparative genomics of <i>Campylobacter jejuni</i> from clinical campylobacteriosis stool specimens. <i>Cut Pathogens</i> , 2022, 14, .	1.6	4
23033	The Phylogenetic Relationships of the Family Sciaenidae Based on Genome-Wide Data Analysis. <i>Animals</i> , 2022, 12, 3386.	1.0	0
23034	Gene Loss may have Shaped the Cnidarian and Bilaterian Hox and ParaHox Complement. <i>Genome Biology and Evolution</i> , 2023, 15, .	1.1	5
23035	Cyclitol metabolism is a central feature of <i>Burkholderia</i> leaf symbionts. <i>Environmental Microbiology</i> , 2023, 25, 454-472.	1.8	5
23036	Genome-wide association studies reveal distinct genetic correlates and increased heritability of antimicrobial resistance in <i>Vibrio cholerae</i> under anaerobic conditions. <i>Microbial Genomics</i> , 2022, 8, .	1.0	2
23037	Characterization of HIV-1 Transmission Clusters Inferred from the Brazilian Nationwide Genotyping Service Database. <i>Viruses</i> , 2022, 14, 2768.	1.5	0
23039	Tandem metalloenzymes gate plant cell entry by pathogenic fungi. <i>Science Advances</i> , 2022, 8, .	4.7	5
23040	Systematics of the <i>Trembleya</i> sensu stricto clade of <i>Microlicia</i> (Melastomataceae, Lavoisieraeae). <i>PhytoKeys</i> , 0, 216, 1-101.	0.4	1
23042	A New Hope: A Hermaphroditic Nematode Enables Analysis of a Recent Whole Genome Duplication Event. <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	3
23044	Unveiling mesophotic diversity in Hawaii: two new species in the genera <i>Halopeltis</i> and <i>Leptofauchea</i> (Rhodymeniales). <i>Tropical Overlook</i> 10 Tf 50		
23045	First DNA barcode efficiency assessment for an important ingredient in the Amazonian ayahuasca tea: <i>mariri/jagube</i> , <i>Banisteriopsis</i> (Malpighiaceae). <i>Genetic Resources and Crop Evolution</i> , 2023, 70, 1605-1616.	0.8	1

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23046	Whole Genome Sequencing and Comparative Genomics of Indian Isolates of Wheat Spot Blotch Pathogen <i>Bipolaris sorokiniana</i> Reveals Expansion of Pathogenicity Gene Clusters. <i>Pathogens</i> , 2023, 12, 1.	1.2	0
23047	The demographic history of house mice (<i>Mus musculus domesticus</i>) in eastern North America. <i>G3: Genes, Genomes, Genetics</i> , 2023, 13, .	0.8	8
23048	S-alleles and mating system in natural populations of <i>Capsella grandiflora</i> (Brassicaceae) and its congeneric relatives. <i>Flora: Morphology, Distribution, Functional Ecology of Plants</i> , 2023, 299, 152206.	0.6	1
23050	Genomic comparison of two strains of <i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i> with contrasting pathogenic phenotype. <i>Tuberculosis</i> , 2023, 138, 102299.	0.8	0
23051	Evolution and diversification of Mountain voles (Rodentia: Cricetidae). <i>Communications Biology</i> , 2022, 5, .	2.0	4
23052	Systematic evaluation of genome-wide metabolic landscapes in lactic acid bacteria reveals diet- and strain-specific probiotic idiosyncrasies. <i>Cell Reports</i> , 2022, 41, 111735.	2.9	8
23053	Shedding light on the origin of <i>Acanthocystidae</i> : <i>Ricksol blepharistes</i> gen. n., sp. n. (Ricksolidae fam.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf Ozanamia gen. n. (Ozanamiidae fam. n.), and “Heterophrys-like organisms” <i>Organisms Diversity and Evolution</i> , 0, , .	0.7	1
23055	Revising the taxonomic placement of <i>Laetiporus persicinus</i> within the Laetiporaceae. <i>Mycologia</i> , 2023, 115, 107-121.	0.8	1
23056	Three new species of <i>Nigrograna</i> (Dothideomycetes, Pleosporales) associated with Arabica coffee from Yunnan Province, China. <i>MycKeys</i> , 0, 94, 51-71.	0.8	3
23058	Impacts of climate change on species distribution patterns of <i>Polyspora</i> sweet in China. <i>Ecology and Evolution</i> , 2022, 12, .	0.8	8
23059	Existence of biogeographic barriers for the long-term Neogene–Quaternary divergence and differentiation of <i>Koenigia forrestii</i> in the Himalaya–Hengduan Mountains. <i>Botanical Journal of the Linnean Society</i> , 2023, 201, 230-253.	0.8	7
23060	Multi-gene phylogeny and morphology of <i>Ophiocordyceps laotii</i> sp. nov. and a new record of <i>O. buquetii</i> (Ophiocordycipitaceae, Hypocreales) on ants from Thailand. <i>Mycological Progress</i> , 2023, 22, .	0.5	4
23061	Early Genomic Surveillance and Phylogeographic Analysis of Getah Virus, a Reemerging Arbovirus, in Livestock in China. <i>Journal of Virology</i> , 2023, 97, .	1.5	5
23062	Chromosomal-level genome assembly of potato tuberworm, <i>Phthorimaea operculella</i> : a pest of solanaceous crops. <i>Scientific Data</i> , 2022, 9, .	2.4	5
23063	A pipeline for assembling low copy nuclear markers from plant genome skimming data for phylogenetic use. <i>PeerJ</i> , 0, 10, e14525.	0.9	2
23064	Faecal carriage of ESBL producing and colistin resistant <i>Escherichia coli</i> in avian species over a 2-year period (2017-2019) in Zimbabwe. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	3
23065	Chitin contributes to the formation of a feeding structure in a predatory nematode. <i>Current Biology</i> , 2023, 33, 15-27.e6.	1.8	8
23066	Comprehensive profiling of antibody responses to the human anellome using programmable phage display. <i>Cell Reports</i> , 2022, 41, 111754.	2.9	7

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23067	Description of a New Cobra (<i>Naja Laurenti</i> , 1768; Squamata, Elapidae) from China with Designation of a Neotype for <i>Naja atra</i> . <i>Animals</i> , 2022, 12, 3481.	1.0	4
23068	Complete Chloroplast Genome Sequence of Endangered Species in the Genus <i>Opisthopappus</i> C. Shih: Characterization, Species Identification, and Phylogenetic Relationships. <i>Genes</i> , 2022, 13, 2410.	1.0	1
23069	Multiple introgressions shape mitochondrial evolutionary history in <i>Drosophila paulistorum</i> and the <i>Drosophila willistoni</i> group. <i>Molecular Phylogenetics and Evolution</i> , 2023, 180, 107683.	1.2	2
23070	A multitude of spots! Five new microendemic species of the <i>Cnemaspis gracilis</i> group (Squamata:) Tj ETQq1 1 0.784314 rgBT /Overlo 1137-1186.	2.0	3
23071	Added Value of Next Generation over Sanger Sequencing in Kenyan Youth with Extensive HIV-1 Drug Resistance. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	2
23072	Taxonomy and phylogeny of <i>Sanguinoderma rugosum</i> complex with descriptions of a new species and a new combination. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
23073	Molecular ecology of the sleeper shark subgenus <i>Somniosus</i> (<i>Somniosus</i>) reveals genetic homogeneity within species and lack of support for <i>S. antarcticus</i> . <i>Journal of Heredity</i> , 2023, 114, 152-164.	1.0	2
23074	Impact of international travel and diarrhea on gut microbiome and resistome dynamics. <i>Nature Communications</i> , 2022, 13, .	5.8	9
23075	<i>Leveillula taurica</i> causing powdery mildew of chickpea in Brazil. <i>Journal of Phytopathology</i> , 2023, 171, 63-66.	0.5	0
23076	<i>Levilactobacillus humaensis</i> sp. nov. and <i>Lapidilactobacillus luobeiensis</i> sp. nov., isolated from traditional Chinese pickle. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	1
23077	<i>Brevibacillus daliensis</i> sp. nov., Isolated From Soil in Machangqing Nature Reserve. <i>Current Microbiology</i> , 2023, 80, .	1.0	0
23078	New globally distributed bacterial phyla within the FCB superphylum. <i>Nature Communications</i> , 2022, 13, .	5.8	4
23079	Time-calibrated phylogeny and ecological niche models indicate Pliocene aridification drove intraspecific diversification of brushtail possums in Australia. <i>Ecology and Evolution</i> , 2022, 12, .	0.8	1
23081	Dual Domestication, Diversity, and Differential Introgression in Old World Cotton Diploids. <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	3
23084	Constraining the composition and quantity of organic matter used by abundant marine Thaumarchaeota. <i>Environmental Microbiology</i> , 2023, 25, 689-704.	1.8	5
23086	Long-term host-pathogen evolution of endogenous beta- and gammaretroviruses in mouse lemurs with little evidence of recent retroviral introgression. <i>Virus Evolution</i> , 2023, 9, .	2.2	1
23087	18S rDNA sequence-structure phylogeny of the <i>Euglenophyceae</i> (Euglenozoa, Euglenida). <i>Journal of Eukaryotic Microbiology</i> , 2023, 70, .	0.8	2
23088	The Hercules pseudoscorpions from Madagascar: A systematic study of Feallidae (Pseudoscorpiones:) Tj ETQq1 1 0.784314 rgBT /Over Arthropod Systematics and Phylogeny, 0, 80, 649-691.	5.5	3

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23089	Draft Genome Sequence Resource of <i>Xylella fastidiosa</i> Strain Alm_Lz_1 Associated with a New Outbreak in Lazio, Italy. <i>Phytopathology</i> , 2023, 113, 108-111.	1.1	2
23090	Complete chloroplast genome and phylogenetic analysis of <i>Anemone shikokiana</i> . <i>Molecular Biology Reports</i> , 0, , .	1.0	0
23092	On the validity of <i>Hebius sauteri maximus</i> (Malnate, 1962) (Squamata, Natricidae), with the redescription of <i>H. maximus</i> comb. nov. and <i>H. sauteri</i> (Boulenger, 1909). <i>Herpetozoa</i> , 0, 35, 265-282.	1.0	3
23093	Molecular evolution and signatures of selective pressures on Bos, focusing on the Nelore breed (Bos) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 427	1.1	0
23094	Phylogeny-wide analysis of G-protein coupled receptors in social amoebas and implications for the evolution of multicellularity. <i>Open Research Europe</i> , 0, 2, 134.	2.0	0
23095	<i>Pontisma blauvikense</i> sp. nov. the first member of the early-diverging oomycete genus <i>Pontisma</i> parasitizing brown algae. <i>Journal of Eukaryotic Microbiology</i> , 2023, 70, .	0.8	3
23098	Genomics Analysis to Identify Multiple Genetic Determinants That Drive the Global Transmission of the Pandemic ST95 Lineage of Extraintestinal Pathogenic <i>Escherichia coli</i> (ExPEC). <i>Pathogens</i> , 2022, 11, 1489.	1.2	1
23099	<i>Ephedra kardangensis</i> , a New Synonym of <i>Ephedra gerardiana</i> (Ephedraceae). <i>Systematic Botany</i> , 2022, 47, 903-914.	0.2	0
23100	Host-plant affinities of stem-boring weevils and moths associated with fireweed (<i>Senecio</i>) using DNA barcoding. <i>Biocontrol Science and Technology</i> , 0, , 1-13.	0.5	2
23101	Recent speciation associated with range expansion and a shift to self-fertilization in North American <i>Arabidopsis</i> . <i>Nature Communications</i> , 2022, 13, .	5.8	4
23102	teiphy: A Python Package for Converting TEI XML Collations to NEXUS and Other Formats. <i>Journal of Open Source Software</i> , 2022, 7, 4879.	2.0	1
23104	Integration of mitogenomic and morphological data disentangles the systematics of <i>Pollenia</i> and establishes a revised phylogenetic hypothesis for the Polleniidae. <i>Systematic Entomology</i> , 2023, 48, 296-315.	1.7	2
23105	Genome sequence resources for <i>Verticillium dahliae</i> inhibiting <i>Streptomyces</i> spp. isolated from agricultural soil. <i>PhytoFrontiers</i> , 0, , .	0.8	0
23106	Characterization of Two New Apodemus Mitogenomes (Rodentia: Muridae) and Mitochondrial Phylogeny of Muridae. <i>Diversity</i> , 2022, 14, 1089.	0.7	2
23107	The unheeded existence of the tubular greens: molecular analyses reveal the distribution of a new <i>Ulva</i> species (Ulvophyceae, Chlorophyta), <i>Ulva capillata</i> sp. nov. in the Atlantic-Baltic Sea transect. <i>Journal of Applied Phycology</i> , 2023, 35, 509-522.	1.5	2
23108	Comparative analysis of mitochondrial genomes reveals marine adaptation in seagrasses. <i>BMC Genomics</i> , 2022, 23, .	1.2	2
23109	<i>Diatrype genheensis</i> sp. nov. a new wood-inhabiting species of Diatrypaceae (Xylariales) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 427	0.8	0
23110	Flower-like meristem conditions and spatial constraints shape architecture of floral pseudanthia in Apioideae. <i>EvoDevo</i> , 2022, 13, .	1.3	3

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23111	General principles for assignments of communities from <scp>eDNA</scp>: Open versus closed taxonomic databases. <i>Environmental DNA</i> , 2023, 5, 326-342.	3.1	4
23112	<i>Ramaria barenthalensis</i> a new record from western Himalayas, Azad Jammu and Kashmir, Pakistan. <i>Italian Botanist</i> , 0, 14, 133-143.	0.0	0
23113	Mapping HPV 16 Sub-Lineages in Anal Cancer and Implications for Disease Outcomes. <i>Diagnostics</i> , 2022, 12, 3222.	1.3	2
23115	Out of Madagascar, repeatedly: The phylogenetics and biogeography of Dombeyoideae (Malvaceae s.l.). <i>Molecular Phylogenetics and Evolution</i> , 2023, 182, 107687.	1.2	2
23116	Genome-Wide Identification and Expression Analysis of the 14-3-3 (TFT) Gene Family in Tomato, and the Role of S1TFT4 in Salt Stress. <i>Plants</i> , 2022, 11, 3491.	1.6	1
23118	Taxonomic, Genomic, and Functional Variation in the Gut Microbiomes of Wild Spotted Hyenas Across 2 Decades of Study. <i>MSystems</i> , 0, , .	1.7	1
23119	Alternative telomere maintenance mechanism in <i>Alligator sinensis</i> provides insights into aging evolution. <i>IScience</i> , 2023, 26, 105850.	1.9	2
23120	Codonoblepharontaeae, a New Major Lineage among Orthotrichoideae (Orthotrichaceae, Bryophyta). <i>Plants</i> , 2022, 11, 3557.	1.6	1
23121	Symbiotic Microorganisms and Their Different Association Types in Aquatic and Semiaquatic Bugs. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	0
23122	A new unique genus of Macrosiphini (Aphididae: Aphidinae) feeding on <i>Lonicera</i> from China. <i>Zoologischer Anzeiger</i> , 2023, 302, 186-197.	0.4	0
23123	The blackgrass genome reveals patterns of non-parallel evolution of polygenic herbicide resistance. <i>New Phytologist</i> , 2023, 237, 1891-1907.	3.5	14
23124	Long-Read Sequencing Improves Recovery of Picoeukaryotic Genomes and Zooplankton Marker Genes from Marine Metagenomes. <i>MSystems</i> , 2022, 7, .	1.7	7
23125	High-quality chromosome-level genome assembly of Pacific cod, <i>Gadus macrocephalus</i> . <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	0
23126	Inhibition of mitochondrial alternative oxidase causes lifecycle arrest of early-stage <i>Trachipleistophora hominis</i> meronts during intracellular infection of mammalian cells. <i>PLoS Pathogens</i> , 2022, 18, e1011024.	2.1	1
23127	A scalable model for simulating multi-round antibody evolution and benchmarking of clonal tree reconstruction methods. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	3
23128	Phylogenetic relationships and taxonomy of <i>Grifola</i> (Polyporales). <i>Mycological Progress</i> , 2023, 22, .	0.5	3
23129	<i>Neospongodes atlantica</i> , a potential case of an early biological introduction in the Southwestern Atlantic. <i>PeerJ</i> , 0, 10, e14347.	0.9	2
23130	Population structure and genetic connectivity of the scalloped hammerhead shark (<i>Sphyrna lewini</i>) across nursery grounds from the Eastern Tropical Pacific: Implications for management and conservation. <i>PLoS ONE</i> , 2022, 17, e0264879.	1.1	2

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23131	Convergent evolution and horizontal gene transfer in Arctic Ocean microalgae. <i>Life Science Alliance</i> , 2023, 6, e202201833.	1.3	6
23132	Functional characterization reveals a diverse array of metazoan fatty acid biosynthesis genes. <i>Molecular Ecology</i> , 2023, 32, 970-982.	2.0	9
23133	Molecular and cytogenetic evidence for sibling species in the Chagas disease vector <i>Triatoma maculata</i> . <i>Medical and Veterinary Entomology</i> , 2023, 37, 316-329.	0.7	1
23134	Karyotype evolution of the Asterids insights from the first genome sequences of the family Cornaceae. <i>DNA Research</i> , 2023, 30, .	1.5	2
23135	Plastome Characterization, Phylogenetic Relationships, and Regional Conservation Status of <i>Ficus populifolia</i> Vahl. (Moraceae), a Peripherally Isolated Plant Population in the Arabian Peninsula. <i>Forests</i> , 2022, 13, 2063.	0.9	1
23136	Vegetable biology and breeding in the genomics era. <i>Science China Life Sciences</i> , 2023, 66, 226-250.	2.3	10
23137	A new contribution to <i>Megasporoporia</i> sensu lato: Six new species and three new combinations. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	6
23138	Climate warming causes photobiont degradation and carbon starvation in a boreal climate sentinel lichen. <i>American Journal of Botany</i> , 2023, 110, .	0.8	5
23139	New Insights into <i>Lymphocystis</i> Disease Virus Genome Diversity. <i>Viruses</i> , 2022, 14, 2741.	1.5	3
23140	Evolution and Introductions of Influenza A Virus H1N1 in a Farrow-to-Finish Farm in Guatemala. <i>Microbiology Spectrum</i> , 0, , .	1.2	0
23141	Effects of discordance between species and gene trees on phylogenetic diversity conservation. <i>Journal of Mathematical Biology</i> , 2023, 86, .	0.8	1
23142	<i>Caldovatus aquaticus</i> sp. nov., a moderately thermophilic bacterium isolated from hot spring microbial mat. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	0
23143	Genomic Legacies of Ancient Adaptation Illuminate GC-Content Evolution in Bacteria. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	7
23145	Genomic Characterization of Skin and Soft Tissue <i>Streptococcus pyogenes</i> Isolates from a Low-Income and a High-Income Setting. <i>MSphere</i> , 2023, 8, .	1.3	4
23146	Convergent Genomic Signatures of High-Altitude Adaptation among Six Independently Evolved Mammals. <i>Animals</i> , 2022, 12, 3572.	1.0	1
23147	Leaf spot caused by <i>Neopestalotiopsis</i> species on <i>Arecaceae</i> in Brazil. <i>Australasian Plant Pathology</i> , 2023, 52, 47-62.	0.5	2
23148	How Important Are Functional and Developmental Constraints on Phenotypic Evolution? An Empirical Test with the Stomatal Anatomy of Flowering Plants. <i>American Naturalist</i> , 2023, 201, 794-812.	1.0	3
23149	Complete mitochondrial genome of the forensically important carrion beetle, <i>Necrodes nigricornis</i> (Coleoptera: Silphidae). <i>Journal of Asia-Pacific Entomology</i> , 2023, 26, 102033.	0.4	2

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23150	Comprehensive Genome Analysis of <i>Neisseria meningitidis</i> from South America Reveals a Distinctive Pathogenicity-Related Prophage Repertoire. <i>International Journal of Molecular Sciences</i> , 2022, 23, 15731.	1.8	0
23151	Natural infection of chiromyzinae larvae (diptera: Stratiomyidae) in southern Chile by <i>Tolypocladium valdiviae</i> sp. nov. <i>Fungal Biology</i> , 2022, , .	1.1	0
23152	Strong species structure but weak geographical structure in demersal Lake Victoria cichlids. <i>Ecology and Evolution</i> , 2022, 12, .	0.8	1
23153	Morphological and molecular reinvestigation of acanthoecid species III. “ <i>Kalathoea cupula</i> (Leadbeater, 1972) gen. et comb. nov. (= <i>Stephanoeca cupula</i> (Leadbeater) Thomsen, 1988). <i>European Journal of Protistology</i> , 2022, , 125943.	0.5	0
23154	Paratype: a genotyping tool for <i>Salmonella</i> Paratyphi A reveals its global genomic diversity. <i>Nature Communications</i> , 2022, 13, .	5.8	6
23156	The <i>Macrobotus persimilis-polonicus</i> complex (Eutardigrada, Macrobiotidae), another example of problematic species identification, with the description of four new species. <i>Organisms Diversity and Evolution</i> , 2023, 23, 329-368.	0.7	3
23157	Diverse Methylmercury (MeHg) Producers and Degraders Inhabit Acid Mine Drainage Sediments, but Few Taxa Correlate with MeHg Accumulation. <i>MSystems</i> , 2023, 8, .	1.7	1
23159	Time to update the sectional classification of <i>Ilex</i> (<i>Aquifoliaceae</i>): new insights from <i>Ilex</i> phylogeny, morphology, and distribution. <i>Journal of Systematics and Evolution</i> , 0, , .	1.6	2
23160	Draft Genome of White-Blotched River Stingray Provides Novel Clues for Niche Adaptation and Skeleton Formation. <i>Genomics, Proteomics and Bioinformatics</i> , 2023, 21, 501-514.	3.0	1
23161	Extensive gene flow in secondary sympatry after allopatric speciation. <i>National Science Review</i> , 2022, 9, .	4.6	8
23162	Cultivation-independent genomes greatly expand taxonomic-profiling capabilities of mOTUs across various environments. <i>Microbiome</i> , 2022, 10, .	4.9	22
23164	New reports, new species, and high diversity of <i>Cantharellus</i> in the southern Appalachians. <i>Mycologia</i> , 0, , 1-25.	0.8	0
23165	Glomerales Dominate Arbuscular Mycorrhizal Fungal Communities Associated with Spontaneous Plants in Phosphate-Rich Soils of Former Rock Phosphate Mining Sites. <i>Microorganisms</i> , 2022, 10, 2406.	1.6	3
23166	Induction of Multiple Immune Signaling Pathways in <i>Grylodes sigillatus</i> Crickets during Overt Viral Infections. <i>Viruses</i> , 2022, 14, 2712.	1.5	0
23167	Phylogenetic revision of Dennstaedtiodeae (Dennstaedtiaceae: Polypodiales) with description of <i>Mucura</i> , gen. nov.. <i>Taxon</i> , 0, , .	0.4	0
23168	Genomic Analysis of <i>Pseudomonas asiatica</i> JP233: An Efficient Phosphate-Solubilizing Bacterium. <i>Genes</i> , 2022, 13, 2290.	1.0	1
23169	Comparing the Efficiency of Single-Locus Species Delimitation Methods within Trochoidea (Gastropoda: Vetigastropoda). <i>Genes</i> , 2022, 13, 2273.	1.0	6
23170	Super-Mitobarcoding in Plant Species Identification? It Can Work! The Case of Leafy Liverworts Belonging to the Genus <i>Calypogeia</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 15570.	1.8	7

#	ARTICLE	IF	CITATIONS
23171	Two canonically aerobic foraminifera express distinct peroxisomal and mitochondrial metabolisms. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	2
23172	A reappraisal of the phylogeny and historical biogeography of <i>Sparganium</i> (Typhaceae) using complete chloroplast genomes. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	4
23174	First record of the human infection of <i>Brucella melitensis</i> in Kyrgyzstan: evidence from whole-genome sequencing-based analysis. <i>Infectious Diseases of Poverty</i> , 2022, 11, .	1.5	2
23175	Genomic innovation and regulatory rewiring during evolution of the cotton genus <i>Gossypium</i> . <i>Nature Genetics</i> , 2022, 54, 1959-1971.	9.4	33
23176	<i>Baldinia droopii</i> sp. nov. (Suessiales, Dinophyceae), a new species from a small rainwater rock pool near TvÄrminne, south-western Finland. <i>Phycologia</i> , 2023, 62, 68-82.	0.6	2
23177	Plastid phylogenomics sheds light on divergence time and ecological adaptations of the tribe Persicarieae (Polygonaceae). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
23180	Genome of <i>Paspalum vaginatum</i> and the role of trehalose mediated autophagy in increasing maize biomass. <i>Nature Communications</i> , 2022, 13, .	5.8	4
23182	The LEA gene family in tomato and its wild relatives: genome-wide identification, structural characterization, expression profiling, and role of SILEA6 in drought stress. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	7
23183	Phylogenomic analyses based on the plastid genome and concatenated nrDNA sequence data reveal cytonuclear discordance in genus <i>Atractylodes</i> (Asteraceae: Carduoideae). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	5
23184	Structural Diversities and Phylogenetic Signals in Plastomes of the Early-Divergent Angiosperms: A Case Study in Saxifragales. <i>Plants</i> , 2022, 11, 3544.	1.6	4
23185	Diversity of interstitial nemertean of the genus <i>Ototyphlonemertes</i> (Nemertea: Monostilifera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 34 genus. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	0
23186	<i>Sinapis</i> genomes provide insights into whole-genome triplication and divergence patterns within tribe Brassiceae. <i>Plant Journal</i> , 2023, 113, 246-261.	2.8	5
23187	Not all bad: Gyromitrin has a limited distribution in the false morels as determined by a new ultra high-performance liquid chromatography method. <i>Mycologia</i> , 2023, 115, 1-15.	0.8	3
23188	<i>Syringa oblata</i> genome provides new insights into molecular mechanism of flower color differences among individuals and biosynthesis of its flower volatiles. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	0
23189	Molecular and Structural Evolution of Porcine Epidemic Diarrhea Virus. <i>Animals</i> , 2022, 12, 3388.	1.0	2
23190	Diversity and Prevalence of <i>Clostridium innocuum</i> in the Human Gut Microbiota. <i>MSphere</i> , 2023, 8, .	1.3	6
23191	New perspectives on an old grouping: The genomic and phenotypic variability of <i>Oxalobacter formigenes</i> and the implications for calcium oxalate stone prevention. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
23192	Host's genetic background determines the outcome of reciprocal faecal transplantation on life-history traits and microbiome composition. <i>Animal Microbiome</i> , 2022, 4, .	1.5	2

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23193	Chromosome-scale genome assembly of <i>Glycyrrhiza uralensis</i> revealed metabolic gene cluster centred specialized metabolites biosynthesis. <i>DNA Research</i> , 2022, 29, .	1.5	3
23194	The Phylogeny of <i>Errazurizia</i> (Fabaceae: Amorpeae) and Description of the New Monotypic Genus <i>Pictarena</i> . <i>Systematic Botany</i> , 2022, 47, 1012-1024.	0.2	3
23195	Within-Host Genotypic and Phenotypic Diversity of Contemporaneous Carbapenem-Resistant <i>Klebsiella pneumoniae</i> from Blood Cultures of Patients with Bacteremia. <i>MBio</i> , 2022, 13, .	1.8	7
23196	An endogenous lentivirus in the germline of a rodent. <i>Retrovirology</i> , 2022, 19, .	0.9	1
23198	Across the highest mountain on earth: discordant phylogeographic patterns and recent dispersal of Tibetan stone loaches (<i>Triplophysa</i>) in the Himalayas. <i>Journal of Fish Biology</i> , 2024, 104, 374-386.	0.7	2
23199	Competitive Transmission of Carbapenem-Resistant <i>Klebsiella pneumoniae</i> in a Newly Opened Intensive Care Unit. <i>MSystems</i> , 2022, 7, .	1.7	1
23200	Evolution of 101 Apocynaceae plastomes and phylogenetic implications. <i>Molecular Phylogenetics and Evolution</i> , 2023, 180, 107688.	1.2	5
23201	Target sequence data shed new light on the infrafamilial classification of Araceae. <i>American Journal of Botany</i> , 2023, 110, .	0.8	3
23202	Repeated evolution of blanched coloration in a lizard across independent white-sand habitats. <i>Ecology and Evolution</i> , 2022, 12, .	0.8	1
23203	Species of <i>Zymoseptoria</i> (Dothideomycetes) as a Model System to Study Plant Pathogen Genome Evolution. , 2023, , 349-370.		0
23204	Genomic analysis of hypoxia inducible factor alpha in ray-finned fishes reveals missing Ohnologs and evidence of widespread positive selection. <i>Scientific Reports</i> , 2022, 12, .	1.6	9
23205	Epidemiological survey and genetic characterization of type 3 vaccine-derived poliovirus isolated from a patient with four doses of inactivated polio vaccine in Henan Province, China. <i>Infectious Diseases of Poverty</i> , 2022, 11, .	1.5	1
23206	Revised molecular phylogeny, global biogeography, and diversification of palms subfamily Coryphoideae (Arecaceae) based on low copy nuclear and plastid regions. <i>Journal of Plant Research</i> , 2023, 136, 159-177.	1.2	2
23207	Response to the detection of an exotic fungal pathogen, <i>Fusarium commune</i> , in a <i>Pinus radiata</i> production nursery in Australia. <i>Australian Forestry</i> , 0, , 1-12.	0.3	1
23208	The draft genome of the Tibetan partridge (<i>Perdix hodgsoniae</i>) provides insights into its phylogenetic position and high-altitude adaptation. <i>Journal of Heredity</i> , 0, , .	1.0	2
23210	A New Endemic Species of <i>Loasa</i> ser. <i>Macrospermae</i> (Loasaceae) from Northern Chile. <i>Systematic Botany</i> , 2022, 47, 1065-1079.	0.2	0
23211	Isolation and endemism in the subterranean aquatic snails of the genus <i>Belgrandiella</i> A. J. Wagner, 1928 (Caenogastropoda: Truncatelloidea: Hydrobiidae). <i>Hydrobiologia</i> , 2023, 850, 4089-4113.	1.0	4
23212	Dynamic evolution of the plastome in the Elm family (Ulmaceae). <i>Planta</i> , 2023, 257, .	1.6	6

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23213	Degree of Dietary Specialization on Furanocoumarin-Containing Hostplants in a Newly Invasive Web Building Caterpillar. <i>Journal of Chemical Ecology</i> , 0, , .	0.9	0
23214	Island life accelerates geographic radiation in the white-eyes (<i>Zosteropidae</i>). <i>Ibis</i> , 2023, 165, 817-828.	1.0	4
23215	Comparative phylogenetic analysis of oolong tea (Phoenix Dancong tea) using complete chloroplast genome sequences. <i>Heliyon</i> , 2022, 8, e12557.	1.4	4
23216	Post-vaccine epidemiology of serotype 3 pneumococci identifies transformation inhibition through prophage-driven alteration of a non-coding RNA. <i>Genome Medicine</i> , 2022, 14, .	3.6	4
23217	Epidemiological and Evolutionary Analysis of West Nile Virus Lineage 2 in Italy. <i>Viruses</i> , 2023, 15, 35.	1.5	1
23218	Reekekee- and roodoodooviruses, two different <i>Microviridae</i> clades constituted by the smallest DNA phages. <i>Virus Evolution</i> , 2023, 9, .	2.2	5
23219	Genomic Consequences of and Demographic Response to Pervasive Hybridization Over Time in Climate-Sensitive Pikas. <i>Molecular Biology and Evolution</i> , 2023, 40, .	3.5	4
23220	The complete chloroplast genome of <i>Dendrobium moschatum</i> (Buch.-Ham.) Sw. 1805 (Orchidaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 2027-2030.	0.2	0
23221	Genetic and demographic signatures accompanying the evolution of the selfing syndrome in <i>Daphne kiusiana</i> , an evergreen shrub. <i>Annals of Botany</i> , 2023, 131, 751-767.	1.4	5
23222	Identification of a conserved maxicircle and unique minicircles as part of the mitochondrial genome of <i>Leishmania martiniquensis</i> strain PCM3 in Thailand. <i>Parasites and Vectors</i> , 2022, 15, .	1.0	0
23223	Comprehensive re-analysis of hairpin small RNAs in fungi reveals loci with conserved links. <i>ELife</i> , 0, 11, .	2.8	4
23224	The antigen recognition portion of African buffalo class I MHC is highly polymorphic, consistent with a complex pathogen challenge environment, and the 3â€™ region suggests distinct haplotype configurations. <i>Immunogenetics</i> , 0, , .	1.2	0
23225	Molecular Characteristics of an NDM-4 and OXA-181 Co-Producing K51-ST16 Carbapenem-Resistant <i>Klebsiella pneumoniae</i> : Study of Its Potential Dissemination Mediated by Conjugative Plasmids and Insertion Sequences. <i>Antimicrobial Agents and Chemotherapy</i> , 2023, 67, .	1.4	3
23226	Gene expressions between obligate bamboo-eating pandas and non-herbivorous mammals reveal converged specialized bamboo diet adaptation. <i>BMC Genomics</i> , 2023, 24, .	1.2	1
23227	Evolution of a hybrid zone of two willow species (<i>Salix</i> L.) in the European Alps analyzed by RAD-seq and morphometrics. <i>Ecology and Evolution</i> , 2023, 13, .	0.8	2
23229	<i>Phaeotubakia lithocarpicola</i> gen. et sp. nov. (Tubakiaceae, Diaporthales) from leaf spots in China. <i>MycKeys</i> , 0, 95, 15-25.	0.8	0
23230	A first look at sea-lavenders genomics “ can genome wide SNP information tip the scales of controversy in the <i>Limonium vulgare</i> species complex?. <i>BMC Plant Biology</i> , 2023, 23, .	1.6	1
23231	Endophytic Fungi Associated with Mango Show In Vitro Antagonism against Bacterial and Fungal Pathogens. <i>Agronomy</i> , 2023, 13, 169.	1.3	4

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23232	The plastid genome of twenty-two species from <i>Ferula</i> , <i>Talassia</i> , and <i>Soranthus</i> : comparative analysis, phylogenetic implications, and adaptive evolution. <i>BMC Plant Biology</i> , 2023, 23, .	1.6	3
23233	Dissemination of Metallo- β -Lactamase-Producing <i>Pseudomonas aeruginosa</i> in Serbian Hospital Settings: Expansion of ST235 and ST654 Clones. <i>International Journal of Molecular Sciences</i> , 2023, 24, 1519.	1.8	5
23234	Epidemiological Analysis on the Occurrence of <i>Salmonella enterica</i> Subspecies <i>enterica</i> Serovar Dublin in the German Federal State Schleswig-Holstein Using Whole-Genome Sequencing. <i>Microorganisms</i> , 2023, 11, 122.	1.6	2
23235	Two new records of <i>Tricholoma</i> species from Pakistan based on morphological features and phylogenetic analysis. <i>Plant and Fungal Systematics</i> , 2022, 67, 25-33.	0.7	0
23236	Unraveling the macroevolution of horseshoe bats (Chiroptera: Rhinolophidae): Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 582 Td (<i>>Rh	0.9	1
23237	High-quality genome of <i>Diaphanosoma dubium</i> provides insights into molecular basis of its broad ecological adaptation. <i>IScience</i> , 2023, 26, 106006.	1.9	0
23238	Phylogeny based generic reclassification of <i>Muscari</i> sensu lato (Asparagaceae) using plastid and genomic DNA. <i>Taxon</i> , 2023, 72, 261-277.	0.4	5
23239	Antimicrobial Resistance of and Genomic Insights into <i>Pasteurella multocida</i> Strains Isolated from Australian Pigs. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	5
23243	No Tail No Fail: Life Cycles of the Zoogonidae (Digenea). <i>Diversity</i> , 2023, 15, 121.	0.7	0
23244	Fbxl4 Regulates the Photic Entrainment of Circadian Locomotor Rhythms in the Cricket <i>Gryllus bimaculatus</i> . <i>Zoological Science</i> , 2023, 40, .	0.3	2
23245	Chromosome-level haplotype-resolved genome assembly for <i>Takifugu ocellatus</i> using PacBio and Hi-C technologies. <i>Scientific Data</i> , 2023, 10, .	2.4	2
23246	Insights into the Genomic and Phenotypic Landscape of the Oleaginous Yeast <i>Yarrowia lipolytica</i> . <i>Journal of Fungi (Basel, Switzerland)</i> , 2023, 9, 76.	1.5	1
23247	Integrative taxonomy reveals that not all European reddish runcinids are the same: the case of the <i>Runcina ferruginea</i> Kress, 1977 (Gastropoda, Heterobranchia, Runcinida) species-complex, with the description of a new genus. <i>Invertebrate Systematics</i> , 2023, 37, 61.	0.5	0
23248	A new species of the genus <i>Eubranchus</i> (Gastropoda: Nudibranchia) from Vietnamese coastal waters. <i>Ruthenica</i> , 2023, 33, 1-8.	0.2	0
23250	Longitudinal, Multi-Platform Metagenomics Yields a High-Quality Genomic Catalog and Guides an <i>In Vitro</i> Model for Cheese Communities. <i>MSystems</i> , 2023, 8, .	1.7	4
23251	Neotropical <i>Clavulina</i> : Two new species from Mexico and a re-evaluation of <i>Clavulina floridana</i> . <i>Mycologia</i> , 2023, 115, 135-152.	0.8	2
23253	Improving Orthologous Signal and Model Fit in Datasets Addressing the Root of the Animal Phylogeny. <i>Molecular Biology and Evolution</i> , 2023, 40, .	3.5	7
23254	Mycoparasites, Gut Dwellers, and Saprotrophs: Phylogenomic Reconstructions and Comparative Analyses of Kickxellomycotina Fungi. <i>Genome Biology and Evolution</i> , 2023, 15, .	1.1	6

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23255	Characterization and phylogenetic analysis of the complete mitochondrial genome sequence of <i>Photinia serratifolia</i> . <i>Scientific Reports</i> , 2023, 13, .	1.6	10
23256	<i>Gymnopilus rubellus</i> sp. nov. from the coniferous forests of Azad Jammu and Kashmir, Pakistan. <i>Plant Systematics and Evolution</i> , 2023, 309, .	0.3	1
23257	The male-heterogametic sex determination system on chromosome 15 of <i>Salix triandra</i> and <i>Salix arbutifolia</i> reveals ancestral male heterogamety and subsequent turnover events in the genus <i>Salix</i> . <i>Heredity</i> , 2023, 130, 122-134.	1.2	3
23258	A chromosome-level genome assembly of the <i>Henosepilachna vigintioctomaculata</i> provides insights into the evolution of ladybird beetles. <i>DNA Research</i> , 2023, 30, .	1.5	2
23259	Egg parasitoids (Hymenoptera: Mymaridae and Trichogrammatidae) of okra leafhopper, <i>Amrasca biguttula</i> (Ishida) (Hemiptera: Cicadellidae), in southern Japan. <i>Journal of Asia-Pacific Entomology</i> , 2023, 26, 102041.	0.4	1
23260	The complete chloroplast genome of an endangered plant <i>Artemisia borotalensis</i> (Asteraceae) and phylogenetic analysis. <i>Mitochondrial DNA Part B: Resources</i> , 2023, 8, 145-148.	0.2	0
23262	Taxonomy, Phylogeny, Divergence Time Estimation, and Biogeography of the Family Pseudoplagiostomataceae (Ascomycota, Diaporthales). <i>Journal of Fungi (Basel, Switzerland)</i> , 2023, 9, 82.	1.5	3
23263	Pleiotropy Structures Plant Height and Seed Weight Scaling in Barley despite Long History of Domestication and Breeding Selection. <i>Plant Phenomics</i> , 2023, 5, .	2.5	2
23264	Taxonomy and Phylogeny of <i>Peniophora</i> Sensu Lato (Russulales, Basidiomycota). <i>Journal of Fungi (Basel, Switzerland)</i> , 2023, 9, 93.	1.5	3
23265	Mammarenavirus Genetic Diversity and Its Biological Implications. <i>Current Topics in Microbiology and Immunology</i> , 2023, , 265-303.	0.7	0
23266	Phylogenetic and morphological evidence reveals the association between diet and the evolution of the venom delivery system in Neotropical goo-eating snakes. <i>Systematics and Biodiversity</i> , 2023, 21, .	0.5	3
23267	Ancient DNA elucidates the lost world of western Indian Ocean giant tortoises and reveals a new extinct species from Madagascar. <i>Science Advances</i> , 2023, 9, .	4.7	5
23268	A chromosome-scale genome assembly of <i>Artemisia argyi</i> reveals unbiased subgenome evolution and key contributions of gene duplication to volatile terpenoid diversity. <i>Plant Communications</i> , 2023, 4, 100516.	3.6	16
23269	The gestational membrane microbiome in the presence or absence of intraamniotic infection. <i>American Journal of Obstetrics & Gynecology MFM</i> , 2023, 5, 100837.	1.3	1
23270	A deeply conserved protease, acylamino acid-releasing enzyme (AARE), acts in ageing in <i>Physcomitrella</i> and <i>Arabidopsis</i> . <i>Communications Biology</i> , 2023, 6, .	2.0	3
23271	<i>Cytospora paraplurivora</i> sp. nov. isolated from orchards with fruit tree decline syndrome in Ontario, Canada. <i>PLoS ONE</i> , 2023, 18, e0279490.	1.1	3
23272	Heterogeneity in diagnostic characters across ecoregions: A case study with <i>Botrynuma</i> (Hydrozoa: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.2	2
23273	Biased mutations and gene losses underlying diploidization of the tetraploid broomcorn millet genome. <i>Plant Journal</i> , 2023, 113, 787-801.	2.8	4

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23274	The complete chloroplast genome of a fast-growing tree <i>Lophostemon confertus</i> (Myrtaceae). Mitochondrial DNA Part B: Resources, 2023, 8, 26-29.	0.2	1
23275	Genomic Characterization of <i>Salmonella enterica</i> serovar Weltevreden Associated with Human Diarrhea. Microbiology Spectrum, 2023, 11, .	1.2	4
23276	<i>Myxobolus shuifuensis</i> sp. n. (Myxozoa: Myxobolidae) infecting the exotic mrigal <i>Cirrhinus mrigala</i> feral in China. Parasitology International, 2023, , 102732.	0.6	0
23277	Molecular characterization and comparisons of potato wart (<i>Synchytrium endobioticum</i>) in historic collections to recent findings in Canada and the Netherlands. , 0, , .		1
23278	The <i>Aphelenchoides</i> genomes reveal substantial horizontal gene transfers in the last common ancestor of free-living and major plant-parasitic nematodes. Molecular Ecology Resources, 2023, 23, 905-919.	2.2	2
23279	Taxonomic Study of Three Novel <i>Paenibacillus</i> Species with Cold-Adapted Plant Growth-Promoting Capacities Isolated from Root of <i>Larix gmelinii</i> . Microorganisms, 2023, 11, 130.	1.6	1
23281	Molecular phylogeny and genetic diversity of some <i>Lepidagathis</i> species (Acanthaceae) based on nuclear and chloroplast regions. Plant Biosystems, 2023, 157, 455-464.	0.8	0
23283	Insights into chloroplast genome structure, intraspecific variation, and phylogeny of <i>Cyclamen</i> species (Myrsinoideae). Scientific Reports, 2023, 13, .	1.6	2
23284	New record of <i>Pholiota multicingulata</i> (Strophariaceae) from India based on morphological data and phylogenetic analyses. Studies in Fungi, 2023, 8, 1-5.	0.5	0
23286	Overexpression of <i>Liriodendron</i> WOX5 in <i>Arabidopsis</i> Leads to Ectopic Flower Formation and Altered Root Morphology. International Journal of Molecular Sciences, 2023, 24, 906.	1.8	1
23287	The complete chloroplast genome of <i>Urtica angustifolia</i> Fisch. ex Hornem. (Urticaceae), an important kind of traditional Chinese medicine in China. Mitochondrial DNA Part B: Resources, 2023, 8, 116-118.	0.2	0
23289	Genomic basis of Y-linked dwarfism in cichlids pursuing alternative reproductive tactics. Molecular Ecology, 2023, 32, 1592-1607.	2.0	3
23290	<i>Fusculimoides kohtsukai</i> gen. et sp. nov., a Minute Eulimid Gastropod Parasitic on the Little Brittle Star <i>Ophiactis savignyi</i> in Central Japan. Zoological Science, 2023, 40, .	0.3	2
23294	A New Species from the Canary Islands Increases the Diversity of the Red Algal Genus <i>Pterocliadiella</i> in the Northeastern Atlantic. Plants, 2023, 12, 416.	1.6	0
23297	Biogeography of the Sunda Shelf revisited: Insights from <i>Macaranga</i> section <i>Pruinosae</i> (Euphorbiaceae). Frontiers in Ecology and Evolution, 0, 10, .	1.1	2
23298	Phylogeny and Morphology of Novel Species and New Collections Related to <i>Sarcoscyphaceae</i> (Pezizales, Ascomycota) from Southwestern China and Thailand. Biology, 2023, 12, 130.	1.3	1
23299	Exploring the diversity of microorganisms and potential pectinase activity isolated from wet fermentation of coffee in northeastern Peru. Food Science and Technology, 0, 43, .	0.8	0
23300	Phylogeny of <i>Saxifraga</i> section <i>Saxifraga</i> subsection <i>Arachnoideae</i> (Saxifragaceae) and the origin of low elevation shade-dwelling species. Ecology and Evolution, 2023, 13, .	0.8	2

#	ARTICLE	IF	CITATIONS
23301	Novel CaLB-like Lipase Found Using ProspectBIO, a Software for Genome-Based Bioprospection. <i>BioTech</i> , 2023, 12, 6.	1.3	0
23302	The complete chloroplast genome of <i>Crataegus scabrifolia</i> (Franch.) Rehd (Rosaceae), a medicinal and edible plant in Southwest China. <i>Mitochondrial DNA Part B: Resources</i> , 2023, 8, 81-85.	0.2	0
23303	Linking breadfruit cultivar names across the globe connects histories after 230 years of separation. <i>Current Biology</i> , 2023, 33, 287-297.e3.	1.8	2
23305	Skinks of Oceania, New Guinea, and Eastern Wallacea: an underexplored biodiversity hotspot. <i>Pacific Conservation Biology</i> , 2023, 29, 526-543.	0.5	4
23306	The complete chloroplast genome of <i>Cynoglossum amabile</i> Stapf & J. R. Drumm., 1906 (Boraginaceae), a traditional Chinese herbal medicine. <i>Mitochondrial DNA Part B: Resources</i> , 2023, 8, 52-56.	0.2	0
23307	CanB is a metabolic mediator of antibiotic resistance in <i>Neisseria gonorrhoeae</i> . <i>Nature Microbiology</i> , 2023, 8, 28-39.	5.9	3
23308	Similar evolutionary trajectories in an environmental <i>Cryptococcus neoformans</i> isolate after human and murine infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2023, 120, .	3.3	5
23309	The Mitochondrial Genomes of Two Parasitoid Wasps <i>Protapanteles immunis</i> and <i>Parapanteles hyposidrae</i> (Hymenoptera: Braconidae) with Phylogenetic Implications and Novel Gene Rearrangements. <i>Genes</i> , 2023, 14, 230.	1.0	0
23310	Diversity and evolution of computationally predicted T cell epitopes against human respiratory syncytial virus. <i>PLoS Computational Biology</i> , 2023, 19, e1010360.	1.5	2
23311	Phylogenetic Conservation of Soil Microbial Responses to Elevated Tropospheric Ozone and Nitrogen Fertilization. <i>MSystems</i> , 2023, 8, .	1.7	4
23312	Evaluating impacts of syntenic block detection strategies on rearrangement phylogeny using <i>Mycobacterium tuberculosis</i> isolates. <i>Bioinformatics</i> , 2023, 39, .	1.8	1
23313	Chromosome genome assembly for the meagre, <i>Argyrosomus regius</i> , reveals species adaptations and sciaenid sex-related locus evolution. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	3
23314	Correlation with a limited set of behavioral niches explains the convergence of somatic morphology in mygalomorph spiders. <i>Ecology and Evolution</i> , 2023, 13, .	0.8	5
23315	Spatiotemporal process of long-distance seed dispersal in a pantropically distributed sea hibiscus group. <i>Molecular Ecology</i> , 0, , .	2.0	1
23316	<i>Commelina danxiaensis</i> (Commelinaceae), a new species from Guangdong, China. <i>PhytoKeys</i> , 0, 218, 117-126.	0.4	2
23317	Genomic evidence for three distinct species in the <i>Erebia manto</i> complex in Central Europe (Lepidoptera, Nymphalidae). <i>Conservation Genetics</i> , 2023, 24, 293-304.	0.8	3
23318	The chromosome-scale genome assembly of the yellowtail clownfish <i>Amphiprion clarkii</i> provides insights into the melanistic pigmentation of anemonefish. <i>G3: Genes, Genomes, Genetics</i> , 2023, 13, .	0.8	4
23319	Taxonomic review of <i>Saguinus mystax</i> (Spix, 1823) (Primates, Callitrichidae), and description of a new species. <i>PeerJ</i> , 0, 11, e14526.	0.9	3

#	ARTICLE	IF	CITATIONS
23320	Resolving a nearly 90-year-old enigma: The rare <i>Fagus chienii</i> is conspecific with <i>F. hayatae</i> based on molecular and morphological evidence. <i>Plant Diversity</i> , 2023, 45, 544-551.	1.8	0
23321	The genome of the oomycete <i>Peronosclerospora sorghi</i> , a cosmopolitan pathogen of maize and sorghum, is inflated with dispersed pseudogenes. <i>G3: Genes, Genomes, Genetics</i> , 2023, 13, .	0.8	2
23322	Blood parasites (<i>Trypanosoma</i> , <i>Leucocytozoon</i> , <i>Haemoproteus</i>) in the Eurasian sparrowhawk (<i>Accipiter nisus</i>): diversity, incidence and persistence of infection at the individual level. <i>Parasites and Vectors</i> , 2023, 16, .	1.0	3
23324	Reference-Based RADseq Unravels the Evolutionary History of Polar Species in the Crux Lichenogorurum™ Genus <i>Usnea</i> (Parmeliaceae, Ascomycota). <i>Journal of Fungi (Basel, Switzerland)</i> , 2023, 9, 99.	1.5	1
23325	Integrative omics analyses of the ligninolytic <i>Rhodospiridium fluviale</i> LM-2 disclose catabolic pathways for biobased chemical production. , 2023, 16, .		2
23326	Myxozoans (Cnidaria) do not retain key oxygen-sensing and homeostasis toolkit genes. <i>Genome Biology and Evolution</i> , 0, , .	1.1	0
23327	Infection by SARS-CoV-2 with alternate frequencies of mRNA vaccine boosting. <i>Journal of Medical Virology</i> , 2023, 95, .	2.5	13
23330	Comparative genomics and molecular epidemiology of colistin-resistant <i>Acinetobacter baumannii</i> . <i>Computational and Structural Biotechnology Journal</i> , 2023, 21, 574-585.	1.9	10
23331	Phylogenetic relationships and systematics of the bamboo specialist <i>Amaurospiza</i> blue seedeaters. <i>Ibis</i> , 2023, 165, 844-861.	1.0	3
23332	A chromosome-level genome assembly of radish (<i>Raphanus sativus</i> L.) reveals insights into genome adaptation and differential bolting regulation. <i>Plant Biotechnology Journal</i> , 2023, 21, 990-1004.	4.1	14
23333	Best BLAST hit alone cannot be used as evidence of fraud. <i>Scientific Reports</i> , 2023, 13, .	1.6	0
23334	Exploring Evolutionary Relationships within Neodermata Using Putative Orthologous Groups of Proteins, with Emphasis on Peptidases. <i>Tropical Medicine and Infectious Disease</i> , 2023, 8, 59.	0.9	2
23335	A new and efficient enrichment method for metagenomic sequencing of Monkeypox virus. <i>BMC Genomics</i> , 2023, 24, .	1.2	2
23336	Nuclear Genome Sequence and Gene Expression of an Intracellular Fungal Endophyte Stimulating the Growth of Cranberry Plants. <i>Journal of Fungi (Basel, Switzerland)</i> , 2023, 9, 126.	1.5	2
23337	The complete chloroplast genome of <i>Pseudotsuga sinensis</i> , a China endemic species. <i>Mitochondrial DNA Part B: Resources</i> , 2023, 8, 23-25.	0.2	0
23338	Genomic evidence for contrasting patterns of host-associated genetic differentiation across shared host-plant species in leaf- and bud-galling sawflies. <i>Molecular Ecology</i> , 2023, 32, 1791-1809.	2.0	3
23340	The role of functional and phylogenetic diversity in riparian tree vegetation on leaf litter breakdown in rivers. <i>Oikos</i> , 2023, 2023, .	1.2	1
23341	<i>Legionella maioricensis</i> sp. nov., a new species isolated from the hot water distribution systems of a hospital and a shopping center during routine sampling. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2023, 73, .	0.8	3

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23342	Annotation of the <i>Turnera subulata</i> (Passifloraceae) Draft Genome Reveals the S-Locus Evolved after the Divergence of Turneroideae from Passifloroideae in a Stepwise Manner. <i>Plants</i> , 2023, 12, 286.	1.6	2
23343	Utilizing evolutionary conservation to detect deleterious mutations and improve genomic prediction in cassava. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
23344	Draft Metagenome-Assembled Genome Sequence of a Novel <i>Citricoccus</i> Species from Agricultural Soil in Western Colorado. <i>Microbiology Resource Announcements</i> , 0, , .	0.3	0
23345	Discovery of novel Mamastroviruses in Bactrian camels and dromedaries reveals complex recombination history. <i>Virus Evolution</i> , 2023, 9, .	2.2	2
23346	Natural Recombination among Type I Restriction-Modification Systems Creates Diverse Genomic Methylation Patterns among <i>Xylella fastidiosa</i> Strains. <i>Applied and Environmental Microbiology</i> , 2023, 89, .	1.4	1
23347	Constraints to speciation despite divergence in an old haplochromine cichlid lineage. <i>Evolution; International Journal of Organic Evolution</i> , 2023, 77, 823-835.	1.1	1
23348	Biochemical and Genomic Characterization of Two New Strains of <i>Lactobacillus paracasei</i> Isolated from the Traditional Corn-Based Beverage of South Africa, Mahewu, and Their Comparison with Strains Isolated from Kefir Grains. <i>Foods</i> , 2023, 12, 223.	1.9	5
23349	Reconstruction of Plastid Proteomes of Apicomplexans and Close Relatives Reveals the Major Evolutionary Outcomes of Cryptic Plastids. <i>Molecular Biology and Evolution</i> , 2023, 40, .	3.5	11
23350	The chloroplast genome of <i>Lappula myosotis</i> V. Wolf, a medicinal species. <i>Mitochondrial DNA Part B: Resources</i> , 2023, 8, 30-33.	0.2	0
23351	Comprehensive characterization of aerobic groundwater biotreatment media. <i>Water Research</i> , 2023, 230, 119587.	5.3	2
23352	Molecular, morphological, and life history data to support research of huntsman spiders (Araneae: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.5	0
23353	High-quality genome sequence reveals a young polyploidization and provides insights into cellulose and lignin biosynthesis in water dropwort (<i>Oenanthe sinensis</i>). <i>Industrial Crops and Products</i> , 2023, 193, 116203.	2.5	7
23354	Invasive <i>Vaucheria</i> aff. <i>compacta</i> (Xanthophyceae) and its distribution over a high Arctic tidal flat in Svalbard. <i>Estuarine, Coastal and Shelf Science</i> , 2023, 281, 108206.	0.9	2
23355	The evolutionary journey of freshwater crabs of the genus <i>Potamon</i> (Decapoda: Brachyura: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	1.2	0
23356	Phylogeny and historical biogeography of the water boatmen (Insecta: Hemiptera: Heteroptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 1	1.2	2
23357	Integrative analysis reveals the divergence and speciation between sister Sooty Copper butterflies <i>Lycaena bleusei</i> and <i>L. tityrus</i> . <i>Molecular Phylogenetics and Evolution</i> , 2023, 180, 107699.	1.2	1
23358	Homoploid hybrids are common but evolutionary dead ends, whereas polyploidy is not linked to hybridization in a group of Pyrenean saxifrages. <i>Molecular Phylogenetics and Evolution</i> , 2023, 180, 107703.	1.2	2
23359	Genome-wide identification glutathione-S-transferase gene superfamily in <i>Daphnia pulex</i> and its transcriptional response to nanoplastics. <i>International Journal of Biological Macromolecules</i> , 2023, 230, 123112.	3.6	10

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23360	Insights into the evolutionary history and taxonomic status of <i>Sinopteris</i> (Pteridaceae). <i>Molecular Phylogenetics and Evolution</i> , 2023, 180, 107672.	1.2	0
23361	Genomic divergence and introgression among three <i>Populus</i> species. <i>Molecular Phylogenetics and Evolution</i> , 2023, 180, 107686.	1.2	5
23362	Genome-resolved metagenomics reveals depth-related patterns of microbial community structure and functions in a highly stratified, AMD overlaying mine tailings. <i>Journal of Hazardous Materials</i> , 2023, 447, 130774.	6.5	4
23363	Whole-genome sequencing for genetic diversity analysis of Iranian <i>Brucella</i> spp. isolated from humans and livestock. <i>One Health</i> , 2023, 16, 100483.	1.5	3
23364	A phylogeny of <i>Calligonum</i> L. (Polygonaceae) yields challenges to current taxonomic classifications. <i>Acta Botanica Brasilica</i> , 2021, 35, 310-322.	0.8	1
23365	Phylogenomic resolution of order- and family-level monocot relationships using 602 single-copy nuclear genes and 1375 BUSCO genes. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	10
23366	Phylogenetic Analysis of Wild Pomegranate (<i>Punica granatum</i> L.) Based on Its Complete Chloroplast Genome from Tibet, China. <i>Agronomy</i> , 2023, 13, 126.	1.3	4
23367	<i>Escherichia Coli</i> : What Is and Which Are? <i>Molecular Biology and Evolution</i> , 2023, 40, .	3.5	5
23368	In situ cultivation of deep-sea water with bicarbonate fueled a different microbial community. <i>Acta Oceanologica Sinica</i> , 2022, 41, 98-104.	0.4	0
23369	Mitogenomic Codon Usage Patterns of Superfamily Certhioidea (Aves, Passeriformes): Insights into Asymmetrical Bias and Phylogenetic Implications. <i>Animals</i> , 2023, 13, 96.	1.0	4
23370	An Integrative Approach for the Identification of Native and Exotic Lymnaeids from Brazil. <i>Malacologia</i> , 2022, 65, .	0.2	1
23371	Comprehensive analysis of the metabolic and genomic features of tannin-transforming <i>Lactiplantibacillus plantarum</i> strains. <i>Scientific Reports</i> , 2022, 12, .	1.6	1
23372	Phylogenomics, divergence time estimation, and adaptive evolution in the Polygonoideae (Polygonaceae). <i>Journal of Systematics and Evolution</i> , 2023, 61, 1004-1019.	1.6	0
23373	A time relic: a new species of dwarf boa, <i>Tropidophis Bibron</i> , 1840 (Serpentes: Amerophidia), from the Upper Amazon Basin. <i>European Journal of Taxonomy</i> , 0, 854, 1-107.	0.6	1
23374	Metagenomic analysis reveals unexplored diversity of archaeal virome in the human gut. <i>Nature Communications</i> , 2022, 13, .	5.8	14
23375	Molecular machineries of ciliogenesis, cell survival, and vasculogenesis are differentially expressed during regeneration in explants of the demosponge <i>Halichondria panicea</i> . <i>BMC Genomics</i> , 2022, 23, .	1.2	3
23376	High-Quality Genomes of Pangolins: Insights into the Molecular Basis of Scale Formation and Adaption to Myrmecophagous Diet. <i>Molecular Biology and Evolution</i> , 2023, 40, .	3.5	4
23377	Plastid Phylogenomics Provide Evidence to Accept Two New Members of <i>Ligusticopsis</i> (Apiaceae.) <i>Tj ETQq1 1 0.784314 rgBT₀Overlo</i>	1.8	0

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23378	Mediterranean Matters: Revision of the Family Onchidorididae (Mollusca, Nudibranchia) with the Description of a New Genus and a New Species. <i>Diversity</i> , 2023, 15, 38.	0.7	4
23380	<i>Fusarium</i> diversity associated with the <i>Sorghum-Striga</i> interaction in Ethiopia. <i>Fungal Systematics and Evolution</i> , 2022, 10, 177-215.	0.9	4
23381	Phylotranscriptomic Analyses of Mycoheterotrophic Monocots Show a Continuum of Convergent Evolutionary Changes in Expressed Nuclear Genes From Three Independent Nonphotosynthetic Lineages. <i>Genome Biology and Evolution</i> , 2023, 15, .	1.1	5
23383	Distribution and New Records of the Bluntnose Sixgill Shark, <i>Hexanchus griseus</i> (Hexanchiformes: Tj ETQq1 1 0.784314 rgBT ₂ /Overlook	1.0	
23384	A one-year genomic investigation of <i>Escherichia coli</i> epidemiology and nosocomial spread at a large US healthcare network. <i>Genome Medicine</i> , 2022, 14, .	3.6	17
23385	Global gene expression analysis reveals complex cuticle organization of the <i>Tribolium</i> compound eye. <i>Genome Biology and Evolution</i> , 0, , .	1.1	0
23386	Genomic insight into <i>Myroides oncorhynchi</i> sp. nov., a new member of the <i>Myroides</i> genus, isolated from the internal organ of rainbow trout (<i>Oncorhynchus mykiss</i>). <i>Antonie Van Leeuwenhoek</i> , 2023, 116, 291-302.	0.7	1
23387	Bringing Plant Immunity to Light: A Genetically Encoded, Bioluminescent Reporter of Pattern-Triggered Immunity in <i>Nicotiana benthamiana</i>. <i>Molecular Plant-Microbe Interactions</i> , 2023, 36, 139-149.	1.4	3
23388	Variation in heat shock protein 40kDa relates to divergence in thermotolerance among cryptic rotifer species. <i>Scientific Reports</i> , 2022, 12, .	1.6	1
23389	Plastid Phylogenomic Analyses Reveal the Taxonomic Position of <i>Peucedanum franchetii</i> . <i>Plants</i> , 2023, 12, 97.	1.6	1
23390	Assessing Species Boundaries in the Freshwater Snail Family Physidae Using Coalescent-Based Delimitation Methods. <i>Malacologia</i> , 2022, 65, .	0.2	1
23391	A choline-releasing glycerophosphodiesterase essential for phosphatidylcholine biosynthesis and blood stage development in the malaria parasite. <i>ELife</i> , 0, 11, .	2.8	8
23392	Ancestral reconstruction reveals catalytic inactivation of activation-induced cytidine deaminase concomitant with cold water adaption in the Gadiformes bony fish. <i>BMC Biology</i> , 2022, 20, .	1.7	3
23393	Population Genomic Evidence for the Diversification of <i>Bellamyia aeruginosa</i> in Different River Systems in China. <i>Biology</i> , 2023, 12, 29.	1.3	0
23394	One in, one out: Generic circumscription within subtribe Manilkarinae (Sapotaceae). <i>Taxon</i> , 0, , .	0.4	2
23395	An atypical NLR protein modulates the NRC immune receptor network in <i>Nicotiana benthamiana</i> . <i>PLoS Genetics</i> , 2023, 19, e1010500.	1.5	19
23396	Comparative and expression analyses of AP2/ERF genes reveal copy number expansion and potential functions of ERF genes in Solanaceae. <i>BMC Plant Biology</i> , 2023, 23, .	1.6	4
23398	Two New <i>Ferula</i> (Apiaceae) Species from Central Anatolia: <i>Ferula turcica</i> and <i>Ferula latialata</i> . <i>Horticulturae</i> , 2023, 9, 144.	1.2	3

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23399	A novel probe set for the phylogenomics and evolution of <sc>RTA</sc> spiders. <i>Cladistics</i> , 2023, 39, 116-128.	1.5	5
23400	Chloroplast genomes of four <i>Carex</i> species: Long repetitive sequences trigger dramatic changes in chloroplast genome structure. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	8
23401	<i>Microstrobilinia castrans</i> , a new genus and species of the Sclerotiniaceae parasitizing pollen cones of <i>Picea</i> spp.. <i>Mycological Progress</i> , 2023, 22, .	0.5	0
23403	Response of an alpine plant to Quaternary climate change: a phylogeographic study of <i>Saxifraga tangutica</i> (Saxifragaceae) in the Qinghai-Tibetan Plateau and Himalayas. <i>Revista Brasileira De Botanica</i> , 0, , .	0.5	0
23404	Polyploid hybrid speciation in the <i>Calcarata</i> species complex of <i>Viola</i> section <i>Melanium</i> (Violaceae): relating hybrid species to parent species distribution and ecology. <i>Botanical Journal of the Linnean Society</i> , 2023, 201, 309-328.	0.8	3
23405	Recovery of the family status of <i>Pericambalidae</i> Silvestri, 1909, stat. nov. (Diplopoda: Spirostreptida.) <i>Tj ETQq1 1 0.784314 rgBT /Overlock</i> 78-100.	0.5	1
23406	Systematic revision of the snorkel snail genus <i>Rhiostoma</i> Benson, 1860 (Gastropoda,) <i>Tj ETQq0 0 0 rgBT /Overlock</i> 10 Tf 50 502 Td (0.5	3
23407	<i>Pseudomonas</i> spp. associated with tomato pith necrosis in the Salto area, Northwest Uruguay. <i>European Journal of Plant Pathology</i> , 0, , .	0.8	0
23408	Evaluation of Genomic Typing Methods in the Salmonella Reference Laboratory in Public Health, England, 2012â€“2020. <i>Pathogens</i> , 2023, 12, 223.	1.2	5
23409	Phylotranscriptomics Shed Light on Intrageneric Relationships and Historical Biogeography of <i>Ceratozamia</i> (Cycadales). <i>Plants</i> , 2023, 12, 478.	1.6	1
23410	Comparisons of genetic population structures of copepods <i>Pseudocalanus</i> spp. in the Okhotsk Sea: the first record of <i>P. acuspes</i> in coastal waters off Japan. <i>Marine Biodiversity</i> , 2023, 53, .	0.3	0
23411	SCORPIOs, a Novel Method to Reconstruct Gene Phylogenies in the Context of a Known WGD Event. <i>Methods in Molecular Biology</i> , 2023, , 155-173.	0.4	0
23413	<i>Diplosphaera elongata</i> sp. nova: Morphology and Phenotypic Plasticity of this New Microalga Isolated from Lichen Thalli. <i>Diversity</i> , 2023, 15, 168.	0.7	1
23414	<i>Klebsiella pneumoniae</i> carrying multiple alleles of antigen 43-encoding gene of <i>Escherichia coli</i> associated with biofilm formation. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2023, 42, 371-377.	1.3	0
23415	New evidence to demystify the supposed holoplanktonic life cycle in <i>Ceriantharia</i> (Cnidaria). <i>Marine Biodiversity</i> , 2023, 53, .	0.3	2
23416	Multiple transitions between realms shape relict lineages of <i>Proteus</i> cave salamanders. <i>Molecular Ecology</i> , 0, , .	2.0	3
23418	The <i>Gynandropsis gynandra</i> genome provides insights into whole-genome duplications and the evolution of C4 photosynthesis in Cleomaceae. <i>Plant Cell</i> , 2023, 35, 1334-1359.	3.1	8
23419	<i>Peronosclerospora neglecta</i> sp. nov.â€”a widespread and overlooked threat to corn (maize) production in the tropics. <i>Mycological Progress</i> , 2023, 22, .	0.5	1

#	ARTICLE	IF	CITATIONS
23420	Cryptic diversity in Zoraptera: <i>Latinozoros barberi</i> (Gurney, 1938) is a complex of at least three species (Zoraptera: Spiralizoridae). <i>PLoS ONE</i> , 2023, 18, e0280113.	1.1	1
23421	Full-length transcriptome sequencing reveals the molecular mechanism of monoterpene and sesquiterpene biosynthesis in <i>Cinnamomum burmannii</i> . <i>Frontiers in Genetics</i> , 0, 13, .	1.1	2
23422	Phylogeographic patterns of <i>Deschampsia cespitosa</i> (Poaceae) in Europe inferred from genomic data. <i>Botanical Journal of the Linnean Society</i> , 2023, 201, 341-360.	0.8	2
23424	Diversification and Biogeography of North American Thistles (<i>Cirsium</i> : Carduoideae): Tj ETQq1 1 0.784314 rgBT /Overlock 10 T 5 2023, 184, 322-341.	0.6	4
23425	Staying in situ or shifting range under ongoing climate change: A case of an endemic herb in the Himalaya-Hengduan Mountains across elevational gradients. <i>Diversity and Distributions</i> , 2023, 29, 524-542.	1.9	3
23426	Evolutionary diversification of methanotrophic ANME-1 archaea and their expansive virome. <i>Nature Microbiology</i> , 2023, 8, 231-245.	5.9	14
23427	Phylodynamics and migration data help describe HIV transmission dynamics in internally displaced people who inject drugs in Ukraine. , 2023, 2, .		3
23428	Suspensions of two bridgehead invasions of <i>Xylella fastidiosa</i> subsp. <i>multiplex</i> in France. <i>Communications Biology</i> , 2023, 6, .	2.0	9
23429	Wild deer (<i>Pudu puda</i>) from Chile harbor a novel ecotype of <i>Anaplasma phagocytophilum</i> . <i>Parasites and Vectors</i> , 2023, 16, .	1.0	3
23430	RAD51 and RAD51B Play Diverse Roles in the Repair of DNA Double Strand Breaks in <i>Physcomitrium patens</i> . <i>Genes</i> , 2023, 14, 305.	1.0	4
23431	Frizzled 7 modulates goblet and Paneth cell fate, and maintains homeostasis in mouse intestine. <i>Development (Cambridge)</i> , 2023, 150, .	1.2	2
23432	Historic samples reveal loss of wild genotype through domestic chicken introgression during the Anthropocene. <i>PLoS Genetics</i> , 2023, 19, e1010551.	1.5	4
23433	“ <i>Allium sunhangii</i> ” a new species from section <i>Brevidentia</i> F.O.Khass. & lengal. (Amaryllidaceae) from Southern Pamir-Alay, Uzbekistan. <i>PhytoKeys</i> , 0, 219, 35-48.	0.4	2
23434	The computational implementation of a platform of relative identity-by-descent scores algorithm for introgressive mapping. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	0
23435	Chromosome-Level Genome Assembly of <i>Herpetospermum pedunculosum</i> (Cucurbitaceae). <i>Genome Biology and Evolution</i> , 2023, 15, .	1.1	1
23436	Re-Evaluating Botryosphaerales: Ancestral State Reconstructions of Selected Characters and Evolution of Nutritional Modes. <i>Journal of Fungi (Basel, Switzerland)</i> , 2023, 9, 184.	1.5	7
23437	High-quality <i>Fagopyrum esculentum</i> genome provides insights into the flavonoid accumulation among different tissues and self-incompatibility. <i>Journal of Integrative Plant Biology</i> , 2023, 65, 1423-1441.	4.1	8
23438	Molecular structures reveal the origin of spectral variation in cryptophyte light harvesting antenna proteins. <i>Protein Science</i> , 2023, 32, .	3.1	6

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23439	Molecular Genetic Mechanisms of Heterosis in Sugarcane Cultivars Using a Comparative Transcriptome Analysis of Hybrids and Ancestral Parents. <i>Agronomy</i> , 2023, 13, 348.	1.3	1
23440	The Chromosome-Level Genome of <i>Hestina assimilis</i> (Lepidoptera: Nymphalidae) Reveals the Evolution of Saprophygy-Related Genes in Brush-Footed Butterflies. <i>International Journal of Molecular Sciences</i> , 2023, 24, 2087.	1.8	0
23441	Uncovering a miltiradiene biosynthetic gene cluster in the Lamiaceae reveals a dynamic evolutionary trajectory. <i>Nature Communications</i> , 2023, 14, .	5.8	13
23442	To Kill or to Be Killed: How Does the Battle between the UPS and Autophagy Maintain the Intracellular Homeostasis in Eukaryotes?. <i>International Journal of Molecular Sciences</i> , 2023, 24, 2221.	1.8	2
23443	Phenotypic and Genomic Characterization of Nine String-Positive Carbapenem-Resistant <i>Acinetobacter baumannii</i> Isolates from Israel. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	1
23444	Comparative Analyses Reveal the Genetic Mechanism of Ambergris Production in the Sperm Whale Based on the Chromosome-Level Genome. <i>Animals</i> , 2023, 13, 361.	1.0	1
23445	Regulation of inositol 1,2,4,5,6-pentakisphosphate and inositol hexakisphosphate levels in <i>Gossypium hirsutum</i> by IPK1. <i>Planta</i> , 2023, 257, .	1.6	0
23447	Characterization and Expression of Holothurian Wnt Signaling Genes during Adult Intestinal Organogenesis. <i>Genes</i> , 2023, 14, 309.	1.0	2
23448	PlantTribes2: Tools for comparative gene family analysis in plant genomics. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	5
23449	Functional roles of nematodes associated with the walnut twig beetle and eastern black walnut in the inland northwest. <i>Forest Pathology</i> , 0, , .	0.5	0
23450	The evolution of ovary-biased gene expression in Hawaiian <i>Drosophila</i> . <i>PLoS Genetics</i> , 2023, 19, e1010607.	1.5	1
23451	Gap-free genome assembly and comparative analysis reveal the evolution and anthocyanin accumulation mechanism of <i>Rhodomyrtus tomentosa</i> . <i>Horticulture Research</i> , 2023, 10, .	2.9	10
23452	Ultraconserved elements resolve the phylogeny and corroborate patterns of molecular rate variation in herons (Aves: Ardeidae). <i>Auk</i> , 2023, 140, .	0.7	9
23453	Two new species of Hymenochaetaceae from tropical Asia and America. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	1
23454	<i>Villoboletus persicinus</i> , gen. et sp. nov. (Boletaceae), a bolete with flocculent-covered stipe from northern China. <i>Mycologia</i> , 2023, 115, 255-262.	0.8	1
23456	Prevalence and genetic characteristics of fosB-positive <i>Staphylococcus aureus</i> in duck farms in Guangdong, China in 2020. <i>Journal of Antimicrobial Chemotherapy</i> , 2023, 78, 802-809.	1.3	2
23457	Isolates of <i>Colletotrichum truncatum</i> with Resistance to Multiple Fungicides from Soybean in Northern Thailand. <i>Plant Disease</i> , 2023, 107, 2736-2750.	0.7	3
23458	<i>Methanocaldococcus lauensis</i> sp. nov., a novel deep-sea hydrothermal vent hyperthermophilic methanogen. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2023, 73, .	0.8	0

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23459	Reclassification of <i>Clostridium cocleatum</i> , <i>Clostridium ramosum</i> , <i>Clostridium spiroforme</i> and <i>Clostridium saccharogumia</i> as <i>Thomasclavelia cocleata</i> gen. nov., comb. nov., <i>Thomasclavelia ramosa</i> comb. nov., gen. nov., <i>Thomasclavelia spiroformis</i> comb. nov. and <i>Thomasclavelia saccharogumia</i> comb. nov. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2023, 73, .	0.8	5
23460	Complete mitochondrial genome assembly and comparison of <i>Camellia sinensis</i> var. <i>Assamica</i> cv. Duntsa. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	10
23462	First Report, Characterization and Pathogenicity of <i>Vibrio chagasii</i> Isolated from Diseased Reared Larvae of Chilean Scallop, <i>Argopecten purpuratus</i> (Lamarck, 1819). <i>Pathogens</i> , 2023, 12, 183.	1.2	6
23463	Improving Performance of Hardware Accelerators by Optimizing Data Movement: A Bioinformatics Case Study. <i>Electronics (Switzerland)</i> , 2023, 12, 586.	1.8	0
23464	Population structure of the fireworm <i>Hermodice carunculata</i> in the wider Caribbean, Atlantic and Mediterranean Sea. <i>Journal of the Marine Biological Association of the United Kingdom</i> , 2023, 103, .	0.4	1
23465	Additions to <i>Rhytidhysterion</i> (Hysteriales, Dothideomycetes) in China. <i>Journal of Fungi (Basel)</i> , Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 5	1.5	3
23466	Traditional taxonomy underestimates the number of species of <i>Bokermannohyla</i> (Amphibia:) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5</i> <i>Biodiversity</i> , 2023, 21, .	0.5	0
23467	Pre-epidemic evolution of the MRSA USA300 clade and a molecular key for classification. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 13, .	1.8	1
23468	Exploring the Potential Molecular Mechanisms of Interactions between a Probiotic Consortium and Its Coral Host. <i>MSystems</i> , 2023, 8, .	1.7	4
23469	Complete chloroplast genomes of three sand-fixing <i>Salix</i> shrubs from Northwest China: comparative and phylogenetic analysis and interspecific identification. <i>Trees - Structure and Function</i> , 0, , .	0.9	0
23471	Genome Assembly and Comparative Analysis of the Egg Parasitoid Wasp <i>Trichogramma dendrolimi</i> Shed Light on the Composition and Evolution of Olfactory Receptors and Venoms. <i>Insects</i> , 2023, 14, 144.	1.0	0
23472	The complete chloroplast genome and phylogenetic analysis of <i>Christella dentata</i> (Forssk.) Brownsey & Jermy (Thelypteridaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2023, 8, 181-185.	0.2	1
23473	Morphological and phylogenetic analyses reveal two new species and a new record of <i>Apiospora</i> (Amphisphaerales, Apiosporaceae) in China. <i>MycKeys</i> , 0, 95, 27-45.	0.8	3
23474	Self-recycling and partially conservative replication of mycobacterial methylmannose polysaccharides. <i>Communications Biology</i> , 2023, 6, .	2.0	2
23476	Phylogeny and biogeography of <i>Tiliacoreae</i> (Menispermaceae), a tribe restricted to tropical rainforests. <i>Annals of Botany</i> , 2023, 131, 685-695.	1.4	2
23477	Retracing Phylogenetic, Host and Geographic Origins of Coronaviruses with Coloured Genomic Bootstrap Barcodes: SARS-CoV and SARS-CoV-2 as Case Studies. <i>Viruses</i> , 2023, 15, 406.	1.5	0
23478	Integrative Taxonomy Approach Reveals Cryptic Diversity within the Phoretic Pseudoscorpion Genus <i>Lamprochernes</i> (Pseudoscorpiones: Chernetidae). <i>Insects</i> , 2023, 14, 122.	1.0	6
23479	An Estuarine Cyanophage S-CREM1 Encodes Three Distinct Antitoxin Genes and a Large Number of Non-Coding RNA Genes. <i>Viruses</i> , 2023, 15, 380.	1.5	1

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23480	First report of canker caused by <i>Chrysosporthe austroafricana</i> on the plantation-grown eucalypt <i>Corymbia henryi</i> in South Africa. <i>Forestry</i> , 0, , .	1.2	1
23481	Alien species revises systematic status: integrative species delimitation of two similar taxa of <i>Symbrenthia</i> HÅ¼bner, [1819] (Lepidoptera, Nymphalidae). <i>PeerJ</i> , 0, 11, e14644.	0.9	0
23483	Origin and Evolution of Marsupial-specific Imprinting Clusters Through Lineage-specific Gene Duplications and Acquisition of Promoter Differential Methylation. <i>Molecular Biology and Evolution</i> , 2023, 40, .	3.5	6
23484	Climacocystaceae fam. nov. and Gloeoporellaceae fam. nov., two new families of Polyporales (Basidiomycota). <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	2
23486	Molecular phylogenetics of <i>Maranta</i> (Marantaceae: Zingiberales): non-monophyly and support for a wider circumscription. <i>Botanical Journal of the Linnean Society</i> , 2023, 202, 181-194.	0.8	1
23487	Characterization and phylogenetic implication of complete mitochondrial genome of the <i>Cataglyphis aenescens</i> (Hymenoptera: Formicidae): Genomic comparisons in Formicinae. <i>Entomological Research</i> , 2023, 53, 45-54.	0.6	0
23488	Morphology and phylogenetic position of three anaerobic ciliates from the classes Odontostomatea and Muranotrichea (Ciliophora). <i>Journal of Eukaryotic Microbiology</i> , 2023, 70, .	0.8	1
23489	Fungi in hair roots of <i>Vaccinium</i> spp. (Ericaceae) growing on decomposing wood: colonization patterns, identity, and in vitro symbiotic potential. <i>Mycorrhiza</i> , 2023, 33, 69-86.	1.3	9
23490	Barbel regeneration and function divergence in red-tail catfish (<i>Hemibagrus wyckioides</i>) based on the chromosome-level genomes and comparative transcriptomes. <i>International Journal of Biological Macromolecules</i> , 2023, 232, 123374.	3.6	1
23491	Diatom endemism and taxonomic turnover: Assessment in high-altitude alpine lakes covering a large geographical range. <i>Science of the Total Environment</i> , 2023, 871, 161970.	3.9	6
23492	Strain and serovar variants of <i>Salmonella enterica</i> exhibit diverse tolerance to food chain-related stress. <i>Food Microbiology</i> , 2023, 112, 104237.	2.1	7
23493	<i>Diploschistes viridis</i> sp. nov. (Lichenized Ascomycota, Thelotremataceae) from Pakistan. <i>Biology Bulletin</i> , 2022, 49, S77-S82.	0.1	0
23494	<i>Termitomyces islamabadensis</i> sp. nov. (Lyophyllaceae, Agaricales) from the Foothills of the Pakistani Himalayas. <i>Biology Bulletin</i> , 2022, 49, S66-S76.	0.1	1
23495	Extension of the known range of the snapping shrimp <i>Alpheus christofferseni</i> Anker, Hurt and Knowlton, 2007 (Caridea: Alpheidae). <i>Nauplius</i> , 0, 31, .	0.3	0
23496	<i>Hydnum atlanticum</i> , a new species from Eastern North America. <i>Fungal Systematics and Evolution</i> , 2023, , .	0.9	0
23497	Plastid phylogenomics and molecular evolution of Thismiaceae (Dioscoreales). <i>American Journal of Botany</i> , 2023, 110, .	0.8	3
23498	Independent Innexin Radiation Shaped Signaling in Ctenophores. <i>Molecular Biology and Evolution</i> , 2023, 40, .	3.5	2
23499	Characterization of Two Transposable Elements and an Ultra-Conserved Element Isolated in the Genome of <i>Zootoca vivipara</i> (Squamata, Lacertidae). <i>Life</i> , 2023, 13, 637.	1.1	1

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23500	The Hyphosphere of Leaf-Cutting Ant Cultivars Is Enriched with Helper Bacteria. <i>Microbial Ecology</i> , 2023, 86, 1773-1788.	1.4	3
23501	Evolutionary Patterns of the Chloroplast Genome in Vanilloid Orchids (Vanilloideae, Orchidaceae). <i>International Journal of Molecular Sciences</i> , 2023, 24, 3808.	1.8	2
23502	Hybrid de novo genome assembly and comparative genomics of three different isolates of <i>Gnomoniopsis castaneae</i> . <i>Scientific Reports</i> , 2023, 13, .	1.6	0
23503	Nitrogen cycling activities during decreased stratification in the coastal oxygen minimum zone off Namibia. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	2
23504	A polyphasic approach to the taxonomy of <i>Backusella</i> reveals two new species. <i>Mycological Progress</i> , 2023, 22, .	0.5	0
23505	Two new species of <i>Exidia sensu lato</i> (Auriculariales, Basidiomycota) based on morphology and DNA sequences. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	0
23506	Best practice for wildlife gut microbiome research: A comprehensive review of methodology for 16S rRNA gene investigations. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	5
23507	Phylogenomics and phylogeography of <i>Menispermum</i> (Menispermaceae). <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	0
23508	Speciation Underpinned by Unexpected Molecular Diversity in the Mycorrhizal Fungal Genus <i>Pisolithus</i> . <i>Molecular Biology and Evolution</i> , 2023, 40, .	3.5	11
23509	High-resolution phylogenetic analysis reveals long-term microbial dynamics and microdiversity in phytoplankton microbiome. <i>Journal of Eukaryotic Microbiology</i> , 2023, 70, .	0.8	2
23510	Evidence for an early green/red photocycle that precedes the diversification of GAF domain photoreceptor cyanobacteriochromes. <i>Photochemical and Photobiological Sciences</i> , 2023, 22, 1415-1427.	1.6	2
23511	Extensive crop-wild hybridization during <i>Brassica</i> evolution and selection during the domestication and diversification of <i>Brassica</i> crops. <i>Genetics</i> , 2023, 223, .	1.2	4
23513	DNA barcoding of Chinese snakes reveals hidden diversity and conservation needs. <i>Molecular Ecology Resources</i> , 2023, 23, 1124-1141.	2.2	2
23514	Complete chloroplast and mitochondrial genomes of <i>Ditrichum rhynchostegium</i> Kindb. (Ditrichaceae, Bryophyta). <i>Mitochondrial DNA Part B: Resources</i> , 2023, 8, 383-388.	0.2	0
23515	Revised classification of the Cyanidiophyceae based on plastid genome data with descriptions of the Cavernicolales ord. nov. and Galdieriales ord. nov. (Rhodophyta). <i>Journal of Phycology</i> , 2023, 59, 444-466.	1.0	11
23517	Discovery of the Streamlined Haloarchaeon <i>Halorutilus salinus</i> , Comprising a New Order Widespread in Hypersaline Environments across the World. <i>MSystems</i> , 2023, 8, .	1.7	5
23518	Continent-wide recent emergence of a global pathogen in African amphibians. <i>Frontiers in Conservation Science</i> , 0, 4, .	0.9	3
23519	Genomic divergence between two sister <i>Medicago</i> species triggered by the quaternary climatic oscillations on the Qinghai-Tibet plateau and northern China. <i>Molecular Ecology</i> , 2023, 32, 3118-3132.	2.0	1

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23520	New Taxonomic Arrangement of <i>Dicranella</i> s.l. and <i>Aongstroemia</i> s.l. (Dicranidae, Bryophyta). <i>Plants</i> , 2023, 12, 1360.	1.6	1
23521	<i>Collybiopsis pakistanica</i> (Omphalotaceae, Agaricales, Basidiomycota), a new mushroom species from Margalla Hills, Pakistan and two new combinations. <i>Nordic Journal of Botany</i> , 0, , .	0.2	0
23522	<i>Phyllactinia cornicola</i> , a new species of powdery mildews from Pakistan. <i>Nordic Journal of Botany</i> , 0, , .	0.2	0
23523	New corticioid taxa in Phanerochaetaceae (Polyporales, Basidiomycota) from East Asia. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	3
23525	Report of two distinct ribotypes in ITS sequences of <i>Phalaris arundinacea</i> (Poaceae) in western Canada and Alaska. <i>Biodiversity Data Journal</i> , 0, 11, .	0.4	0
23526	The species coalescent indicates possible bat and pangolin origins of the COVID-19 pandemic. <i>Scientific Reports</i> , 2023, 13, .	1.6	3
23527	Identification of three cultivated varieties of <i>Scutellaria baicalensis</i> using the complete chloroplast genome as a super-barcode. <i>Scientific Reports</i> , 2023, 13, .	1.6	4
23528	Chromosome-scale genome assembly of marigold (<i>Tagetes erecta</i> L.): An ornamental plant and feedstock for industrial lutein production. <i>Horticultural Plant Journal</i> , 2023, 9, 1119-1130.	2.3	2
23530	Analyses of a chromosome-scale genome assembly reveal the origin and evolution of cultivated chrysanthemum. <i>Nature Communications</i> , 2023, 14, .	5.8	25
23531	Phylogenomics of <i>Aralia</i> sect. <i>Aralia</i> (Araliaceae): Signals of hybridization and insights into its species delimitations and intercontinental biogeography. <i>Molecular Phylogenetics and Evolution</i> , 2023, 181, 107727.	1.2	4
23533	Phylogenomics reveal extensive phylogenetic discordance due to incomplete lineage sorting following the rapid radiation of alpine butterflies (Papilionidae: <i>Parnassius</i>). <i>Systematic Entomology</i> , 2023, 48, 585-599.	1.7	2
23534	Mass mortality among colony-breeding seabirds in the German Wadden Sea in 2022 due to distinct genotypes of HPAIV H5N1 clade 2.3.4.4b. <i>Journal of General Virology</i> , 2023, 104, .	1.3	9
23535	Characterisation and Cultivation of New Lineages of Colponemids, a Critical Assemblage for Inferring Alveolate Evolution. <i>Protist</i> , 2023, 174, 125949.	0.6	4
23536	<i>Elaphomyces castilloi</i> (Elaphomycetaceae, Ascomycota) and <i>Entoloma secotioides</i> (Entolomataceae, Tj ETQq1 1 0.784314 rgBT /Ove MycoKeys, 0, 96, 127-142.	0.8	1
23537	Proteomic Study of the Interactions between Phages and the Bacterial Host <i>Klebsiella pneumoniae</i> . <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	8
23539	Adaptive Evolution of the Spike Protein in Coronaviruses. <i>Molecular Biology and Evolution</i> , 2023, 40, .	3.5	6
23540	<i>Pseudobangia corderoi</i> sp. nov. (Bangiales, Rhodophyta) from the Philippines. <i>Phycologia</i> , 0, , 1-7.	0.6	0
23541	Legume-wide comparative analysis of pod shatter locus <i>PDH1</i> reveals phaseoloid specificity, high cowpea expression, and stress responsive genomic context. <i>Plant Journal</i> , 2023, 115, 68-80.	2.8	5

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23542	Biodiversity of Basidiomycetous Yeasts Associated with <i>Cladonia rei</i> Lichen in Japan, with a Description of <i>Microsporomyces cladoniophilus</i> sp. nov. <i>Journal of Fungi</i> (Basel, Switzerland), 2023, 9, 473.	1.5	0
23545	The genome sequence and demographic history of <i>Przewalskia tangutica</i> (Solanaceae), an endangered alpine plant on the Qinghai-Tibet Plateau. <i>DNA Research</i> , 2023, 30, .	1.5	1
23546	A dated phylogeny of the Neotropical Dipterygeae clade reveals 30 million years of winged papilionate floral conservatism in the otherwise florally labile early-branching papilionoid legumes. <i>Botanical Journal of the Linnean Society</i> , 2023, 202, 449-475.	0.8	1
23547	Diversity of <i>Monochaetia</i> Species from Fagaceous Leaf Spots in China and Pathogenicity for Chinese Chestnut. <i>Microbiology Spectrum</i> , 0, , .	1.2	0
23548	Molecular phylogeny and inflorescence evolution of <i>Prunus</i> (Rosaceae) based on RAD-seq and genome skimming analyses. <i>Plant Diversity</i> , 2023, 45, 397-408.	1.8	6
23549	<i>Burkholderia semiarida</i> sp. nov. and <i>Burkholderia sola</i> sp. nov., two novel <i>B. cepacia</i> complex species causing onion sour skin. <i>Systematic and Applied Microbiology</i> , 2023, 46, 126415.	1.2	3
23550	Features and evolution of control regions in leafroller moths (Lepidoptera: Tortricidae) inferred from mitochondrial genomes and phylogeny. <i>International Journal of Biological Macromolecules</i> , 2023, 236, 123928.	3.6	6
23551	Functional genome annotation and transcriptome analysis of <i>Pseudozyma hubeiensis</i> BOT-O, an oleaginous yeast that utilizes glucose and xylose at equal rates. <i>Fungal Genetics and Biology</i> , 2023, 166, 103783.	0.9	1
23552	Phylogenomic analyses of <i>Camellia</i> support reticulate evolution among major clades. <i>Molecular Phylogenetics and Evolution</i> , 2023, 182, 107744.	1.2	3
23553	Diversification of the African legless skinks in the subfamily Acontinae (Family Scincidae). <i>Molecular Phylogenetics and Evolution</i> , 2023, 182, 107747.	1.2	1
23554	A plastome phylogeny of <i>Rumex</i> (Polygonaceae) illuminates the divergent evolutionary histories of docks and sorrels. <i>Molecular Phylogenetics and Evolution</i> , 2023, 182, 107755.	1.2	1
23555	The hybridization origin of the Chinese endemic herb genus <i>Notopterygium</i> (Apiaceae): Evidence from population genomics and ecological niche analysis. <i>Molecular Phylogenetics and Evolution</i> , 2023, 182, 107736.	1.2	1
23556	The complete mitochondrial genome and phylogenetic characterization of two putative subspecies of golden jackal (<i>Canis aureus cruesemanni</i> and <i>Canis aureus moreotica</i>). <i>Gene</i> , 2023, 866, 147303.	1.0	3
23557	Emergence of a novel genotype of class II New Castle Disease virus in North Eastern States of India. <i>Gene</i> , 2023, 864, 147315.	1.0	0
23558	Diversification and introgression in four chromosomal taxa of the Pearson's horseshoe bat (<i>Rhinolophus pearsoni</i>) group. <i>Molecular Phylogenetics and Evolution</i> , 2023, 183, 107784.	1.2	0
23559	<i>Metarhizium indicum</i> , a new species of entomopathogenic fungus infecting leafhopper, <i>Busonomimus manjunathi</i> from India. <i>Journal of Invertebrate Pathology</i> , 2023, 198, 107919.	1.5	1
23560	The first genomic insight into <i>Chlamydia psittaci</i> sequence type (ST)24 from a healthy captive psittacine host in Australia demonstrates evolutionary proximity with strains from psittacine, human, and equine hosts. <i>Veterinary Microbiology</i> , 2023, 280, 109704.	0.8	2
23561	Deep genome-wide divergences among species in White Cloud Mountain minnow <i>Tanichthys albonubes</i> (Cypriniformes: Tanichthyidae) complex: Conservation and species management implications. <i>Molecular Phylogenetics and Evolution</i> , 2023, 182, 107734.	1.2	1

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23562	Phylogenomics and biogeography of arid-adapted <i>Chlamydogobius</i> goby fishes. <i>Molecular Phylogenetics and Evolution</i> , 2023, 182, 107757.	1.2	2
23563	Molecular characterization and phylogenetic analysis of <i>Paratrichodina africana</i> Kazubski and El-Tantawy, 1986 based on 18S rRNA gene data with the evolutionary hypothesis of trichodinids. <i>Parasitology International</i> , 2023, 94, 102735.	0.6	0
23564	Multiple introgression events during the diversification history of the edible Mexican grasshopper genus <i>Sphenarium</i> (Orthoptera: Pyrgomorphidae). <i>Molecular Phylogenetics and Evolution</i> , 2023, 183, 107774.	1.2	0
23565	Is it inappropriate to ask for your age? Evaluating parameter impact on tree dating in a challenging clade (Macroselidea). <i>Molecular Phylogenetics and Evolution</i> , 2023, 183, 107756.	1.2	0
23566	Evolution of <i>cox2</i> introns in angiosperm mitochondria and efficient splicing of an elongated <i>cox2i691</i> intron. <i>Gene</i> , 2023, 869, 147393.	1.0	0
23567	Cencurut virus: A novel Orthonairovirus from Asian house shrews (<i>Suncus murinus</i>) in Singapore. <i>One Health</i> , 2023, 16, 100529.	1.5	4
23568	Diversity and phylogeny of seagrasses in Singapore. <i>Aquatic Botany</i> , 2023, 187, 103648.	0.8	0
23569	A new species of <i>Anthophila</i> Haworth, 1811 with variable male genitalia from the Canary Islands (Spain) (Lepidoptera: Choreutidae). , 2020, 48, 671-681.		2
23570	The chromosome-level genome of double-petal phenotype jasmine provides insights into the biosynthesis of floral scent. <i>Horticultural Plant Journal</i> , 2024, 10, 259-272.	2.3	1
23571	Environmental formation of methylmercury is controlled by synergy of inorganic mercury bioavailability and microbial mercury methylation capacity. <i>Environmental Microbiology</i> , 2023, 25, 1409-1423.	1.8	7
23572	Algal ciguatera toxin identified as source of ciguatera poisoning in the Caribbean. <i>Chemosphere</i> , 2023, 330, 138659.	4.2	15
23573	Whole-Genome Sequencing-Based Characterization of Clinical <i>Listeria monocytogenes</i> Isolates in China, 2013–2019. <i>Foodborne Pathogens and Disease</i> , 2023, 20, 158-168.	0.8	5
23574	The genome and transcriptome of <i>Sarocladium terricola</i> provide insight into ergosterol biosynthesis. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 13, .	1.8	0
23575	Genomic characterization of Lumpy Skin Disease virus (LSDV) from India: Circulation of Kenyan-like LSDV strains with unique kelch-like proteins. <i>Acta Tropica</i> , 2023, 241, 106838.	0.9	4
23576	Nuclear import of IRF11 via the importin β pathway is essential for its antiviral activity. <i>Developmental and Comparative Immunology</i> , 2023, 141, 104649.	1.0	0
23577	Phylogenomic Analysis of Two Species of <i>Parasenecio</i> and Comparative Analysis within Tribe Senecioneae (Asteraceae). <i>Diversity</i> , 2023, 15, 563.	0.7	2
23578	Insights into identifying resistance genes for cold and disease stresses through chromosome-level reference genome analyses of <i>Poncirus polyandra</i> . <i>Genomics</i> , 2023, 115, 110617.	1.3	1
23579	Plant Receptor-like proteins (RLPs): Structural features enabling versatile immune recognition. <i>Physiological and Molecular Plant Pathology</i> , 2023, 125, 102004.	1.3	8

#	ARTICLE	IF	CITATIONS
23589	A new species of <i>Stigmatodiscus</i> (Ascomycota, Dothideomycetes, Stigmatodiscaceae) from Juan de Nova (Mozambique Channel, Scattered Islands, French Southern and Antarctic Lands). <i>Plant and Fungal Systematics</i> , 2022, 67, 55-62.	0.7	1
23590	Development of a diagnostic single nucleotide polymorphism (SNP) panel for identifying geographic origins of <i>Cochliomyia hominivorax</i> , the New World screwworm. <i>Veterinary Parasitology</i> , 2023, 315, 109884.	0.7	0
23591	Multi-gene phylogeny reveals a new genus and species of Hapalidiales (Rhodophyta) from Antarctica: <i>Thalassolithon adeliense</i> gen. nov. & sp. nov. <i>Phycologia</i> , 2023, 62, 83-98.	0.6	1
23592	Identification of novel RNA mycoviruses from wild mushroom isolates in Japan. <i>Virus Research</i> , 2023, 325, 199045.	1.1	4
23593	Genome-wide analyzation and functional characterization on the TPS family provide insight into the biosynthesis of mono-terpenes in the camphor tree. <i>Plant Physiology and Biochemistry</i> , 2023, 196, 55-64.	2.8	3
23594	More than meets no eyes: Taxonomic status of a <i>Liotyphlops</i> (Serpentes: Anomalepididae) blindsnake from the Atlantic Rainforest. <i>Zoologischer Anzeiger</i> , 2023, 303, 10-25.	0.4	1
23595	The austral biflagellate <i>Chloromonas rubroleosa</i> (Chlorophyceae) is the closest relative of the unusual quadriflagellate genus <i>Chlainomonas</i> , both found in snow. <i>Journal of Phycology</i> , 2023, 59, 342-355.	1.0	5
23596	Genomic and phylogenetic characterization of <i>Elizabethkingia anophelis</i> strains: The first two cases of life-threatening infection in Japan. <i>Journal of Infection and Chemotherapy</i> , 2023, 29, 376-383.	0.8	2
23597	Small population of the largest water strider after the late Pleistocene and the implications for its conservation. <i>Gene</i> , 2023, 859, 147219.	1.0	0
23598	Predicting functions of putative fungal sesquiterpene synthase genes based on multiomics data analysis. <i>Fungal Genetics and Biology</i> , 2023, 165, 103779.	0.9	3
23599	Still Many to Be Named: An Integrative Analysis of the Genus <i>Dendronotus</i> (Gastropoda: Nudibranchia) in the North Pacific Revealed Seven New Species. <i>Diversity</i> , 2023, 15, 162.	0.7	0
23600	Not all clusters are equal: dynamics of molecular HIV-1 clusters in a statewide Rhode Island epidemic. <i>Aids</i> , 2023, 37, 389-399.	1.0	1
23601	The use of Anchored Hybrid Enrichment data to resolve higher-level phylogenetic relationships: A proof-of-concept applied to Asterales (Eudicotyledoneae; Angiosperms). <i>Molecular Phylogenetics and Evolution</i> , 2023, 181, 107714.	1.2	0
23602	Allopatric mosaics in the Indo-West Pacific crab subfamily Chlorodiellinae reveal correlated patterns of sympatry, genetic divergence, and genitalic disparity. <i>Molecular Phylogenetics and Evolution</i> , 2023, 181, 107710.	1.2	1
23603	Genome Analysis Identifies a Novel Type III Secretion System (T3SS) Category in <i>Vibrio</i> Species. <i>Microorganisms</i> , 2023, 11, 290.	1.6	0
23604	A reversible mutation in a genomic hotspot saves bacterial swarms from extinction. <i>IScience</i> , 2023, 26, 106043.	1.9	5
23605	Annelid functional genomics reveal the origins of bilaterian life cycles. <i>Nature</i> , 2023, 615, 105-110.	13.7	34
23606	First report of <i>Paramyrothecium foliicola</i> causing leaf spots on hop. <i>Australasian Plant Disease Notes</i> , 2023, 18, .	0.4	1

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23607	A Physcomitrella <sc>PIN</sc> protein acts in spermatogenesis and sporophyte retention. New Phytologist, 2023, 237, 2118-2135.	3.5	2
23608	MAMMLE: A Framework for Phylogeny Estimation Based on Multiobjective Application-aware Multiple Sequence Alignment and Maximum Likelihood Ensemble. Journal of Computational Biology, 2023, 30, 245-249.	0.8	0
23609	Mechanistic and microbial ecological insights into the impacts of micro- and nano-Plastics on microbial reductive dehalogenation of organohalide pollutants. Journal of Hazardous Materials, 2023, 448, 130895.	6.5	8
23610	Novelties in Microthyriaceae (Microthyriales): Two New Asexual Genera with Three New Species from Freshwater Habitats in Guizhou Province, China. Journal of Fungi (Basel, Switzerland), 2023, 9, 178.	1.5	2
23611	<i>Hypochnicium</i> sensu lato (<i>Polyporales</i>,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 587 Td (<i>Basidiomycota</i>). Mycoscience, 2023, 64, 19-34.	0.3	2
23612	Sequence analysis of SARS-CoV-2 Delta variant isolated from Makassar, South Sulawesi, Indonesia. Heliyon, 2023, 9, e13382.	1.4	3
23613	High abundance of hydrocarbon-degrading <i>Alcanivorax</i> in plumes of hydrothermally active volcanoes in the South Pacific Ocean. ISME Journal, 2023, 17, 600-610.	4.4	5
23614	Phylogeny, Morphology, Distribution, and Pathogenicity of Seven <i>Calonectria</i> Species from Leaf-Blighted <i>Eucalyptus</i> in HaiNan Island, China. Plant Disease, 2023, 107, 2579-2605.	0.7	3
23615	Characterization of the Plastid Genome of the Vulnerable Endemic Indosasa lipoensis and Phylogenetic Analysis. Diversity, 2023, 15, 197.	0.7	3
23616	Diversity and pathogenicity of species of <i>Botrytis</i>, <i>Cladosporium</i>, <i>Neopestalotiopsis</i> and <i>Pestalotiopsis</i> causing flower diseases of macadamia in Australia. Plant Pathology, 2023, 72, 881-899.	1.2	2
23617	The chromosome-level genome and key genes associated with mud-dwelling behavior and adaptations of hypoxia and noxious environments in loach (Misgurnus anguillicaudatus). BMC Biology, 2023, 21, .	1.7	2
23619	DNA Barcoding of Fish Species Diversity in Guizhou, China. Diversity, 2023, 15, 203.	0.7	1
23620	Phylogeny and adaptive evolution of subgenus Rhizirideum (Amaryllidaceae, Allium) based on plastid genomes. BMC Plant Biology, 2023, 23, .	1.6	5
23623	A morphological analysis of <i>Syzygium</i>, with a focus on fibre bundles and description of a new subgenus. Botanical Journal of the Linnean Society, 0, , .	0.8	0
23625	Applying a modified metabarcoding approach for the sequencing of macrofungal specimens from fungarium collections. Applications in Plant Sciences, 2023, 11, .	0.8	1
23626	Whole-Genome Sequencing to Predict Antimicrobial Susceptibility Profiles in <i>Neisseria gonorrhoeae</i>. Journal of Infectious Diseases, 2023, 227, 917-925.	1.9	2
23627	Molecular evolution analysis of three species gyroviruses in China from 2018 to 2019. Virus Research, 2023, 326, 199058.	1.1	2
23628	Pan-genome and transcriptome analyses provide insights into genomic variation and differential gene expression profiles related to disease resistance and fatty acid biosynthesis in eastern black walnut (<i>Juglans nigra</i>). Horticulture Research, 2023, 10, .	2.9	11

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23629	Symbiont diversity in the eukaryotic microbiomes of marine crustacean zooplankton. <i>Journal of Plankton Research</i> , 2023, 45, 338-359.	0.8	2
23630	Chromosome-Level Assembly of Flowering Cherry (<i>Prunus campanulata</i>) Provides Insight into Anthocyanin Accumulation. <i>Genes</i> , 2023, 14, 389.	1.0	1
23631	Diversification of spiny-throated reed frogs (<i>Anura: Hyperoliidae</i>) with the description of a new, range-restricted species from the Ukaguru Mountains, Tanzania. <i>PLoS ONE</i> , 2023, 18, e0277535.	1.1	1
23632	Genome-wide association and dissociation studies in <i>Pantoea ananatis</i> reveal potential virulence factors affecting <i>Allium porrum</i> and <i>Allium fistulosum</i> × <i>Allium cepa</i> hybrid. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	0
23633	The complete chloroplast genome sequence of the medicinal plant, <i>Dracocephalum rupestre</i> (<i>Lamiaceae</i>). <i>Mitochondrial DNA Part B: Resources</i> , 2023, 8, 229-232.	0.2	0
23634	Diversity and Distribution of <i>Calonectria</i> Species in Soils from <i>Eucalyptus</i> × <i>Aurophylla</i> × <i>E. grandis</i> , <i>Pinus massoniana</i> , and <i>Cunninghamia lanceolata</i> Plantations in Four Provinces in Southern China. <i>Journal of Fungi (Basel, Switzerland)</i> , 2023, 9, 198.	1.5	2
23635	Mitochondrial genomes in the iconic reindeer lichens: Architecture, variation, and synteny across multiple evolutionary scales. <i>Mycologia</i> , 2023, 115, 187-205.	0.8	1
23636	Photographic Checklist, DNA Barcoding, and New Species of Sea Slugs and Snails from the Faafu Atoll, Maldives (<i>Gastropoda: Heterobranchia</i> and <i>Vetigastropoda</i>). <i>Diversity</i> , 2023, 15, 219.	0.7	3
23637	Chromosome-level genome assembly of goose provides insight into the adaptation and growth of local goose breeds. <i>GigaScience</i> , 2022, 12, .	3.3	2
23638	<i>Proteus mirabilis</i> isolated from untreated hospital wastewater, Ibadan, Southwestern Nigeria showed low-level resistance to fluoroquinolone and carried <i>qnrD3</i> on Col3M plasmids. <i>Environmental Science and Pollution Research</i> , 2023, 30, 47158-47167.	2.7	0
23639	Description of a new oxytrichid ciliate, <i>Oxytricha buxai</i> n. sp. and redescription of <i>O. quadricirrata</i> Blatterer and Foissner, 1988 based on morphology and 18S rDNA analyses. <i>European Journal of Protistology</i> , 2023, 88, 125959.	0.5	1
23642	A chromosome-level genome assembly of the beet armyworm <i>Spodoptera exigua</i> . <i>Genomics</i> , 2023, 115, 110571.	1.3	4
23643	<i>Lecanora neobarkmaniana</i> (<i>Lecanorales, Lecanoraceae</i>), A New Lichen Species from South Korea. <i>Mycobiology</i> , 2023, 51, 16-25.	0.6	1
23644	Putative source and niche shift pattern of a new alien ant species (<i>Odontomachus troglodytes</i>) in Taiwan. <i>PeerJ</i> , 0, 11, e14718.	0.9	0
23645	Newly identified sex chromosomes in the <i>Sphagnum</i> (peat moss) genome alter carbon sequestration and ecosystem dynamics. <i>Nature Plants</i> , 2023, 9, 238-254.	4.7	18
23646	Ancestral Sequence Reconstruction Enhances Gene Mining Efforts for Industrial Ene Reductases by Expanding Enzyme Panels with Thermostable Catalysts. <i>ACS Catalysis</i> , 2023, 13, 2576-2585.	5.5	12
23647	Phylogeny and Historical Biogeography of the East Asian <i>Clematis</i> Group, Sect. <i>Tubulosae</i> , Inferred from Phylogenomic Data. <i>International Journal of Molecular Sciences</i> , 2023, 24, 3056.	1.8	2
23648	Comparative Genomic Analyses of Cellulolytic Machinery Reveal Two Nutritional Strategies of Marine <i>Labrynthulomycetes</i> Protists. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	1

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23649	Phylogeny of sea spiders (Arthropoda: Pycnogonida) inferred from mitochondrial genome and 18S ribosomal RNA gene sequences. <i>Molecular Phylogenetics and Evolution</i> , 2023, 182, 107726.	1.2	5
23651	A nontuberculous mycobacterium could solve the mystery of the lady from the Franciscan church in Basel, Switzerland. <i>BMC Biology</i> , 2023, 21, .	1.7	1
23652	Study of Genetic Variation in Bermuda Grass along Longitudinal and Latitudinal Gradients Using Spectral Reflectance. <i>Remote Sensing</i> , 2023, 15, 896.	1.8	3
23653	Integrative taxonomy reveals new, widely distributed tardigrade species of the genus <i>Paramacrotius</i> (Eutardigrada: Macrobiotidae). <i>Scientific Reports</i> , 2023, 13, .	1.6	9
23654	<i>Pseudomonas nunensis</i> sp. nov. isolated from a suppressive potato field in Greenland. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2023, 73, .	0.8	2
23655	Plastid Phylogenomic Insights into the Inter-Tribal Relationships of Plantaginaceae. <i>Biology</i> , 2023, 12, 263.	1.3	2
23656	Redundant potassium transporter systems guarantee the survival of <i>Enterococcus faecalis</i> under stress conditions. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	2
23657	Morphology and Phylogeny Reveal Three <i>Montagnula</i> Species from China and Thailand. <i>Plants</i> , 2023, 12, 738.	1.6	2
23658	Pan-Plastome of Greater Yam (<i>Dioscorea alata</i>) in China: Intraspecific Genetic Variation, Comparative Genomics, and Phylogenetic Analyses. <i>International Journal of Molecular Sciences</i> , 2023, 24, 3341.	1.8	5
23659	Identification and characterization of the causative agents of Focal Ulcerative Dermatitis in commercial laying hens. <i>Frontiers in Veterinary Science</i> , 0, 10, .	0.9	2
23660	Paraphlomis yingdeensis (Lamiaceae), a new species from Guangdong (China). <i>PhytoKeys</i> , 0, 219, 107-120.	0.4	2
23661	Morphological and molecular analyses reveal two new species of <i>Termitomyces</i> (Agaricales). <i>Tj ETQq1 1 0.784314 rgBT /Oyerlock 10</i>	0.8	1
23662	Macroevolutionary diversity of traits and genomes in the model yeast genus <i>Saccharomyces</i> . <i>Nature Communications</i> , 2023, 14, .	5.8	8
23664	264. The complete mitochondrial genome of a Peruvian creole cattle (<i>Bos taurus</i>) and its phylogenetic analysis. , 2022, , .		0
23665	Global epidemiology and clinical outcomes of carbapenem-resistant <i>Pseudomonas aeruginosa</i> and associated carbapenemases (POP): a prospective cohort study. <i>Lancet Microbe</i> , The, 2023, 4, e159-e170.	3.4	55
23666	Salinity determines performance, functional populations, and microbial ecology in consortia attenuating organohalide pollutants. <i>ISME Journal</i> , 2023, 17, 660-670.	4.4	15
23669	Deciphering the mitochondrial genome of <i>Juglans mandshurica</i> (Juglandaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2023, 8, 249-254.	0.2	1
23670	Molecular phylogeny of Spirotrichonympha (Parabasalia) with emphasis on <i>Spirotrichonympha</i> , <i>Spirotrichonympha</i> , and three new genera <i>Pseudospironympha</i> , <i>Nanospirotrichonympha</i> , and <i>Brugerollina</i> . <i>Journal of Eukaryotic Microbiology</i> , 2023, 70, .	0.8	2

#	ARTICLE	IF	CITATIONS
23671	On the mysterious Seychellois endemic spider genus <i>Cenemus</i> (Araneae, Pholcidae). <i>Arthropod Systematics and Phylogeny</i> , 0, 81, 179-200.	5.5	3
23672	Blue-Winged Teals in Guatemala and Their Potential Role in the Ecology of H14 Subtype Influenza A Viruses. <i>Viruses</i> , 2023, 15, 483.	1.5	3
23673	Two new species of miniature tetras of the fish genus <i>Priocharax</i> from the Rio Juruá drainage, Acre, Brazil (Teleostei: Characiformes: Characidae). <i>Canadian Journal of Zoology</i> , 2023, 101, 248-266.	0.4	2
23674	Insights on the evolution and conservation of Appalachian burrowing crayfishes, with the description of a new species of <i>Cambarus</i> Erichson, 1846 (Decapoda: Astacidea: Cambaridae). <i>Journal of Crustacean Biology</i> , 2023, 43, .	0.3	1
23675	Whole-Genome Duplication Reshaped Adaptive Evolution in a Relict Plant Species, <i>Cyclocarya paliurus</i> . <i>Genomics, Proteomics and Bioinformatics</i> , 2023, 21, 455-469.	3.0	6
23676	Climate-influenced boreotropical survival and rampant introgressions explain the thriving of New World grapes in the north temperate zone. <i>Journal of Integrative Plant Biology</i> , 2023, 65, 1183-1203.	4.1	9
23677	Evidence of phenotypic plasticity in <i>Alloteuthis media</i> (Linnaeus, 1758) from morphological analyses on North Sea specimens and DNA barcoding of the genus <i>Alloteuthis</i> Walker, 1920 across its latitudinal range. <i>Marine Biology</i> , 2023, 170, .	0.7	2
23678	Intercross population study reveals that co-mutation of <i>mitfa</i> genes in two subgenomes induces red skin color in common carp (<i>Cyprinus carpio wuyuanensis</i>). <i>Zoological Research</i> , 2023, 44, 276-286.	0.9	0
23679	Complete functional analysis of type IV pilus components of a reemergent plant pathogen reveals neofunctionalization of paralog genes. <i>PLoS Pathogens</i> , 2023, 19, e1011154.	2.1	0
23681	Minus-C subfamily has diverged from Classic odorant-binding proteins in honeybees. <i>Apidologie</i> , 2023, 54, .	0.9	2
23682	Capsular Polysaccharide Is Essential for the Virulence of the Antimicrobial-Resistant Pathogen <i>Enterobacter hormaechei</i> . <i>MBio</i> , 2023, 14, .	1.8	2
23683	The Complete Mitochondrial Genome of the Hermit Crab <i>Diogenes edwardsii</i> (Anomura: Diogenidae) and Phylogenetic Relationships within Infraorder Anomura. <i>Genes</i> , 2023, 14, 470.	1.0	2
23684	Multiple mutations in the Nav1.4 sodium channel of New Guinean toxic birds provide autoresistance to deadly batrachotoxin. <i>Molecular Ecology</i> , 0, , .	2.0	3
23685	Genomic insights into antibiotic resistance and mobilome of lactic acid bacteria and bifidobacteria. <i>Life Science Alliance</i> , 2023, 6, e202201637.	1.3	2
23686	Two new species of the lichenized genus <i>Lasioloma</i> (<i>Byssolomataceae</i>) from Asia. <i>Lichenologist</i> , 2023, 55, 27-33.	0.5	0
23687	Clustering pattern and evolution characteristic of microRNAs in grass carp (<i>Ctenopharyngodon</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.2	1
23688	Genotypic Characteristics and Antimicrobial Resistance of <i>Escherichia coli</i> ST141 Clonal Group. <i>Antibiotics</i> , 2023, 12, 382.	1.5	1
23689	Comparative mitogenomes reveal diverse and novel gene rearrangements in the genus <i>Meteorus</i> (Hymenoptera: Braconidae). <i>Frontiers in Genetics</i> , 0, 14, .	1.1	1

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23691	Tundra Soil Viruses Mediate Responses of Microbial Communities to Climate Warming. <i>MBio</i> , 2023, 14, .	1.8	5
23692	Intra-Host Evolution Provides for the Continuous Emergence of SARS-CoV-2 Variants. <i>MBio</i> , 2023, 14, .	1.8	5
23693	The <i>baseless</i> mutant links protein phosphatase 2A with basal cell identity in the brown alga <i>Ectocarpus</i> . <i>Development (Cambridge)</i> , 2023, 150, .	1.2	2
23694	A gap-free and haplotype-resolved lemon genome provides insights into flavor synthesis and huanglongbing (HLB) tolerance. <i>Horticulture Research</i> , 2023, 10, .	2.9	6
23695	Plasmids manipulate bacterial behaviour through translational regulatory crosstalk. <i>PLoS Biology</i> , 2023, 21, e3001988.	2.6	10
23696	Host phylogeny and ecological associations best explain <i>Wolbachia</i> host shifts in scale insects. <i>Molecular Ecology</i> , 2023, 32, 2351-2363.	2.0	3
23697	Transcriptome and Proteome of Methicillin-Resistant <i>Staphylococcus aureus</i> Small-Colony Variants Reveal Changed Metabolism and Increased Immune Evasion. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	5
23698	Deciphering the Tangible Spatio-Temporal Spread of a 25-Year Tuberculosis Outbreak Boosted by Social Determinants. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	1
23699	A chromosome-level genome assembly of <i>Ostrea denselamellosa</i> provides initial insights into its evolution. <i>Genomics</i> , 2023, 115, 110582.	1.3	3
23700	<i>Umbelopsis</i> (Mucoromycota) from Patagonia, Argentina: identification, phylogenetic analysis, and expression profiling of lipase activity and lipid accumulation in selected isolates. <i>Mycological Progress</i> , 2023, 22, .	0.5	1
23702	Recent transposable element bursts are associated with the proximity to genes in a fungal plant pathogen. <i>PLoS Pathogens</i> , 2023, 19, e1011130.	2.1	15
23704	Phylogeny-wide analysis of G-protein coupled receptors in social amoebas and implications for the evolution of multicellularity. <i>Open Research Europe</i> , 0, 2, 134.	2.0	1
23705	Genome-Wide Identification of G Protein-Coupled Receptors in Ciliated Eukaryotes. <i>International Journal of Molecular Sciences</i> , 2023, 24, 3869.	1.8	2
23706	On the origin and evolution of RNA editing in metazoans. <i>Cell Reports</i> , 2023, 42, 112112.	2.9	17
23707	Genomic insight into <i>Campylobacter jejuni</i> isolated from commercial turkey flocks in Germany using whole-genome sequencing analysis. <i>Frontiers in Veterinary Science</i> , 0, 10, .	0.9	5
23708	The complete chloroplast genome of <i>Holarrhena pubescens</i> and its phylogenetic analysis. <i>Mitochondrial DNA Part B: Resources</i> , 2023, 8, 266-269.	0.2	0
23709	Genome analysis and genomic comparison of a fungal cultivar of the nonsocial weevil <i>Euops chinensis</i> reveals its plant decomposition and protective roles in fungus-farming mutualism. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	1
23710	Untargeted Metabolomics for Integrative Taxonomy: Metabolomics, DNA Marker-Based Sequencing, and Phenotype Bioimaging. <i>Plants</i> , 2023, 12, 881.	1.6	3

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23711	Parallel expansion and divergence of an adhesin family in pathogenic yeasts. <i>Genetics</i> , 2023, 223, .	1.2	4
23712	Trends in the evolution of intronless genes in Poaceae. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	0
23714	Comparing the transmission potential from sequence and surveillance data of 2009 North American influenza pandemic waves. <i>Infectious Disease Modelling</i> , 2023, 8, 240-252.	1.2	0
23715	Genetic analysis of the frozen microbiome at 7900 m a.s.l., on the South Col of Sagarmatha (Mount) Tj ETQq1 1 0.784314 rgBT /Overdo	0.4	0
23716	A new species of <i>Neofavolus</i> (&i>Polyporales, Basidiomycota&i>) from Brazil. <i>Mycoscience</i> , 2023, 64, 69-73.	0.3	0
23717	Genomics and biochemical analyses reveal a metabolon key to $\hat{1}^2$ -L-ODAP biosynthesis in <i>Lathyrus sativus</i> . <i>Nature Communications</i> , 2023, 14, .	5.8	10
23718	First record of North Italian roach, <i>Leucos aula</i> (Bonaparte, 1841) on the Pag Island, Croatiaâ€”relict of the last glacial maximum?. <i>Organisms Diversity and Evolution</i> , 2023, 23, 543-553.	0.7	2
23719	Chromosomeâ€scale genome assembly and insights into the metabolome and gene regulation of leaf color transition in an important oak species, <i>Quercus dentata</i> . <i>New Phytologist</i> , 2023, 238, 2016-2032.	3.5	13
23721	Amazonian birds in more dynamic habitats have less population genetic structure and higher gene flow. <i>Molecular Ecology</i> , 2023, 32, 2186-2205.	2.0	8
23722	A biallelic variant of DCAF13 implicated in a neuromuscular disorder in humans. <i>European Journal of Human Genetics</i> , 2023, 31, 629-637.	1.4	3
23723	Using PhyloSuite for molecular phylogeny and treeâ€based analyses. , 2023, 2, .		46
23724	Punctaâ€localized <i>TRAF</i> domain protein <i>TC1b</i> contributes to the autoimmunity of <i>snc1</i> . <i>Plant Journal</i> , 2023, 114, 591-612.	2.8	0
23725	Broad protective vaccination against systemic <i>Escherichia coli</i> with autotransporter antigens. <i>PLoS Pathogens</i> , 2023, 19, e1011082.	2.1	5
23726	Precipitation is the main axis of tropical plant phylogenetic turnover across space and time. <i>Science Advances</i> , 2023, 9, .	4.7	12
23727	Identification and Comparative Expression Profiles of Candidate Olfactory Receptors in the Transcriptomes of the Important Egg Parasitoid Wasp <i>Anastatus japonicus</i> Ashmead (Hymenoptera:) Tj ETQq0 0 0 rgBT /Overdock 10 Tf		
23728	Parallel evolution and cryptic diversification in a common and widespread Amazonian tree, <i>Protium suberratum</i> . <i>Molecular Ecology</i> , 0, , .	2.0	0
23729	Resolving the <i>Sticta fuliginosa</i> Morphodeme (Lichenized Ascomycota: Peltigeraceae) in Northwestern North America. <i>Bryologist</i> , 2023, 126, .	0.1	1
23730	A subfamily classification to choreograph the diverse activities within glycoside hydrolase family 31. <i>Journal of Biological Chemistry</i> , 2023, 299, 103038.	1.6	6

#	ARTICLE	IF	CITATIONS
23731	Nitrogenase resurrection and the evolution of a singular enzymatic mechanism. <i>ELife</i> , 0, 12, .	2.8	8
23732	Revision of the leachella group of Megachile subgenus Eutricharaea in the Western Palaearctic (Hymenoptera, Apoidea, Megachilidae): A renewed plea for DNA barcoding type material. <i>Journal of Hymenoptera Research</i> , 0, 95, 143-198.	0.8	6
23733	Estimating phylogenies from genomes: A beginners review of commonly used genomic data in vertebrate phylogenomics. <i>Journal of Heredity</i> , 2023, 114, 1-13.	1.0	2
23734	Phyllosticta rizhaoensis sp. nov. causing leaf blight of Ophiopogon japonicus in China. <i>Fungal Systematics and Evolution</i> , 2023, , .	0.9	1
23735	Emergence, phylogeography, and adaptive evolution of mpox virus. <i>New Microbes and New Infections</i> , 2023, 52, 101102.	0.8	7
23736	Diverse Marine T4-like Cyanophage Communities Are Primarily Comprised of Low-Abundance Species Including Species with Distinct Seasonal, Persistent, Occasional, or Sporadic Dynamics. <i>Viruses</i> , 2023, 15, 581.	1.5	3
23737	Multi-omics Investigation of Freeze Tolerance in the Amur Sleeper, an Aquatic Ectothermic Vertebrate. <i>Molecular Biology and Evolution</i> , 2023, 40, .	3.5	4
23738	Evolutionary History of the <i>Poecilia picta</i> Sex Chromosomes. <i>Genome Biology and Evolution</i> , 2023, 15, .	1.1	4
23739	Niche evolution in a northern temperate tree lineage: biogeographical legacies in cork oaks (<i>Quercus</i> section <i>Cerris</i>). <i>Annals of Botany</i> , 2023, 131, 769-787.	1.4	4
23740	Genomic Epidemiology and Transmission Dynamics of Global Coxsackievirus B4. <i>Viruses</i> , 2023, 15, 569.	1.5	1
23741	Genome Size Changes by Duplication, Divergence, and Insertion in <i>Caenorhabditis</i> Worms. <i>Molecular Biology and Evolution</i> , 2023, 40, .	3.5	0
23742	Whole-Genome Comparison Reveals Structural Variations behind Heading Leaf Trait in Brassica oleracea. <i>International Journal of Molecular Sciences</i> , 2023, 24, 4063.	1.8	3
23743	Computational Insight into Intraspecies Distinctions in <i>Pseudoalteromonas distincta</i> : Carotenoid-like Synthesis Traits and Genomic Heterogeneity. <i>International Journal of Molecular Sciences</i> , 2023, 24, 4158.	1.8	2
23744	Molecular Species Delimitation Using COI Barcodes of Mealybugs (Hemiptera: Pseudococcidae) from Coffee Plants in Espírito Santo, Brazil. <i>Diversity</i> , 2023, 15, 305.	0.7	3
23745	Whole genome sequencing and phylogenetic analysis of African swine fever virus detected in a backyard pig in Mongolia, 2019. <i>Frontiers in Veterinary Science</i> , 0, 10, .	0.9	1
23746	Chromosome-level genome assembly and population genomics of Mongolian racerunner (<i>Eremias</i>) Tj ETQq1 1 0.784314 rgBT ₂ /Overlook	1.7	1
23747	Comparison of plastid genomes and ITS of two sister species in <i>Gentiana</i> and a discussion on potential threats for the endangered species from hybridization. <i>BMC Plant Biology</i> , 2023, 23, .	1.6	4
23748	Insights into the systematics of <i>Alluaudinella</i> and allied <i>Aethiopomyia</i> and <i>Ochromusca</i> (Muscidae, Diptera). <i>Zoologica Scripta</i> , 2023, 52, 279-297.	0.7	0

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23750	Genomic analysis, trajectory tracking, and field surveys reveal sources and long-distance dispersal routes of wheat stripe rust pathogen in China. <i>Plant Communications</i> , 2023, 4, 100563.	3.6	2
23751	Two new chasmophytic species of <i>Silene</i> (Caryophyllaceae, sect. <i>Siphonomorpha</i>) from Iran. <i>European Journal of Taxonomy</i> , 0, 860, 42-61.	0.6	0
23752	Nanopore adaptive sampling for targeted mitochondrial genome sequencing and bloodmeal identification in hematophagous insects. <i>Parasites and Vectors</i> , 2023, 16, .	1.0	5
23753	Genetic differentiation between two subspecies of <i>Emberiza schoeniclus</i> and open forest bunting's evolution inferred from mitogenomes. <i>Journal of Avian Biology</i> , 2023, 2023, .	0.6	0
23755	Enlarged fins of Tibetan catfish provide new evidence of adaptation to high plateau. <i>Science China Life Sciences</i> , 2023, 66, 1554-1568.	2.3	2
23756	High-quality <i>Cymbidium mannii</i> genome and multifaceted regulation of crassulacean acid metabolism in epiphytes. <i>Plant Communications</i> , 2023, 4, 100564.	3.6	5
23757	A comparative plastomic analysis of <i>Ziziphus jujuba</i> var. <i>spinosa</i> (Bunge) Hu ex H. F. Chow and implication of the origin of Chinese jujube. <i>AoB PLANTS</i> , 2023, 15, .	1.2	3
23758	Genomic Epidemiological Analysis of Antimicrobial-Resistant Bacteria with Nanopore Sequencing. <i>Methods in Molecular Biology</i> , 2023, , 227-246.	0.4	0
23759	Genomic, transcriptomic, and metabolomic analysis of <i>Oldenlandia corymbosa</i> reveals the biosynthesis and mode of action of anti-cancer metabolites. <i>Journal of Integrative Plant Biology</i> , 2023, 65, 1442-1466.	4.1	7
23761	Two new species of <i>Haploporus</i> (Polyporales, Basidiomycota) from China and Ecuador based on morphology and phylogeny. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 13, .	1.8	2
23762	Taxonomic composition, community structure and molecular novelty of microeukaryotes in a temperate oligomesotrophic lake as revealed by metabarcoding. <i>Scientific Reports</i> , 2023, 13, .	1.6	1
23763	Chloroplast genomic comparison provides insights into the evolution of seagrasses. <i>BMC Plant Biology</i> , 2023, 23, .	1.6	2
23764	Myrmecophily of the enigmatic stag beetle <i>Torynognathus chrysomelinus</i> (Coleoptera: Lucanidae: Lucaninae) with remarks on adult morphology, immature stages, and systematic position. <i>Entomological Science</i> , 2023, 26, .	0.3	1
23765	Mitochondrial RNA editing sites affect the phylogenetic reconstruction of gymnosperms. <i>Plant Diversity</i> , 2023, 45, 485-489.	1.8	0
23766	Importance of mobile genetic element immunity in numerically abundant <i>Trichodesmium</i> clades. <i>ISME Communications</i> , 2023, 3, .	1.7	4
23767	Endophytic <i>Colletotrichum</i> (Sordariomycetes, Glomerellaceae) species associated with <i>Citrus grandis</i> cv. 'Tomentosa' in China. <i>MycKeys</i> , 0, 95, 163-188.	0.8	4
23768	High-Throughput Mutagenesis Reveals a Role for Antimicrobial Resistance- and Virulence-Associated Mobile Genetic Elements in <i>Staphylococcus aureus</i> Host Adaptation. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	2
23769	Subspecies-level genome comparison of <i>Lactobacillus delbrueckii</i> . <i>Scientific Reports</i> , 2023, 13, .	1.6	7

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23770	Phylogeography and population structure of the global, wide host-range hybrid pathogen <i>Phytophthora cambivora</i> . <i>IMA Fungus</i> , 2023, 14, .	1.7	1
23771	The First Complete Chloroplast Genome Sequence of <i>Morti</i> (<i>Vaccinium floribundum</i>) and Comparative Analyses with Other <i>Vaccinium</i> Species. <i>Horticulturae</i> , 2023, 9, 302.	1.2	3
23772	Long divergent haplotypes introgressed from wild sheep are associated with distinct morphological and adaptive characteristics in domestic sheep. <i>PLoS Genetics</i> , 2023, 19, e1010615.	1.5	10
23773	<i>Fusarium</i> diversity associated with diseased cereals in China, with an updated phylogenomic assessment of the genus. <i>Studies in Mycology</i> , 2023, 104, 87-148.	4.5	8
23774	A Global Survey of Hypervirulent <i>Aeromonas hydrophila</i> (vAh) Identified vAh Strains in the Lower Mekong River Basin and Diverse Opportunistic Pathogens from Farmed Fish and Other Environmental Sources. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	2
23775	Transcript annotation of Chinese sturgeon (<i>Acipenser sinensis</i>) using Iso-seq and RNA-seq data. <i>Scientific Data</i> , 2023, 10, .	2.4	2
23776	Fungal diversity notes 1512–1610: taxonomic and phylogenetic contributions on genera and species of fungal taxa. <i>Fungal Diversity</i> , 2022, 117, 1-272.	4.7	20
23777	Species delimitation, molecular phylogeny and historical biogeography of the sweetlips fish (Perciformes, Haemulidae). <i>Zoosystematics and Evolution</i> , 2023, 99, 135-147.	0.4	1
23778	Analysis of the complete mitogenome of <i>Daphnia galeata</i> from the Han River, South Korea: structure comparison and control region evolution. <i>Functional and Integrative Genomics</i> , 2023, 23, .	1.4	1
23779	Extending and improving metagenomic taxonomic profiling with uncharacterized species using MetaPhlan 4. <i>Nature Biotechnology</i> , 2023, 41, 1633-1644.	9.4	132
23781	Diversity of the genus <i>Avrainvillea</i> (Dichotomosiphonaceae, Chlorophyta): new insights and eight new species. <i>European Journal of Phycology</i> , 0, , 1-28.	0.9	1
23782	Evolution of enzyme functionality in the flavin-containing monooxygenases. <i>Nature Communications</i> , 2023, 14, .	5.8	11
23783	Comparative Analyses of Chloroplast Genomes for Parasitic Species of Santalales in the Light of Two Newly Sequenced Species, <i>Taxillus nigrans</i> and <i>Scurrula parasitica</i> . <i>Genes</i> , 2023, 14, 560.	1.0	0
23784	Synteny Identifies Reliable Orthologs for Phylogenomics and Comparative Genomics of the Brassicaceae. <i>Genome Biology and Evolution</i> , 2023, 15, .	1.1	3
23785	Ancient Rapid Radiation Explains Most Conflicts Among Gene Trees and Well-Supported Phylogenomic Trees of Nostoclean Cyanobacteria. <i>Systematic Biology</i> , 2023, 72, 694-712.	2.7	2
23786	Evolution of the Growth Hormone Gene Duplication in Passerine Birds. <i>Genome Biology and Evolution</i> , 2023, 15, .	1.1	0
23787	Roadmap to the study of gene and protein phylogeny and evolution—A practical guide. <i>PLoS ONE</i> , 2023, 18, e0279597.	1.1	4
23788	Genomic characterization and molecular dating of the novel bacterium <i>Permianibacter aggregans</i> HW001T, which originated from Permian ground water. <i>Marine Life Science and Technology</i> , 2023, 5, 12-27.	1.8	0

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23789	Phylogenetic placement of the protosteloid amoeba <i>Microglomus paxillus</i> identifies another case of sporocarpic fruiting in Discosea (Amoebozoa). <i>Journal of Eukaryotic Microbiology</i> , 2023, 70, .	0.8	3
23790	<i>Thermomonas paludicola</i> sp. nov., isolated from a lotus wetland. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2023, 73, .	0.8	1
23791	Combining multiple lines of evidence to elucidate the origin and introduction pathway of bitou bush (<i>Chrysanthemoides monilifera</i> subsp. <i>rotundata</i>) in Australia. <i>Biological Invasions</i> , 0, , .	1.2	0
23792	Low genetic diversity among introduced axis deer: comments on the genetic paradox and invasive species. <i>Journal of Mammalogy</i> , 2023, 104, 603-618.	0.6	1
23793	Comparative analyses of five complete chloroplast genomes from the endemic genus <i>Cremanthodium</i> (Asteraceae) in Himalayan and adjacent areas. <i>Physiology and Molecular Biology of Plants</i> , 2023, 29, 409-420.	1.4	1
23794	The molecular phylogenetic position of <i>Harpagocarpus</i> (Polygonaceae) sheds new light on the infrageneric classification of <i>Fagopyrum</i> . <i>PhytoKeys</i> , 0, 220, 109-126.	0.4	0
23796	A global phylogenomic analysis of the shiitake genus <i>Lentinula</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2023, 120, .	3.3	5
23797	Phylogenomic insights into the origin and evolutionary history of evergreen broadleaved forests in East Asia under Cenozoic climate change. <i>Molecular Ecology</i> , 2023, 32, 2850-2868.	2.0	4
23798	Fungal Pathogens Associated with Aerial Symptoms of Avocado (<i>Persea americana</i> Mill.) in Tenerife (Canary Islands, Spain) Focused on Species of the Family Botryosphaeriaceae. <i>Microorganisms</i> , 2023, 11, 585.	1.6	5
23799	Evolutionary origin and establishment of a dioecious diploid-tetraploid complex. <i>Molecular Ecology</i> , 2023, 32, 2732-2749.	2.0	3
23800	A new species of Bush frog (<i>Anura</i> , Rhacophoridae, <i>Raorchestes</i>) from southeastern Yunnan, China. <i>ZooKeys</i> , 0, 1151, 47-65.	0.5	1
23801	Molecular exploration of fossil eggshell uncovers hidden lineage of giant extinct bird. <i>Nature Communications</i> , 2023, 14, .	5.8	2
23806	Two new species of <i>Diaporthe</i> (Diaporthaceae, Diaporthales) in China. <i>MycKeys</i> , 0, 95, 209-228.	0.8	4
23807	The complete chloroplast genome of <i>Elsholtzia fruticosa</i> (D. Don) Rehd. (Labiatae), an ornamental plant with high medicinal value. <i>Mitochondrial DNA Part B: Resources</i> , 2023, 8, 336-341.	0.2	2
23808	Genetic Characterization of a Novel Equus caballus Papillomavirus Isolated from a Thoroughbred Mare. <i>Viruses</i> , 2023, 15, 650.	1.5	2
23809	Investigating an Unknown Biodiversity: Evidence of Distinct Lineages of the Endemic Chola Guitarfish <i>Pseudobatos percellens</i> Walbaum, 1792 in the Western Atlantic Ocean. <i>Diversity</i> , 2023, 15, 344.	0.7	1
23810	Multi-gene phylogeny and morphology of two new <i>Phyllosticta</i> (Phyllostictaceae, Botryosphaeriales) species from China. <i>MycKeys</i> , 0, 95, 189-207.	0.8	2
23811	The majority of microorganisms in gas hydrate-bearing subseafloor sediments ferment macromolecules. <i>Microbiome</i> , 2023, 11, .	4.9	7

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23812	Species delimitation in a recently diverged species complex of <i>Eryngium</i> (Apiaceae: Saniculoideae) from the Chilean Mediterranean and the Atacama Desert: morphological, environmental and molecular coalescent-based analyses. <i>Botanical Journal of the Linnean Society</i> , 0, , .	0.8	0
23813	Insights into the Taxonomically Challenging Hexaploid Alpine Shrub Willows of <i>Salix</i> Sections <i>Phylicifoliae</i> and <i>Nigricantes</i> (Salicaceae). <i>Plants</i> , 2023, 12, 1144.	1.6	0
23814	Chromosome-level reference genome of <i>Tetrastigma hemsleyanum</i> (Vitaceae) provides insights into genomic evolution and the biosynthesis of phenylpropanoids and flavonoids. <i>Plant Journal</i> , 2023, 114, 805-823.	2.8	5
23815	<i>Gambierdiscus</i> (Gonyaulacales, Dinophyceae) diversity in Vietnamese waters with description of <i>G. vietnamensis</i> sp. nov.. <i>Journal of Phycology</i> , 2023, 59, 496-517.	1.0	2
23816	Transcriptome Analysis of Cyclooctasulfur Oxidation and Reduction by the Neutrophilic Chemolithoautotrophic <i>Sulfurovum indicum</i> from Deep-Sea Hydrothermal Ecosystems. <i>Antioxidants</i> , 2023, 12, 627.	2.2	4
23817	Phylogeography of Solomon Islands blossom bats reflects oceanic divides and Pleistocene connections. <i>Journal of Biogeography</i> , 2023, 50, 920-931.	1.4	1
23818	Immunogenic Properties and Antigenic Similarity of Virus-like Particles Derived from Human Polyomaviruses. <i>International Journal of Molecular Sciences</i> , 2023, 24, 4907.	1.8	0
23819	A molecular framework for grain number determination in barley. <i>Science Advances</i> , 2023, 9, .	4.7	10
23820	Phylogeny of the flea beetles (Galerucinae: Alticini) and the position of <i>Aulacothorax</i> elucidated through anchored phylogenomics (Coleoptera: Chrysomelidae: Alticini). <i>Systematic Entomology</i> , 2023, 48, 361-386.	1.7	5
23821	Evolutionary trend of bovine β -defensin proteins toward functionality prediction: A domain-based bioinformatics study. <i>Heliyon</i> , 2023, 9, e14158.	1.4	1
23822	Formation of the Holarctic Fauna: Dated molecular phylogenetic and biogeographic insights from the <i>Quedius</i> -lineage of Ground-Dwelling Rove Beetles (Coleoptera, Staphylinidae). <i>Molecular Phylogenetics and Evolution</i> , 2023, 182, 107749.	1.2	2
23823	Dispersal syndromes mediate phylogenetic distance decay relationships in a dendritic stream network. <i>Journal of Biogeography</i> , 2023, 50, 897-908.	1.4	0
23824	Assessment of the Diversity, Distinctiveness and Conservation of Australia's Central Queensland Coastal Rainforests Using DNA Barcoding. <i>Diversity</i> , 2023, 15, 378.	0.7	0
23825	A New Parasitic <i>Archamoeba</i> Causing Systemic Granulomatous Disease in Goldfish Extends the Diversity of Pathogenic <i>Endolimax</i> spp.. <i>Animals</i> , 2023, 13, 935.	1.0	0
23826	Re-Examination of the Holotype of <i>Ganoderma sichuanense</i> (Ganodermataceae, Polyporales) and a Clarification of the Identity of Chinese Cultivated Lingzhi. <i>Journal of Fungi (Basel, Switzerland)</i> , 2023, 9, 323.	1.5	1
23828	Molecular phylogenetics coupled with morphological analyses of Arctic and Antarctic strains place <i>Chamaepinnularia</i> (Bacillariophyta) within the Sellaphoraceae. <i>Fottea</i> , 2024, 24, 1-22.	0.4	2
23829	DNA barcoding of the genus <i>Alburnoides</i> Jetteles, 1861 (Actinopterygii, Cyprinidae) from Anatolia, Turkey. <i>Zoosystematics and Evolution</i> , 2023, 99, 185-194.	0.4	1
23830	Integrative approach resolves the systematics of barred wolf snakes in the <i>Lycodon striatus</i> complex (Reptilia, Colubridae). <i>Zoologica Scripta</i> , 2023, 52, 370-393.	0.7	2

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23831	The abundance of the potential pathogen <i>Staphylococcus hominis</i> in the air microbiome in a dental clinic and its susceptibility to far-UV light. <i>MicrobiologyOpen</i> , 2023, 12, .	1.2	0
23833	Taxonomy of <i>Thelidium auruntii</i> and <i>T. incavatum</i> complexes (lichenized Ascomycota, Verrucariales) in Finland. <i>MycKeys</i> , 0, 96, 1-23.	0.8	0
23835	Genetic differentiation within species exhibiting widespread gene flow; phylogeography of the downstream-inhabiting species <i>Ephemera orientalis</i> (Insecta: Ephemeroptera). <i>Biological Journal of the Linnean Society</i> , 2023, 138, 351-364.	0.7	1
23836	Evolution of mitogenomic gene order in Orthoptera. <i>Insect Molecular Biology</i> , 2023, 32, 387-399.	1.0	2
23837	Discovery of Avian Paramyxoviruses APMV-1 and APMV-6 in Shorebirds and Waterfowl in Southern Ukraine. <i>Viruses</i> , 2023, 15, 699.	1.5	2
23840	A broadly distributed predicted helicase/nuclease confers phage resistance via abortive infection. <i>Cell Host and Microbe</i> , 2023, 31, 343-355.e5.	5.1	6
23841	2b or not 2b? <i>2bRAD</i> is an effective alternative to <i>ddRAD</i> for phylogenomics. <i>Ecology and Evolution</i> , 2023, 13, .	0.8	1
23842	Molecular evolution, diversity, and adaptation of foot-and-mouth disease virus serotype O in Asia. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	2
23843	Molecular phylogeny of the Pseudaliidae (Nematoda) and the origin of associations between lungworms and marine mammals. <i>International Journal for Parasitology: Parasites and Wildlife</i> , 2023, 20, 192-202.	0.6	2
23844	Development of the oral resistome during the first decade of life. <i>Nature Communications</i> , 2023, 14, .	5.8	7
23845	<i>Hedyotis konhanungensis</i> (Rubiaceae): A new species from the central highlands of Vietnam. <i>PhytoKeys</i> , 0, 221, 73-84.	0.4	1
23846	Aneuploidy and gene dosage regulate filamentation and host colonization by <i>Candida albicans</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2023, 120, .	3.3	1
23847	Two novel recombinant human mastadenovirus D genotypes associated with acute respiratory illness. <i>Journal of Medical Virology</i> , 2023, 95, .	2.5	1
23848	Genetic Diversity and Phylogeography of a Turf-Forming Cosmopolitan Marine Alga, <i>Gelidium crinale</i> (Gelidiales, Rhodo-Phyta). <i>International Journal of Molecular Sciences</i> , 2023, 24, 5263.	1.8	0
23849	Type 1 vomeronasal receptor expression in juvenile and adult lungfish olfactory organ. <i>Zoological Letters</i> , 2023, 9, .	0.7	2
23850	Climate Cycles, Habitat Stability, and Lineage Diversification in an African Biodiversity Hotspot. <i>Diversity</i> , 2023, 15, 394.	0.7	0
23851	Whole-genome analysis showed the promotion of genetic diversity and coevolution in <i>Staphylococcus aureus</i> lytic bacteriophages and their hosts mediated by prophages via worldwide recombination events. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	1
23852	<i>Acinetobacter nematophilus</i> sp. nov., <i>Alcaligenes nematophilus</i> sp. nov., <i>Enterobacter nematophilus</i> sp. nov., and <i>Kaistia nematophila</i> sp. nov., Isolated from Soil-Borne Nematodes and Proposal for the Elevation of <i>Alcaligenes faecalis</i> subsp. <i>faecalis</i> , <i>Alcaligenes faecalis</i> subsp. <i>parafaecalis</i> , and <i>Alcaligenes faecalis</i> subsp. <i>phenolicus</i> to the Species Level. <i>Taxonomy</i> , 2023, 3, 148-168.	0.4	5

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23853	Bizarre Morphology Obscures Real Affiliation: An Integrative Study of Enigmatic Cephalaspid Philine denticulata from Arctic Waters Reveals Its Unique Phylogenetic Position. <i>Diversity</i> , 2023, 15, 395.	0.7	0
23854	Complete chloroplast genome sequence and phylogenetic analysis of <i>Rhododendron molle</i> G. Don, an endangered Ericaceae species located on Dabie Mountains (central China). <i>Plant Biotechnology Reports</i> , 0, , .	0.9	0
23855	Dynamic changes in polioviruses identified by environmental surveillance in Guangzhou, 2009â€“2021. <i>Journal of Medical Virology</i> , 2023, 95, .	2.5	1
23858	Codon Usage Analyses Reveal the Evolutionary Patterns among Plastid Genes of Saxifragales at a Larger-Sampling Scale. <i>Genes</i> , 2023, 14, 694.	1.0	0
23859	An Automated Bioinformatics Pipeline Informing Near-Real-Time Public Health Responses to New HIV Diagnoses in a Statewide HIV Epidemic. <i>Viruses</i> , 2023, 15, 737.	1.5	0
23860	Mitochondrial Genome Sequence of <i>Salvia officinalis</i> (Lamiales: Lamiaceae) Suggests Diverse Genome Structures in Cogeneric Species and Finds the Stop Gain of Genes through RNA Editing Events. <i>International Journal of Molecular Sciences</i> , 2023, 24, 5372.	1.8	6
23861	Litthabitellidae: a new family of the Truncatelloidea (Mollusca: Caenogastropoda). <i>Journal of Natural History</i> , 2023, 57, 299-329.	0.2	1
23862	New record of <i>Halymenia malaysiana</i> (Halymeniaceae, Rhodophyta) from Viet Nam, and its genetic diversity in the western Pacific. <i>Botanica Marina</i> , 2023, 66, 113-123.	0.6	2
23863	Simultaneous production of $\hat{1}^3$ -linolenic acid and carotenoids by a novel microalgal strain isolated from the underexplored habitat of intermittent streams. <i>Algal Research</i> , 2023, 71, 103055.	2.4	1
23864	Exploring More on Dictyosporiaceae: The Species Geographical Distribution and Intriguing Novel Additions from Plant Litter. <i>Diversity</i> , 2023, 15, 410.	0.7	0
23865	Phylogeny of <i>Rubus</i> (Rosaceae): Integrating molecular and morphological evidence into an infrageneric revision. <i>Taxon</i> , 2023, 72, 278-306.	0.4	5
23866	<i>Kengiochloa</i> , a new bamboo genus to accommodate the morphologically unique species, <i>Pseudosasa pubiflora</i> (Poaceae). <i>PhytoKeys</i> , 0, 221, 131-145.	0.4	1
23867	Complete Chloroplast Genome of Four Thai Native Dioscorea Species: Structural, Comparative and Phylogenetic Analyses. <i>Genes</i> , 2023, 14, 703.	1.0	1
23869	The Evolution and Transmission Dynamics of Multidrug-Resistant Tuberculosis in an Isolated High-Plateau Population of Tibet, China. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	3
23870	From oral structure to molecular evidence: new insights into the evolutionary phylogeny of the ciliate order Sessilida (Protista, Ciliophora), with the establishment of two new families and new contributions to the poorly studied family Vaginicolidae. <i>Science China Life Sciences</i> , 2023, 66, 1535-1553.	2.3	6
23871	The Silk roads: phylogeography of Central Asian dice snakes (Serpentes: Natricidae) shaped by rivers in deserts and mountain valleys. <i>Environmental Epigenetics</i> , 0, , .	0.9	1
23872	<i>Carex quixotiana</i> (Cyperaceae), a new Iberian endemic from Don Quixote's land (La Mancha, S Spain). <i>PhytoKeys</i> , 0, 221, 161-186.	0.4	0
23875	Large-Scale Species Tree Estimation. , 2023, , 19-42.		1

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23876	Relationship between Dubas Bug (<i>Ommatissus lybicus</i>) Infestation and the Development of Fungal-Induced Leaf Spots in Date Palms (<i>Phoenix dactylifera</i>). <i>Insects</i> , 2023, 14, 283.	1.0	0
23877	Metabolic Versatility of the Family <i>Haliaceae</i> Revealed by the Genomics of Novel Cultured Isolates. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	0
23878	The first chromosome-level <i>Fallopia multiflora</i> genome assembly provides insights into stilbene biosynthesis. <i>Horticulture Research</i> , 2023, 10, .	2.9	1
23879	Genome sequence and probiotic potential of newly isolated <i>Enterococcus durans</i> strain MN187066. <i>Letters in Applied Microbiology</i> , 2023, 76, .	1.0	2
23880	<i>Calonectria</i> species diversity on eucalypts in Indonesia. <i>Southern Forests</i> , 0, , 1-9.	0.2	1
23881	Natural History of DNA-Dependent DNA Polymerases: Multiple Pathways to the Origins of DNA. <i>Viruses</i> , 2023, 15, 749.	1.5	2
23882	Tracing 100 million years of grass genome evolutionary plasticity. <i>Plant Journal</i> , 2023, 114, 1243-1266.	2.8	3
23883	Genomic Characterization of <i>Staphylococcus aureus</i> in Wildlife. <i>Animals</i> , 2023, 13, 1064.	1.0	6
23884	Revealing evolution of tropane alkaloid biosynthesis by analyzing two genomes in the Solanaceae family. <i>Nature Communications</i> , 2023, 14, .	5.8	12
23885	Taxonomy and phylogeny of brown-rot corticioid fungi in China: <i>Coniophora beijingensis</i> and <i>Veluticeps subfasciculata</i> spp. nov.. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	1
23886	Population genomics unravels the Holocene history of bread wheat and its relatives. <i>Nature Plants</i> , 2023, 9, 403-419.	4.7	28
23887	A Survey of Processing Systems for Phylogenetics and Population Genetics. <i>ACM Transactions on Reconfigurable Technology and Systems</i> , 2023, 16, 1-27.	1.9	0
23888	Deep Structural Analysis of Myriads of Omicron Sub-Variants Revealed Hotspot for Vaccine Escape Immunity. <i>Vaccines</i> , 2023, 11, 668.	2.1	3
23889	<i>Helicobacter kumamotonensis</i> sp. nov., isolated from human clinical specimens. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2023, 73, .	0.8	0
23890	Genome assembly of the deep-sea coral <i>Lophelia pertusa</i> . <i>GigaByte</i> , 0, 2023, 1-12.	0.0	1
23893	Generic classification of Asian horned toads (Anura: Megophryidae: Megophryinae) and monograph of Chinese species. <i>Zoological Research</i> , 2023, 44, 380-450.	0.9	5
23894	A food poisoning caused by ST7 <i>Staphylococcus aureus</i> harboring sea gene in Hainan province, China. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	5
23896	<i>Salinibacterium sedimenticola</i> sp. nov., Isolated from Tidal Flat Sediment. <i>Current Microbiology</i> , 2023, 80, .	1.0	1

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23897	Polygamy and purifying selection in birds. <i>Evolution; International Journal of Organic Evolution</i> , 2023, 77, 276-288.	1.1	3
23898	<i>De novo</i> genomic analysis of <i>Enterobacter asburiae</i> EBRJ12, a plant growth-promoting rhizobacteria isolated from the rhizosphere of <i>Phaseolus vulgaris</i> L. <i>Journal of Applied Microbiology</i> , 2023, 134, .	1.4	6
23899	<i>Spiranthes hachijoensis</i> (Orchidaceae), a new species within the <i>S. sinensis</i> species complex in Japan, based on morphological, phylogenetic, and ecological evidence. <i>Journal of Plant Research</i> , 2023, 136, 333-348.	1.2	2
23900	Evolution of the rice blast pathogen on spatially structured rice landraces maintains multiple generalist fungal lineages. <i>Molecular Ecology</i> , 2023, 32, 2519-2533.	2.0	4
23901	Two novel endophytic <i>Tolypocladium</i> species identified from native pines in south Florida. <i>Fungal Systematics and Evolution</i> , 2023, , .	0.9	0
23904	Enterococcal <i>Escherichia coli</i> as etiological agent of endemic diarrhea in Spain: A prospective multicenter prevalence study with molecular characterization of isolates. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	1
23905	Resurrection of <i>Leucobryum scalare</i> M. A. J. Hal. ex M. Fleisch. (Bryophyta, Leucobryaceae) based on phylogenetic and morphometric evidence. <i>PhytoKeys</i> , 0, 222, 27-47.	0.4	1
23906	High Andean Steppes of Southern Chile Contain Little-Explored <i>Peltigera</i> Lichen Symbionts. <i>Journal of Fungi</i> (Basel, Switzerland), 2023, 9, 372.	1.5	0
23908	A new species and a new record of the genus <i>Squamulea</i> (<i>Teloschistaceae</i>, lichenized) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.5	0
23910	Vancomycin Resistance in <i>Enterococcus faecium</i> from the Dallas, Texas, Area Is Conferred Predominantly on pRUM-Like Plasmids. <i>MSphere</i> , 2023, 8, .	1.3	2
23911	A tale of two tubeworms: taxonomy of vestimentiferans (Annelida: Siboglinidae) from the Mid-Cayman Spreading Centre. <i>Invertebrate Systematics</i> , 2023, 37, 167-191.	0.5	1
23913	Evolutionary history of two evergreen <i>Rhododendron</i> species as revealed by chromosome-level genome assembly. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	2
23914	Freshwater Lichens, Including New Species in the Genera <i>Verrucaria</i> , <i>Placopyrenium</i> and <i>Circinaria</i> , Associated with <i>Lobothallia hydrocharis</i> (Poelt & Nimis) Sohrabi & Nimis from Watercourses of Sardinia. <i>Journal of Fungi</i> (Basel, Switzerland), 2023, 9, 380.	1.5	2
23915	Colonization order of bacterial isolates on treefrog embryos impacts microbiome structure in tadpoles. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2023, 290, .	1.2	0
23916	A contribution to the genus <i>Steccherinum</i> (Steccherinaceae, Polyporales): Introducing two new species and two new combinations of the genus. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	0
23917	Morphological and molecular investigations shed light on diversity and distribution of <i>Palmariaceae</i> in the north-western Pacific. <i>European Journal of Phycology</i> , 2023, 58, 438-456.	0.9	0
23918	A real data-driven simulation strategy to select an imputation method for mixed-type trait data. <i>PLoS Computational Biology</i> , 2023, 19, e1010154.	1.5	2
23919	Genomic analyses of hair from Ludwig van Beethoven. <i>Current Biology</i> , 2023, 33, 1431-1447.e22.	1.8	20

#	ARTICLE	IF	CITATIONS
23921	From primordial clocks to circadian oscillators. <i>Nature</i> , 2023, 616, 183-189.	13.7	6
23922	Evolutionary differences in gene loss and pseudogenization among mycoheterotrophic orchids in the tribe Vanilleae (subfamily Vanilloideae). <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	0
23923	Aminoacyl-tRNA Synthetase Evolution within the Dynamic Tripartite Translation System of Plant Cells. <i>Genome Biology and Evolution</i> , 2023, 15, .	1.1	2
23924	Lost characters and lost taxonomists: Coelocarteriidae fam. nov., Poecilosclerida with and without chelae, to accommodate supposed phloeodictyids (Haplosclerida). <i>Invertebrate Systematics</i> , 2023, 37, 192-210.	0.5	0
23925	The evolution of white-tailed jackrabbit camouflage in response to past and future seasonal climates. <i>Science</i> , 2023, 379, 1238-1242.	6.0	5
23926	Elucidation of the pathway for biosynthesis of saponin adjuvants from the soapbark tree. <i>Science</i> , 2023, 379, 1252-1264.	6.0	30
23927	Impact of the Dimethyl Sulfoxide Reductase Superfamily on the Evolution of Biogeochemical Cycles. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	4
23928	Genomes of four <i>Streptomyces</i> strains reveal insights into putative new species and pathogenicity of scab-causing organisms. <i>BMC Genomics</i> , 2023, 24, .	1.2	1
23929	The COVID-19 Pandemic Sparked Off a Large-Scale Outbreak of Carbapenem-Resistant <i>Acinetobacter baumannii</i> from the Endemic Strains at an Italian Hospital. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	3
23930	Peribolospomycetes class. nov.: description of a new heat resistant and osmotolerant basidiomycete lineage, represented by <i>Peribolospora</i> gen. nov., <i>P. kevrpleyi</i> sp. nov., and <i>P. baueri</i> sp. nov.. <i>Mycological Progress</i> , 2023, 22, .	0.5	0
23932	Fossil berries reveal global radiation of the nightshade family by the early Cenozoic. <i>New Phytologist</i> , 2023, 238, 2685-2697.	3.5	0
23933	Vaginal microbiota of adolescents and their mothers: A preliminary study of vertical transmission and persistence. , 0, 2, .		0
23934	Freshwater fungi from karst landscapes in China and Thailand. <i>Fungal Diversity</i> , 2023, 119, 1-212.	4.7	10
23935	Analysis of bacterial pangenomes reduces CRISPR dark matter and reveals strong association between membranome and CRISPR-Cas systems. <i>Science Advances</i> , 2023, 9, .	4.7	1
23936	A new, rare, small-ranged, and endangered mountain snake of the genus <i>Elaphe</i> from the Southern Levant. <i>Scientific Reports</i> , 2023, 13, .	1.6	2
23937	Reverse vaccinology-based identification of a novel surface lipoprotein that is an effective vaccine antigen against bovine infections caused by <i>Pasteurella multocida</i> . <i>PLoS Pathogens</i> , 2023, 19, e1011249.	2.1	1
23938	Characterization of Antimicrobial Resistance Genes and Virulence Factors in the Genomes of <i>Escherichia coli</i> ST69 Isolates from Preweaned Dairy Calves and Their Phylogenetic Relationship with Poultry and Human Clinical Strains. <i>Microbial Drug Resistance</i> , 2023, 29, 249-255.	0.9	3
23939	Atomistic simulation of protein evolution reveals sequence covariation and time-dependent fluctuations of site-specific substitution rates. <i>PLoS Computational Biology</i> , 2023, 19, e1010262.	1.5	0

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23940	Global scenario of the RmtE pan-aminoglycoside-resistance mechanism: emergence of the rmtE4 gene in South America associated with a hospital-related IncL plasmid. <i>Microbial Genomics</i> , 2023, 9, .	1.0	0
23941	Upregulation of ENKD1 disrupts cellular homeostasis to promote lymphoma development. <i>Journal of Cellular Physiology</i> , 0, , .	2.0	0
23942	Genomic convergence underlying high-altitude adaptation in alpine plants. <i>Journal of Integrative Plant Biology</i> , 2023, 65, 1620-1635.	4.1	3
23943	Checking the balance between pathogenic and mutualistic pine needle fungi of the genus <i>Lophodermium</i> in forested and urban areas of Slovakia. <i>Scandinavian Journal of Forest Research</i> , 2023, 38, 39-48.	0.5	0
23945	Diversity of Gracilariaceae (Rhodophyta) in China: An integrative morphological and molecular assessment including a description of <i>Gracilaria tsengii</i> sp. nov.. <i>Algal Research</i> , 2023, 71, 103074.	2.4	1
23946	How to start a <i>LINE</i> : 5' switching rejuvenates <i>LINE</i> retrotransposons in tobacco and related <i>Nicotiana</i> species. <i>Plant Journal</i> , 2023, 115, 52-67.	2.8	0
23947	Comprehensive genomic analyses of <i>Vigna unguiculata</i> provide insights into population differentiation and the genetic basis of key agricultural traits. <i>Plant Biotechnology Journal</i> , 2023, 21, 1426-1439.	4.1	2
23949	First report of <i>Erysiphe astragali</i> causing powdery mildew on <i>Astragalus strictus</i> in Tibet, China. <i>Australasian Plant Pathology</i> , 2023, 52, 207-214.	0.5	0
23950	A male-killing gene encoded by a symbiotic virus of <i>Drosophila</i> . <i>Nature Communications</i> , 2023, 14, .	5.8	9
23951	Comparative analysis of complete <i>Artemisia</i> subgenus <i>Seriphidium</i> (Asteraceae: Anthemideae) chloroplast genomes: insights into structural divergence and phylogenetic relationships. <i>BMC Plant Biology</i> , 2023, 23, .	1.6	5
23952	Adeno-Associated Virus 2 and Human Adenovirus F41 in Wastewater during Outbreak of Severe Acute Hepatitis in Children, Ireland. <i>Emerging Infectious Diseases</i> , 2023, 29, 751-760.	2.0	10
23953	Addition of three new lineages in <i>Mycosphaerellaceae</i> : <i>Neoacervuloseptoria</i> gen. nov., <i>Neocercospora</i> gen. nov. and <i>Neoramulariopsis</i> gen. nov.. <i>Mycological Progress</i> , 2023, 22, .	0.5	0
23954	Being Safe, but Not Too Safe: A Nudibranch Feeding on a Bryozoan-Associated Hydrozoan. <i>Diversity</i> , 2023, 15, 484.	0.7	0
23955	Allelic diversity uncovers protein domains contributing to the emergence of antimicrobial resistance. <i>PLoS Genetics</i> , 2023, 19, e1010490.	1.5	2
23956	<i>Neocamarosporium aquaticum</i> (Neocamarosporiaceae, Dothideomycetes), a novel fungus from salt marsh habitats. <i>Botanica Marina</i> , 2023, 66, 271-279.	0.6	2
23957	The Origins of ST11 KL64 <i>Klebsiella pneumoniae</i> : a Genome-Based Study. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	3
23958	High-resolution single-molecule long-fragment rRNA gene amplicon sequencing of bacterial and eukaryotic microbial communities. <i>Cell Reports Methods</i> , 2023, 3, 100437.	1.4	0
23961	Characterization and Genome Analysis of <i>Cladobotryum mycophilum</i> , the Causal Agent of Cobweb Disease of <i>Morchella sextelata</i> in China. <i>Journal of Fungi (Basel, Switzerland)</i> , 2023, 9, 411.	1.5	1

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23962	Evaluating species boundaries using coalescent delimitation in pine-killing <i>Monochamus</i> (Coleoptera: Tj ETQq0 0 0 rgBT /Overlock 10 T	1.2	2
23963	Diversity of RNA editing in chloroplast transcripts across three main plant clades. <i>Plant Systematics and Evolution</i> , 2023, 309, .	0.3	1
23964	Emergence of hypervirulent <i>Pseudomonas aeruginosa</i> pathotypically armed with co-expressed T3SS effectors ExoS and ExoU. , 2023, 1, 44-56.		1
23965	Anthropogenic impacts on threatened species erode functional diversity in chelonians and crocodylians. <i>Nature Communications</i> , 2023, 14, .	5.8	5
23966	Enterococcal Linear Plasmids Adapt to <i>Enterococcus faecium</i> and Spread within Multidrug-Resistant Clades. <i>Antimicrobial Agents and Chemotherapy</i> , 2023, 67, .	1.4	3
23967	High throughput screening of fungal phytopathogens caught in Australian forestry insect surveillance traps. <i>Frontiers in Forests and Global Change</i> , 0, 6, .	1.0	1
23968	A Contribution to the Systematics of Sunda Shelf Angle-Headed Dragons (Agamidae: <i>Gonocephalus</i>) with the Description of New Taxa from Sumatra. <i>Herpetological Monographs</i> , 2023, 37, .	1.1	0
23969	Growth characteristics and phylogenetic analysis of the isolate mycelium, <i>Ophiocordyceps sinensis</i> . , 0, , .		1
23970	<i>Paraphyton mirabile</i> "A rare geophilic dermatophyte" with unclear relation to nail disease. <i>Journal of the European Academy of Dermatology and Venereology</i> , 2023, 37, .	1.3	1
23971	The biology of an isolated <i>Mashona</i> mole-rat population from southern Malawi, with implications for the diversity and biogeography of the genus <i>Fukomys</i> . <i>Organisms Diversity and Evolution</i> , 0, , .	0.7	0
23972	<i>Marsupella lusitanica</i> (Gymnomitriaceae, Marchantiophyta), a New Species of Sect. <i>Ustulatae</i> from Mountain Ranges of Portugal. <i>Plants</i> , 2023, 12, 1468.	1.6	0
23974	Src inhibition induces mitotic arrest associated with chromosomal passenger complex. <i>Cell and Tissue Research</i> , 0, , .	1.5	0
23975	The complete chloroplast genome of <i>Ligusticopsis acaulis</i> (Shan et Sheh) Pimenov (Apiaceae), an endemic species from China. <i>Mitochondrial DNA Part B: Resources</i> , 2023, 8, 451-456.	0.2	0
23976	The role of geography, ecology, and hybridisation in the evolutionary history of Canary Island <i>Descurainia</i> . <i>American Journal of Botany</i> , 0, , .	0.8	0
23977	New Zealand isolates from snow of the widespread algal genus <i>Raphidonema</i> assigned to a single species. <i>New Zealand Journal of Botany</i> , 2024, 62, 83-94.	0.8	2
23979	Description of a Novel Fish Pathogen, <i>Plesiomonas shigelloides</i> subsp. <i>oncorhynchi</i> , Isolated from Rainbow Trout (<i>Oncorhynchus mykiss</i>): First Genome Analysis and Comparative Genomics. <i>Fishes</i> , 2023, 8, 179.	0.7	4
23980	Phylogenomics and morphological evolution of the mega-diverse genus <i>Artemisia</i> (Asteraceae: Tj ETQq0 0 0 rgBT /Overlock 10 T 131, 867-883.	1.4	5
23981	Phylogeography of <i>Falagonia mexicana</i> Sharp, 1883 (Coleoptera, Staphylinidae, Aleocharinae). <i>ZooKeys</i> , 0, 1156, 107-131.	0.5	0

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23982	Genome-Wide Pathway Exploration of the Epidermidibacterium keratini EPI-7T. Microorganisms, 2023, 11, 870.	1.6	1
23983	A molecular and morphological study of <i>Leucobryum</i> in Britain and Europe: the presence of <i>L. albidum</i> (P.Beauv.) Lindb. confirmed. Journal of Bryology, 2023, 45, 1-29.	0.4	0
23985	<i>Carya luana</i> C. Deng et X. Xiang, sp. nov. (Juglandaceae), a new species from Guizhou, China, identified based on whole plastome phylogeny and morphometrics. Nordic Journal of Botany, 2023, .	0.2	1
23986	Genomic Diversity and Phenotypic Variation in Fungal Decomposers Involved in Bioremediation of Persistent Organic Pollutants. Journal of Fungi (Basel, Switzerland), 2023, 9, 418.	1.5	2
23987	Parallel host shifts in a bacterial plant pathogen suggest independent genetic solutions. Molecular Plant Pathology, 2023, 24, 527-535.	2.0	5
23988	Infection strategies of different chytrids in a diatom spring bloom. Freshwater Biology, 2023, 68, 972-986.	1.2	2
23989	Cryo-tomography reveals rigid-body motion and organization of apicomplexan invasion machinery. Nature Communications, 2023, 14, .	5.8	8
23990	Phylogenetic position and low genomic diversity of <i>Candidatus Rickettsia kotlanii</i> inferred by complete genome sequences of two Japanese isolates. Microbiology and Immunology, 2023, 67, 275-280.	0.7	1
23991	Genome structures resolve the early diversification of teleost fishes. Science, 2023, 379, 572-575.	6.0	18
23992	<i>Polydomus karssenii</i> gen. nov. sp. nov. is a dark septate endophyte with a bifunctional lifestyle parasitising eggs of plant parasitic cyst nematodes (Heterodera spp.). IMA Fungus, 2023, 14, .	1.7	2
23993	Prevalence of foodborne viruses and influenza A virus from poultry processing plants to retailled chickens. Frontiers in Sustainable Food Systems, 0, 7, .	1.8	0
23994	Studies on the Genus <i>Pyrenopolyporus</i> (Hypoxylaceae) in Thailand Using a Polyphasic Taxonomic Approach. Journal of Fungi (Basel, Switzerland), 2023, 9, 429.	1.5	0
23995	Integrating Fossil Flowers into the Angiosperm Phylogeny Using Molecular and Morphological Evidence. Systematic Biology, 2023, 72, 837-855.	2.7	4
23996	Tracing the Origin of Genotype II African Swine Fever Virus in China by Genomic Epidemiology Analysis. Transboundary and Emerging Diseases, 2023, 2023, 1-14.	1.3	4
23997	The first two mitochondrial genomes from <i>Apiotrichum</i> reveal mitochondrial evolution and different taxonomic assignment of Trichosporonales. IMA Fungus, 2023, 14, .	1.7	4
23998	Genomics of the <i>œtumorigenes</i> clade of the family <i>Rhizobiaceae</i> and description of <i>Rhizobium rhododendri</i> sp. nov.. MicrobiologyOpen, 2023, 12, .	1.2	4
23999	Gene loss during a transition to multicellularity. Scientific Reports, 2023, 13, .	1.6	3
24000	Comparative genomics reveals unique features of two <i>Babesia motasi</i> subspecies: <i>Babesia motasi lintanensis</i> and <i>Babesia motasi hebeiensis</i> . International Journal for Parasitology, 2023, 53, 265-283.	1.3	2

#	ARTICLE	IF	CITATIONS
24001	Taxonomic and phylogenetic study of the genus <i>Diploschistes</i> (Ostropales, Thelotremataceae) reveals one new species from Pakistan. <i>Acta Botanica Brasilica</i> , 0, 37, .	0.8	0
24002	Effects of Environmental Variation in Structuring Population Genetic Variation in the False-Water Cobras (<i>Xenodontinae</i> : <i>Hydrodynastes</i>). <i>Evolutionary Biology</i> , 0, , .	0.5	0
24004	What is <i>Salvinia molesta</i> (<i>Salviniaceae</i>)? Determining the maternal progenitor and genetic diversity of the clonal invasive fern giant salvinia. <i>Biological Invasions</i> , 0, , .	1.2	0
24005	<i>Aquitalea palustris</i> sp. nov., isolated from a wild cranberry bog in the Cape Cod National Seashore. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2023, 73, .	0.8	0
24006	Confirmation of <i>Stemphylium vesicarium</i> , the causal agent of brown spot of tomato in Germany. <i>Journal of Plant Diseases and Protection</i> , 0, , .	1.6	0
24007	The complete chloroplast genome of <i>Pseudostellaria davidii</i> (franch.) Pax, 1934. <i>Mitochondrial DNA Part B: Resources</i> , 2023, 8, 471-474.	0.2	0
24008	Fortuitously compatible protein surfaces primed allosteric control in cyanobacterial photoprotection. <i>Nature Ecology and Evolution</i> , 2023, 7, 756-767.	3.4	6
24009	The complete plastid genome and nuclear ribosomal transcription unit sequences of <i>Spiraea prunifolia</i> f. <i>simpliciflora</i> (<i>Rosaceae</i>). <i>Korean Journal of Plant Taxonomy</i> , 2023, 53, 32-37.	0.3	1
24010	Back-to-Africa introductions of <i>Mycobacterium tuberculosis</i> as the main cause of tuberculosis in Dar es Salaam, Tanzania. <i>PLoS Pathogens</i> , 2023, 19, e1010893.	2.1	4
24011	Ancestral reconstruction of the MotA stator subunit reveals that conserved residues far from the pore are required to drive flagellar motility. <i>MicroLife</i> , 2023, 4, .	1.0	3
24012	High-Quality Assembly and Comparative Analysis of <i>Actinidia latifolia</i> and <i>A. valvata</i> Mitogenomes. <i>Genes</i> , 2023, 14, 863.	1.0	1
24013	Comparative genomics of <i>Viola selkirkii</i> and <i>V. ulleungdoensis</i> (<i>Violaceae</i>). <i>Korean Journal of Plant Taxonomy</i> , 2023, 53, 38-46.	0.3	1
24014	The complete mitochondrial genome of the Critically Endangered Saba Green Iguana, <i>Iguana iguana</i> (Squamata: Iguanidae). <i>Mitochondrial DNA Part B: Resources</i> , 2023, 8, 475-478.	0.2	0
24017	<i>Gerhardtia tomentosa</i> and <i>Ossicaulis borealis</i> (<i>Agaricales</i> , <i>Lyophyllaceae</i>)—Two new species from northeast China. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	0
24018	First insights into antimicrobial resistance, toxigenic profiles, and genetic diversity in <i>Bacillus cereus</i> isolated from Chinese sausages. <i>LWT - Food Science and Technology</i> , 2023, 181, 114717.	2.5	2
24019	Insight into the evolutionary and domesticated history of the most widely cultivated mushroom <i>Agaricus bisporus</i> via mitogenome sequences of 361 global strains. <i>BMC Genomics</i> , 2023, 24, .	1.2	0
24020	Effect of environmental and spatial factors on the phylogenetic and functional diversity of the Mediterranean tree communities of Europe. <i>Plant Biology</i> , 2023, 25, 631-645.	1.8	2
24021	Drivers of strong isolation and small effective population size at a leading range edge of a widespread plant. <i>Heredity</i> , 2023, 130, 347-357.	1.2	2

#	ARTICLE	IF	CITATIONS
24022	A high-quality chromosome-level <i>Eutrema salsugineum</i> genome, an extremophile plant model. <i>BMC Genomics</i> , 2023, 24, .	1.2	4
24023	Hepatitis E virus in pork meat products and exposure assessment in Belgium. <i>International Journal of Food Microbiology</i> , 2023, 397, 110198.	2.1	4
24024	Diversity of Pholcus Spiders (Araneae: Pholcidae) in China's Lǎliang Mountains: An Integrated Morphological and Molecular Approach. <i>Insects</i> , 2023, 14, 364.	1.0	5
24025	Increased public health threat of avian-origin H3N2 influenza virus caused by its evolution in dogs. <i>ELife</i> , 0, 12, .	2.8	6
24027	Plastid phylogenomics and species discrimination in the "Chinese" clade of <i>Roscoea</i> (Zingiberaceae). <i>Plant Diversity</i> , 2023, , .	1.8	0
24028	Survival and Genome Evolution Signatures of <i>Klebsiella pneumoniae</i> Isolates Originated in Seven Species of Aquatic Animals. <i>Diversity</i> , 2023, 15, 527.	0.7	1
24029	Nuclear DNA Amounts in Chinese Bryophytes Estimated by Flow Cytometry: Variation Patterns and Biological Significances. <i>Plants</i> , 2023, 12, 1564.	1.6	0
24030	<i>Astrothelium subsiamense</i> sp. nov. from Fujian, China. <i>Mycotaxon</i> , 2022, 137, 477-484.	0.1	0
24031	Plant DNA barcode library for native flowering plants in the arid region of northwestern China. <i>Molecular Ecology Resources</i> , 2023, 23, 1389-1402.	2.2	2
24032	Three New <i>Gesneria</i> Species (Gesneriaceae) Support Parc National Pic Macaya (Haiti) as an Important Biodiversity Hotspot. <i>Systematic Botany</i> , 2023, 48, 34-43.	0.2	2
24033	Evolutionarily Young African Rhinoceros Gammaretroviruses. <i>Journal of Virology</i> , 0, , .	1.5	0
24034	Genomic Relationships of <i>Glycine remota</i> , a Recently Discovered Perennial Relative of Soybean, within <i>Glycine</i> . <i>Systematic Botany</i> , 2023, 48, 78-87.	0.2	4
24035	Texas microfungi: on the taxonomic placement of <i>Flosculomyces floridaensis</i> in <i>Zygosporiaceae</i> . <i>Mycotaxon</i> , 2022, 137, 521-536.	0.1	0
24036	<i>Tuber rugosum</i> , a new species from northeastern North America: Slug mycophagy aides in electron microscopy of ascospores. <i>Mycologia</i> , 0, , 1-17.	0.8	1
24037	Target Capture Methods Offer Insight into the Evolution of Rapidly Diverged Taxa and Resolve Allopolyploid Homeologs in the Fern Genus <i>Polypodium</i> s.s.. <i>Systematic Botany</i> , 2023, 48, 96-109.	0.2	1
24039	Genome wide identification and characterization of MATE family genes in mangrove plants. <i>Genetica</i> , 2023, 151, 241-249.	0.5	1
24040	MutaGAN: A sequence-to-sequence GAN framework to predict mutations of evolving protein populations. <i>Virus Evolution</i> , 2023, 9, .	2.2	0
24041	Six decades of museum collections reveal disruption of native ant assemblages by introduced species. <i>Current Biology</i> , 2023, 33, 2088-2094.e6.	1.8	5

#	ARTICLE	IF	CITATIONS
24042	Population structure and genome-wide evolutionary signatures reveal putative climate-driven habitat change and local adaptation in the large yellow croaker. <i>Marine Life Science and Technology</i> , 2023, 5, 141-154.	1.8	2
24043	Evolutionary history of New World crakes (Aves: Rallidae) with emphasis on the tribe Laterallini. <i>Zoologica Scripta</i> , 2023, 52, 394-412.	0.7	1
24044	Foodborne Outbreak of Extended Spectrum Beta-lactamase Producing <i>Shigella sonnei</i> Associated with Contaminated Spring Onions in the United Kingdom. <i>Journal of Food Protection</i> , 2023, 86, 100074.	0.8	4
24045	The mitochondrial genome of <i>Dendrobaena tellermanica</i> Perel, 1966 (Annelida: Tj ETQq1 1 0.784314 rgBT 0/Overloc	0.4	0
24046	The relative transmission fitness of multidrug-resistant <i>Mycobacterium tuberculosis</i> in a drug resistance hotspot. <i>Nature Communications</i> , 2023, 14, .	5.8	11
24047	Metagenomic analysis reveals the short-term influences on conjugation of bla _{NDM-1} and microbiome in hospital wastewater by silver nanoparticles at environmental-related concentration. <i>Environmental Research</i> , 2023, 228, 115866.	3.7	1
24048	Phylogenomics revealed migration routes and adaptive radiation timing of Holarctic malaria mosquito species of the <i>Maculipennis</i> Group. <i>BMC Biology</i> , 2023, 21, .	1.7	0
24049	First national record of <i>Microhyla hmongorum</i> Hoang, Nguyen, Phan, Pham, Ninh, Wang, Jiang, Ziegler and Nguyen, 2022 (Anura, Microhylidae, Microhyla) in China. <i>Biodiversity Data Journal</i> , 0, 11, .	0.4	1
24050	Two new species of genus <i>Leucoagaricus</i> (Agaricaceae, Agaricales) from Pakistan. <i>MycKeys</i> , 0, 96, 159-171.	0.8	1
24051	Genome-Wide Identification and Expression Analysis of the TCP Genes in <i>Jatropha curcas</i> L. Reveals Its Roles in Involvement of Leaf Shape. <i>Forests</i> , 2023, 14, 780.	0.9	1
24052	Functional characterization of xanthorhodopsin in <i>Salinivibrio socompensis</i> , a novel halophile isolated from modern stromatolites. <i>Photochemical and Photobiological Sciences</i> , 0, , .	1.6	0
24053	Distribution and abundance of tetraether lipid cyclization genes in terrestrial hot springs reflect pH . <i>Environmental Microbiology</i> , 2023, 25, 1644-1658.	1.8	2
24054	Bacterial origin of a key innovation in the evolution of the vertebrate eye. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2023, 120, .	3.3	7
24055	Maximum likelihood pandemic-scale phylogenetics. <i>Nature Genetics</i> , 2023, 55, 746-752.	9.4	11
24056	Population genomics reveals demographic history and selection signatures of hazelnut (<i>Corylus</i>). <i>Horticulture Research</i> , 0, , .	2.9	0
24057	Macroevolutionary decline in mycorrhizal colonization and chemical defense responsiveness to mycorrhization. <i>IScience</i> , 2023, 26, 106632.	1.9	4
24058	Molecular mechanisms underlying hematophagia revealed by comparative analyses of leech genomes. <i>GigaScience</i> , 2022, 12, .	3.3	3
24059	Genome-wide association reveals host-specific genomic traits in <i>Escherichia coli</i> . <i>BMC Biology</i> , 2023, 21, .	1.7	7

#	ARTICLE	IF	CITATIONS
24061	Where to set the bar? Recent descriptions inflate species number in South American toad-headed turtles (<i>Mesoclemmys</i>). <i>Zootaxa</i> , 2023, 5263, 566-574.	0.2	3
24062	<i>Phytophthora alticola</i> and <i>P. boodjera</i> associated with decline of young <i>Eucalyptus smithii</i> trees in Uruguay. <i>Forest Pathology</i> , 2023, 53, .	0.5	0
24063	Identification of hidden associations among eukaryotic genes through statistical analysis of coevolutionary transitions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2023, 120, .	3.3	7
24064	On-person adaptive evolution of <i>Staphylococcus aureus</i> during treatment for atopic dermatitis. <i>Cell Host and Microbe</i> , 2023, 31, 593-603.e7.	5.1	14
24065	Characterizing nrDNA ITS1, 5.8S and ITS2 secondary structures and their phylogenetic utility in the legume tribe Hedysareae with special reference to <i>Hedysarum</i> . <i>PLoS ONE</i> , 2023, 18, e0283847.	1.1	0
24066	Genomic analysis of two phlebotomine sand fly vectors of <i>Leishmania</i> from the New and Old World. <i>PLoS Neglected Tropical Diseases</i> , 2023, 17, e0010862.	1.3	4
24067	Comparing genomic variant identification protocols for <i>Candida auris</i> . <i>Microbial Genomics</i> , 2023, 9, .	1.0	2
24068	Genome sequencing and multifaceted taxonomic analysis of novel strains of violacein-producing bacteria and non-violacein-producing close relatives. <i>Microbial Genomics</i> , 2023, 9, .	1.0	0
24069	Genomic and transcriptomic analyses support a silk gland origin of spider venom glands. <i>BMC Biology</i> , 2023, 21, .	1.7	5
24070	Phylogenetic relationship and comparative analysis of the main <i>Bupleuri Radix</i> species in China. <i>PeerJ</i> , 0, 11, e15157.	0.9	0
24071	A widespread Ponto-Caspian invader with a mistaken identity: integrative taxonomy elucidates the confusing taxonomy of <i>Trichogammarus trichiatus</i> (= <i>Echinogammarus</i>) (Crustacea: Tj ETQq0 0 0 rgBT.0 Overlock 10 Tf 50	1.0	0
24072	Mito-nuclear discordance in the phenotypically variable Andean hummingbirds <i>Coeligena bonapartei</i> and <i>Coeligena helianthea</i> (Trochilidae). <i>Biological Journal of the Linnean Society</i> , 0, , .	0.7	1
24073	Genetic Characterization of Raspberry Bushy Dwarf Virus Isolated from Red Raspberry in Kazakhstan. <i>Viruses</i> , 2023, 15, 975.	1.5	1
24076	<i>Actinophytocola gossypii</i> sp. nov. and <i>Streptomyces gossypii</i> sp. nov., two novel actinomycetes isolated from rhizosphere soil of cotton. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2023, 73, .	0.8	0
24077	Haplotype-resolved genomes of two buckwheat crops provide insights into their contrasted rutin concentrations and reproductive systems. <i>BMC Biology</i> , 2023, 21, .	1.7	4
24078	Phylogenomics of the <i>Olea europaea</i> complex using 15 whole genomes supports recurrent genetic admixture together with differentiation into seven subspecies. <i>BMC Biology</i> , 2023, 21, .	1.7	4
24079	HMMerge: an ensemble method for multiple sequence alignment. <i>Bioinformatics Advances</i> , 2023, 3, .	0.9	1
24080	Variation in <i>Sphingomonas</i> traits across habitats and phylogenetic clades. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	0

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24082	Rich but morphologically problematic: an integrative approach to taxonomic resolution of the genus <i>Neospororchis</i> (Trematoda: Schistosomatoidea). <i>International Journal for Parasitology</i> , 2023, 53, 363-380.	1.3	2
24083	Novelties in Macrofungi of the Tropical Montane Cloud Forest in Mexico. <i>Journal of Fungi (Basel)</i> , 2023, 9, 1070.	1.5	0
24084	Comparative mitogenomic and evolutionary analysis of Lycaenidae (Insecta: Lepidoptera): Potential association with high-altitude adaptation. <i>Frontiers in Genetics</i> , 2023, 14, .	1.1	1
24085	Probable airborne transmission of <i>Burkholderia pseudomallei</i> causing an urban outbreak of melioidosis during typhoon season in Hong Kong, China. <i>Emerging Microbes and Infections</i> , 2023, 12, .	3.0	2
24086	Plastid Phylogenomic Analyses Reveal a Cryptic Species of <i>Ligusticopsis</i> (Apiaceae, Angiosperms). <i>International Journal of Molecular Sciences</i> , 2023, 24, 7419.	1.8	1
24089	The microbiome of the endosymbiotic Symbiodiniaceae in corals exposed to thermal stress. <i>Hydrobiologia</i> , 2023, 850, 3685-3704.	1.0	4
24090	Neotypification of <i>Muyocopron dipterocarpi</i> , a new host record on <i>Zanthoxylum fagara</i> (Rutaceae) and the potential for secondary metabolite production in <i>Muyocopronaceae</i> . <i>Studies in Fungi</i> , 2023, 8, 0-0.	0.5	0
24091	First mitogenome phylogeny of the sun bear <i>Helarctos malayanus</i> reveals a deep split between Indochinese and Sundaic lineages. <i>Ecology and Evolution</i> , 2023, 13, .	0.8	3
24092	MRF: a tool to overcome the barrier of inconsistent genome annotations and perform comparative genomics studies for the largest animal DNA virus. <i>Virology Journal</i> , 2023, 20, .	1.4	1
24093	Helper-embedded satellites from an integrase clade that repeatedly targets prophage late genes. <i>NAR Genomics and Bioinformatics</i> , 2023, 5, .	1.5	0
24094	Multigene phylogeny reveals a cryptic diversity in the genus <i>Dinobryon</i> (Chrysophyceae) with integrative description of five new species. <i>Frontiers in Plant Science</i> , 2023, 14, .	1.7	0
24095	Identifying Climatic Drivers of Hybridization with a New Ancestral Niche Reconstruction Method. <i>Systematic Biology</i> , 2023, 72, 856-873.	2.7	2
24096	Phylogeny and structural insights of lipase from <i>Halopseudomonas maritima</i> sp. nov., isolated from sea sand. <i>International Microbiology</i> , 2023, 0, .	1.1	0
24097	The evolutionary history of rice azaleas (<i>Rhododendron tschonoskii</i> alliance) involved niche evolution to a montane environment. <i>American Journal of Botany</i> , 2023, 0, .	0.8	0
24098	Genomic insight of sulfate reducing bacterial genus <i>Desulfofaba</i> reveals their metabolic versatility in biogeochemical cycling. <i>BMC Genomics</i> , 2023, 24, .	1.2	0
24099	Viruses of sulfur oxidizing phototrophs encode genes for pigment, carbon, and sulfur metabolisms. <i>Communications Earth & Environment</i> , 2023, 4, .	2.6	3
24100	Species Delimitation, Phylogenomics, and Biogeography of Sulawesi Flying Lizards: A Diversification History Complicated by Ancient Hybridization, Cryptic Species, and Arrested Speciation. <i>Systematic Biology</i> , 2023, 0, .	2.7	4
24101	Phylogenomics of One of the World's Most Intriguing Groups of CAM Plants, the Opuntioids (Opuntioideae: Cactaceae): Adaptation to Tropical Dry Forests Helped Drive Prominent Morphological Features in the Clade. <i>Diversity</i> , 2023, 15, 570.	0.7	2

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24102	Genome-environment associations along elevation gradients in two snowbed species of the North-Eastern Calcareous Alps. <i>BMC Plant Biology</i> , 2023, 23, .	1.6	0
24103	Description of four new <i>Medeopteryx</i> Ballantyne (Coleoptera, Lampyridae, Luciolinae) species from Thailand and their phylogenetic placements based on mitochondrial DNA. <i>Journal of Asia-Pacific Entomology</i> , 2023, 26, 102084.	0.4	2
24104	Human CEACAM1 is targeted by a <i>Streptococcus pyogenes</i> adhesin implicated in puerperal sepsis pathogenesis. <i>Nature Communications</i> , 2023, 14, .	5.8	4
24105	Unrecognized diversity, genetic structuring, and phylogeography of the genus <i>Triplophysa</i> (Cypriniformes: Nemacheilidae) sheds light on two opposite colonization routes during Quaternary glaciation that occurred in the Qilian Mountains. <i>Ecology and Evolution</i> , 2023, 13, .	0.8	1
24106	Extensive genome analysis identifies novel plasmid families in <i>Clostridium perfringens</i> . <i>Microbial Genomics</i> , 2023, 9, .	1.0	0
24107	Systematics and biogeography of the Old World fern genus <i>Antrophyum</i> . <i>Cladistics</i> , 2023, 39, 249-272.	1.5	0
24108	Dissecting the genotypic features of a fluoroquinolone-resistant <i>Pseudomonas aeruginosa</i> ST316 sublineage causing ear infections in Shanghai, China. <i>Microbial Genomics</i> , 2023, 9, .	1.0	1
24110	Attack of the clones: Population genetics reveals clonality of <i>Colletotrichum lupini</i> , the causal agent of lupin anthracnose. <i>Molecular Plant Pathology</i> , 2023, 24, 616-627.	2.0	2
24111	Taxonomy and phylogeny of <i>Sidera</i> (Hymenochaetales, Rickenella clade) from China and North America revealing two new species. <i>MycoKeys</i> , 0, 96, 173-191.	0.8	1
24113	A global genomic perspective on the multidrug-resistant <i>Streptococcus pneumoniae</i> 15A-CC63 sub-lineage following pneumococcal conjugate vaccine introduction. <i>Microbial Genomics</i> , 2023, 9, .	1.0	1
24114	Comparative genomics identifies conserved and variable TAL effectors in African strains of the cotton pathogen <i>Xanthomonas citri</i> pv. <i>malvacearum</i> . <i>Phytopathology</i> , 0, , .	1.1	0
24115	Metapangenomics of wild and cultivated banana microbiome reveals a plethora of host-associated protective functions. <i>Environmental Microbiomes</i> , 2023, 18, .	2.2	3
24116	First Isolation and Genome Sequence Analysis of West Nile Virus in Mosquitoes in Brazil. <i>Tropical Medicine and Infectious Disease</i> , 2023, 8, 237.	0.9	2
24117	Microbial Processes of Methane Oxidation at the Kara Sea Sites of Gas Prospecting. <i>Microbiology</i> , 2023, 92, 171-182.	0.5	1
24118	Effects of recurrent summer droughts on arbuscular mycorrhizal and total fungal communities in experimental grasslands differing in plant diversity and community composition. <i>Frontiers in Soil Science</i> , 0, 3, .	0.8	1
24119	Parallel Shifts in Trout Feeding Morphology Suggest Rapid Adaptation to Alpine Lake Environments. <i>Evolution; International Journal of Organic Evolution</i> , 0, , .	1.1	0
24120	Lineage diversity in a widely distributed New World passerine bird, the House Wren. <i>Auk</i> , 2023, 140, .	0.7	3
24121	Identification and pathogenicity analysis of leaf brown spot of <i>Juglans regia</i> in China. <i>Scientific Reports</i> , 2023, 13, .	1.6	1

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24122	The phylogenetic structure and coalescent species delimitation of an endemic trapdoor spider genus, <i>Stasimopus</i> (Araneae, Mygalomorphae, Stasimopidae) in the Karoo region of South Africa. <i>Molecular Phylogenetics and Evolution</i> , 2023, 184, 107798.	1.2	2
24200	Protocols to Study Host-Pathosystems. , 2023, , 831-913.		0
24304	Phylogenetic Analysis of Bacterial Pathogen Genomes. <i>Methods in Molecular Biology</i> , 2023, , 87-99.	0.4	0
24445	Kurze Einfhrung in die phylogenetische Analyse von molekularen Sequenzdaten. , 2023, , 117-137.		0
24679	Case report: A successfully treated case of community-acquired urinary tract infection due to <i>Klebsiella aerogenes</i> in Bangladesh. <i>Frontiers in Medicine</i> , 0, 10, .	1.2	3
25035	The NLR Family of Disease Resistance Genes in Cultivated Watermelon and Other Cucurbits: Opportunities and Challenges. <i>Compendium of Plant Genomes</i> , 2023, , 37-67.	0.3	0
25046	Data-Mining with Three Genome-Scale Approaches Supports that Lungfish is the Closest Living Relative of Land Vertebrate, but not Coelacanth. , 2022, , .		0
25473	Phylogenetic Placement of Aligned Genomes and Metagenomes with Non-tree-like Evolutionary Histories. , 2023, , .		0
25480	Reconstructing Phylogenies Using Branch-Variable Substitution Models and Unaligned Biomolecular Sequences: A Performance Study and New Resampling Method. , 2023, , .		0
25506	Reducing the Impact of Domain Rearrangement on Sequence Alignment and Phylogeny Reconstruction. <i>Lecture Notes in Computer Science</i> , 2023, , 337-350.	1.0	0
25514	Approaches to increase the validity of gene family identification using manual homology search tools. <i>Genetica</i> , 0, , .	0.5	0
25615	Case report: tularaemia in a white-handed gibbon (<i>Hylobates lar</i>), Germany. <i>International Journal of Veterinary Science and Medicine</i> , 2023, 11, 121-125.	0.8	1
25676	Occurrence and characterization of <i>Pectobacterium brasiliense</i> causing soft rot on <i>Zamioculcas zamiifolia</i> plants in Greece. , 2024, 106, 245-250.		0
25790	An Exploratory Study of Deep Learning for Predicting Computational Tasks Behavior in HPC Systems. , 2023, , .		0
25843	First report of <i>Trichoderma guizhouense</i> isolated from soil in Trkiye. <i>Journal of Plant Diseases and Protection</i> , 2024, 131, 619-625.	1.6	0
25870	Detection and Analysis of <i>Wolbachia</i> in Plant-Parasitic Nematodes and Insights into <i>Wolbachia</i> Evolution. <i>Methods in Molecular Biology</i> , 2024, , 115-134.	0.4	0
26180	Powdery mildew of ash trees caused by the non-native <i>Erysiphe salmonii</i> in Hungary. <i>Journal of Plant Diseases and Protection</i> , 0, , .	1.6	0
26275	Bioinformatics in the study of microbial infections. , 2024, , 1975-1992.		0

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