

Improvement of Phylogenies after Removing Divergent from Protein Sequence Alignments

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Semaphorin and neuropilin expression during early morphogenesis of <i>Xenopus laevis</i> . <i>Developmental Dynamics</i> , 2008, 237, 3853-3863.	0.8	25
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5	Using ESTs for phylogenomics: can one accurately infer a phylogenetic tree from a gappy alignment?. <i>BMC Evolutionary Biology</i> , 2008, 8, 95.	3.2	106
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58	The Tree and Net Components of Prokaryote Evolution. <i>Genome Biology and Evolution</i> , 2010, 2, 745-756.	1.1	221
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124	Morphological and Molecular Evolution Are Not Linked in <i>Lamellogaster</i> (Platyhelminthes,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 1.1 28		
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147	Regional Selection Acting on the OFD1 Gene Family. PLoS ONE, 2011, 6, e26195.	1.1	9

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952	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
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955	Comparative Mitogenomics of Leeches (Annelida: Clitellata): Genome Conservation and <i>Placobdella</i> -Specific <i>trnD</i> Gene Duplication. <i>PLoS ONE</i> , 2016, 11, e0155441.	1.1	18
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958	A Radical Solution: The Phylogeny of the Nudibranch Family Fionidae. <i>PLoS ONE</i> , 2016, 11, e0167800.	1.1	37
959	Primitive Extracellular Lipid Components on the Surface of the Charophytic Alga <i>Klebsormidium flaccidum</i> and Their Possible Biosynthetic Pathways as Deduced from the Genome Sequence. <i>Frontiers in Plant Science</i> , 2016, 7, 952.	1.7	37
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962	The genus <i>Cyclops</i> (Copepoda, Cyclopoida) in Europe. Zoologica Scripta, 2016, 45, 671-682.	0.7	14
963	Limited sharing of tick-borne hemoparasites between sympatric wild and domestic ungulates. Veterinary Parasitology, 2016, 226, 167-173.	0.7	9
964	The neutral metallopeptidase NMP1 of <i>Trichoderma guizhouense</i> is required for mycotrophy and self-defence. Environmental Microbiology, 2016, 18, 580-597.	1.8	50
965	One note samba: the biogeographical history of the relict Brazilian butterfly <i>Elkalyce cogina</i> . Journal of Biogeography, 2016, 43, 727-737.	1.4	5
966	A molecular phylogeny of the temperate Gondwanan family Pettalidae (Arachnida, Opiliones, Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 178, 523-545.	1.0	26
967	The true identity of <i>Oobama</i> (Platyhelminthes: Geoplanidae) flatworm spreading across Europe. Zoological Journal of the Linnean Society, 2016, 177, 5-28.	1.0	36
968	Out of Africa: Phylogeny and biogeography of the widespread genus <i>Acanthodactylus</i> (Reptilia: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 1.2 63	1.2	63
969	<i>Aeolidia papillosa</i> (Linnaeus, 1761) (Mollusca: Heterobranchia: Nudibranchia), single species or a cryptic species complex? A morphological and molecular study. Zoological Journal of the Linnean Society, 2016, 177, 481-506.	1.0	39
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972	NFAP2, a novel cysteine-rich anti-yeast protein from <i>Neosartorya fischeri</i> NRRL 181: isolation and characterization. AMB Express, 2016, 6, 75.	1.4	43
973	Whole Genome Comparison of <i>Thermus</i> sp. NMX2.A1 Reveals Principal Carbon Metabolism Differences with Closest Relation <i>Thermus scotoductus</i> SA-01. G3: Genes, Genomes, Genetics, 2016, 6, 2791-2797.	0.8	5
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975	Mass spectrometry analysis and transcriptome sequencing reveal glowing squid crystal proteins are in the same superfamily as firefly luciferase. Scientific Reports, 2016, 6, 27638.	1.6	18
976	Porcelain crabs of the genera <i>Pachycheles</i> Stimpson and <i>Neopisosoma</i> Haig (Decapoda : Anomura : Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 0.5 2	0.5	2
977	Large-scale mitogenomics enables insights into <i>Schizophora</i> (Diptera) radiation and population diversity. Scientific Reports, 2016, 6, 21762.	1.6	66
978	The mitogenome of the amphipod <i>Hyaella lucifugax</i> (Crustacea) and its phylogenetic placement. Mitochondrial DNA Part B: Resources, 2016, 1, 755-756.	0.2	7

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980	The complete mitochondrial genome of the broad-winged damselfly <i>Mnais costalis</i> Selys (Odonata: Calopterygidae) obtained by next-generation sequencing. <i>International Journal of Odonatology</i> , 2016, 19, 191-198.	0.5	6
981	<i>Cercospora</i> cf. <i>flagellaris</i> and <i>Cercospora</i> cf. <i>sigesbeckiae</i> Are Associated with <i>Cercospora</i> Leaf Blight and Purple Seed Stain on Soybean in North America. <i>Phytopathology</i> , 2016, 106, 1376-1385.	1.1	38
982	A Novel Ilarvirus Is Associated with Privet Necrotic Ringspot Disease in the Southern United States. <i>Phytopathology</i> , 2016, 106, 87-93.	1.1	8
983	Next-generation systematics: An innovative approach to resolve the structure of complex prokaryotic taxa. <i>Scientific Reports</i> , 2016, 6, 38392.	1.6	114
984	The complete genome sequence of the African buffalo (<i>Syncerus caffer</i>). <i>BMC Genomics</i> , 2016, 17, 1001.	1.2	21
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989	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
990	Evolutionary study of <i>Yersinia</i> genomes deciphers emergence of human pathogenic species. <i>Scientific Reports</i> , 2016, 6, 36116.	1.6	14
991	Mitochondrial Phylogenomics yields Strongly Supported Hypotheses for Ascaridomorph Nematodes. <i>Scientific Reports</i> , 2016, 6, 39248.	1.6	26
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993	Proteomic analysis of scallop hepatopancreatic extract provides insights into marine polysaccharide digestion. <i>Scientific Reports</i> , 2016, 6, 34866.	1.6	12
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995	A draft genome sequence of <i>Pseudomonas veronii</i> R4: a grapevine (<i>Vitis vinifera</i> L.) root-associated strain with high biocontrol potential. <i>Standards in Genomic Sciences</i> , 2016, 11, 76.	1.5	12
996	Comparative Omics of the <i>Fusarium fujikuroi</i> Species Complex Highlights Differences in Genetic Potential and Metabolite Synthesis. <i>Genome Biology and Evolution</i> , 2016, 8, 3574-3599.	1.1	124

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998	Characterization of the complete mitochondrial genome of the cloacal tapeworm <i>Cloacotaenia megalops</i> (Cestoda: Hymenolepididae). <i>Parasites and Vectors</i> , 2016, 9, 490.	1.0	11
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1001	Elucidating the triplicated ancestral genome structure of radish based on chromosome-level comparison with the Brassica genomes. <i>Theoretical and Applied Genetics</i> , 2016, 129, 1357-1372.	1.8	110
1002	The evolutionary origin of CIPK16: A gene involved in enhanced salt tolerance. <i>Molecular Phylogenetics and Evolution</i> , 2016, 100, 135-147.	1.2	10
1003	Complex Ancestries of Isoprenoid Synthesis in Dinoflagellates. <i>Journal of Eukaryotic Microbiology</i> , 2016, 63, 123-137.	0.8	17
1004	Plastid genomes reveal support for deep phylogenetic relationships and extensive rate variation among palms and other commelinid monocots. <i>New Phytologist</i> , 2016, 209, 855-870.	3.5	181
1005	<i>Bifidobacterium aerophilum</i> sp. nov., <i>Bifidobacterium avesanii</i> sp. nov. and <i>Bifidobacterium ramosum</i> sp. nov.: Three novel taxa from the faeces of cotton-top tamarin (<i>Saguinus oedipus</i> L.). <i>Systematic and Applied Microbiology</i> , 2016, 39, 229-236.	1.2	38
1006	Molecular evidence for cryptic species in <i>Pteroclava krempfi</i> (Hydrozoa, Cladocorynidae) living in association with alcyonaceans. <i>Systematics and Biodiversity</i> , 2016, 14, 484-493.	0.5	24
1007	The complete mitochondrial genome of <i>Pseudanoplocephala crawfordi</i> and a comparison with closely related cestode species. <i>Journal of Helminthology</i> , 2016, 90, 588-595.	0.4	13
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1009	Taxonomy and molecular phylogeny of <i>Diatrypaceae</i> (Ascomycota, Xylariales) species from the Brazilian semi-arid region, including four new species. <i>Mycological Progress</i> , 2016, 15, 1.	0.5	27
1010	Bacterial Î ² -Kdo glycosyltransferases represent a new glycosyltransferase family (GT99). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E3120-9.	3.3	43
1011	Ectomycorrhizal fungi decompose soil organic matter using oxidative mechanisms adapted from saprotrophic ancestors. <i>New Phytologist</i> , 2016, 209, 1705-1719.	3.5	264
1012	Integration of multi-omics data of a genome-reduced bacterium: Prevalence of post-transcriptional regulation and its correlation with protein abundances. <i>Nucleic Acids Research</i> , 2016, 44, 1192-1202.	6.5	35
1013	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
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1015	Molecular Evolution of Alternative Oxidase Proteins: A Phylogenetic and Structure Modeling Approach. <i>Journal of Molecular Evolution</i> , 2016, 82, 207-218.	0.8	27
1016	<i>Salmones chadwickae</i> , a new alpheid shrimp (Crustacea: Decapoda: Alpheidae) from the Red Sea, with remarks on related or regional congeners. <i>Marine Biodiversity</i> , 2016, 46, 773-793.	0.3	15
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1018	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
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1025	Cutaneous hyalohyphomycosis due to <i>Parengyodontium album</i> gen. et comb. nov.. <i>Medical Mycology</i> , 2016, 54, 699-713.	0.3	29
1026	De novo transcriptome assembly and identification of the gene conferring a "pandan-like" aroma in coconut (<i>Cocos nucifera</i> L.). <i>Plant Science</i> , 2016, 252, 324-334.	1.7	42
1027	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
1028	bcgTree: automatized phylogenetic tree building from bacterial core genomes. <i>Genome</i> , 2016, 59, 783-791.	0.9	151
1029	Soil microbial communities as potential regulators of in situ N ₂ O fluxes in annual and perennial cropping systems. <i>Soil Biology and Biochemistry</i> , 2016, 103, 262-273.	4.2	39
1030	Phylogenomic re-assessment of the thermophilic genus <i>Geobacillus</i> . <i>Systematic and Applied Microbiology</i> , 2016, 39, 527-533.	1.2	116
1031	A molecular analysis of the phylogenetic position of the suborder <i>Cavernicola</i> within the <i>Tricladida</i> (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
1032	A systematic study of the whole genome sequence of <i>Amycolatopsis methanolica</i> strain 239 T provides an insight into its physiological and taxonomic properties which correlate with its position in the genus. <i>Synthetic and Systems Biotechnology</i> , 2016, 1, 169-186.	1.8	29

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1034	Population structure and gene flow in the global pest, <i>Helicoverpa armigera</i> . <i>Molecular Ecology</i> , 2016, 25, 5296-5311.	2.0	71
1035	A plant biologists' guide to phylogenetic analysis of biological macromolecule sequences. <i>Biologia Plantarum</i> , 2016, 60, 619-627.	1.9	1
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1037	Reprint of "Sequence and phylogenetic analyses of novel totivirus-like double-stranded RNAs from field-collected powdery mildew fungi". <i>Virus Research</i> , 2016, 219, 39-50.	1.1	1
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1039	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
1040	Depth as a driver of evolution in the deep sea: Insights from grenadiers (Gadiformes: Macrouridae) of the genus <i>Coryphaenoides</i> . <i>Molecular Phylogenetics and Evolution</i> , 2016, 104, 73-82.	1.2	26
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1042	Co-evolution of SNF spliceosomal proteins with their RNA targets in trans-splicing nematodes. <i>Genetica</i> , 2016, 144, 487-496.	0.5	1
1043	A novel uncultured bacterium of the family Gallionellaceae: Description and genome reconstruction based on metagenomic analysis of microbial community in acid mine drainage. <i>Microbiology</i> , 2016, 85, 449-461.	0.5	23
1044	Morphology and molecular phylogeny of a new freshwater ciliate <i>Urosomoida sejongensis</i> n. sp. (Ciliophora, Sporadotrichida, Oxytrichidae) from King George Island, Antarctica. <i>Zootaxa</i> , 2016, 4072, 254-62.	0.2	6
1045	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
1046	Incorporating tree-thinking and evolutionary time scale into developmental biology. <i>Development Growth and Differentiation</i> , 2016, 58, 131-142.	0.6	17
1047	Taxonomy and biogeography of <i>Bunopus spatulurus</i> (Reptilia; Gekkonidae) from the Arabian Peninsula. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2016, 54, 67-81.	0.6	24
1048	Animal Mitochondrial DNA as We Do Not Know It: mt-Genome Organization and Evolution in Nonbilaterian Lineages. <i>Genome Biology and Evolution</i> , 2016, 8, 2896-2913.	1.1	154
1049	Positive selection on panpulmonate mitogenomes provide new clues on adaptations to terrestrial life. <i>BMC Evolutionary Biology</i> , 2016, 16, 164.	3.2	41
1050	Phylogenetic evidence places the coraloid jelly fungus <i>Tremellodendropsis tuberosa</i> (Tremellodendropsidales) among early diverging Agaricomycetes. <i>Mycological Progress</i> , 2016, 15, 939-946.	0.5	4

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1053	Multilocus phylogenetic reconstruction of the Clavariaceae (Agaricales) reveals polyphyly of agaricoid members. <i>Mycologia</i> , 2016, 108, 860-868.	0.8	20
1054	Complete mitochondrial genomes of four entomopathogenic nematode species of the genus <i>Steinernema</i> . <i>Parasites and Vectors</i> , 2016, 9, 430.	1.0	8
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1057	Characterization of an O-methyltransferase specific to guaiacol-type benzenoids from the flowers of loquat (<i>Eriobotrya japonica</i>). <i>Journal of Bioscience and Bioengineering</i> , 2016, 122, 679-684.	1.1	16
1058	Energy efficiency trade-offs drive nucleotide usage in transcribed regions. <i>Nature Communications</i> , 2016, 7, 11334.	5.8	104
1059	<i>Streptomyces thermoautotrophicus</i> does not fix nitrogen. <i>Scientific Reports</i> , 2016, 6, 20086.	1.6	31
1060	Residue management leading to higher field-scale N ₂ O flux is associated with different soil bacterial nitrifier and denitrifier gene community structures. <i>Applied Soil Ecology</i> , 2016, 108, 288-299.	2.1	19
1061	Morphology, morphogenesis and molecular phylogeny of a novel saline soil ciliate, <i>Lamtostyla salina</i> n. sp. (Ciliophora, Hypotricha). <i>European Journal of Protistology</i> , 2016, 56, 219-231.	0.5	19
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1065	The complete mitochondrial genome of the land snail <i>Cerion incanum</i> (Gastropoda). <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50</i> <i>Molluscan Studies</i> , 2016, 82, 525-533.	0.4	8
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1067	Trends in the sand: Directional evolution in the shell shape of recessing scallops (Bivalvia). <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50</i> 34	1.1	34
1068	Molecular data show that <i>Hypotrachyna sorocheila</i> (Parmeliaceae) is not monophyletic. <i>Bryologist</i> , 2016, 119, 172-180.	0.1	5
1069	Basidiomycete yeasts in the cortex of ascomycete macrolichens. <i>Science</i> , 2016, 353, 488-492.	6.0	409

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1071	Multi-locus fossil-calibrated phylogeny, biogeography and a subgeneric revision of the Margaritiferidae (Mollusca: Bivalvia: Unionoidea). <i>Molecular Phylogenetics and Evolution</i> , 2016, 103, 104-121.	1.2	52
1072	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
1073	Potential steps in the evolution of a fused trimeric all- β dUTPase involve a catalytically competent fused dimeric intermediate. <i>FEBS Journal</i> , 2016, 283, 3268-3286.	2.2	5
1074	Human Survivors of Disease Outbreaks Caused by Ebola or Marburg Virus Exhibit Cross-Reactive and Long-Lived Antibody Responses. <i>Vaccine Journal</i> , 2016, 23, 717-724.	3.2	40
1075	Hidden diversity before our eyes: Delimiting and describing cryptic lichen-forming fungal species in camouflage lichens (Parmeliaceae, Ascomycota). <i>Fungal Biology</i> , 2016, 120, 1374-1391.	1.1	32
1076	The genomic content and context of auxiliary metabolic genes in marine cyanomyoviruses. <i>Virology</i> , 2016, 499, 219-229.	1.1	99
1077	Pathogen-dependent role of turbot (<i>Scophthalmus maximus</i>) interferon-gamma. <i>Fish and Shellfish Immunology</i> , 2016, 59, 25-35.	1.6	29
1078	Species- α -function relationships shape ecological properties of the human gut microbiome. <i>Nature Microbiology</i> , 2016, 1, 16088.	5.9	279
1079	Impact of donor-recipient phylogenetic distance on bacterial genome transplantation. <i>Nucleic Acids Research</i> , 2016, 44, 8501-8511.	6.5	60
1080	Anterior sensory organs in Sabellariidae (Annelida). <i>Invertebrate Biology</i> , 2016, 135, 423-447.	0.3	11
1081	An integrated genomic and transcriptomic survey of mucormycosis-causing fungi. <i>Nature Communications</i> , 2016, 7, 12218.	5.8	103
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1104	Plastid phylogenomics and molecular evolution of Alismatales. Cladistics, 2016, 32, 160-178.	1.5	98
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1108	Molecular characterization of <i>Potato mop-top virus</i> isolates from China and Canada and development of RT-PCR differentiation of two sequence variant groups. <i>Canadian Journal of Plant Pathology</i> , 2016, 38, 231-242.	0.8	7
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1116	Phylogenetic relationships of species of the oesophageal parasitic nematode genera <i>Cyclostrongylus</i> and <i>Spirostrongylus</i> (Strongyloidea: Chabertiidae: Cloacininae) with their wallaby hosts (Marsupialia: <i>Tj ETQq0 0 OugBT /Overlock 10 Tf</i>)		
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1122	Characterization and Complete Genome Sequences of Three N4-Like Roseobacter Phages Isolated from the South China Sea. <i>Current Microbiology</i> , 2016, 73, 409-418.	1.0	21
1123	<i>Enterobius</i> (<i>Enterobius</i>) <i>shriveri</i> n. sp. (Nematoda: Oxyuridae: Enterobiinae) from <i>Macaca fascicularis</i> Raffles, 1821 (Primates: Cercopithecoidea: Cercopithecinae) and Three Other Cercopithecoid Primate Species: With Additional Information on <i>Enterobius</i> (<i>Enterobius</i>) <i>macaci</i> Yen, 1973. <i>Comparative Parasitology</i> , 2016, 83, 54-73.	0.0	1

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1125	Phylogenetic hypothesis of Sphaerodoridae Malmgren, 1867 (Annelida) and its position within Phyllococida. <i>Cladistics</i> , 2016, 32, 335-350.	1.5	6
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1130	Sequence and phylogenetic analyses of novel totivirus-like double-stranded RNAs from field-collected powdery mildew fungi. <i>Virus Research</i> , 2016, 213, 353-364.	1.1	35
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1132	Regulation of cell wall remodeling in grapevine (<i>Vitis vinifera</i> L.) callus under individual mineral stress deficiency. <i>Journal of Plant Physiology</i> , 2016, 190, 95-105.	1.6	16
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1134	Combined phylogenetic and morphological studies of true morels (Pezizales, Ascomycota) in Cyprus reveal significant diversity, including <i>Morchella arbutiphila</i> and <i>M. disparilis</i> spp. nov.. <i>Mycological Progress</i> , 2016, 15, 1.	0.5	32
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1137	Complete mitochondrial genome of the scleractinian coral <i>Porites rus</i> . <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 3695-3696.	0.7	1
1138	Detection and genome analysis of a novel (dima)rhabdovirus (Riverside virus) from <i>Ochlerotatus</i> sp. mosquitoes in Central Europe. <i>Infection, Genetics and Evolution</i> , 2016, 39, 336-341.	1.0	17
1139	The genome of <i>Bacillus aryabhatai</i> T61 reveals its adaptation to Tibetan Plateau environment. <i>Genes and Genomics</i> , 2016, 38, 293-301.	0.5	12
1140	Distinct Processes Drive Diversification in Different Clades of Gesneriaceae. <i>Systematic Biology</i> , 2016, 65, 662-684.	2.7	72
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1148	A Global Genomic Characterization of Nairoviruses Identifies Nine Discrete Genogroups with Distinctive Structural Characteristics and Host-Vector Associations. <i>American Journal of Tropical Medicine and Hygiene</i> , 2016, 94, 1107-1122.	0.6	45
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1152	Evolution around the Red Sea: Systematics and biogeography of the agamid genus <i>Pseudotrappelus</i> (Squamata: Agamidae) from North Africa and Arabia. <i>Molecular Phylogenetics and Evolution</i> , 2016, 97, 55-68.	1.2	33
1153	Effects of DNA Methylation and Chromatin State on Rates of Molecular Evolution in Insects. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 357-363.	0.8	37
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1157	Untangling the phylogeny of <i>Leandra</i> s.str. (Melastomataceae, Miconieae). <i>Molecular Phylogenetics and Evolution</i> , 2016, 96, 17-32.	1.2	48
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1161	Phylogenetic and genomic analysis of <i>Methanomassiliicoccales</i> in wetlands and animal intestinal tracts reveals clade-specific habitat preferences. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiv149.	1.3	110
1162	Genome organisation and expression profiling of ABC protein-encoding genes in <i>Heterobasidion annosum</i> s.l. complex. <i>Fungal Biology</i> , 2016, 120, 376-384.	1.1	9
1163	Genetic diversity of <i>Aspergillus</i> species isolated from onychomycosis and <i>Aspergillus hongkongensis</i> sp. nov., with implications to antifungal susceptibility testing. <i>Diagnostic Microbiology and Infectious Disease</i> , 2016, 84, 125-134.	0.8	43
1164	Multiple sequence alignment modeling: methods and applications. <i>Briefings in Bioinformatics</i> , 2016, 17, 1009-1023.	3.2	153
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1166	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
1167	New Boletaceae taxa from Guyana: <i>Binderoboletus segoi</i> gen. and sp. nov., <i>Guyanaporus albipodus</i> gen. and sp. nov., <i>Singerocomus rubriflavus</i> gen. and sp. nov., and a new combination for <i>Xerocomus inundabilis</i> . <i>Mycologia</i> , 2016, 108, 157-173.	0.8	36
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1174	Peste Des Petits Ruminants in Benin: Persistence of a Single Virus Genotype in the Country for Over 42 Years. <i>Transboundary and Emerging Diseases</i> , 2017, 64, 1037-1044.	1.3	32
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1180	The complete chloroplast genome sequence of <i>Ulva linza</i> . <i>Conservation Genetics Resources</i> , 2017, 9, 463-466.	0.4	12
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1190	An integrative approach underscores the taxonomic status of <i>Lamellidens exolecens</i> , a freshwater mussel from the Oriental tropics (Bivalvia: Unionidae). <i>Systematics and Biodiversity</i> , 2017, 15, 204-217.	0.5	22
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1198	Morphology and Morphogenesis of a Novel Saline Soil Hypotrichous Ciliate, <i>Gonostomum sinicum</i> nov. spec. (Ciliophora, Hypotrichia, Gonostomatidae), Including a Report on the Small Subunit <i>rDNA</i> Sequence. <i>Journal of Eukaryotic Microbiology</i> , 2017, 64, 632-646.	0.8	14
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1205	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
1206	SAGA complex mediates the transcriptional up-regulation of antiviral RNA silencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E3499-E3506.	3.3	50
1207	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
1208	Using a temporal phylogenetic method to harmonize family- and genus-level classification in the largest clade of lichen-forming fungi. <i>Fungal Diversity</i> , 2017, 84, 101-117.	4.7	75
1209	Increased taxon sampling reveals thousands of hidden orthologs in flatworms. <i>Genome Research</i> , 2017, 27, 1263-1272.	2.4	39
1210	Unique mitochondrial localization of arginase 1 and 2 in hepatocytes of air-breathing walking catfish, <i>Clarias batrachus</i> and their differential expression patterns under hyper-ammonia stress. <i>Gene</i> , 2017, 622, 13-22.	1.0	14
1211	Two <i>Pisidium</i> species inhabit freshwater lakes of Novaya Zemlya Archipelago: the first molecular evidence. <i>Polar Biology</i> , 2017, 40, 2119-2126.	0.5	7
1212	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
1213	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

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1214	Ancient Recombination Events between Human Herpes Simplex Viruses. <i>Molecular Biology and Evolution</i> , 2017, 34, 1713-1721.	3.5	49
1215	Phylogenetic and phenotypic characterisation of <i>Sirococcus castaneae</i> comb. nov. (synonym <i>Diplodina</i>) Tj ETQq1 1,0,784314,rgBT /Ove 1.1 135	1.1	135
1216	<i>Ambrosiella</i> in Taiwan including one new species. <i>Mycoscience</i> , 2017, 58, 242-252.	0.3	10
1217	A possible occurrence of genome reassortment among bipartite rhabdoviruses. <i>Virology</i> , 2017, 508, 18-25.	1.1	39
1218	Diversity and evolution of sex determination systems in terrestrial isopods. <i>Scientific Reports</i> , 2017, 7, 1084.	1.6	35
1219	Multilocus phylogeny and statistical biogeography clarify the evolutionary history of major lineages of turtles. <i>Molecular Phylogenetics and Evolution</i> , 2017, 113, 59-66.	1.2	120
1220	Rearranged Biosynthetic Gene Cluster and Synthesis of Hassallidin E in <i>Planktothrix serbia</i> PCC 8927. <i>ACS Chemical Biology</i> , 2017, 12, 1796-1804.	1.6	25
1221	When molecules and morphology work together: lines of evidence for the validity of <i>Caridina buehleri</i> Roux (Crustacea : Decapoda : Atyidae) and for <i>C. gueryi</i> Marquet, Keith & Kalfatak as its junior synonym. <i>Invertebrate Systematics</i> , 2017, 31, 220.	0.5	4
1222	Mitochondrial genome sequences effectively reveal deep branching events in aphids (Insecta:) Tj ETQq0 0 0 rgBT /Overlock 10,Tf 50 422 0.7 12	0.7	12
1223	Scaling Up the Phylogenetic Detection of Lateral Gene Transfer Events. <i>Methods in Molecular Biology</i> , 2017, 1525, 421-432.	0.4	2
1224	Comprehensive identification and clustering of CLV3/ESR-related (CLE) genes in plants finds groups with a potentially shared function. <i>New Phytologist</i> , 2017, 216, 605-616.	3.5	101
1225	The genome and transcriptome of Japanese flounder provide insights into flatfish asymmetry. <i>Nature Genetics</i> , 2017, 49, 119-124.	9.4	178
1226	Molecular epidemiology of Avian Rotaviruses Group A and D shed by different bird species in Nigeria. <i>Virology Journal</i> , 2017, 14, 111.	1.4	21
1227	New data of two trichodinid ectoparasites (Ciliophora: Trichodinidae) from farmed freshwater fishes in Hubei, China. <i>European Journal of Protistology</i> , 2017, 60, 50-59.	0.5	16
1228	In Planta Recapitulation of Isoprene Synthase Evolution from Ocimene Synthases. <i>Molecular Biology and Evolution</i> , 2017, 34, 2583-2599.	3.5	26
1229	Host influence in the genomic composition of flaviviruses: A multivariate approach. <i>Biochemical and Biophysical Research Communications</i> , 2017, 492, 572-578.	1.0	18
1230	Recent origin and rapid speciation of Neotropical orchids in the world's richest plant biodiversity hotspot. <i>New Phytologist</i> , 2017, 215, 891-905.	3.5	170
1231	Discovery of a Highly Divergent Coronavirus in the Asian House Shrew from China Illuminates the Origin of the Alphacoronaviruses. <i>Journal of Virology</i> , 2017, 91, .	1.5	37

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1232	The Evolution of Venom by Co-option of Single-Copy Genes. <i>Current Biology</i> , 2017, 27, 2007-2013.e8.	1.8	99
1233	The Mitochondrial Genome of the Guanaco Louse, <i>Microthoracius praelongiceps</i> : Insights into the Ancestral Mitochondrial Karyotype of Sucking Lice (Anoplura, Insecta). <i>Genome Biology and Evolution</i> , 2017, 9, 431-445.	1.1	27
1234	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
1235	Quantification of novel geosmin-producing bacteria in aquaculture systems. <i>Aquaculture</i> , 2017, 479, 304-310.	1.7	27
1236	Positive diversifying selection is a pervasive adaptive force throughout the <i>Drosophila</i> radiation. <i>Molecular Phylogenetics and Evolution</i> , 2017, 112, 230-243.	1.2	26
1237	The draft genome of blunt snout bream (<i>Megalobrama amblycephala</i>) reveals the development of intermuscular bone and adaptation to herbivorous diet. <i>GigaScience</i> , 2017, 6, 1-13.	3.3	95
1238	The diversity of CO ₂ -concentrating mechanisms in marine diatoms as inferred from their genetic content. <i>Journal of Experimental Botany</i> , 2017, 68, 3937-3948.	2.4	27
1239	Rapidly Evolving Toll-3/4 Genes Encode Male-Specific Toll-Like Receptors in <i>Drosophila</i> . <i>Molecular Biology and Evolution</i> , 2017, 34, 2307-2323.	3.5	21
1240	Evolution of foraging behaviour: Deep intra-generic genetic divergence between territorial and non-territorial southern African patellid limpets. <i>Molecular Phylogenetics and Evolution</i> , 2017, 117, 95-101.	1.2	5
1241	Ancient River Inference Explains Exceptional Oriental Freshwater Mussel Radiations. <i>Scientific Reports</i> , 2017, 7, 2135.	1.6	75
1242	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
1243	Correlated evolutionary rates across genomic compartments in Annonaceae. <i>Molecular Phylogenetics and Evolution</i> , 2017, 114, 63-72.	1.2	13
1244	Taxonomy of the corticolous, shrubby, esorediate, neotropical species of <i>Usnea</i> Adans. (<i>Parmeliaceae</i>) with an emphasis on southern Brazil. <i>Lichenologist</i> , 2017, 49, 199-238.	0.5	14
1245	The genus <i>Relicinopsis</i> is nested within <i>Relicina</i> (<i>Parmeliaceae</i> , Ascomycota). <i>Lichenologist</i> , 2017, 49, 189-197.	0.5	6
1246	Ultraconserved elements show utility in phylogenetic inference of <i>Adephaga</i> (<i>Coleoptera</i>) and suggest paraphyly of "Hydradephaga". <i>Systematic Entomology</i> , 2017, 42, 786-795.	1.7	77
1247	Systematic revision of <i>Acanthodactylus busacki</i> (Squamata: Lacertidae) with a description of a new species from Morocco. <i>Zootaxa</i> , 2017, 4276, 357.	0.2	5
1248	Understanding disjunct distribution patterns in lichen-forming fungi: insights from <i>Parmelina</i> (<i>Parmeliaceae</i> : Ascomycota). <i>Botanical Journal of the Linnean Society</i> , 2017, 184, 238-253.	0.8	7
1249	<i>Luciobarbus chelifensis</i> and <i>L. mascarensis</i> , two new species from Algeria (Teleostei: Cyprinidae). <i>Zootaxa</i> , 2017, 4277, 32.	0.2	5

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1251	Molecular phylogeny of the <i>Trichodactylus fluviatilis</i> Latreille, 1828 (Brachyura: Trichodactylidae) species complex. <i>Journal of Crustacean Biology</i> , 2017, 37, 187-194.	0.3	11
1252	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
1253	Extensive diversity of coronaviruses in bats from China. <i>Virology</i> , 2017, 507, 1-10.	1.1	97
1254	Listerimics: an Interactive Web Platform for Systems Biology of <i>Listeria</i> . <i>MSystems</i> , 2017, 2, .	1.7	37
1255	<i>Buellia numerosa</i> and <i>B. subnumerosa</i> , two new species of the lichen genus <i>Buellia</i> (Caliciaceae) from Japan. <i>Bryologist</i> , 2017, 120, 25.	0.1	3
1256	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
1257	Phylogenomic evolutionary surveys of subtilase superfamily genes in fungi. <i>Scientific Reports</i> , 2017, 7, 45456.	1.6	48
1258	Model-based analyses reveal insular population diversification and cryptic frog species in the <i>Ischnocnema parva</i> complex in the Atlantic forest of Brazil. <i>Molecular Phylogenetics and Evolution</i> , 2017, 112, 68-78.	1.2	20
1259	Parallel evolution of genes controlling mitonuclear balance in short-lived annual fishes. <i>Aging Cell</i> , 2017, 16, 488-496.	3.0	29
1260	Phylogenetic relationships and divergence dates of softshell turtles (Testudines: Trionychidae) inferred from complete mitochondrial genomes. <i>Journal of Evolutionary Biology</i> , 2017, 30, 1011-1023.	0.8	20
1261	Phylogenetic systematics of <i>Syncephalis</i> (Zoopagales, Zoopagomycotina), a genus of ubiquitous mycoparasites. <i>Mycologia</i> , 2017, 109, 333-349.	0.8	20
1262	Estimation of main diversification time-points of hantaviruses using phylogenetic analyses of complete genomes. <i>Virus Research</i> , 2017, 233, 60-69.	1.1	8
1263	<i>Moniezia benedeni</i> and <i>Moniezia expansa</i> are distinct cestode species based on complete mitochondrial genomes. <i>Acta Tropica</i> , 2017, 166, 287-292.	0.9	14
1264	â€ˆ Candidatus <i>Dichloromethanomonas elyunquensis</i> â€™ gen. nov., sp. nov., a dichloromethane-degrading anaerobe of the Peptococcaceae family. <i>Systematic and Applied Microbiology</i> , 2017, 40, 150-159.	1.2	50
1265	Insight into the Genome of <i>Brochothrix thermosphacta</i> , a Problematic Meat Spoilage Bacterium. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	61
1266	Ecomorphological adaptations in Collembola in relation to feeding strategies and microhabitat. <i>European Journal of Soil Biology</i> , 2017, 78, 82-91.	1.4	35
1267	Mitochondrial genome of the Christmas tree worm <i>Spirobranchus giganteus</i> (Annelida: Serpulidae) reveals a high substitution rate among annelids. <i>Gene</i> , 2017, 605, 43-53.	1.0	24

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1269	Phylogeny of the conifer pathogen <i>Heterobasidion irregulare</i> : Inventory, phylogeny, and transcriptional analysis of the response to biocontrol. <i>Fungal Biology</i> , 2017, 121, 158-171.	1.1	9
1270	Novel species of <i>Gliocladiopsis</i> (Nectriaceae, Hypocreales, Ascomycota) from avocado roots (<i>Persea</i>). <i>Trends in Microbiology</i> , 2017, 25, 107-110.	0.3	6
1271	Detection and characterization of a novel rhabdovirus in <i>Aedes cantans</i> mosquitoes and evidence for a mosquito-associated new genus in the family Rhabdoviridae. <i>Infection, Genetics and Evolution</i> , 2017, 55, 260-268.	1.0	15
1272	Genome sequencing of the winged midge, <i>Parochlus steinenii</i> , from the Antarctic Peninsula. <i>GigaScience</i> , 2017, 6, 1-8.	3.3	15
1273	Endemics or strangers? The integrative re-appraisal of taxonomy and phylogeny of the Greenland <i>Lymnaeidae</i> (Mollusca: Gastropoda). <i>Comptes Rendus - Biologies</i> , 2017, 340, 541-557.	0.1	13
1274	Phylogenetic relationships of millipedes in the subclass <i>Penicillata</i> (Diplopoda) with a key to the genera. <i>Journal of Natural History</i> , 2017, 51, 2443-2461.	0.2	10
1275	New taxa of freshwater mussels (Unionidae) from a species-rich but overlooked evolutionary hotspot in Southeast Asia. <i>Scientific Reports</i> , 2017, 7, 11573.	1.6	67
1276	Wholly reconstructed Metabolic Profile of the Quintessential Bacterial Parasite of Eukaryotic Cells. <i>MBio</i> , 2017, 8, .	1.8	121
1277	Chromatin-associated regulation of sorbitol synthesis in flower buds of peach. <i>Plant Molecular Biology</i> , 2017, 95, 507-517.	2.0	22
1278	<i>Panax ginseng</i> genome examination for ginsenoside biosynthesis. <i>GigaScience</i> , 2017, 6, 1-15.	3.3	150
1279	Draft genome of the gayal, <i>Bos frontalis</i> . <i>GigaScience</i> , 2017, 6, 1-7.	3.3	23
1280	Unique pleuroproctid taxa of the nudibranch family <i>Aeolidiidae</i> from the Atlantic and Pacific Oceans, with description of a new genus and species. <i>Journal of Molluscan Studies</i> , 2017, 83, 409-421.	0.4	12
1281	A customized contamination controlling approach for culturing oleaginous <i>Nannochloropsis oceanica</i> . <i>Algal Research</i> , 2017, 27, 376-382.	2.4	23
1282	Phylogenetically conserved resource partitioning in the coastal microbial loop. <i>ISME Journal</i> , 2017, 11, 2781-2792.	4.4	82
1283	First global molecular phylogeny and biogeographical analysis of two arachnid orders (Schizomida). <i>Biogeography</i> , 2017, 44, 2660-2672.	1.4	37
1284	Molecular and morphological evidence for a new genus of small trapdoor spiders from arid Western Australia (Araneae : Mygalomorphae : Nemesiidae : Anaminae). <i>Invertebrate Systematics</i> , 2017, 31, 492.	0.5	18
1285	The systematics and biogeography of the mite harvestman family <i>Sironidae</i> (Arachnida : Opiliones :). <i>Trends in Microbiology</i> , 2017, 25, 107-110.	0.5	3

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1287	Limited locomotive ability relaxed selective constraints on molluscs mitochondrial genomes. <i>Scientific Reports</i> , 2017, 7, 10628.	1.6	21
1288	An integrative taxonomic study of <i>Pavanelliella</i> spp. (Monogeneoidea, Dactylogyridae) with the description of a new species from the nasal cavities of an Amazon pimelodid catfish. <i>Parasitology International</i> , 2017, 66, 777-788.	0.6	12
1289	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
1290	Mitochondrial phylogenomics of Hemiptera reveals adaptive innovations driving the diversification of true bugs. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20171223.	1.2	218
1291	Climate-related environmental variation in a visual signalling device: the male and female dewlap in <i>Anolis sagrei</i> lizards. <i>Journal of Evolutionary Biology</i> , 2017, 30, 1846-1861.	0.8	19
1292	Novel Alphacoronaviruses and Paramyxoviruses Cocirculate with Type 1 and Severe Acute Respiratory System (SARS)-Related Betacoronaviruses in Synanthropic Bats of Luxembourg. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	30
1293	A genomic investigation of ecological differentiation between free-living and <i>Drosophila</i> -associated bacteria. <i>Molecular Ecology</i> , 2017, 26, 4536-4550.	2.0	52
1294	Culture-Free Detection of Crop Pathogens at the Single-Cell Level by Micro-Raman Spectroscopy. <i>Advanced Science</i> , 2017, 4, 1700127.	5.6	22
1295	Optimization of production conditions for xylanase production by newly isolated strain <i>Aspergillus niger</i> through solid state fermentation of oil palm empty fruit bunches. <i>Biocatalysis and Agricultural Biotechnology</i> , 2017, 11, 239-247.	1.5	33
1296	Cutting the Gordian Knot: Phylogenetic and ecological diversification of the <i>Mesalina brevirostris</i> species complex (Squamata, Lacertidae). <i>Zoologica Scripta</i> , 2017, 46, 649-664.	0.7	17
1297	Large Variation in the Ratio of Mitochondrial to Nuclear Mutation Rate across Animals: Implications for Genetic Diversity and the Use of Mitochondrial DNA as a Molecular Marker. <i>Molecular Biology and Evolution</i> , 2017, 34, 2762-2772.	3.5	240
1298	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
1299	Phylogenetic convergence and multiple shell shape optima for gliding scallops (Bivalvia: Pectinidae). <i>Journal of Evolutionary Biology</i> , 2017, 30, 1736-1747.	0.8	29
1300	Description of a New Species of <i>Vinathela</i> Ono, 2000 (Araneae: Mesothelae: Liphistiidae), Based on Morphological and Molecular Characters. <i>Arachnology</i> , 2017, 17, 229-237.	0.4	1
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1302	Diversity of MHC class II DRB alleles in the Eurasian population of the least weasel, <i>Mustela nivalis</i> (Mustelidae: Mammalia). <i>Biological Journal of the Linnean Society</i> , 2017, 121, 28-37.	0.7	11
1303	Kanyawara Virus: A Novel Rhabdovirus Infecting Newly Discovered Nycteribiid Bat Flies Infesting Previously Unknown Pteropodid Bats in Uganda. <i>Scientific Reports</i> , 2017, 7, 5287.	1.6	32

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1304	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
1305	Phylogenetic placement of the enigmatic worm-like Rhodopemorpha slugs as basal Heterobranchia. <i>Journal of Molluscan Studies</i> , 2017, 83, 399-408.	0.4	9
1306	Two <i>Radix</i> spp. (Gastropoda: Lymnaeidae) endemic to thermal springs around Lake Baikal represent ecotypes of the widespread <i>Radix auricularia</i> . <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2017, 55, 298-309.	0.6	20
1307	Evolution, gene expression profiling and 3D modeling of CSLD proteins in cotton. <i>BMC Plant Biology</i> , 2017, 17, 119.	1.6	26
1308	The draft genome sequence of a desert tree <i>Populus pruinosa</i> . <i>GigaScience</i> , 2017, 6, 1-7.	3.3	61
1309	A second species of the genus <i>Vietnamorpha</i> Golovatch, 1984 (Polydesmida: Paradoxosomatidae) and notes on the generic relationship. <i>Journal of Natural History</i> , 2017, 51, 2331-2343.	0.2	1
1310	Interferon-independent antiviral activity of 25-hydroxycholesterol in a teleost fish. <i>Antiviral Research</i> , 2017, 145, 146-159.	1.9	31
1311	The complete mitochondrial genome of <i>Cerion uva uva</i> (Gastropoda: Panpulmonata: Tj ETQq1 1 0.784314 rgBT/Overlock 10 Tf 50	0.2	4
1312	Genomic Analysis of the Evolution of Phototrophy among Haloalkaliphilic Rhodobacterales. <i>Genome Biology and Evolution</i> , 2017, 9, 1950-1962.	1.1	25
1313	Complete mitochondrial genome of the freshwater prawn <i>Palaemon capensis</i> (Crustacea: Tj ETQq1 1 0.784314 rgBT/Overlock 10 Tf 50	0.2	3
1314	The Plastid Genome in Cladophorales Green Algae Is Encoded by Hairpin Chromosomes. <i>Current Biology</i> , 2017, 27, 3771-3782.e6.	1.8	45
1315	<i>Ricasolia amplissima</i> (Lobariaceae): one species, three genotypes and a new taxon from south-eastern Alaska. <i>Lichenologist</i> , 2017, 49, 579-596.	0.5	7
1316	Aligning evidence: concerns regarding multiple sequence alignments in estimating the phylogeny of the Nudibranchia suborder Doridina. <i>Royal Society Open Science</i> , 2017, 4, 171095.	1.1	31
1317	Process optimization of ^{13}C -Hexachlorocyclohexane degradation using three novel <i>Bacillus</i> sp. strains. <i>Biocatalysis and Agricultural Biotechnology</i> , 2017, 11, 97-107.	1.5	24
1318	Description of <i>Turritopsoides marhei</i> sp. nov. (Hydrozoa, Anthoathecata) from the Maldives and its phylogenetic position. <i>Marine Biology Research</i> , 2017, 13, 983-992.	0.3	6
1319	Integrative taxonomy and biogeography of the genus <i>Bulbaeolidia</i> (Nudibranchia: Aeolidida). <i>Journal of Molluscan Studies</i> , 2017, 83, 440-450.	0.4	2
1320	Sulfide Generation by Dominant <i>Halanaerobium</i> Microorganisms in Hydraulically Fractured Shales. <i>MSphere</i> , 2017, 2, .	1.3	62
1321	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

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1323	Peculiar citric acid cycle of hydrothermal vent chemolithoautotroph <i>Hydrogenovibrio crunogenus</i> , and insights into carbon metabolism by obligate autotrophs. <i>FEMS Microbiology Letters</i> , 2017, 364, .	0.7	8
1324	Involvement of aurantiactinomycin in the life cycle of <i>Thelohanellus testudineus</i> (Cnidaria: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 667 T) ultrastructural, and molecular analysis. <i>Parasitology Research</i> , 2017, 116, 2449-2456.	0.6	3
1325	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
1326	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
1327	Evolution of immune chemoreceptors into sensors of the outside world. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 7397-7402.	3.3	24
1328	Molecular Evidence of <i>Apatococcus</i> , including <i>A. fuscidea</i> sp. nov., as Photobiont in the Genus <i>Fuscidea</i> . <i>Protist</i> , 2017, 168, 425-438.	0.6	12
1329	In silico approach to designing rational metagenomic libraries for functional studies. <i>BMC Bioinformatics</i> , 2017, 18, 267.	1.2	19
1330	Fossils matter: improved estimates of divergence times in <i>Pinus</i> reveal older diversification. <i>BMC Evolutionary Biology</i> , 2017, 17, 95.	3.2	76
1331	MARS: improving multiple circular sequence alignment using refined sequences. <i>BMC Genomics</i> , 2017, 18, 86.	1.2	35
1332	Genome-wide characterization and expression analyses of superoxide dismutase (SOD) genes in <i>Gossypium hirsutum</i> . <i>BMC Genomics</i> , 2017, 18, 376.	1.2	101
1333	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
1334	Cleavage modification did not alter blastomere fates during bryozoan evolution. <i>BMC Biology</i> , 2017, 15, 33.	1.7	29
1335	Comparative genomic analysis reveals genetic features related to the virulence of <i>Bacillus cereus</i> FORC_013. <i>Gut Pathogens</i> , 2017, 9, 29.	1.6	7
1336	Superoxide-responsive gene expression in <i>Arabidopsis thaliana</i> and <i>Zea mays</i> . <i>Plant Physiology and Biochemistry</i> , 2017, 117, 51-60.	2.8	19
1337	Multiple introns in a deep-sea Annelid (Decemunciger: Ampharetidae) mitochondrial genome. <i>Scientific Reports</i> , 2017, 7, 4295.	1.6	21
1338	Morphology and molecular phylogeny of three heterotrichid species (Ciliophora, Heterotrichea), including a new species of <i>Anigsteinia</i> . <i>European Journal of Protistology</i> , 2017, 61, 278-293.	0.5	20
1339	The durable wheat disease resistance gene <i>Lr34</i> confers common rust and northern corn leaf blight resistance in maize. <i>Plant Biotechnology Journal</i> , 2017, 15, 489-496.	4.1	75

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1340	<i>Pseudonotohymena antarctica</i> n. g., n. sp. (Ciliophora, Hypotricha), a New Species from Antarctic Soil. <i>Journal of Eukaryotic Microbiology</i> , 2017, 64, 447-456.	0.8	9
1341	Genome of <i>Ca. Desulfovibrio trichonymphae</i> TM , an H ₂ -oxidizing bacterium in a tripartite symbiotic system within a protist cell in the termite gut. <i>ISME Journal</i> , 2017, 11, 766-776.	4.4	38
1342	Molecular phylogenetic analysis of <i>œpirate spiders</i> (Araneae, Mimetidae) with the description of a new African genus and the first report of maternal care in the family. <i>Cladistics</i> , 2017, 33, 375-405.	1.5	20
1343	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
1344	Description of a New Freshwater Ciliate <i>Epistylis wuhanensis</i> n. sp. (Ciliophora, Peritrichia) from China, with a Focus on Phylogenetic Relationships within Family Epistylididae. <i>Journal of Eukaryotic Microbiology</i> , 2017, 64, 394-406.	0.8	28
1345	Neogene diversification in the temperate lichen-forming fungal genus <i>Parmelia</i> (Parmeliaceae, Tj ETQq1 1 0.784314 rgBT /Ove	0.5	14
1346	Biosynthesis of the psychotropic plant diterpene salvinorin A: Discovery and characterization of the <i>Salvia divinorum</i> clerodienyl diphosphate synthase. <i>Plant Journal</i> , 2017, 89, 885-897.	2.8	55
1347	A six-gene phylogeny provides new insights into choanoflagellate evolution. <i>Molecular Phylogenetics and Evolution</i> , 2017, 107, 166-178.	1.2	59
1348	The family Rhabdoviridae: mono- and bipartite negative-sense RNA viruses with diverse genome organization and common evolutionary origins. <i>Virus Research</i> , 2017, 227, 158-170.	1.1	200
1349	High phylogenetic utility of an ultraconserved element probe set designed for Arachnida. <i>Molecular Ecology Resources</i> , 2017, 17, 812-823.	2.2	99
1350	A first higher-level time-calibrated phylogeny of antlions (Neuroptera: Myrmeleontidae). <i>Molecular Phylogenetics and Evolution</i> , 2017, 107, 103-116.	1.2	30
1351	Genomic Basis of Adaptive Evolution: The Survival of <i>Amur Ide</i> (<i>Leuciscu</i> <i>waleckii</i>) in an Extremely Alkaline Environment. <i>Molecular Biology and Evolution</i> , 2017, 34, 145-159.	3.5	66
1352	Phylogeny of the <i>jacchus</i> group of <i>Callithrix</i> marmosets based on complete mitochondrial genomes. <i>American Journal of Physical Anthropology</i> , 2017, 162, 157-169.	2.1	15
1353	Evolution and Cryo-electron Microscopy Capsid Structure of a North American Bat Adenovirus and Its Relationship to Other Mastadenoviruses. <i>Journal of Virology</i> , 2017, 91, .	1.5	26
1354	<i>Almendravirus</i> : A Proposed New Genus of Rhabdoviruses Isolated from Mosquitoes in Tropical Regions of the Americas. <i>American Journal of Tropical Medicine and Hygiene</i> , 2017, 96, 100-109.	0.6	27
1355	Phylogenetic relationships of two Cuban spleenworts with unusual morphology: <i>Asplenium</i> (<i>Schaffneria</i>) <i>nigripes</i> and <i>Asplenium pumilum</i> (<i>Aspleniaceae</i> , leptosporangiate ferns). <i>Plant Systematics and Evolution</i> , 2017, 303, 165-176.	0.3	4
1356	A whole genome analysis reveals the presence of a plant PR1 sequence in the potato pathogen <i>Streptomyces scabies</i> and other <i>Streptomyces</i> species. <i>Molecular Phylogenetics and Evolution</i> , 2017, 114, 346-352.	1.2	8
1357	A new Antarctic heterobranch clade is sister to all other Cephalaspidea (Mollusca: Gastropoda). <i>Zoologica Scripta</i> , 2017, 46, 127-137.	0.7	11

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1359	<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
1360	Thiol oxidation of hemolymph proteins in oysters <i>Crassostrea brasiliana</i> as markers of oxidative damage induced by urban sewage exposure. <i>Environmental Toxicology and Chemistry</i> , 2017, 36, 1833-1845.	2.2	9
1361	A cryptic species in the <i>Pteroclava krempfi</i> species complex (Hydrozoa, Cladocorynidae) revealed in the Caribbean. <i>Marine Biodiversity</i> , 2017, 47, 83-89.	0.3	25
1362	New species of Ampharetidae (Annelida: Polychaeta) from the Arctic Loki Castle vent field. <i>Deep-Sea Research Part II: Topical Studies in Oceanography</i> , 2017, 137, 232-245.	0.6	19
1363	<i>Paramytha ossicola</i> sp. nov. (Polychaeta, Ampharetidae) from mammal bones: Reproductive biology and population structure. <i>Deep-Sea Research Part II: Topical Studies in Oceanography</i> , 2017, 137, 349-358.	0.6	6
1364	Morphology and molecular phylogeny of a new <i>Myxidium</i> species (Cnidaria: Myxosporea) infecting the farmed turtle <i>Podocnemis expansa</i> (Testudines: Podocnemididae) in the Brazilian Amazon. <i>Parasitology International</i> , 2017, 66, 825-830.	0.6	10
1365	Bacteriomes of the corn leafhopper, <i>Dalbulus maidis</i> (DeLong & Wolcott, 1923) (Insecta, Hemiptera,) and transovarial transmission. <i>Protoplasma</i> , 2017, 254, 1421-1429.	1.0	12
1366	Evolutionary processes and environmental factors underlying the genetic diversity and lifestyles of <i>Bacillus cereus</i> group bacteria. <i>Research in Microbiology</i> , 2017, 168, 309-318.	1.0	43
1367	Endemic diversification in the mountains: genetic, morphological, and geographical differentiation of the <i>Hemidactylus</i> geckos in southwestern Arabia. <i>Organisms Diversity and Evolution</i> , 2017, 17, 267-285.	0.7	22
1368	MYB transcription factor gene involved in sex determination in <i>Asparagus officinalis</i> . <i>Genes To Cells</i> , 2017, 22, 115-123.	0.5	59
1369	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
1370	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
1371	The transition from somatic to germline identity shows conserved and specialized features during angiosperm evolution. <i>New Phytologist</i> , 2017, 216, 495-509.	3.5	41
1372	Phylogeography of a freshwater crustacean species complex reflects a long-gone archipelago. <i>Journal of Biogeography</i> , 2017, 44, 421-432.	1.4	43
1373	An integrative approach to the evolution of shrimps of the genus <i>Palaemon</i> (Decapoda,). <i>Tj ETQq1 1 0.784314 rgBT / Overlock 10</i>	0.7	17
1374	Exploring the evolution of the proteins of the plant nuclear envelope. <i>Nucleus</i> , 2017, 8, 46-59.	0.6	46
1375	The genus <i>Elaphomyces</i> (Ascomycota, Eurotiales): a ribosomal DNA-based phylogeny and revised systematics of European 'deer truffles'. <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2017, 38, 197-239.	1.6	30

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1376	The impact of phenotypic and molecular data on the inference of <i>Colletotrichum</i> diversity associated with <i>Musa</i> . <i>Mycologia</i> , 2017, 109, 912-934.	0.8	53
1377	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
1378	Plastid Phylogenomics Resolve Deep Relationships among Eupolypod II Ferns with Rapid Radiation and Rate Heterogeneity. <i>Genome Biology and Evolution</i> , 2017, 9, 1646-1657.	1.1	67
1379	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
1380	The identity of <i>Monomia argentata</i> (Crustacea : Brachyura : Portunidae) resolved by X-ray, computed tomography scanning and molecular comparisons. <i>Invertebrate Systematics</i> , 2017, 31, 797.	0.5	9
1381	Identification of very small open reading frames in the genomes of Holmes Jungle virus, Ord River virus, and Wongabel virus of the genus <i>Hapavirus</i> , family <i>Rhabdoviridae</i> . <i>Evolutionary Bioinformatics</i> , 2017, 13, 117693431771348.	0.6	3
1383	Phylogenomic analysis of <i>Balantidium ctenopharyngodoni</i> (Ciliophora, Litostomatea) based on single-cell transcriptome sequencing. <i>Parasite</i> , 2017, 24, 43.	0.8	9
1384	South Florida microfungi: a new species of <i>Taeniolella</i> (anamorphic Sordariomycetes) isolated from cabbage palm. <i>Nova Hedwigia</i> , 2017, 105, 1-14.	0.2	4
1385	Genome-Based Analyses of Six Hexacorallian Species Reject the "Naked Coral" Hypothesis. <i>Genome Biology and Evolution</i> , 2017, 9, 2626-2634.	1.1	8
1386	Phylogeny, taxonomy and biogeography of Neotropical Quiinoideae (Ochnaceae s.l.). <i>Taxon</i> , 2017, 66, 855-867.	0.4	13
1387	Male Mutation Bias Is the Main Force Shaping Chromosomal Substitution Rates in Monotreme Mammals. <i>Genome Biology and Evolution</i> , 2017, 9, 2198-2210.	1.1	6
1388	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
1389	Compensatory Evolution of Intrinsic Transcription Terminators in <i>Bacillus Cereus</i> . <i>Genome Biology and Evolution</i> , 2017, 9, 340-349.	1.1	1
1390	<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
1391	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
1392	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
1393	MICROORGANISMS AS CHEMICAL FACTORIES FOR ISOLATION OF META-BOLOMES FROM MESOPHILIC SOIL. <i>International Journal of Pharmacy and Pharmaceutical Sciences</i> , 2017, 9, 121.	0.3	4
1394	Molecular systematics of <i>Haploginglymus</i> , a genus of subterranean amphipods endemic to the Iberian Peninsula (Amphipoda: Niphargidae). <i>Contributions To Zoology</i> , 2017, 86, 239-260.	0.2	12

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1396	Characterization of the Polycomb-Group Mark H3K27me3 in Unicellular Algae. <i>Frontiers in Plant Science</i> , 2017, 8, 607.	1.7	38
1397	Diversity and Functional Analysis of the FeMo-Cofactor Maturase NifB. <i>Frontiers in Plant Science</i> , 2017, 8, 1947.	1.7	17
1398	Draft sequencing and assembly of the genome of the world's largest fish, the whale shark: <i>Rhincodon typus</i> Smith 1828. <i>BMC Genomics</i> , 2017, 18, 532.	1.2	91
1399	The purplish bifurcate mussel <i>Mytilisepta virgata</i> gene expression atlas reveals a remarkable tissue functional specialization. <i>BMC Genomics</i> , 2017, 18, 590.	1.2	32
1400	New species and phylogeny of landhoppers in the genus <i>Waematau</i> Duncan, 1994 (Crustacea: Tj ETQq1 1 0.784314 rgBT /Overlock 10 0.2 3		
1401	Comment: Characterization of Two Historic Smallpox Specimens from a Czech Museum. <i>Viruses</i> , 2017, 9, 276.	1.5	13
1402	A phylogenetically-based nomenclature for <i>Cordycipitaceae</i> (Hypocreales). <i>IMA Fungus</i> , 2017, 8, 335-353.	1.7	216
1403	In silico Comparison of 19 <i>Porphyromonas gingivalis</i> Strains in Genomics, Phylogenetics, Phylogenomics and Functional Genomics. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 28.	1.8	25
1404	Horizontally Acquired Biosynthesis Genes Boost <i>Coxiella burnetii</i> 's Physiology. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 174.	1.8	20
1405	Developmental Cycle and Genome Analysis of <i>Protochlamydia massiliensis</i> sp. nov. a New Species in the Parachlamydiaceae Family. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 385.	1.8	11
1406	Comparative Pan-Genome Analysis of <i>Piscirickettsia salmonis</i> Reveals Genomic Divergences within Genogroups. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 459.	1.8	52
1407	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
1408	Genome-Wide Analyses Reveal Genes Subject to Positive Selection in <i>Pasteurella multocida</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 961.	1.5	36
1409	Phylogenomic, Pan-genomic, Pathogenomic and Evolutionary Genomic Insights into the Agronomically Relevant Enterobacteria <i>Pantoea ananatis</i> and <i>Pantoea stewartii</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 1755.	1.5	20
1410	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
1411	Biochemical Function, Molecular Structure and Evolution of an Atypical Thioredoxin Reductase from <i>Desulfovibrio vulgaris</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 1855.	1.5	20
1412	Comparative Genomics of Sibling Species of <i>Fonsecaea</i> Associated with Human Chromoblastomycosis. <i>Frontiers in Microbiology</i> , 2017, 8, 1924.	1.5	31

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1413	Ecogenomics and Taxonomy of Cyanobacteria Phylum. <i>Frontiers in Microbiology</i> , 2017, 8, 2132.	1.5	99
1414	Comparative analyses of plastid genomes from fourteen Cornales species: inferences for phylogenetic relationships and genome evolution. <i>BMC Genomics</i> , 2017, 18, 956.	1.2	40
1415	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
1416	An in silico pan-genomic probe for the molecular traits behind <i>Lactobacillus ruminis</i> gut autochthony. <i>PLoS ONE</i> , 2017, 12, e0175541.	1.1	13
1417	Genetic variation and factors affecting the genetic structure of the lichenicolous fungus <i>Heterocephalacia bachmannii</i> (Filobasidiales, Basidiomycota). <i>PLoS ONE</i> , 2017, 12, e0189603.	1.1	9
1418	Who's there? – First morphological and DNA barcoding catalogue of the shallow Hawaiian sponge fauna. <i>PLoS ONE</i> , 2017, 12, e0189357.	1.1	15
1419	Comparative genomics of geographically distant <i>Fusarium fujikuroi</i> isolates revealed two distinct pathotypes correlating with secondary metabolite profiles. <i>PLoS Pathogens</i> , 2017, 13, e1006670.	2.1	58
1420	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
1421	<i>Cortinarius</i> section <i>Bicolores</i> and section <i>Saturnini</i> (<i>Basidiomycota</i> , <i>Tj ETQq0 0 0 rgBT /Overlock 10 T</i>) <i>Molecular Phylogeny and Evolution of Fungi</i> , 2017, 39, 175-200.	1.6	13
1422	Diversification of <i>Orientia tsutsugamushi</i> genotypes by intragenic recombination and their potential expansion in endemic areas. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005408.	1.3	57
1423	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
1424	The influence of molecular markers and methods on inferring the phylogenetic relationships between the representatives of the Arini (parrots, Psittaciformes), determined on the basis of their complete mitochondrial genomes. <i>BMC Evolutionary Biology</i> , 2017, 17, 166.	3.2	15
1425	A novel Coltivirus-related virus isolated from free-tailed bats from Côte d'Ivoire is able to infect human cells in vitro. <i>Virology Journal</i> , 2017, 14, 181.	1.4	21
1426	Genetic diversity of <i>Haemonchus contortus</i> isolated from sympatric wild blue sheep (Pseudois) <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 T</i>	1.0	10
1427	Phylogenetic analyses reveal that <i>Schellackia</i> parasites (Apicomplexa) detected in American lizards are closely related to the genus <i>Lankesterella</i> : is the range of <i>Schellackia</i> restricted to the Old World?. <i>Parasites and Vectors</i> , 2017, 10, 470.	1.0	11
1428	The phylogenetic position of the enigmatic Balkan <i>Aulopyge huegelii</i> (Teleostei: Cyprinidae) from the perspective of host-specific <i>Dactylogyrus</i> parasites (Monogenea), with a description of <i>Dactylogyrus omenti</i> n. sp.. <i>Parasites and Vectors</i> , 2017, 10, 547.	1.0	21
1429	Host-specific <i>Dactylogyrus</i> parasites revealing new insights on the historical biogeography of Northwest African and Iberian cyprinid fish. <i>Parasites and Vectors</i> , 2017, 10, 589.	1.0	32
1430	Phylogenomics of Colombian <i>Helicobacter pylori</i> isolates. <i>Gut Pathogens</i> , 2017, 9, 52.	1.6	18

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1432	Biosynthesis of volatile terpenes that accumulate in the secretory cavities of young leaves of Japanese pepper (<i>Zanthoxylum piperitum</i>): Isolation and functional characterization of monoterpene and sesquiterpene synthase genes. Plant Biotechnology, 2017, 34, 17-28.	0.5	12
1433	Polyphyly of the traditional family Flabellinidae affects a major group of Nudibranchia: aeolidacean taxonomic reassessment with descriptions of several new families, genera, and species (Mollusca, Tj ETQq0 0 0 rg0Tf Overlook 10 Tf 50	0.5	10
1434	Berlin Squirrelpox Virus, a New Poxvirus in Red Squirrels, Berlin, Germany. Emerging Infectious Diseases, 2017, 23, 1726-1729.	2.0	9
1435	Divergent HIV-1 strains (CRF92_C2U and CRF93_cpx) co-circulating in the Democratic Republic of the Congo: Phylogenetic insights on the early evolutionary history of subtype C. Virus Evolution, 2017, 3, vex032.	2.2	14
1436	Parallel Miocene-dominated diversification of the lichen-forming fungal genus <i>Oropogon</i> (Ascomycota: Parmeliaceae) in different continents. Taxon, 2017, 66, 1269-1281.	0.4	6
1437	Genomic analysis of endemic clones of toxigenic and non-toxigenic Corynebacterium diphtheriae in Belarus during and after the major epidemic in 1990s. BMC Genomics, 2017, 18, 873.	1.2	41
1438	The Small Noncoding RNA Processing Machinery of Two Living Fossil Species, Lungfish and Coelacanth, Gives New Insights into the Evolution of the Argonaute Protein Family. Genome Biology and Evolution, 2017, 9, 438-453.	1.1	11
1439	First Description of the Causal Agent of Taproot Decline of Soybean, an Emerging Disease in the Southern United States. Plant Health Progress, 2017, 18, 35-40.	0.8	7
1440	Rediscovery of the <i>Ochromonas</i> type species <i>Ochromonas triangulata</i> (Chrysophyceae) from its type locality (Lake Veysove, Donetsk region, Ukraine). Phycologia, 2017, 56, 591-604.	0.6	40
1441	SCREENING, ISOLATION, AND ANTIBACTERIAL ACTIVITY OF ANTIBIOTIC PRODUCING BACTERIA OBTAINED FROM SAPROPHYTIC SOIL SAMPLES. Asian Journal of Pharmaceutical and Clinical Research, 2017, 10, 92.	0.3	4
1442	Hidden diversity of forest birds in Madagascar revealed using integrative taxonomy. Molecular Phylogenetics and Evolution, 2018, 124, 16-26.	1.2	24
1443	Estimating evolutionary rates in giant viruses using ancient genomes. Virus Evolution, 2018, 4, vey006.	2.2	7
1444	Discovery, Biosynthesis and Stress-Related Accumulation of Dolabradiene-Derived Defenses in Maize. Plant Physiology, 2018, 176, 2677-2690.	2.3	94
1445	A cytochrome P450 <sc>CYP</sc>71 enzyme expressed in <i>Sorghum bicolor</i> root hair cells participates in the biosynthesis of the benzoquinone allelochemical sorgoleone. New Phytologist, 2018, 218, 616-629.	3.5	28
1446	Diversity and evolution of four-domain voltage-gated cation channels of eukaryotes and their ancestral functional determinants. Scientific Reports, 2018, 8, 3539.	1.6	24
1447	Genomes of ubiquitous marine and hypersaline <i>Hydrogenovibrio</i>, <i>Thiomicrothabodus</i> and <i>Thiomicrospira</i> spp. encode a diversity of mechanisms to sustain chemolithoautotrophy in heterogeneous environments. Environmental Microbiology, 2018, 20, 2686-2708.	1.8	32
1448	New virus of the family Flaviviridae detected in lumpfish (Cyclopterus lumpus). Archives of Virology, 2018, 163, 679-685.	0.9	55

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1449	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
1450	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
1451	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
1452	FasParser2: a graphical platform for batch manipulation of tremendous amount of sequence data. <i>Bioinformatics</i> , 2018, 34, 2493-2495.	1.8	17
1453	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
1454	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
1455	Characterization and Pathogenicity of Botryosphaeriaceae Fungi Associated with Declining Urban Stands of Coast Redwood in California. <i>Plant Disease</i> , 2018, 102, 1950-1957.	0.7	13
1456	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
1457	Mitogenomics reveals phylogenetic relationships of caudofoveate aplacophoran molluscs. <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 429-436.	1.2	17
1458	Genomic insights into the <i>Agromyces</i> -like symbiont of earthworms and its distribution among host species. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	9
1459	The Genome Sequence of <i>Candidatus Fokinia solitaria</i> : Insights on Reductive Evolution in Rickettsiales. <i>Genome Biology and Evolution</i> , 2018, 10, 1120-1126.	1.1	40
1460	Survival in northern microrefugia in an endemic Carpathian gammarid (Crustacea: Amphipoda). <i>Zoologica Scripta</i> , 2018, 47, 357-372.	0.7	18
1461	Consequences of Asexuality in Natural Populations: Insights from Stick Insects. <i>Molecular Biology and Evolution</i> , 2018, 35, 1668-1677.	3.5	63
1462	Genetic diversity of MHC class II DRB alleles in the continental and Japanese populations of the sable <i>Martes zibellina</i> (Mustelidae, Carnivora, Mammalia). <i>Mammal Research</i> , 2018, 63, 369-378.	0.6	5
1463	Phylogeny, evolution and mitochondrial gene order rearrangement in scale worms (Aphroditiformia). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5</i>	1.2	67
1464	Disentangling the Causes for Faster-X Evolution in Aphids. <i>Genome Biology and Evolution</i> , 2018, 10, 507-520.	1.1	42
1465	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
1466	More diverse than expected: distributional patterns of <i>Oecidiobanchus</i> Hessler, 1970 (Isopoda). <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 5</i>	0.3	10

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1467	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
1468	Terminal Uridyltransferases Execute Programmed Clearance of Maternal Transcriptome in Vertebrate Embryos. <i>Molecular Cell</i> , 2018, 70, 72-82.e7.	4.5	87
1469	Differential Evolution of Antiretroviral Restriction Factors in Pteropid Bats as Revealed by APOBEC3 Gene Complexity. <i>Molecular Biology and Evolution</i> , 2018, 35, 1626-1637.	3.5	59
1470	Anchored phylogenomics of burrowing mayflies (Ephemeroptera) and the evolution of tusks. <i>Systematic Entomology</i> , 2018, 43, 692-701.	1.7	12
1471	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
1472	Description of <i>Myolaimus mycophilus</i> Slos & Bert sp. n. (Rhabditida: Myolaimidae). <i>Nematology</i> , 2018, 20, 175-186.	0.2	3
1473	The epibiotic life of the cosmopolitan diatom <i>Fragilariopsis doliolus</i> on heterotrophic ciliates in the open ocean. <i>ISME Journal</i> , 2018, 12, 1094-1108.	4.4	26
1474	Phylogenetic position of the enigmatic deep-sea nematode order Rhaptothyreida: A molecular analysis. <i>Molecular Phylogenetics and Evolution</i> , 2018, 122, 29-36.	1.2	9
1475	Clonal genome evolution and rapid invasive spread of the marbled crayfish. <i>Nature Ecology and Evolution</i> , 2018, 2, 567-573.	3.4	168
1476	Molecular species delimitation and its implications for species descriptions using desmosomatid and nannoniscid isopods from the VEMA fracture zone as example taxa. <i>Deep-Sea Research Part II: Topical Studies in Oceanography</i> , 2018, 148, 180-207.	0.6	25
1477	Filtering of target sequence capture individuals facilitates species tree construction in the plant subtribe <i>Lochrominae</i> (Solanaceae). <i>Molecular Phylogenetics and Evolution</i> , 2018, 123, 26-34.	1.2	9
1478	<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
1479	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
1480	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
1481	Lytic xylan oxidases from wood-decay fungi unlock biomass degradation. <i>Nature Chemical Biology</i> , 2018, 14, 306-310.	3.9	269
1482	Multiple Roots of Fruiting Body Formation in Amoebozoa. <i>Genome Biology and Evolution</i> , 2018, 10, 591-606.	1.1	39
1483	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
1484	Keeping an eye on coloration: ecological correlates of the evolution of pitcher traits in the genus <i>Nepenthes</i> (Caryophyllales). <i>Biological Journal of the Linnean Society</i> , 2018, 123, 321-337.	0.7	16

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1486	Large-scale phylogenomic analysis resolves a backbone phylogeny in ferns. <i>GigaScience</i> , 2018, 7, 1-11.	3.3	90
1487	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
1488	Morphology, Morphogenesis, and Molecular Phylogeny of a New Soil Ciliate, <i>Sterkiella multicirrata</i> sp. nov. (Ciliophora, Hypotrichia) from China. <i>Journal of Eukaryotic Microbiology</i> , 2018, 65, 627-636.	0.8	6
1489	Analysis of Homologs of Cry-toxin Receptor-Related Proteins in the Midgut of a Non-Bt Target, <i>Nilaparvata lugens</i> (Stål) (Hemiptera: Delphacidae). <i>Journal of Insect Science</i> , 2018, 18, .	0.6	9
1490	Novel, diverse RNA viruses from Mediterranean isolates of the phytopathogenic fungus, <i>Rosellinia necatrix</i> : insights into evolutionary biology of fungal viruses. <i>Environmental Microbiology</i> , 2018, 20, 1464-1483.	1.8	92
1491	New insights into the molecular phylogeny of the swimming crabs of the genera <i>Portunus</i> Weber, 1795 and <i>Achelous</i> De Haan, 1833 (Brachyura: Portunidae) of the Americas. <i>Journal of Crustacean Biology</i> , 2018, 38, 190-197.	0.3	11
1492	Draft genome sequence of ramie, <i>Boehmeria nivea</i> (L.) Gaudich. <i>Molecular Ecology Resources</i> , 2018, 18, 639-645.	2.2	46
1493	Latitudinal variation in genome size in crustaceans. <i>Biological Journal of the Linnean Society</i> , 2018, 123, 348-359.	0.7	24
1494	High intraspecific genome diversity in the model arbuscular mycorrhizal symbiont <i>Rhizophagus irregularis</i> . <i>New Phytologist</i> , 2018, 220, 1161-1171.	3.5	206
1495	<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
1496	Genetic and molecular basis of the immune system in the brachiopod <i>Lingula anatina</i> . <i>Developmental and Comparative Immunology</i> , 2018, 82, 7-30.	1.0	31
1497	Evolutionary history of spiny-tailed lizards (Agamidae: <i>Uromastix</i>) from the Sahara-Arabian region. <i>Zoologica Scripta</i> , 2018, 47, 159-173.	0.7	29
1498	Genome sequencing of <i>Pediococcus acidilactici</i> (NRCC1), a novel isolate from dromedary camel (<i>Camelus dromedarius</i>) rumen fluid. <i>Annals of Microbiology</i> , 2018, 68, 103-110.	1.1	4
1499	Coelacanth-specific adaptive genes give insights into primitive evolution for water-to-land transition of tetrapods. <i>Marine Genomics</i> , 2018, 38, 89-95.	0.4	1
1500	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
1501	Dispersion Profiles and Gene Associations of Repetitive DNAs in the Euchromatin of the Beetle <i>Tribolium castaneum</i> . <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 875-886.	0.8	21
1502	Molecular phylogeny of the Aglajidae head-shield sea slugs (Heterobranchia: Cephalaspidea): new evolutionary lineages revealed and proposal of a new classification. <i>Zoological Journal of the Linnean Society</i> , 2018, 183, 1-51.	1.0	16

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1503	Vibrio ferrin production by the food spoilage bacterium <i>Pseudomonas fragi</i> . <i>FEMS Microbiology Letters</i> , 2018, 365, .	0.7	19
1504	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
1505	Genome mining for peptidases in heat-tolerant and mesophilic fungi and putative adaptations for thermostability. <i>BMC Genomics</i> , 2018, 19, 152.	1.2	14
1506	Identification of novel MITEs (miniature inverted-repeat transposable elements) in <i>Coxiella burnetii</i> : implications for protein and small RNA evolution. <i>BMC Genomics</i> , 2018, 19, 247.	1.2	14
1507	Grapevine rootstocks shape underground bacterial microbiome and networking but not potential functionality. <i>Microbiome</i> , 2018, 6, 3.	4.9	194
1508	Hidden diversity uncovered in <i>Hygrophorus</i> sect. <i>Aurei</i> (Hygrophoraceae), including the Mediterranean <i>H. meridionalis</i> and the North American <i>H. boyeri</i> , spp. nov.. <i>Fungal Biology</i> , 2018, 122, 817-836.	1.1	11
1509	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
1510	Molecular phylogenetics reveals novel relationships within <i>Empidoidea</i> (<i>Diptera</i>). <i>Systematic Entomology</i> , 2018, 43, 619-636.	1.7	27
1511	Virulence factors of <i>Moraxella catarrhalis</i> outer membrane vesicles are major targets for cross-reactive antibodies and have adapted during evolution. <i>Scientific Reports</i> , 2018, 8, 4955.	1.6	26
1512	Phylogenetic relationships of the Australasian open-holed trapdoor spiders (Araneae: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 387 classification of a highly diverse fauna. <i>Zoological Journal of the Linnean Society</i> , 2018, 184, 407-452.	1.0	28
1513	Multiple Factors Confounding Phylogenetic Detection of Selection on Codon Usage. <i>Molecular Biology and Evolution</i> , 2018, 35, 1463-1472.	3.5	10
1514	Evidence for a novel negative-stranded RNA mycovirus isolated from the plant pathogenic fungus <i>Fusarium graminearum</i> . <i>Virology</i> , 2018, 518, 232-240.	1.1	41
1515	Betaine Lipid Is Crucial for Adapting to Low Temperature and Phosphate Deficiency in <i>Nannochloropsis</i> . <i>Plant Physiology</i> , 2018, 177, 181-193.	2.3	83
1516	The genomic and functional landscapes of developmental plasticity in the American cockroach. <i>Nature Communications</i> , 2018, 9, 1008.	5.8	113
1517	Comparative genomic analysis of <i>Lactobacillus plantarum</i> GB-LP4 and identification of evolutionarily divergent genes in high-osmolarity environment. <i>Genes and Genomics</i> , 2018, 40, 217-223.	0.5	12
1518	Isolation and characterization of pathogenic leptospires associated with cattle. <i>Veterinary Microbiology</i> , 2018, 218, 25-30.	0.8	41
1519	Taitaia, a novel lichenicolous fungus in tropical montane forests in Kenya (East Africa). <i>Lichenologist</i> , 2018, 50, 173-184.	0.5	13
1520	Species-specific serine-threonine protein kinase Pkb2 of <i>Bifidobacterium longum</i> subsp. <i>longum</i> : Genetic environment and substrate specificity. <i>Anaerobe</i> , 2018, 51, 26-35.	1.0	18

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1521	Isolation and identification of burn wound superbugs by molecular technique and their susceptibility to silver nanoparticles. IOP Conference Series: Materials Science and Engineering, 2018, 310, 012146.	0.3	0
1522	Characterization and comparative analysis of the genome of <i>Puccinia sorghi</i> Schwein, the causal agent of maize common rust. Fungal Genetics and Biology, 2018, 112, 31-39.	0.9	31
1523	Bat Systematics in the Light of Unconstrained Analyses of a Comprehensive Molecular Supermatrix. Journal of Mammalian Evolution, 2018, 25, 37-70.	1.0	123
1524	Integrative species delimitation in the deep-sea genus <i>Thaumastosoma</i> Hessler, 1970 (Isopoda, Asellota.) Tj ETQq1 1 0.784314 rgBT / Overlock 10, Tf 50 182 Research Part II: Topical Studies in Oceanography, 2018, 148, 151-179.	0.6	21
1525	Mitogenomics phylogenetic relationships of the current slothâ€™s genera and species (Bradypodidae and) Tj ETQq0 0 0 rgBT / Overlock 10, Tf 50 182	0.7	9
1526	Phylogeny of the hyperâ€™diverse rove beetle subtribe <i>Philonthina</i> with implications for classification of the tribe <i>Staphylinini</i> (Coleoptera: Staphylinidae). Cladistics, 2018, 34, 1-40.	1.5	40
1527	Host specificity versus plasticity: testing the morphology-based taxonomy of the endoparasitic copepod family <i>Splanchnotrophidae</i> with COI barcoding. Journal of the Marine Biological Association of the United Kingdom, 2018, 98, 231-243.	0.4	2
1528	Phylogeny and systematics of <i>Aphroditiformia</i> . Cladistics, 2018, 34, 225-259.	1.5	42
1529	Resurrection and emendation of the <i>Hypoxylaceae</i> , recognised from a multigene phylogeny of the <i>Xylariales</i> . Mycological Progress, 2018, 17, 115-154.	0.5	144
1530	Low genetic variation in the MHC class II DRB gene and MHC-linked microsatellites in endangered island populations of the leopard cat (<i>Prionailurus bengalensis</i>) in Japan. Immunogenetics, 2018, 70, 115-124.	1.2	11
1531	The revenant: rediscovery of <i>Margaritifera homsensis</i> from Orontes drainage with remarks on its taxonomic status and conservation (Bivalvia: Margaritiferidae). Systematics and Biodiversity, 2018, 16, 69-80.	0.5	11
1532	Know your farmer: Ancient origins and multiple independent domestications of ambrosia beetle fungal cultivars. Molecular Ecology, 2018, 27, 2077-2094.	2.0	67
1533	Multiple reversals of strand asymmetry in molluscs mitochondrial genomes, and consequences for phylogenetic inferences. Molecular Phylogenetics and Evolution, 2018, 118, 222-231.	1.2	20
1534	When the ribosomal DNA does not tell the truth: The case of the taxonomic position of <i>Kurtia argillacea</i> , an ericoid mycorrhizal fungus residing among <i>Hymenochaetales</i> . Fungal Biology, 2018, 122, 1-18.	1.1	30
1535	Molecular phylogeny and biogeography of the Westâ€™Palearctic <i>Velia</i> (Heteroptera: Tj ETQq0 0 0 rgBT / Overlock 10, Tf 50 182	1.7	9
1536	Adenovirus infection in savanna chimpanzees (<i>Pan troglodytes schweinfurthii</i>) in the Issa Valley, Tanzania. Archives of Virology, 2018, 163, 191-196.	0.9	6
1537	A multilocus view on Mediterranean aeolid nudibranchs (Mollusca): Systematics and cryptic diversity of <i>Flabellinidae</i> and <i>Piseinotecidae</i> . Molecular Phylogenetics and Evolution, 2018, 118, 13-22.	1.2	18
1538	Small spotted bodies with multiple specific mitochondrial DNAs: existence of diverse and differentiated tigrina lineages or species (<i>Leopardus</i> spp: Felidae, Mammalia) throughout Latin America. Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2018, 29, 993-1014.	0.7	11

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1539	Convergent evolution of bilaterian nerve cords. <i>Nature</i> , 2018, 553, 45-50.	13.7	140
1540	Climatic suitability, isolation by distance and river resistance explain genetic variation in a Brazilian whiptail lizard. <i>Heredity</i> , 2018, 120, 251-265.	1.2	39
1541	Rolling into the deep of the land planarian genus <i>Choeradoplana</i> (Tricladida, Continenticola). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 662</i>	0.7	9
1542	Coexistence of poribacterial phylotypes among geographically widespread and phylogenetically divergent sponge hosts. <i>Environmental Microbiology Reports</i> , 2018, 10, 80-91.	1.0	5
1543	On the importance of homology in the age of phylogenomics. <i>Systematics and Biodiversity</i> , 2018, 16, 210-228.	0.5	78
1544	A bacterial pioneer produces cellulase complexes that persist through community succession. <i>Nature Microbiology</i> , 2018, 3, 99-107.	5.9	38
1545	The complex pattern of codon usage evolution in the family Comamonadaceae. <i>Ecological Genetics and Genomics</i> , 2018, 6, 1-8.	0.3	5
1546	Characterization of the complete mitochondrial genome of <i>Marshallagia marshalli</i> and phylogenetic implications for the superfamily Trichostrongyloidea. <i>Parasitology Research</i> , 2018, 117, 307-313.	0.6	7
1547	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
1548	Characterization of a <i>Heterobasidion irregulare</i> endo- α -D-galacturonase that mediate growth on pectin. <i>Journal of Phytopathology</i> , 2018, 166, 34-43.	0.5	1
1549	First record of the fungus <i>Battarreia phalloides</i> (Agariaceae) in New Zealand. <i>New Zealand Journal of Botany</i> , 2018, 56, 109-114.	0.8	3
1550	Contribution to the phylogeny and a new species of <i>Cocodiella</i> (Phyllachorales). <i>Mycological Progress</i> , 2018, 17, 205-213.	0.5	7
1551	Extensive diversity and evolution of hepadnaviruses in bats in China. <i>Virology</i> , 2018, 514, 88-97.	1.1	16
1552	Sequence and structure insights of kazal type thrombin inhibitor protein: Studied with phylogeny, homology modeling and dynamic MM/GBSA studies. <i>International Journal of Biological Macromolecules</i> , 2018, 108, 1045-1052.	3.6	9
1553	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
1554	The complete mitochondrial genome of the alvinocaridid shrimp <i>Shinkaicaris leurokolos</i> (Decapoda). <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 662</i> shrimp. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2018, 25, 42-52.	0.4	45
1555	Transcriptional Profiles of Secondary Metabolite Biosynthesis Genes and Cytochromes in the Leaves of Four Papaver Species. <i>Data</i> , 2018, 3, 55.	1.2	7
1556	Endophytic and endolichenic fungal diversity in maritime Antarctica based on cultured material and their evolutionary position among Dikarya. <i>Fungal Systematics and Evolution</i> , 2018, 2, 263-272.	0.9	12

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1558	A phylogenomic resolution of the sea urchin tree of life. BMC Evolutionary Biology, 2018, 18, 189.	3.2	42
1559	Dye-tolerant marine <i>Acinetobacter baumannii</i> -mediated biodegradation of reactive red. Water Science and Engineering, 2018, 11, 265-275.	1.4	38
1560	Overview of Phacidiales, including <i>Aotearoamyces</i> gen. nov. on <i>Nothofagus</i> . IMA Fungus, 2018, 9, 371-382.	1.7	8
1561	<i>Singerocomus atlanticus</i> sp. nov., and a first record of <i>Singerocomus rubriflavus</i> (Boletaceae,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 582	0.8	10
1562	Molecular phylogenetics reveals a complex history underlying cryptic diversity in the Bush Squeaker Frog (<i>Arthroleptis wahlbergii</i>) in southern Africa. African Zoology, 2018, 53, 83-97.	0.2	10
1563	The genome of an underwater architect, the caddisfly <i>Stenopsyche tienmushanensis</i> Hwang (Insecta: Trichoptera). GigaScience, 2018, 7, .	3.3	41
1564	Assembly of a Complete Mitogenome of <i>Chrysanthemum nankingense</i> Using Oxford Nanopore Long Reads and the Diversity and Evolution of Asteraceae Mitogenomes. Genes, 2018, 9, 547.	1.0	34
1565	Plant rhabdoviruses—their origins and vector interactions. Current Opinion in Virology, 2018, 33, 198-207.	2.6	70
1566	foxF-1 Controls Specification of Non-body Wall Muscle and Phagocytic Cells in Planarians. Current Biology, 2018, 28, 3787-3801.e6.	1.8	49
1567	Diversity of phytobeneficial traits revealed by whole-genome analysis of worldwide-isolated phenazine-producing <i>Pseudomonas</i> spp.. Environmental Microbiology, 2019, 21, 437-455.	1.8	66
1568	Fungi between extremotolerance and opportunistic pathogenicity on humans. Fungal Diversity, 2018, 93, 195-213.	4.7	73
1569	Rapid Expansion of a Highly Germline-Expressed <i>Mariner</i> Element Acquired by Horizontal Transfer in the Fire Ant Genome. Genome Biology and Evolution, 2018, 10, 3262-3278.	1.1	6
1570	A new species of <i>Gyroporus</i> (Gyroporaceae, Boletales) from Atlantic Forest in Southern Brazil. Nova Hedwigia, 2018, 107, 291-301.	0.2	6
1571	Annotation and analysis of the mitochondrial genome of <i>Coniothyrium glycinis</i> , causal agent of red leaf blotch of soybean, reveals an abundance of homing endonucleases. PLoS ONE, 2018, 13, e0207062.	1.1	15
1572	A multigene typing system for human adenoviruses reveals a new genotype in a collection of Swedish clinical isolates. PLoS ONE, 2018, 13, e0209038.	1.1	13
1573	A Phylogenomic Framework and Divergence History of Cephalochordata Amphioxus. Frontiers in Physiology, 2018, 9, 1833.	1.3	11
1574	Molecular and morphological characterization of new species of hypogean <i>Paradraculoides</i> (Schizomida: Hubbardiidae) from the arid Pilbara bioregion of Western Australia. Journal of Arachnology, 2018, 46, 507.	0.3	6

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1575	Genome sequence of walking catfish (<i>Clarias batrachus</i>) provides insights into terrestrial adaptation. <i>BMC Genomics</i> , 2018, 19, 952.	1.2	36
1576	Insights into the transcriptional and post-transcriptional regulation of the rice SUMOylation machinery and into the role of two rice SUMO proteases. <i>BMC Plant Biology</i> , 2018, 18, 349.	1.6	18
1577	Systematic revision, diversity patterns and trophic ecology of the tropical Indo-West Pacific sea slug genus <i>Phanerophthalmus</i> A. Adams, 1850 (Cephalaspidea, Haminoeidae). <i>Invertebrate Systematics</i> , 2018, 32, 1336.	0.5	9
1578	A Comparative View on Sex Differentiation and Gametogenesis Genes in Lungfish and Coelacanths. <i>Genome Biology and Evolution</i> , 2018, 10, 1430-1444.	1.1	17
1579	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
1580	Ice ages and butterflyfishes: Phylogenomics elucidates the ecological and evolutionary history of reef fishes in an endemism hotspot. <i>Ecology and Evolution</i> , 2018, 8, 10989-11008.	0.8	8
1581	Evolution of Oviposition Techniques in Stick and Leaf Insects (Phasmatodea). <i>Frontiers in Ecology and Evolution</i> , 2018, 6, .	1.1	85
1582	High Throughput Identification of Antihypertensive Peptides from Fish Proteome Datasets. <i>Marine Drugs</i> , 2018, 16, 365.	2.2	12
1583	Phylogenetic position of Alvinocarididae (Crustacea: Decapoda: Caridea): New insights into the origin and evolutionary history of the hydrothermal vent alvinocarid shrimps. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2018, 141, 93-105.	0.6	14
1584	Genome-wide analysis of <i>Borrelia turcica</i> and <i>Candidatus Borrelia tachyglossi</i> TM 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
1585	<i>Kaviengella jeffkinchi</i> , a new genus and species of symbiotic shrimp (Crustacea: Decapoda: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 342 T	0.2	2
1586	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
1587	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
1588	<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
1589	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
1590	New insight into parrots TM mitogenomes indicates that their ancestor contained a duplicated region. <i>Molecular Biology and Evolution</i> , 2018, 35, 2989-3009.	3.5	19
1591	Activity of native and commercial strains of <i>Metarhizium</i> spp. against the poultry red mite <i>Dermanyssus gallinae</i> under different environmental conditions. <i>Veterinary Parasitology</i> , 2018, 262, 20-25.	0.7	20
1592	The complete mitochondrial genomes of two skipper genera (Lepidoptera: Hesperidae) and their associated phylogenetic analysis. <i>Scientific Reports</i> , 2018, 8, 15762.	1.6	19

#	ARTICLE	IF	CITATIONS
1593	Bacterial endosymbiont <i>Cardinium</i> cSfur genome sequence provides insights for understanding the symbiotic relationship in <i>Sogatella furcifera</i> host. <i>BMC Genomics</i> , 2018, 19, 688.	1.2	32
1594	Hoshinoamides A and B, Acyclic Lipopeptides from the Marine Cyanobacterium <i>Caldora penicillata</i> . <i>Journal of Natural Products</i> , 2018, 81, 2545-2552.	1.5	17
1595	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
1596	The dilemma of bacterial expansins evolution. The unusual case of <i>Streptomyces acidiscabies</i> and <i>Kutzneria</i> sp. 744. <i>Communicative and Integrative Biology</i> , 2018, 11, e1539612.	0.6	2
1597	Adaptation and Constraint in the Atypical Chemokine Receptor Family in Mammals. <i>BioMed Research International</i> , 2018, 2018, 1-9.	0.9	3
1598	The threonine-tRNA ligase gene region is applicable in classification, typing, and phylogenetic analysis of bifidobacteria. <i>Journal of Microbiology</i> , 2018, 56, 713-721.	1.3	6
1599	Phylogenetic Diversity and Single-Cell Genome Analysis of <i>Melainabacteria</i> , a Non-Photosynthetic Cyanobacterial Group, in the Termite Gut. <i>Microbes and Environments</i> , 2018, 33, 50-57.	0.7	33
1600	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 ETQq1 1 0.784314 rgBT /@verlock</i>	1.4	10
1601	Enzymatic analysis, structural study and molecular docking of laccase and catalase from <i>B. subtilis</i> SK1 after textile dye exposure. <i>Ecological Informatics</i> , 2018, 48, 269-280.	2.3	15
1602	First evidence of polychaete intermediate hosts for <i>Neospororchis</i> spp. marine turtle blood flukes (Trematoda: Spirorchidae). <i>International Journal for Parasitology</i> , 2018, 48, 1097-1106.	1.3	20
1603	Potential of Herbariomics for Studying Repetitive DNA in Angiosperms. <i>Frontiers in Ecology and Evolution</i> , 2018, 6, .	1.1	7
1604	The pathogenic mechanisms of <i>Tilletia horrida</i> as revealed by comparative and functional genomics. <i>Scientific Reports</i> , 2018, 8, 15413.	1.6	17
1605	Diversity and taxonomy of <i>Tricholoma</i> species from Yunnan, China, and notes on species from Europe and North America. <i>Mycologia</i> , 2018, 110, 1081-1109.	0.8	18
1606	Diversity of Diatom Communities in Delaware Tidal Wetland and Their Relationship to Water Quality. <i>Frontiers in Environmental Science</i> , 2018, 6, .	1.5	4
1607	Transcriptome Profiling of Two Ornamental and Medicinal Papaver Herbs. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3192.	1.8	9
1608	Investigation of inter- and intraspecies variation through genome sequencing of <i>Aspergillus</i> section Nigri. <i>Nature Genetics</i> , 2018, 50, 1688-1695.	9.4	160
1609	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
1610	Draft genome sequence of wild <i>Prunus yedoensis</i> reveals massive inter-specific hybridization between sympatric flowering cherries. <i>Genome Biology</i> , 2018, 19, 127.	3.8	89

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1611	Whole Genome Sequencing of the Pirarucu (<i>Arapaima gigas</i>) Supports Independent Emergence of Major Teleost Clades. <i>Genome Biology and Evolution</i> , 2018, 10, 2366-2379.	1.1	33
1612	Mitogenomics of the jaguarundi (<i>Puma yagouaroundi</i> , Felidae, Carnivora): Disagreement between morphological subspecies and molecular data. <i>Mammalian Biology</i> , 2018, 93, 153-168.	0.8	8
1613	New neotropical species of Phyllachorales based on molecular, morphological, and ecological data. <i>Mycologia</i> , 2018, 110, 835-859.	0.8	4
1614	Chromosome-level reference genome and alternative splicing atlas of moso bamboo (<i>Phyllostachys</i>) Tj ETQq1 1 0.784314 rgBT /Overl	3.3	98
1615	Molecular evidence for the paraphyly of Scolecophidia and its evolutionary implications. <i>Journal of Evolutionary Biology</i> , 2018, 31, 1782-1793.	0.8	52
1616	Transient genetic transformation of <i>Mougeotia scalaris</i> (<i>Zygnematophyceae</i>) mediated by the endogenous α -tubulin1 promoter. <i>Journal of Phycology</i> , 2018, 54, 840-849.	1.0	17
1617	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
1618	The Evolution Force of Genome Reduction in Carnivorous Plants. <i>American Journal of Biochemistry and Biotechnology</i> , 2018, 14, 154-161.	0.1	1
1619	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
1620	Hidden diversity in mushrooms explored: A new nematode species, <i>Neodiplogaster unguispiculata</i> sp. n. (<i>Rhabditida</i> , <i>Diplogastridae</i>), with a key to the species of <i>Neodiplogaster</i> . <i>Zoologischer Anzeiger</i> , 2018, 276, 71-85.	0.4	4
1621	Molecular phylogeny and bioprospecting of Endolichenic Fungi (ELF) inhabiting in the lichens collected from a mangrove ecosystem in Sri Lanka. <i>PLoS ONE</i> , 2018, 13, e0200711.	1.1	21
1622	New contributions to <i>Gruberia lanceolata</i> (Gruber, 1884) Kahl, 1932 based on analyses of multiple populations and genes (<i>Ciliophora</i> , <i>Heterotrichea</i> , <i>Gruberiidae</i>). <i>European Journal of Protistology</i> , 2018, 65, 16-30.	0.5	10
1623	The zoogeography of extant rhabdopleurid hemichordates (<i>Pterobranchia</i> : <i>Graptolithina</i>), with a new species from the Mediterranean Sea. <i>Invertebrate Systematics</i> , 2018, 32, 100.	0.5	14
1624	Horizontal operon transfer, plasmids, and the evolution of photosynthesis in <i>Rhodobacteraceae</i> . <i>ISME Journal</i> , 2018, 12, 1994-2010.	4.4	75
1625	An integrative taxonomic approach reveals the first marine triclad (<i>Platyhelminthes</i>) trapped in a cave from a semiarid Neotropical environment. <i>Invertebrate Systematics</i> , 2018, 32, 627.	0.5	8
1626	Comparative analyses of the mitochondrial genome of the sheep ked <i>Melophagus ovinus</i> (<i>Diptera</i>): Tj ETQq1 1 0.784314 rgBT /Overl	0.6	10
1627	The mitochondrial genome of the oribatid mite <i>Paraleius leontonychus</i> : new insights into tRNA evolution and phylogenetic relationships in acariform mites. <i>Scientific Reports</i> , 2018, 8, 7558.	1.6	22
1628	Components of a new gene family of ferroxidases involved in virulence are functionally specialized in fungal dimorphism. <i>Scientific Reports</i> , 2018, 8, 7660.	1.6	47

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1629	Investigation of genetic diversity and epidemiological characteristics of <i>Pasteurella multocida</i> isolates from poultry in southwest China by population structure, multi-locus sequence typing and virulence-associated gene profile analysis. <i>Journal of Veterinary Medical Science</i> , 2018, 80, 921-929.	0.3	15
1630	Secondary metabolites of Antarctic fungi antagonistic to aquatic pathogenic bacteria. <i>Open Life Sciences</i> , 2018, 13, 11-21.	0.6	2
1631	Differential expression of multiple glutamine synthetase genes in air-breathing magur catfish, <i>Clarias magur</i> and their induction under hyper-ammonia stress. <i>Gene</i> , 2018, 671, 85-95.	1.0	16
1632	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
1633	Population genomic data reveal genes related to important traits of quail. <i>GigaScience</i> , 2018, 7, .	3.3	38
1634	De novo genome assembly of the red silk cotton tree (<i>Bombax ceiba</i>). <i>GigaScience</i> , 2018, 7, .	3.3	27
1635	Broad Genomic Sampling Reveals a Smut Pathogenic Ancestry of the Fungal Clade Ustilaginomycotina. <i>Molecular Biology and Evolution</i> , 2018, 35, 1840-1854.	3.5	43
1636	<i>Monomia lucida</i> sp. nov., a new swimming crab (Crustacea: Decapoda: Portunidae) from the South China Sea. <i>Zootaxa</i> , 2018, 4387, 567.	0.2	2
1637	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
1638	Genus-wide comparison of <i>Pseudovibrio</i> bacterial genomes reveal diverse adaptations to different marine invertebrate hosts. <i>PLoS ONE</i> , 2018, 13, e0194368.	1.1	50
1639	Functional analysis of African <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> TALomes reveals a new susceptibility gene in bacterial leaf blight of rice. <i>PLoS Pathogens</i> , 2018, 14, e1007092.	2.1	86
1640	<i>Luciobarbus lanigarensis</i> and <i>L. numidiensis</i> , two new species of barbels from the Mediterranean Sea basin in North Africa (Teostei: Cyprinidae). <i>Zootaxa</i> , 2018, 4433, 542.	0.2	3
1641	Feline Aspergillosis. , 2018, , 337-356.		1
1642	Patterns of Conservation and Diversification in the Fungal Polarization Network. <i>Genome Biology and Evolution</i> , 2018, 10, 1765-1782.	1.1	15
1643	Gene family innovation, conservation and loss on the animal stem lineage. <i>ELife</i> , 2018, 7, .	2.8	149
1644	DNA methylation in adults and during development of the self-fertilizing mangrove rivulus, <i>Kryptolebias marmoratus</i> . <i>Ecology and Evolution</i> , 2018, 8, 6016-6033.	0.8	31
1645	In silico modelling and molecular dynamics simulation studies on L-Asparaginase isolated from bacterial endophyte of <i>Ocimum tenuiflorum</i> . <i>Enzyme and Microbial Technology</i> , 2018, 117, 32-40.	1.6	26
1646	Geometric morphometric on a new species of Trichodinidae. A tool to discriminate trichodinid species combined with traditional morphology and molecular analysis. <i>International Journal for Parasitology: Parasites and Wildlife</i> , 2018, 7, 228-236.	0.6	10

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1647	Improved phylogenetic resolution within Siphonophora (Cnidaria) with implications for trait evolution. <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 823-833.	1.2	25
1648	TERribly Difficult: Searching for Telomerase RNAs in Saccharomycetes. <i>Genes</i> , 2018, 9, 372.	1.0	12
1649	Comparative genomic investigation of high-elevation adaptation in ectothermic snakes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 8406-8411.	3.3	119
1650	Pattern of DNA Methylation in Daphnia: Evolutionary Perspective. <i>Genome Biology and Evolution</i> , 2018, 10, 1988-2007.	1.1	47
1651	A Tangled Web: Origins of Reproductive Parasitism. <i>Genome Biology and Evolution</i> , 2018, 10, 2292-2309.	1.1	47
1652	Mitochondrial Glycolysis in a Major Lineage of Eukaryotes. <i>Genome Biology and Evolution</i> , 2018, 10, 2310-2325.	1.1	62
1653	CO-dependent hydrogen production by the facultative anaerobe <i>Parageobacillus thermoglucosidasius</i> . <i>Microbial Cell Factories</i> , 2018, 17, 108.	1.9	37
1654	Comparison of the response of <i>Symbiodinium</i> in hospite and <i>Symbiodinium</i> ex hospite to elevated temperature. <i>Marine and Freshwater Behaviour and Physiology</i> , 2018, 51, 93-108.	0.4	5
1655	Enigmatic Diphyllatea eukaryotes: culturing and targeted PacBio RS amplicon sequencing reveals a higher order taxonomic diversity and global distribution. <i>BMC Evolutionary Biology</i> , 2018, 18, 115.	3.2	10
1656	Flatfish monophyly refuted by the relationship of Psettodes in Carangimorphariae. <i>BMC Genomics</i> , 2018, 19, 400.	1.2	18
1657	Comparative mitogenomics supports synonymy of the genera <i>Ligula</i> and <i>Digramma</i> (Cestoda: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 34).	1.0	17
1658	Genomic evidence for intraspecific hybridization in a clonal and extremely halotolerant yeast. <i>BMC Genomics</i> , 2018, 19, 364.	1.2	47
1659	Plastid Genome Evolution in the Early-Diverging Legume Subfamily Cercidoideae (Fabaceae). <i>Frontiers in Plant Science</i> , 2018, 9, 138.	1.7	97
1660	The Zinc-Finger Thylakoid-Membrane Protein FIP Is Involved With Abiotic Stress Response in <i>Arabidopsis thaliana</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 504.	1.7	15
1661	A revision of <i>Leptogium</i> (Collemales, lichenized Ascomycota) from Antarctica with a key to species. <i>Lichenologist</i> , 2018, 50, 467-485.	0.5	12
1662	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
1663	Pan-genome analyses of 24 <i>Shewanella</i> strains re-emphasize the diversification of their functions yet evolutionary dynamics of metal-reducing pathway. <i>Biotechnology for Biofuels</i> , 2018, 11, 193.	6.2	59
1664	Divergent evolution and clade-specific duplications of the Insulin-like Receptor in malacostracan crustaceans. <i>General and Comparative Endocrinology</i> , 2018, 268, 34-39.	0.8	9

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1665	Endosymbiont genomes yield clues of tubeworm success. <i>ISME Journal</i> , 2018, 12, 2785-2795.	4.4	33
1666	Rapid Viral Symbiogenesis via Changes in Parasitoid Wasp Genome Architecture. <i>Molecular Biology and Evolution</i> , 2018, 35, 2463-2474.	3.5	44
1667	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
1668	Dichorhviruses in their Host Plants and Mite Vectors. <i>Advances in Virus Research</i> , 2018, 102, 119-148.	0.9	51
1669	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
1670	<i>Labilibaculum manganireducens</i> gen. nov., sp. nov. and <i>Labilibaculum filiforme</i> sp. nov., Novel Bacteroidetes Isolated from Subsurface Sediments of the Baltic Sea. <i>Frontiers in Microbiology</i> , 2017, 8, 2614.	1.5	25
1671	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
1672	Comparative Genomics of Environmental and Clinical <i>Burkholderia cenocepacia</i> Strains Closely Related to the Highly Transmissible Epidemic ET12 Lineage. <i>Frontiers in Microbiology</i> , 2018, 9, 383.	1.5	16
1673	Metabolic and Evolutionary Insights in the Transformation of Diphenylamine by a <i>Pseudomonas putida</i> Strain Unravalled by Genomic, Proteomic, and Transcription Analysis. <i>Frontiers in Microbiology</i> , 2018, 9, 676.	1.5	4
1674	Evolutionary History of Bacteriophages in the Genus <i>Paraburkholderia</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 835.	1.5	13
1675	The invasive MED/Q <i>Bemisia tabaci</i> genome: a tale of gene loss and gene gain. <i>BMC Genomics</i> , 2018, 19, 68.	1.2	41
1676	Assembly of the <i>Boechera retrofracta</i> Genome and Evolutionary Analysis of Apomixis-Associated Genes. <i>Genes</i> , 2018, 9, 185.	1.0	24
1677	Genome Sequence of the Freshwater Yangtze Finless Porpoise. <i>Genes</i> , 2018, 9, 213.	1.0	16
1679	Hidden diversity in forest soils: Characterization and comparison of terrestrial flatworms' communities in two national parks in Spain. <i>Ecology and Evolution</i> , 2018, 8, 7386-7400.	0.8	2
1680	Phylogeny of the <i>Inula</i> group (Asteraceae: Inuleae): Evidence from nuclear and plastid genomes and a recircumscription of <i>Pentanema</i> . <i>Taxon</i> , 2018, 67, 149-164.	0.4	33
1681	Microbial Diversity and Toxin Risk in Tropical Freshwater Reservoirs of Cape Verde. <i>Toxins</i> , 2018, 10, 186.	1.5	8
1682	Cytomegaloviruses in a Community of Wild Nonhuman Primates in Taï National Park, Côte d'Ivoire. <i>Viruses</i> , 2018, 10, 11.	1.5	13
1683	Sequencing of two mitochondrial genomes of endangered form of the Sevan trout <i>Salmo ischchan aestivalis</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 469-471.	0.2	2

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1684	Convergent evolution of unusual complex I homologs with increased proton pumping capacity: energetic and ecological implications. <i>ISME Journal</i> , 2018, 12, 2668-2680.	4.4	33
1685	The genome assembly of the fungal pathogen <i>Pyrenochaeta lycopersici</i> from Single-Molecule Real-Time sequencing sheds new light on its biological complexity. <i>PLoS ONE</i> , 2018, 13, e0200217.	1.1	19
1686	Inferring Ancient Relationships with Genomic Data: A Commentary on Current Practices. <i>Integrative and Comparative Biology</i> , 2018, 58, 623-639.	0.9	14
1687	Phylogenomic analysis on the exceptionally diverse fish clade Gobioidae (Actinopterygii: Gobiiformes) and data-filtering based on molecular clocklikeness. <i>Molecular Phylogenetics and Evolution</i> , 2018, 128, 192-202.	1.2	32
1688	<i>Madangella altirostris</i> , a new genus and species of palaemonid shrimps (Crustacea: Decapoda: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 58	0.2	1
1689	Comparative genomics of the miniature wasp and pest control agent <i>Trichogramma pretiosum</i> . <i>BMC Biology</i> , 2018, 16, 54.	1.7	57
1690	Complete mitochondrial genome of the first deep-sea spongicolid shrimp <i>Spongiocaris panglao</i> (Decapoda: Stenopodidea): Novel gene arrangement and the phylogenetic position and origin of Stenopodidea. <i>Gene</i> , 2018, 676, 123-138.	1.0	14
1691	Phylogeny and morphological evolution of the so-called bougainvilliids (Hydrozoa, Hydroidolina). <i>Zoologica Scripta</i> , 2018, 47, 608-622.	0.7	7
1692	The End of a 60-year Riddle: Identification and Genomic Characterization of an Iridovirus, the Causative Agent of White Fat Cell Disease in Zooplankton. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 1259-1272.	0.8	12
1693	Hemoparasites and immunological parameters in Snow Bunting (<i>Plectrophenax nivalis</i>) nestlings. <i>Polar Biology</i> , 2018, 41, 1855-1866.	0.5	12
1694	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
1695	Assessing phylogeny and historical biogeography of the largest genus of lichen-forming fungi, <i>Xanthoparmelia</i> (Parmeliaceae, Ascomycota). <i>Lichenologist</i> , 2018, 50, 299-312.	0.5	20
1696	Within-host speciation events in yoyo clams, obligate commensals with mantis shrimps, including one that involves a change in microhabitat and a loss of specialized traits. <i>Biological Journal of the Linnean Society</i> , 2018, 124, 504-517.	0.7	5
1697	Two complete mitochondrial genomes of extinct form of the Sevan trout <i>Salmo ischchan danilewskii</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 40-41.	0.2	5
1698	Expect the unexpected: a new large species of <i>Marionia</i> (Heterobranchia : Nudibranchia : Tritoniidae) from western Europe. <i>Invertebrate Systematics</i> , 2018, 32, 892.	0.5	5
1699	Identification of novel <i>Legionella</i> genes required for endosymbiosis in <i>Paramecium</i> based on comparative genome analysis with <i>Holospora</i> spp.. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	8
1700	A Phylogenomic and Molecular Markers Based Analysis of the Class Acidimicrobiia. <i>Frontiers in Microbiology</i> , 2018, 9, 987.	1.5	28
1701	Isolation of Jahanene and Jahanane, and Total Synthesis of the Jahanyne Family. <i>Journal of Organic Chemistry</i> , 2018, 83, 9592-9603.	1.7	12

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1702	Genetic Diversity among Isolates of <i>Phytophthora sojae</i> in Anhui Province of China based on ISSR-PCR Markers. <i>Journal of the American Society for Horticultural Science</i> , 2018, 143, 304-309.	0.5	4
1703	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
1704	Molecular Evolution and Phylogeny of <i>Leishmania</i> . , 2018, , 19-57.		4
1705	A new species of spotted leaf frog, genus <i>Phasmahyla</i> (Amphibia, Phyllomedusidae) from Southeast Brazil. <i>PeerJ</i> , 2018, 6, e4900.	0.9	7
1706	A Freeloader? The Highly Eroded Yet Large Genome of the <i>Serratia symbiotica</i> Symbiont of <i>Cinara strobi</i> . <i>Genome Biology and Evolution</i> , 2018, 10, 2178-2189.	1.1	29
1707	Evolutionary gain of red blood cells in a commensal bivalve (Galeommatoidae) as an adaptation to a hypoxic shrimp burrow. <i>Biological Journal of the Linnean Society</i> , 2018, 125, 368-376.	0.7	2
1708	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
1709	Biology and genome of a newly discovered sibling species of <i>Caenorhabditis elegans</i> . <i>Nature Communications</i> , 2018, 9, 3216.	5.8	102
1710	Phylogenetic analysis of the mitochondrial genomes in bees (Hymenoptera: Apoidea: Anthophila). <i>PLoS ONE</i> , 2018, 13, e0202187.	1.1	11
1711	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
1712	Lethal Respiratory Disease Associated with Human Rhinovirus A in Wild Chimpanzees, Uganda, 2013. <i>Emerging Infectious Diseases</i> , 2018, 24, 267-274.	2.0	80
1713	Unveiling the complete genome sequence of clorodendrum chlorotic spot virus, a putative dichorhavirus infecting ornamental plants. <i>Archives of Virology</i> , 2018, 163, 2519-2524.	0.9	15
1714	CDK-11-Cyclin L is required for gametogenesis and fertility in <i>C. elegans</i> . <i>Developmental Biology</i> , 2018, 441, 52-66.	0.9	2
1715	Phylogenetic conservatism of thermal traits explains dispersal limitation and genomic differentiation of <i>Streptomyces</i> sister-taxa. <i>ISME Journal</i> , 2018, 12, 2176-2186.	4.4	27
1716	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
1717	Generic delimitation in Apocynae (Apocynaceae). <i>Taxon</i> , 2018, 67, 341-358.	0.4	6
1718	First true brackish-water nudibranch mollusc provides new insights for phylogeny and biogeography and reveals paedomorphosis-driven evolution. <i>PLoS ONE</i> , 2018, 13, e0192177.	1.1	29
1719	Genomic insights into the broad antifungal activity, plant-probiotic properties, and their regulation, in <i>Pseudomonas donghuensis</i> strain SVBP6. <i>PLoS ONE</i> , 2018, 13, e0194088.	1.1	42

#	ARTICLE	IF	CITATIONS
1720	Harnessing the power of phylogenomics to disentangle the directionality and signatures of interkingdom host jumping in the parasitic fungal genus <i>Tolyposcladium</i> . <i>Mycologia</i> , 2018, 110, 104-117.	0.8	12
1721	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
1722	Ancient association of cyanobacterial multicellularity with the regulator HetR and an RGSGR pentapeptide-containing protein (PatX). <i>Molecular Microbiology</i> , 2018, 110, 931-954.	1.2	28
1723	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
1724	Insect Retroelements Provide Novel Insights into the Origin of Hepatitis B Viruses. <i>Molecular Biology and Evolution</i> , 2018, 35, 2254-2259.	3.5	13
1725	Molecular footprints of inshore aquatic adaptation in Indo-Pacific humpback dolphin (<i>Sousa</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 347	1.3	10
1726	According to mitochondrial DNA evidence, <i>Parascaris equorum</i> and <i>Parascaris univalens</i> may represent the same species. <i>Journal of Helminthology</i> , 2019, 93, 383-388.	0.4	17
1727	Multiple Sequence Alignment Averaging Improves Phylogeny Reconstruction. <i>Systematic Biology</i> , 2019, 68, 117-130.	2.7	24
1728	Evolution of MHC class I genes in Eurasian badgers, genus <i>Meles</i> (Carnivora, Mustelidae). <i>Heredity</i> , 2019, 122, 205-218.	1.2	9
1729	Tree Evaluation and Robustness Testing. , 2019, , 736-745.		0
1730	Morphological and molecular characterisation of <i>Spirinia antipodea</i> Leduc n. sp. (Nematoda:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 347	0.2	2
1731	A comprehensive molecular phylogeny of tiger beetles (Coleoptera, Carabidae, Cicindelinae). <i>Systematic Entomology</i> , 2019, 44, 305-321.	1.7	31
1732	Fragment of the aspartyl-tRNA synthetase applicable as a shared classification and phylogenetic marker in particular representatives of the order Lactobacillales. <i>Folia Microbiologica</i> , 2019, 64, 113-120.	1.1	5
1733	Phylogenetic systematics of <i>Mylabris</i> blister beetles (Coleoptera, Meloidae): a molecular assessment using species trees and total evidence. <i>Cladistics</i> , 2019, 35, 243-268.	1.5	19
1734	Morphological and molecular confirmation of the validity of <i>Trichuris rhinopittheroxella</i> in the endangered golden snub-nosed monkey (<i>Rhinopithecus roxellana</i>). <i>Journal of Helminthology</i> , 2019, 93, 601-607.	0.4	6
1735	Molecular evidence linking the larval and adult stages of <i>Mexiconema cichlasomae</i> (Dracunculoidea:) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 347	0.4	2
1736	Taxonomic revision of the biotechnologically important species <i>Penicillium oxalicum</i> with the description of two new species from acidic and saline soils. <i>Mycological Progress</i> , 2019, 18, 215-228.	0.5	11
1737	Phylogenetic relationships and biogeographic history of the Australian trapdoor spider genus <i>Conothele</i> (Araneae: Mygalomorphae: Halonoproctidae): diversification into arid habitats in an otherwise tropical radiation. <i>Invertebrate Systematics</i> , 2019, , .	0.5	10

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1738	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
1739	Evolution of the Cholesterol Biosynthesis Pathway in Animals. <i>Molecular Biology and Evolution</i> , 2019, 36, 2548-2556.	3.5	37
1740	Homoplasy 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
1741	Metagenomic insights into production of zero valent sulfur from dissimilatory sulfate reduction in a methanogenic bioreactor. <i>Bioresource Technology Reports</i> , 2019, 8, 100305.	1.5	6
1742	Molecular Systematics and Morphological Analyses of the Subgenus <i>Setihenricia</i> (Echinodermata: Asteroidea: <i>Henricia</i>) from Japan. <i>Species Diversity</i> , 2019, 24, 119-135.	0.1	3
1743	Prediction of the Spatial Origin of Puumala Virus Infections Using L Segment Sequences Derived from a Generic Screening PCR. <i>Viruses</i> , 2019, 11, 694.	1.5	5
1744	Characterization of the complete mitochondrial genome of the echinostome <i>Echinostoma miyagawai</i> and phylogenetic implications. <i>Parasitology Research</i> , 2019, 118, 3091-3097.	0.6	13
1745	Morphology and molecular phylogeny of four <i>Frontonia</i> species from Turkey (Protista, Ciliophora). <i>Zootaxa</i> , 2019, 4609, 548.	0.2	3
1746	<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
1747	Identification of Molecular Markers That Are Specific to the Class Thermoleophilia. <i>Frontiers in Microbiology</i> , 2019, 10, 1185.	1.5	36
1748	<i>Bradyrhizobium nanningense</i> sp. nov., <i>Bradyrhizobium guangzhouense</i> sp. nov. and <i>Bradyrhizobium zhanjiangense</i> sp. nov., isolated from effective nodules of peanut in Southeast China. <i>Systematic and Applied Microbiology</i> , 2019, 42, 126002.	1.2	53
1749	Cytomegalovirus distribution and evolution in hominines. <i>Virus Evolution</i> , 2019, 5, vez015.	2.2	26
1750	Phylogenetic Reconstruction and Divergence Time Estimation of <i>Blumea</i> DC. (Asteraceae: Inuleae) in China Based on nrDNA ITS and cpDNA trnL-F Sequences. <i>Plants</i> , 2019, 8, 210.	1.6	7
1751	Herbivore range expansion triggers adaptation in a subsequently-associated third trophic level species and shared microbial symbionts. <i>Scientific Reports</i> , 2019, 9, 10314.	1.6	4
1752	<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
1753	Clustered Core- and Pan-Genome Content on Rhodobacteraceae Chromosomes. <i>Genome Biology and Evolution</i> , 2019, 11, 2208-2217.	1.1	12
1754	Biochemical characterization and thermodynamic study of β -mannanase from <i>Enterobacter asburiae</i> . <i>Biocatalysis and Agricultural Biotechnology</i> , 2019, 20, 101211.	1.5	5
1755	Exploration of phylogeography of <i>Monacha cantiana</i> s.l. continues: the populations of the Apuan Alps (NW Tuscany, Italy) (Eupulmonata, Stylommatophora, Hygromiidae). <i>ZooKeys</i> , 2019, 814, 115-149.	0.5	5

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1756	A demonstration of unsupervised machine learning in species delimitation. <i>Molecular Phylogenetics and Evolution</i> , 2019, 139, 106562.	1.2	67
1757	Global distribution of mating types shows limited opportunities for mating across populations of fungi causing boxwood blight disease. <i>Fungal Genetics and Biology</i> , 2019, 131, 103246.	0.9	16
1758	Characterization of the complete mitochondrial genome of <i>Centrorhynchus milvus</i> (Acanthocephala: Tj ETQq0 0 0 rgBT /Overlock 10 TF	1.8	9
1759	Taxonomic assignment of uncultured prokaryotes with long range PCR targeting the spectinomycin operon. <i>Research in Microbiology</i> , 2019, 170, 280-287.	1.0	2
1760	A molecular phylogeny of the Indo-West Pacific species of <i>Haloa sensu lato</i> gastropods (Cephalaspidea: Haminoeidae): Tethyan vicariance, generic diversity, and ecological specialization. <i>Molecular Phylogenetics and Evolution</i> , 2019, 139, 106557.	1.2	19
1761	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
1762	Maize Carbohydrate Partitioning Defective33 Encodes an MCTP Protein and Functions in Sucrose Export from Leaves. <i>Molecular Plant</i> , 2019, 12, 1278-1293.	3.9	26
1763	Redescription of the western Balkan species <i>Xerocampylaea waldemari</i> and its phylogenetic relationships to other Urticicolini (Gastropoda: Hygromiidae). <i>Systematics and Biodiversity</i> , 2019, 17, 367-384.	0.5	3
1764	Developmental and Immune Role of a Novel Multiple Cysteine Cluster TLR From <i>Eisenia andrei</i> Earthworms. <i>Frontiers in Immunology</i> , 2019, 10, 1277.	2.2	22
1765	Microbial life cycles link global modularity in regulation to mosaic evolution. <i>Nature Ecology and Evolution</i> , 2019, 3, 1184-1196.	3.4	18
1766	The lichen symbiosis re-viewed through the genomes of <i>Cladonia grayi</i> and its algal partner <i>Asterochloris glomerata</i> . <i>BMC Genomics</i> , 2019, 20, 605.	1.2	98
1767	Evidence for selection events during domestication by extensive mitochondrial genome analysis between japonica and indica in cultivated rice. <i>Scientific Reports</i> , 2019, 9, 10846.	1.6	7
1768	The phylogenetic position of <i>Anacanthorus</i> (Monogenea, Dactylogyridae) parasitizing Brazilian serrasalmids (Characiformes). <i>Parasite</i> , 2019, 26, 44.	0.8	5
1769	Phenotypic and Genetic Variation of an Interspecific <i>Centaurium</i> Hybrid (Gentianaceae) and Its Parental Species. <i>Plants</i> , 2019, 8, 224.	1.6	4
1770	Ancient role of vasopressin/oxytocin-type neuropeptides as regulators of feeding revealed in an echinoderm. <i>BMC Biology</i> , 2019, 17, 60.	1.7	33
1771	The genome assembly and annotation of yellowhorn (<i>Xanthoceras sorbifolium</i> Bunge). <i>GigaScience</i> , 2019, 8, .	3.3	37
1772	Transcriptional and physiological responses to inorganic nutrition in a tropical Pacific strain of <i>Alexandrium minutum</i> : Implications for nutrient uptakes and assimilation. <i>Gene</i> , 2019, 711, 143950.	1.0	5
1773	Structural variation and phylogenetic analysis of the mating-type locus in the genus <i>Morchella</i> . <i>Mycologia</i> , 2019, 111, 551-562.	0.8	15

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1774	The Asianâ€Melanesian bambusicolous genus <i>Myriodiscus</i> is related to the genus <i>Tympanis</i> , the North Americanâ€European tree pathogen. <i>Forest Pathology</i> , 2019, 49, e12532.	0.5	2
1775	Pseudomolecule-level assembly of the Chinese oil tree yellowhorn (<i>Xanthoceras sorbifolium</i>) genome. <i>CigaScience</i> , 2019, 8, .	3.3	47
1776	<i>Mortierella oedorhiza</i> , a new species forming a dichotomously branched rhizoid at the sporangiophore base. <i>Mycoscience</i> , 2019, 60, 361-365.	0.3	5
1777	Evolutionary history of the human multigene families reveals widespread gene duplications throughout the history of animals. <i>BMC Evolutionary Biology</i> , 2019, 19, 128.	3.2	9
1778	Novel Victorivirus from a Pakistani Isolate of <i>Alternaria alternata</i> Lacking a Typical Translational Stop/Restart Sequence Signature. <i>Viruses</i> , 2019, 11, 577.	1.5	35
1779	A stigmatic gene confers interspecies incompatibility in the Brassicaceae. <i>Nature Plants</i> , 2019, 5, 731-741.	4.7	37
1780	Complete mitochondrial genome of the Blotched snake, <i>Elaphe sauromates</i> (Pallas, 1814). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 468-469.	0.2	2
1781	Relaxed Selection Limits Lifespan by Increasing Mutation Load. <i>Cell</i> , 2019, 178, 385-399.e20.	13.5	94
1782	Systematic revision of the <i>Tubifera casparyi</i> â€T <i>dictyoderma</i> complex: Resurrection of the genus <i>Siphoptychium</i> and introduction of the new genus <i>Thecotubifera</i> . <i>Mycologia</i> , 2019, 111, 981-997.	0.8	9
1783	The chromosome-scale reference genome of black pepper provides insight into piperine biosynthesis. <i>Nature Communications</i> , 2019, 10, 4702.	5.8	115
1784	Deciphering Ancestral Sex Chromosome Turnovers Based on Analysis of Male Mutation Bias. <i>Genome Biology and Evolution</i> , 2019, 11, 3054-3067.	1.1	9
1785	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
1786	Novel Lineages of Oxymonad Flagellates from the Termite <i>Porotermes adamsoni</i> (Stolotermitidae): the Genera <i>Oxynympha</i> and <i>Termitimonas</i> . <i>Protist</i> , 2019, 170, 125683.	0.6	5
1787	The complete mitochondrial genomes of two vent squat lobsters, <i>Munidopsis lauensis</i> and <i>M. Áverrilli</i> : Novel gene arrangements and phylogenetic implications. <i>Ecology and Evolution</i> , 2019, 9, 12390-12407.	0.8	16
1788	Description of <i>Echthrogaleus spinulus</i> n. sp. (Copepoda: Pandaridae) parasitic on a torpedo ray from the central Pacific Ocean utilising a morphological and molecular approach. <i>Systematic Parasitology</i> , 2019, 96, 777-788.	0.5	4
1789	Simultaneous Optimization for Ultrasound-Assisted Extraction and Antioxidant Activity of Flavonoids from <i>Sophora flavescens</i> Using Response Surface Methodology. <i>Molecules</i> , 2019, 24, 112.	1.7	36
1790	The PATRIC Bioinformatics Resource Center: expanding data and analysis capabilities. <i>Nucleic Acids Research</i> , 2020, 48, D606-D612.	6.5	552
1791	Novel Polyomaviruses in Mammals from Multiple Orders and Reassessment of Polyomavirus Evolution and Taxonomy. <i>Viruses</i> , 2019, 11, 930.	1.5	23

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1792	Comparative Genomic Analysis of the Biotechnological Potential of the Novel Species <i>Pseudomonas wadsworthii</i> CCOS 864T and <i>Pseudomonas reidholzensis</i> CCOS 865T. <i>Diversity</i> , 2019, 11, 204.	0.7	3
1794	The global diversity of <i>Haemonchus contortus</i> is shaped by human intervention and climate. <i>Nature Communications</i> , 2019, 10, 4811.	5.8	63
1795	Congruence of morphological and molecular phylogenies of the rove beetle subfamily Staphylininae (Coleoptera: Staphylinidae). <i>Scientific Reports</i> , 2019, 9, 15137.	1.6	11
1796	Effect of Seasonal Variation on Bacterial Inhabitants and Diversity in Drinking Water of an Office Building, Delhi. <i>Air, Soil and Water Research</i> , 2019, 12, 117862211988233.	1.2	6
1797	Positive Selection in <i>Bifidobacterium</i> Genes Drives Species-Specific Host-Bacteria Communication. <i>Frontiers in Microbiology</i> , 2019, 10, 2374.	1.5	5
1798	Freshwater mussels house a diverse mussel-associated leech assemblage. <i>Scientific Reports</i> , 2019, 9, 16449.	1.6	30
1799	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
1800	Identification of <i>Cryptosporidium viatorum</i> XVa subtype family in two wild rat species in China. <i>Parasites and Vectors</i> , 2019, 12, 502.	1.0	14
1801	The Complete Mitochondrial Genome of the Caecal Fluke of Poultry, <i>Postharmostomum commutatum</i> , as the First Representative from the Superfamily Brachylaimoidea. <i>Frontiers in Genetics</i> , 2019, 10, 1037.	1.1	13
1802	Evolutionary Conservation of the Orchid MYB Transcription Factors DIV, RAD, and DRIF. <i>Frontiers in Plant Science</i> , 2019, 10, 1359.	1.7	17
1803	The complete mitochondrial genome of <i>Gruberia lanceolata</i> (Gruber, 1884) Kahl, 1932 (Ciliophora: Heterotrichea). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3443-3445.	0.2	3
1804	191 Early weaning in pigs induces long-term alterations in intestinal nutrient transporter function and expression partially via beta adrenergic enteric neural receptors. <i>Journal of Animal Science</i> , 2019, 97, 112-113.	0.2	0
1805	Massive Gene Flux Drives Genome Diversity between Sympatric <i>Streptomyces</i> Conspecifics. <i>MBio</i> , 2019, 10, .	1.8	41
1806	Genomic Variation among Strains of <i>Crithidia bombi</i> and <i>C. expoeki</i> . <i>MSphere</i> , 2019, 4, .	1.3	7
1807	Cycad Coralloid Roots Contain Bacterial Communities Including Cyanobacteria and <i>Caulobacter</i> spp. That Encode Niche-Specific Biosynthetic Gene Clusters. <i>Genome Biology and Evolution</i> , 2019, 11, 319-334.	1.1	57
1808	Influence of forest type on dark-spored myxomycete community in subtropical forest soil, China. <i>Soil Biology and Biochemistry</i> , 2019, 138, 107606.	4.2	11
1809	A multigene and morphological analysis expands the diversity of the seabed shrimp <i>Xiphopenaeus</i> Smith, 1869 (Decapoda: Penaeidae), with descriptions of two new species. <i>Scientific Reports</i> , 2019, 9, 15281.	1.6	16
1810	New species of <i>Bannoa</i> described from the tropics and the first report of the genus in South America. <i>Mycologia</i> , 2019, 111, 953-964.	0.8	3

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1811	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
1812	Observations on Texas hypoxylons, including two new <i>Hypoxylon</i> species and widespread environmental isolates of the <i>H. croceum</i> complex identified by a polyphasic approach. <i>Mycologia</i> , 2019, 111, 832-856.	0.8	18
1813	Phylogenetic placement and new data on the morphology and ecology of <i>Calathella eruciformis</i> (Agaricales, Basidiomycota), a cyphelloid fungus new to Poland. <i>Plant and Fungal Systematics</i> , 2019, 64, 91-99.	0.7	0
1814	Complete mitochondrial genomes of <i>Bittacus strigosus</i> and <i>Panorpa debilis</i> and genomic comparisons of Mecoptera. <i>International Journal of Biological Macromolecules</i> , 2019, 140, 672-681.	3.6	12
1815	The complete mitochondrial genome of a whitefly (Hemiptera: Aleyrodidae) infesting <i>Glycine max</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2011-2012.	0.2	1
1816	Sequence capture phylogenomics of historical ethanol-preserved museum specimens: Unlocking the rest of the vault. <i>Molecular Ecology Resources</i> , 2019, 19, 1531-1544.	2.2	74
1817	Biochemical characterization of diterpene synthases of <i>Taiwania cryptomerioides</i> expands the known functional space of specialized diterpene metabolism in gymnosperms. <i>Plant Journal</i> , 2019, 100, 1254-1272.	2.8	12
1818	<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
1819	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
1820	A New Species Of <i>Ascarophis</i> (Nematoda: Cystidicolidae) Parasitizing <i>Clinocottus analis</i> (Pisces:) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 182 T	0.3	3
1821	The structure of bactofilin filaments reveals their mode of membrane binding and lack of polarity. <i>Nature Microbiology</i> , 2019, 4, 2357-2368.	5.9	30
1822	<p>Worm-riding clam: description of <i>Montacutona sigalionidcola</i> sp. nov. (Bivalvia: Heterodonta: Galeommatidae) from Japan and its phylogenetic position.</p> <i>Zootaxa</i> , 2019, 4652, 473-486.	0.2	0
1823	The millipede genus <i>Antichiropus</i> (Diplopoda: Polydesmida: Paradoxosomatidae), part 3: species of the Pilbara bioregion of Western Australia. <i>Zootaxa</i> , 2019, 4617, zootaxa.4617.1.1.	0.2	3
1824	<p><i>Cinetorhynchus gabonensis</i>, a new species of hinge-beak shrimp (Crustacea: Decapoda: Rhynchocinetidae) from the eastern Atlantic.</p> <i>Zootaxa</i> , 2019, 4664, 191-205.	0.2	1
1825	The complete mitochondrial genome of <i>Calyptogena marissinica</i> (Heterodonta: Veneroida:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 182 T	1.1	26
1826	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
1827	A shared core microbiome in soda lakes separated by large distances. <i>Nature Communications</i> , 2019, 10, 4230.	5.8	75
1828	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

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1829	A chromosome-level genome assembly of <i>Cydia pomonella</i> provides insights into chemical ecology and insecticide resistance. <i>Nature Communications</i> , 2019, 10, 4237.	5.8	102
1830	Open-holed trapdoor spiders of the genus <i>Teyl</i> (Mygalomorphae: Nemesiidae: Anamini) from Western Australia's Pilbara bioregion: a new species and expanded phylogenetic assessment. <i>Zootaxa</i> , 2019, 4674, zootaxa.4674.3.3.	0.2	5
1831	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
1832	Phylogenetic Analyses of Some <i>Melanoleuca</i> Species (Agaricales, Tricholomataceae) in Northern China, With Descriptions of Two New Species and the Identification of Seven Species as a First Record. <i>Frontiers in Microbiology</i> , 2019, 10, 2167.	1.5	9
1833	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
1834	<i>Megalaria yunnanensis</i> sp. nov. from Yunnan, China. <i>Mycotaxon</i> , 2019, 134, 289-294.	0.1	1
1835	Resolving Phylogenetic Relationships within Passeriformes Based on Mitochondrial Genes and Inferring the Evolution of Their Mitogenomes in Terms of Duplications. <i>Genome Biology and Evolution</i> , 2019, 11, 2824-2849.	1.1	32
1836	Two new brackish-water species of <i>Pogaina</i> (Rhabdocoela: Tj ETQq1 1 0.784314 rgBT / Overlock 10 Tf 50 462	0.2	0
1837	New species, diversity, systematics, and conservation assessment of the Puppet Toads of Sumatra (Anura: Bufonidae: <i>Sigalegalephrynus</i>). <i>Zootaxa</i> , 2019, 4679, zootaxa.4679.2.9.	0.2	6
1838	Metagenomic Signatures of Gut Infections Caused by Different <i>Escherichia coli</i> Pathotypes. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	33
1839	Effects of Habitat Partitioning on the Distribution of Bacterioplankton in Deep Lakes. <i>Frontiers in Microbiology</i> , 2019, 10, 2257.	1.5	26
1840	Isolation and Total Synthesis of Mabuniamide, a Lipopeptide from an <i>Okeania</i> sp. Marine Cyanobacterium. <i>Journal of Natural Products</i> , 2019, 82, 2907-2915.	1.5	13
1841	Genomes of Three Closely Related Caribbean Amazons Provide Insight for Species History and Conservation. <i>Genes</i> , 2019, 10, 54.	1.0	8
1842	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
1843	Endemic, endangered and evolutionarily significant: cryptic lineages in Seychelles' frogs (Anura: Tj ETQq0 0 0 rgBT / Overlock 10 Tf 5	0.7	11
1844	The genome of broomcorn millet. <i>Nature Communications</i> , 2019, 10, 436.	5.8	130
1845	Repeated Evolution of Asexuality Involves Convergent Gene Expression Changes. <i>Molecular Biology and Evolution</i> , 2019, 36, 350-364.	3.5	26
1846	First record of <i>Aphanius almiriensis</i> from Italy and notes on the distribution of <i>Aphanius fasciatus</i> (Teleostei: Aphaniidae). <i>Journal of Applied Ichthyology</i> , 2019, 35, 541-550.	0.3	5

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1847	Present status and future of boletoid fungi (Boletaceae) on the island of Cyprus: Cryptic and threatened diversity unravelled by ten-year study. <i>Fungal Ecology</i> , 2019, 41, 65-81.	0.7	11
1848	A phylogeny of Xanthopygina (Insecta, Coleoptera) reveals major lineages and the origin of myrmecophily. <i>Zoologica Scripta</i> , 2019, 48, 494-506.	0.7	10
1849	<i>Stenotrophomonas maltophilia</i> Differential Gene Expression in Synthetic Cystic Fibrosis Sputum Reveals Shared and Cystic Fibrosis Strain-Specific Responses to the Sputum Environment. <i>Journal of Bacteriology</i> , 2019, 201, .	1.0	8
1850	Two novel fungal negative-strand RNA viruses related to mymonaviruses and phenuiviruses in the shiitake mushroom (<i>Lentinula edodes</i>). <i>Virology</i> , 2019, 533, 125-136.	1.1	72
1851	Arsenite Oxidation by a Newly Isolated Betaproteobacterium Possessing arx Genes and Diversity of the arx Gene Cluster in Bacterial Genomes. <i>Frontiers in Microbiology</i> , 2019, 10, 1210.	1.5	11
1852	Mitochondrial Architecture Rearrangements Produce Asymmetrical Nonadaptive Mutational Pressures That Subvert the Phylogenetic Reconstruction in Isopoda. <i>Genome Biology and Evolution</i> , 2019, 11, 1797-1812.	1.1	31
1853	Genome of a Member of the Candidate Archaeal Phylum Verstraetearchaeota from a Subsurface Thermal Aquifer Revealed Pathways of Methyl-Reducing Methanogenesis and Fermentative Metabolism. <i>Microbiology</i> , 2019, 88, 316-323.	0.5	6
1854	Total evidence approach reveals an extinct lineage of Paederinae rove beetles from Cretaceous Burmese amber. <i>Palaeontology</i> , 2019, 62, 935-949.	1.0	12
1855	Diet assessment of two land planarian species using high-throughput sequencing data. <i>Scientific Reports</i> , 2019, 9, 8679.	1.6	5
1856	Molecular evidence for resurrection of <i>Plesiochorus elongatus</i> (Digenea: Gorgoderidae): An urinary bladder parasite of sea turtles. <i>Parasitology International</i> , 2019, 71, 180-185.	0.6	3
1857	What determines host specificity in hyperspecialized plant parasitic nematodes?. <i>BMC Genomics</i> , 2019, 20, 457.	1.2	11
1858	Genomic Evidence of Recombination in the Basidiomycete <i>Walleimia mellicola</i> . <i>Genes</i> , 2019, 10, 427.	1.0	14
1859	Lignocellulose degradation in isopods: new insights into the adaptation to terrestrial life. <i>BMC Genomics</i> , 2019, 20, 462.	1.2	22
1860	A multigene phylogeny toward a new phylogenetic classification of Leotiomyces. <i>IMA Fungus</i> , 2019, 10, 1.	1.7	140
1862	Characterization of the complete mitochondrial genome of <i>Sphaerirostris picae</i> (Rudolphi, 1819) (Acanthocephala: Centrorhynchidae), representative of the genus <i>Sphaerirostris</i> . <i>Parasitology Research</i> , 2019, 118, 2213-2221.	0.6	9
1863	Going Deeper into High and Low Phylogenetic Relationships of Protura. <i>Genes</i> , 2019, 10, 292.	1.0	5
1864	Complete mitochondrial genome of <i>Ophichthus brevicaudatus</i> reveals novel gene order and phylogenetic relationships of Anguilliformes. <i>International Journal of Biological Macromolecules</i> , 2019, 135, 609-618.	3.6	20
1865	The pH sensing receptor AopalH plays important roles in the nematophagous fungus <i>Arthrobotrys oligospora</i> . <i>Fungal Biology</i> , 2019, 123, 547-554.	1.1	15

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1866	Evolution and functional differentiation of recently diverged phytochelatin synthase genes from <i>Arundo donax</i> L.. <i>Journal of Experimental Botany</i> , 2019, 70, 5391-5405.	2.4	15
1867	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
1868	Characterization of the complete mitochondrial genome of <i>Uvitellina</i> sp., representative of the family Cyclocoelidae and phylogenetic implications. <i>Parasitology Research</i> , 2019, 118, 2203-2211.	0.6	14
1869	A homolog of <i>Arabidopsis</i> SDP1 lipase in <i>Nannochloropsis</i> is involved in degradation of de novo-synthesized triacylglycerols in the endoplasmic reticulum. <i>Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids</i> , 2019, 1864, 1185-1193.	1.2	20
1870	An emerging new fowl adenovirus genotype. <i>Heliyon</i> , 2019, 5, e01732.	1.4	38
1871	Dynamism in plastome structure observed across the phylogenetic tree of ferns. <i>Botanical Journal of the Linnean Society</i> , 2019, 190, 229-241.	0.8	15
1872	Genomic erosion and extensive horizontal gene transfer in gut-associated <i>Acetobacteraceae</i> . <i>BMC Genomics</i> , 2019, 20, 472.	1.2	32
1873	Phylogenetic and distributional data on boletoid fungi (<i>Boletaceae</i>) in Cyprus and description of a new sampling methodology. <i>Data in Brief</i> , 2019, 25, 104115.	0.5	0
1874	Evolution and comparative genomics of the most common <i>Trichoderma</i> species. <i>BMC Genomics</i> , 2019, 20, 485.	1.2	181
1875	Too hot to handle: Cenozoic aridification drives multiple independent incursions of <i>Schizomida</i> (<i>Hubbardiidae</i>) into hypogean environments. <i>Molecular Phylogenetics and Evolution</i> , 2019, 139, 106532.	1.2	19
1876	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
1877	Fifty <i>Aureobasidium pullulans</i> genomes reveal a recombining polyextremotolerant generalist. <i>Environmental Microbiology</i> , 2019, 21, 3638-3652.	1.8	39
1878	Comparative Functional and Phylogenomic Analyses of Host Association in the Remoras (<i>Echeneidae</i>), a Family of Hitchhiking Fishes. <i>Integrative Organismal Biology</i> , 2019, 1, obz007.	0.9	7
1879	Comparative analysis of mitochondrial DNA datasets indicates that <i>Toxascaris leonina</i> represents a species complex. <i>Parasites and Vectors</i> , 2019, 12, 194.	1.0	19
1880	Mitochondrial genomes of three kissing bugs (<i>Reduviidae: Triatominae</i>) and their phylogenetic implications. <i>International Journal of Biological Macromolecules</i> , 2019, 134, 36-42.	3.6	19
1881	Resistance Gene-Directed Genome Mining of 50 <i>Aspergillus</i> Species. <i>MSystems</i> , 2019, 4, .	1.7	29
1882	Insights into the phylogeny of Hemiptera from increased mitogenomic taxon sampling. <i>Molecular Phylogenetics and Evolution</i> , 2019, 137, 236-249.	1.2	59
1883	Consensus sequence design as a general strategy to create hyperstable, biologically active proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 11275-11284.	3.3	105

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1884	Genome and Ontogenetic-Based Transcriptomic Analyses of the Flesh Fly, <i>Sarcophaga bullata</i> . <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1313-1320.	0.8	11
1885	Genomic analyses of aminoacyl tRNA synthetases from human-infecting helminths. <i>BMC Genomics</i> , 2019, 20, 333.	1.2	1
1886	Baltic amber Staphylinini (Coleoptera: Staphylinidae: Staphylininae): a rove beetle fauna on the eve of our modern climate. <i>Zoological Journal of the Linnean Society</i> , 2019, 187, 166-197.	1.0	30
1887	Thermo and alkali stable β -mannanase: Characterization and application for removal of food (mannans) Tj ETQq1 1,0,784314 rgBT /Overlock 10 Tf 50 267	3.6	25
1888	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
1889	Elucidating the evolution and diversity of Uroglena-like colonial flagellates (Chrysophyceae): polyphyletic origin of the morphotype. <i>European Journal of Phycology</i> , 2019, 54, 404-416.	0.9	10
1890	What lies beneath? Molecular evolution during the radiation of caecilian amphibians. <i>BMC Genomics</i> , 2019, 20, 354.	1.2	7
1891	The GMC superfamily of oxidoreductases revisited: analysis and evolution of fungal GMC oxidoreductases. <i>Biotechnology for Biofuels</i> , 2019, 12, 118.	6.2	84
1892	De novo assembly of the Indian blue peacock (<i>Pavo cristatus</i>) genome using Oxford Nanopore technology and Illumina sequencing. <i>GigaScience</i> , 2019, 8, .	3.3	25
1893	The Complete Chloroplast Genome of <i>Euphrasia regelii</i> , Pseudogenization of <i>ndh</i> Genes and the Phylogenetic Relationships Within Orobanchaceae. <i>Frontiers in Genetics</i> , 2019, 10, 444.	1.1	31
1894	What is really out there? Review of the genus <i>Okenia</i> Menke, 1830 (Nudibranchia: Goniadorididae) in the Mediterranean Sea with description of two new species. <i>PLoS ONE</i> , 2019, 14, e0215037.	1.1	19
1895	An integrative assessment of the diversity, phylogeny, distribution, and conservation of the terrestrial reptiles (Sauropsida, Squamata) of the United Arab Emirates. <i>PLoS ONE</i> , 2019, 14, e0216273.	1.1	16
1896	Characterization of the complete mitochondrial genome of <i>Plagiorchis maculosus</i> (Digenea), Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 267 International, 2019, 71, 99-105.	0.6	24
1897	The Blue-Light Photoreceptor <i>Sfwc-1</i> Gene Regulates the Phototropic Response and Fruiting-Body Development in the Homothallic Ascomycete <i>Sordaria fimicola</i> . <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	11
1898	Can Sequence Phylogenies Safely Infer the Origin of the Global Virome?. <i>MBio</i> , 2019, 10, .	1.8	37
1899	A comparative study on growth and degradation behavior of <i>C. pyrenoidosa</i> on synthetic phenol and phenolic wastewater of a coal gasification plant. <i>Journal of Environmental Chemical Engineering</i> , 2019, 7, 103079.	3.3	31
1900	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
1901	Complete mitochondrial genome of the four-lined snake, <i>Elaphe quatuorlineata</i> (Bonnaterre, 1790). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 897-898.	0.2	3

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1902	Two new and one known deep-sea Comesomatidae Filipjev, 1918 species (Nematoda: Araeolaimida) from New Zealand's continental margin. <i>Marine Biodiversity</i> , 2019, 49, 1931-1949.	0.3	3
1903	A natural antisense transcript of the <i>fem-1</i> gene was found expressed in female gonads during the characterization, expression profile, and cellular localization of the <i>fem-1</i> gene in Pacific white shrimp <i>Penaeus vannamei</i> . <i>Gene</i> , 2019, 706, 19-31.	1.0	19
1904	<i>Cheilolejeunea morgani</i> Bever. & Glenn (Lejeuneaceae, Marchantiopsida), a newly described species from lowland indigenous forest sites in New Zealand. <i>Journal of Bryology</i> , 2019, 41, 157-165.	0.4	1
1905	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
1906	Adrift across tectonic plates: molecular phylogenetics supports the ancient Laurasian origin of old limnic crangonyctid amphipods. <i>Organisms Diversity and Evolution</i> , 2019, 19, 191-207.	0.7	50
1907	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
1908	Phylogenetic and morphological analyses of species of the Entolomataceae (Agaricales). <i>Trends in Microbiology</i> , 2019, 10, 502-511.	0.1	11
1909	Two new species of marine flatworm from southern China facilitate determination of the phylogenetic position of the genus <i>Nerpa</i> Marcus, 1948 and the histochemical structure of the nervous system in the genus <i>Paucumara</i> Sluys, 1989 (Platyhelminthes, Tricladida, Maricola). <i>Zootaxa</i> , 2019, 4568, 1-9.	0.2	4
1910	Complete genome sequence of a novel member of the family Potyviridae isolated from <i>Phellodendron amurense</i> Rupr. in Liaoning, China. <i>Archives of Virology</i> , 2019, 164, 1705-1709.	0.9	2
1911	Comparative study on <i>Cronobacter sakazakii</i> and <i>Pseudomonas otitidis</i> isolated from septic tank wastewater in microbial fuel cell for bioelectricity generation. <i>Fuel</i> , 2019, 248, 47-55.	3.4	40
1912	Megaphylogeny resolves global patterns of mushroom evolution. <i>Nature Ecology and Evolution</i> , 2019, 3, 668-678.	3.4	187
1913	Six Impossible Things before Breakfast: Assumptions, Models, and Belief in Molecular Dating. <i>Trends in Ecology and Evolution</i> , 2019, 34, 474-486.	4.2	57
1914	The evolution of functional complexity within the α -amylase gene family in land plants. <i>BMC Evolutionary Biology</i> , 2019, 19, 66.	3.2	47
1915	<i>Tricholomopsis badinensis</i> sp. nov. and <i>T. sulphureoides</i> two rare fungi of European old-growth forests. <i>Mycological Progress</i> , 2019, 18, 321-334.	0.5	7
1916	Ultra-Conserved Element Phylogenomics of New World <i>Ponera</i> (Hymenoptera: Formicidae) Illuminates the Origin and Phylogeographic History of the Endemic Exotic Ant <i>Ponera exotica</i> . <i>Insect Systematics and Diversity</i> , 2019, 3, .	0.7	19
1917	Taxonomic update of <i>Clitocybula</i> sensu lato with a new generic classification. <i>Fungal Biology</i> , 2019, 123, 431-447.	1.1	11
1918	Species variability in the response to elevated temperature of select corals in north-western Philippines. <i>Journal of the Marine Biological Association of the United Kingdom</i> , 2019, 99, 1273-1279.	0.4	9
1919	Towards a phylogenetic classification of the Myxomycetes. <i>Phytotaxa</i> , 2019, 399, 209.	0.1	61

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1920	Functional characterization of the cytochrome P450 monooxygenase CYP71AU87 indicates a role in marrubiin biosynthesis in the medicinal plant <i>Marrubium vulgare</i> . <i>BMC Plant Biology</i> , 2019, 19, 114.	1.6	14
1921	Subspecies Typing of <i>Streptococcus agalactiae</i> Based on Ribosomal Subunit Protein Mass Variation by MALDI-TOF MS. <i>Frontiers in Microbiology</i> , 2019, 10, 471.	1.5	17
1922	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
1923	Isolation and partial characterization of a new moderate thermophilic <i>Albidovulum</i> sp. SLM16 with transaminase activity from Deception Island, Antarctica. <i>Biological Research</i> , 2019, 52, 5.	1.5	8
1924	Incorporating alignment uncertainty into Felsenstein's phylogenetic bootstrap to improve its reliability. <i>Bioinformatics</i> , 2021, 37, 1506-1514.	1.8	7
1925	Ecomorphological convergence in <i>Eleutherodactylus</i> frogs: a case of replicate radiations in the Caribbean. <i>Ecology Letters</i> , 2019, 22, 884-893.	3.0	37
1926	Contrasting patterns of molecular evolution in metazoan germ line genes. <i>BMC Evolutionary Biology</i> , 2019, 19, 53.	3.2	8
1927	Comparative genomics and pathogenicity potential of members of the <i>Pseudomonas syringae</i> species complex on <i>Prunus</i> spp. <i>BMC Genomics</i> , 2019, 20, 172.	1.2	30
1928	Improved phylogeny of brown algae <i>Cystoseira</i> (Fucales) from the Atlantic-Mediterranean region based on mitochondrial sequences. <i>PLoS ONE</i> , 2019, 14, e0210143.	1.1	27
1929	Identification of evolutionarily conserved virulence factor by selective pressure analysis of <i>Streptococcus pneumoniae</i> . <i>Communications Biology</i> , 2019, 2, 96.	2.0	26
1930	A detection of benzimidazole resistance-associated SNPs in the isotype-1 β -tubulin gene in <i>Haemonchus contortus</i> from wild blue sheep (<i>Pseudois nayaur</i>) sympatric with sheep in Helan Mountains, China. <i>BMC Veterinary Research</i> , 2019, 15, 89.	0.7	5
1931	A new genus and two new species of freshwater mussels (Unionidae) from western Indochina. <i>Scientific Reports</i> , 2019, 9, 4106.	1.6	28
1932	Consistent bacterial selection by date palm root system across heterogeneous desert oasis agroecosystems. <i>Scientific Reports</i> , 2019, 9, 4033.	1.6	32
1933	Olfactory Proteins in <i>Timema</i> Stick Insects. <i>Frontiers in Ecology and Evolution</i> , 2019, 7, .	1.1	1
1934	A molecular phylogeny of the gastropod family Haminoeidae sensu lato (Heterobranchia): Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 182 Td (0.5	4
1935	A new continent in the geographic distribution of the genus <i>Oregoniplana</i> (Platyhelminthes): Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 182 Td (1.0	5
1936	Welcome back Janolidae and <i>Antiopella</i> : Improving the understanding of Janolidae and Madrellidae (Cladobranchia, Heterobranchia) with description of four new species. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2019, 57, 345-368.	0.6	5
1937	Independent origins of coastal colonization in the tribe Athetini (Coleoptera, Staphylinidae). <i>Zoologica Scripta</i> , 2019, 48, 337-348.	0.7	4

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1938	The Marine Mammal Class II Major Histocompatibility Complex Organization. <i>Frontiers in Immunology</i> , 2019, 10, 696.	2.2	18
1939	Complete plastome sequences of 14 African yam species (<i>Dioscorea</i> spp.). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 74-76.	0.2	4
1940	Diversity of phenotypically non-dermatophyte, non- <i>Aspergillus</i> filamentous fungi causing nail infections: importance of accurate identification and antifungal susceptibility testing. <i>Emerging Microbes and Infections</i> , 2019, 8, 531-541.	3.0	7
1941	Whole-Genome Comparisons Among the Genus <i>Shewanella</i> Reveal the Enrichment of Genes Encoding Ankyrin-Repeats Containing Proteins in Sponge-Associated Bacteria. <i>Frontiers in Microbiology</i> , 2019, 10, 5.	1.5	14
1942	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
1943	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
1944	GeM-Pro: a tool for genome functional mining and microbial profiling. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 3123-3134.	1.7	13
1945	Evolution of squat lobsters (Crustacea, Galatheaidea): mitogenomic data suggest an early divergent Porcellanidae. <i>Hydrobiologia</i> , 2019, 833, 173-184.	1.0	5
1946	The long journey of <i>Orthotrichum shevockii</i> (Orthotrichaceae, Bryopsida): From California to Macaronesia. <i>PLoS ONE</i> , 2019, 14, e0211017.	1.1	12
1947	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
1948	Contrasting Patterns of Rapid Molecular Evolution within the <i>p53</i> Network across Mammal and Sauropsid Lineages. <i>Genome Biology and Evolution</i> , 2019, 11, 629-643.	1.1	7
1949	Mitochondrial and nuclear ribosomal DNA dataset suggests that <i>Hepatiarius sudarikovi</i> Feizullaev, 1961 is a member of the genus <i>Opisthorchis</i> Blanchard, 1895 (Digenea: Opisthorchiidae). <i>Parasitology Research</i> , 2019, 118, 807-815.	0.6	6
1950	Phylomitogenomics reconfirm the phylogenetic position of the genus <i>Metaplex</i> inferred from the two grapsid crabs (Decapoda: Brachyura: Grapsoidea). <i>PLoS ONE</i> , 2019, 14, e0210763.	1.1	18
1951	Red And far€red regulation of filament movement correlates with the expression of phytochrome and <i>scp</i> genes in <i>Spirogyra varians</i> (<i>Zygnematales</i> , <i>Streptophyta</i>). <i>Journal of Phycology</i> , 2019, 55, 688-699.	1.0	10
1952	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
1953	Reproduction of contagious caprine pleuropneumonia reveals the ability of convalescent sera to reduce hydrogen peroxide production in vitro. <i>Veterinary Research</i> , 2019, 50, 10.	1.1	24
1954	Comparative limb bone scaling in turtles: Phylogenetic transitions with changes in functional demands?. <i>Journal of Morphology</i> , 2019, 280, 593-603.	0.6	2
1955	Higher-level molecular phylogeny of jumping plant lice (Hemiptera: Sternorrhyncha: Psylloidea). <i>Systematic Entomology</i> , 2019, 44, 638-651.	1.7	17

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1956	The evolution of gene regulatory networks controlling <i>Arabidopsis thaliana</i> L. trichome development. <i>BMC Plant Biology</i> , 2019, 19, 53.	1.6	40
1957	Wnt Signaling Pathway Linked to Intestinal Regeneration via Evolutionary Patterns and Gene Expression in the Sea Cucumber <i>Apostichopus japonicus</i> . <i>Frontiers in Genetics</i> , 2019, 10, 112.	1.1	27
1958	Viral metagenomics revealed novel betatorquevirus species in pediatric inpatients with encephalitis/meningoencephalitis from Ghana. <i>Scientific Reports</i> , 2019, 9, 2360.	1.6	29
1959	Cryptic diversity and dynamic chromosome evolution in Alpine scorpions (Euscorpidae: Euscorpius). <i>Molecular Phylogenetics and Evolution</i> , 2019, 134, 152-163.	1.2	26
1960	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
1961	Deep segregation in the open ocean: Macaronesia as an evolutionary hotspot for low dispersal marine invertebrates. <i>Molecular Ecology</i> , 2019, 28, 1784-1800.	2.0	20
1962	Phylogenetic Reclassification of Vertebrate Melatonin Receptors To Include Mel1d. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3225-3238.	0.8	20
1963	Comprehensive Analysis Reveals the Evolution and Pathogenicity of <i>Aeromonas</i> , Viewed from Both Single Isolated Species and Microbial Communities. <i>MSystems</i> , 2019, 4, .	1.7	36
1964	Aquatic Hemiptera in Southwest Cameroon: Biodiversity of Potential Reservoirs of <i>Mycobacterium ulcerans</i> and Multiple <i>Wolbachia</i> Sequence Types Revealed by Metagenomics. <i>Diversity</i> , 2019, 11, 225.	0.7	2
1965	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
1966	Morphological phylogeny of Megachilini and the evolution of leaf-cutter behavior in bees (Hymenoptera: Megachilidae). <i>Journal of Melittology</i> , 2019, , 1-123.	0.2	23
1967	Magnetosome Gene Duplication as an Important Driver in the Evolution of Magnetotaxis in the <i>Alphaproteobacteria</i> . <i>MSystems</i> , 2019, 4, .	1.7	16
1968	Characterization of the Complete Chloroplast Genome of <i>Acer truncatum</i> Bunge (Sapindales: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 2019, 2019, 1-13.	0.9	12
1969	A Structurally-Validated Multiple Sequence Alignment of 497 Human Protein Kinase Domains. <i>Scientific Reports</i> , 2019, 9, 19790.	1.6	79
1970	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
1971	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
1972	Unraveling the Genetic Structure of the Coconut Scale Insect Pest (<i>Aspidiotus rigidus</i> Reyne) Outbreak Populations in the Philippines. <i>Insects</i> , 2019, 10, 374.	1.0	6
1973	Draft genome sequences of five <i>Calonectria</i> species from <i>Eucalyptus</i> 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

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1974	Putative circumsporozoite protein (CSP) of <i>Plasmodium vivax</i> is considerably distinct from the well-known CSP and plays a role in the protein ubiquitination pathway. <i>Gene</i> : X, 2019, 4, 100024.	2.3	1
1975	Genetic evidence against monophyly of Oniscidea implies a need to revise scenarios for the origin of terrestrial isopods. <i>Scientific Reports</i> , 2019, 9, 18508.	1.6	33
1976	Two New Species of <i>Placolecis</i> (Lichenized Ascomycota) from China. <i>Mycobiology</i> , 2019, 47, 401-407.	0.6	1
1977	Diversity of <i>Tilletiopsis</i> -Like Fungi in Exobasidiomycetes (Ustilaginomycotina) and Description of Six Novel Species. <i>Frontiers in Microbiology</i> , 2019, 10, 2544.	1.5	13
1978	LMAP_S: Lightweight Multigene Alignment and Phylogeny eStimation. <i>BMC Bioinformatics</i> , 2019, 20, 739.	1.2	1
1979	Complex I and II Subunit Gene Duplications Provide Increased Fitness to Worms. <i>Frontiers in Genetics</i> , 2019, 10, 1043.	1.1	10
1980	Two new species of <i>Rhabdocoela</i> (Polycystididae) and <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 502 Td</i> (<i>Trigonostomidae</i>)	0.2	2
1981	Diversity and Evolution of Novel Invertebrate DNA Viruses Revealed by Meta-Transcriptomics. <i>Viruses</i> , 2019, 11, 1092.	1.5	16
1982	Population Genomics of an Obligately Halophilic Basidiomycete <i>Wallemia ichthyophaga</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 2019.	1.5	9
1983	Highly thermostable carboxylic acid reductases generated by ancestral sequence reconstruction. <i>Communications Biology</i> , 2019, 2, 429.	2.0	34
1984	Multidecade Mortality and a Homolog of Hepatitis C Virus in Bald Eagles (<i>Haliaeetus leucocephalus</i>), the National Bird of the USA. <i>Scientific Reports</i> , 2019, 9, 14953.	1.6	13
1985	Deep ocean seascape and <i>Pseudotanaidae</i> (Crustacea: Tanaidacea) diversity at the Clarion-Clipperton Fracture Zone. <i>Scientific Reports</i> , 2019, 9, 17305.	1.6	24
1986	The complete mitochondrial genome of <i>Harpago chiragra</i> and <i>Lambis lambis</i> (Gastropoda: <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 262 Td</i>)	1.6	8
1987	Variability of mitochondrial ORFans hints at possible differences in the system of doubly uniparental inheritance of mitochondria among families of freshwater mussels (Bivalvia: Unionida). <i>BMC Evolutionary Biology</i> , 2019, 19, 229.	3.2	18
1988	A genome-skimmed phylogeny of a widespread bryozoan family, Adeonidae. <i>BMC Evolutionary Biology</i> , 2019, 19, 235.	3.2	7
1989	<i>Leptolejeunea nigra</i> (<i>Lejeuneaceae</i>), a new species with brownish black ocelli based upon morphology and DNA sequences. <i>Phytotaxa</i> , 2019, 427, 31-42.	0.1	3
1990	Mitogenomics suggests a sister relationship of <i>Relicanthus daphneae</i> (Cnidaria: Anthozoa: <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 102 Td</i>)	1.6	11
1991	A new genus of Staphylinina and a review of major lineages (Staphylinidae: Staphylininae: Staphylinini). <i>Systematics and Biodiversity</i> , 2019, 17, 745-758.	0.5	9

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1992	The complete chloroplast genome sequence of the threatened <i>Cypripedium calceolus</i> (Orchidaceae). Mitochondrial DNA Part B: Resources, 2019, 4, 4220-4222.	0.2	3
1993	PhySpeTree: an automated pipeline for reconstructing phylogenetic species trees. BMC Evolutionary Biology, 2019, 19, 219.	3.2	3
1994	Gene Expression and Sequence Analysis of BADH1 Gene in CLSU Aromatic Rice (<i>Oryza Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 66</i>). Science and Vitaminology, 2019, 65, S196-S199.	0.2	6
1995	Integrative systematics and ecology of a new deep-sea family of tanaidacean crustaceans. Scientific Reports, 2019, 9, 18720.	1.6	13
1996	<p>Two new species of Calocybe (Lyophyllaceae) from northeast China</p>. Phytotaxa, 2019, 425, 219-232.	0.1	3
1997	Mitochondrial genomes of the early land plant lineage liverworts (Marchantiophyta): conserved genome structure, and ongoing low frequency recombination. BMC Genomics, 2019, 20, 953.	1.2	21
1999	Genomic insights into mite phylogeny, fitness, development, and reproduction. BMC Genomics, 2019, 20, 954.	1.2	25
2000	Multiple Origins and Specific Evolution of CRISPR/Cas9 Systems in Minimal Bacteria (Mollicutes). Frontiers in Microbiology, 2019, 10, 2701.	1.5	24
2001	Mitochondrial Genome Fragmentation Unites the Parasitic Lice of Eutherian Mammals. Systematic Biology, 2019, 68, 430-440.	2.7	84
2002	Bryozoan genera Fenestulina and Microporella no longer confamilial; multi-gene phylogeny supports separation. Zoological Journal of the Linnean Society, 2019, 186, 190-199.	1.0	13
2003	Integrative taxonomy reveals a new <i>Gammarus</i> species (Crustacea, Amphipoda) surviving in a previously unknown southeast European glacial refugium. Journal of Zoological Systematics and Evolutionary Research, 2019, 57, 272-297.	0.6	18
2004	<i>Laciniporus arabicus</i> gen. et sp. nov. (Dinophyceae, Peridinales), a new thecate, marine, sand-dwelling dinoflagellate from the northern Indian Ocean (Arabian Sea)¹. Journal of Phycology, 2019, 55, 84-103.	1.0	6
2005	Draft genome of the cotton aphid <i>Aphis gossypii</i> . Insect Biochemistry and Molecular Biology, 2019, 105, 25-32.	1.2	55
2006	Diverse RNA viruses of arthropod origin in the blood of fruit bats suggest a link between bat and arthropod viromes. Virology, 2019, 528, 64-72.	1.1	36
2007	A new surface gliding species of Chironomidae: An independent invasion of marine environments and its evolutionary implications. Zoologica Scripta, 2019, 48, 81-92.	0.7	9
2008	A member of the CONSTANS-Like protein family is a putative regulator of reactive oxygen species homeostasis and spaceflight physiological adaptation. AoB PLANTS, 2019, 11, ply075.	1.2	8
2009	Phylogenomics of Thecamoebida (Discosea, Amoebozoa) with the Description of <i>Stratorugosa tubuloviscum</i> gen. nov. sp. nov., a Freshwater Amoeba with a Perinuclear MTOC. Protist, 2019, 170, 8-20.	0.6	9
2010	The diversification of neopasiphaeine bees during the Cenozoic (Hymenoptera: Colletidae). Zoologica Scripta, 2019, 48, 226-242.	0.7	27

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2011	Contrasting patterns of coding and flanking region evolution in mammalian keratin associated protein-1 genes. <i>Molecular Phylogenetics and Evolution</i> , 2019, 133, 352-361.	1.2	5
2012	An interspecies malateâ€“pyruvate shuttle reconciles redox imbalance in an anaerobic microbial community. <i>ISME Journal</i> , 2019, 13, 1042-1055.	4.4	15
2013	The mitochondrial genome of the ciliate <i>Pseudourostyla cristata</i> (Ciliophora, Urostylida). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 66-67.	0.2	7
2014	A multilocus phylogenetic framework of the tribe Aeromachini (Lepidoptera: Hesperidae: Hesperinae), with implications for taxonomy and biogeography. <i>Systematic Entomology</i> , 2019, 44, 163-178.	1.7	18
2015	Convergent Evolution of the Army Ant Syndrome and Congruence in Big-Data Phylogenetics. <i>Systematic Biology</i> , 2019, 68, 642-656.	2.7	47
2016	Phylogenetic position of the parasitic nematode <i>Trophomera</i> (Nematoda, Benthimermithidae): A molecular analysis. <i>Molecular Phylogenetics and Evolution</i> , 2019, 132, 177-182.	1.2	10
2017	The Origin and Population History of the Endangered Golden Snub-Nosed Monkey (<i>Rhinopithecus</i>)	3.5	20
2018	New systematic position of <i>Itatingamyia</i> Albuquerque (Diptera, Muscidae) based on molecular evidence, and description of the female of <i>I. couriae</i> . <i>Revista Brasileira De Entomologia</i> , 2019, 63, 35-42.	0.1	3
2019	The first mitochondrial genome from Scopuridae (Insecta: Plecoptera) reveals structural features and phylogenetic implications. <i>International Journal of Biological Macromolecules</i> , 2019, 122, 893-902.	3.6	29
2020	Isolation and characterization of soil bacteria able to rapidly degrade the organophosphorus nematicide fosthiazate. <i>Letters in Applied Microbiology</i> , 2019, 68, 149-155.	1.0	11
2021	Molecular phylogeny of Caudofoveata (Mollusca) challenges traditional views. <i>Molecular Phylogenetics and Evolution</i> , 2019, 132, 138-150.	1.2	8
2022	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
2023	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
2024	Reorganising the order Bacillales through phylogenomics. <i>Systematic and Applied Microbiology</i> , 2019, 42, 178-189.	1.2	11
2025	<i>Hypomontagnella</i> (Hypoxylaceae): a new genus segregated from <i>Hypoxylon</i> by a polyphasic taxonomic approach. <i>Mycological Progress</i> , 2019, 18, 187-201.	0.5	38
2026	Unmasking Antarctic mollusc lineages: novel evidence from philinoid snails (Gastropoda:)	1.5	12
2027	A bacterial [2Fe 4S] ferredoxin as redox partner of the plastidic-type ferredoxin-NADP+ reductase from <i>Leptosira</i> interrogans. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2019, 1863, 651-660.	1.1	4
2028	Ion uptake pathways in European sea bass <i>Dicentrarchus labrax</i> . <i>Gene</i> , 2019, 692, 126-137.	1.0	24

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2029	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
2030	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
2031	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
2032	Combining transcriptomes and ultraconserved elements to illuminate the phylogeny of Apidae. <i>Molecular Phylogenetics and Evolution</i> , 2019, 130, 121-131.	1.2	127
2033	Isotope discrimination by form IC RubisCO from <i>Ralstonia eutropha</i> and <i>Rhodobacter sphaeroides</i> , metabolically versatile members of Proteobacteria™ from aquatic and soil habitats. <i>Environmental Microbiology</i> , 2019, 21, 72-80.	1.8	19
2034	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
2035	Insight into the evolution and functional characteristics of the pan-genome assembly from sesame landraces and modern cultivars. <i>Plant Biotechnology Journal</i> , 2019, 17, 881-892.	4.1	79
2036	Fall webworm genomes yield insights into rapid adaptation of invasive species. <i>Nature Ecology and Evolution</i> , 2019, 3, 105-115.	3.4	82
2037	<i>Lichinodium</i> is a new lichenized lineage in the Leotiomycetes. <i>Fungal Diversity</i> , 2019, 94, 23-39.	4.7	20
2038	Increased tolerance to organic xenobiotics following recent allopolyploidy in <i>Spartina</i> (Poaceae). <i>Plant Science</i> , 2019, 280, 143-154.	1.7	22
2039	Phylogeny of the family Cladoniaceae (Lecanoromycetes, Ascomycota) based on sequences of multiple loci. <i>Cladistics</i> , 2019, 35, 351-384.	1.5	29
2040	Mitogenomics Reveals a Novel Genetic Code in Hemichordata. <i>Genome Biology and Evolution</i> , 2019, 11, 29-40.	1.1	20
2041	Diversity in CO ₂ -Concentrating Mechanisms among Chemolithoautotrophs from the Genera <i>Hydrogenovibrio</i> , <i>Thiomicrothrix</i> , and <i>Thiomicrospira</i> , Ubiquitous in Sulfidic Habitats Worldwide. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	25
2042	IGFBP-rP1, a strongly conserved member of the androgenic hormone signalling pathway in Isopoda. <i>General and Comparative Endocrinology</i> , 2019, 272, 9-19.	0.8	4
2043	Enhancing Statistical Multiple Sequence Alignment and Tree Inference Using Structural Information. <i>Methods in Molecular Biology</i> , 2019, 1851, 183-214.	0.4	1
2044	Conservation of mitochondrial genome arrangements in brittle stars (Echinodermata, Ophiuroidea). <i>Molecular Phylogenetics and Evolution</i> , 2019, 130, 115-120.	1.2	18
2045	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
2046	The importance of integrative approaches in nematode taxonomy: the validity of <i>Parapharyngodon</i> and <i>Thelandros</i> as distinct genera. <i>Journal of Helminthology</i> , 2019, 93, 616-628.	0.4	7

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2047	High-Throughput Reconstruction of Ancestral Protein Sequence, Structure, and Molecular Function. <i>Methods in Molecular Biology</i> , 2019, 1851, 135-170.	0.4	15
2048	Diversity and Evolution of Sensor Histidine Kinases in Eukaryotes. <i>Genome Biology and Evolution</i> , 2019, 11, 86-108.	1.1	28
2049	Genetic diversity of MHC class II<i>DRB</i> alleles in the marbled polecat, <i>Vormela peregusna</i>, in Bulgaria. <i>Ethology Ecology and Evolution</i> , 2019, 31, 59-72.	0.6	2
2050	Genome analyses of uncultured TG2/ZB3 bacteria in "Margulisbacteria" specifically attached to ectosymbiotic spirochetes of protists in the termite gut. <i>ISME Journal</i> , 2019, 13, 455-467.	4.4	55
2051	Living with a giant parchment tube worm: a description of a new nudibranch species (Gastropoda: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.3	11
2052	A novel insect-infecting virga/nege-like virus group and its pervasive endogenization into insect genomes. <i>Virus Research</i> , 2019, 262, 37-47.	1.1	49
2053	Assessment of the genetic diversity of Argentinean isolates of <i>Beauveria bassiana</i> (Ascomycota: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.6	3
2054	Phylogeny and historical biogeography of Gondwanan mossbugs (Insecta: Hemiptera: Coleorrhyncha: Tj ETQq1 1 0.784314 rgBT /Ov	1.5	13
2055	Glutamine synthetase type I (glnAI) represents a rewarding molecular marker in the classification of bifidobacteria and related genera. <i>Folia Microbiologica</i> , 2020, 65, 143-151.	1.1	3
2056	Dates and rates in grape" plastomes: evolution in slow motion. <i>Current Genetics</i> , 2020, 66, 123-140.	0.8	10
2057	Whole genome sequencing and genome annotation of the wild edible mushroom, <i>Russula griseocarnosa</i> . <i>Genomics</i> , 2020, 112, 603-614.	1.3	30
2058	Molecular Phylogenetics of <i>Bradypus</i> (Three-Toed Sloth, Pilosa: Bradypodidae, Mammalia) and Phylogeography of <i>Bradypus variegatus</i> (Brown-Throated Three-Toed Sloth) with Mitochondrial Gene Sequences. <i>Journal of Mammalian Evolution</i> , 2020, 27, 461-482.	1.0	4
2059	Gliding Dragons and Flying Squirrels: Diversifying versus Stabilizing Selection on Morphology following the Evolution of an Innovation. <i>American Naturalist</i> , 2020, 195, E51-E66.	1.0	9
2060	Morphological and phylogenetical analysis reveals that a new tapeworm species (Cestoda: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	1.7	1
2061	Phylogeny, genetics, and the partial life cycle of <i>Oncomegas wageneri</i> in the Gulf of Mexico. <i>Environmental Epigenetics</i> , 2020, 66, 275-283.	0.9	4
2062	Serial horizontal transfer of vitamin-biosynthetic genes enables the establishment of new nutritional symbionts in aphids" di-symbiotic systems. <i>ISME Journal</i> , 2020, 14, 259-273.	4.4	79
2063	Sirt6 attenuates hypoxia-induced tubular epithelial cell injury via targeting G2/M phase arrest. <i>Journal of Cellular Physiology</i> , 2020, 235, 3463-3473.	2.0	21
2064	A chromosome-level genome assembly reveals the genetic basis of cold tolerance in a notorious rice insect pest, <i>Chilo suppressalis</i>. <i>Molecular Ecology Resources</i> , 2020, 20, 268-282.	2.2	51

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2065	PhyloSuite: An integrated and scalable desktop platform for streamlined molecular sequence data management and evolutionary phylogenetics studies. <i>Molecular Ecology Resources</i> , 2020, 20, 348-355.	2.2	1,605
2066	Multilocus data reveal deep phylogenetic relationships and intercontinental biogeography of the Eurasian-North American genus <i>Corylus</i> (Betulaceae). <i>Molecular Phylogenetics and Evolution</i> , 2020, 142, 106658.	1.2	13
2067	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
2068	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
2069	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
2070	Revisiting the phylogeny of Dipsacales: New insights from phylogenomic analyses of complete plastomic sequences. <i>Journal of Systematics and Evolution</i> , 2020, 58, 103-117.	1.6	30
2071	Mitochondrial genomes and 28S rDNA contradict the proposed obsolescence of the order Tetraonchidea (Platyhelminthes: Monogenea). <i>International Journal of Biological Macromolecules</i> , 2020, 143, 891-901.	3.6	5
2072	Mitochondrial genome evidence suggests <i>Cooperia</i> sp. from China may represent a distinct species from <i>Cooperia oncophora</i> from Australia. <i>Parasitology International</i> , 2020, 75, 102001.	0.6	3
2073	Resolving the genetic paradox of invasions: Preadapted genomes and postintroduction hybridization of bigheaded carps in the Mississippi River Basin. <i>Evolutionary Applications</i> , 2020, 13, 263-277.	1.5	20
2074	<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
2075	Frontline Science: Antagonism between regular and atypical Cxcr3 receptors regulates macrophage migration during infection and injury in zebrafish. <i>Journal of Leukocyte Biology</i> , 2020, 107, 185-203.	1.5	31
2076	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
2077	Rapid immobilization of viable <i>Bacillus pseudomycoloides</i> in polyvinyl alcohol/glutaraldehyde hydrogel for biological treatment of municipal wastewater. <i>Environmental Science and Pollution Research</i> , 2020, 27, 9167-9180.	2.7	32
2078	<i>Natonodosa speciosa</i> gen. et sp. nov. and rediscovery of <i>Poroisariopsis inornata</i> : neotropical anamorphic fungi in Xylariales. <i>Mycological Progress</i> , 2020, 19, 15-30.	0.5	6
2079	The complete chloroplast genome sequence of yellow mustard (<i>Sinapis alba</i> L.) and its phylogenetic relationship to other Brassicaceae species. <i>Gene</i> , 2020, 731, 144340.	1.0	43
2080	Molecular characterization and ornithine-urea cycle genes expression in air-breathing magur catfish (<i>Clarias magur</i>) during exposure to high external ammonia. <i>Genomics</i> , 2020, 112, 2247-2260.	1.3	12
2081	A new Southern Ocean species in the remarkable and rare amphipod family Podosiridae (Crustacea: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 190, 613-631.	1.0	3
2082	Evolution and molecular epidemiology of polyomaviruses. <i>Infection, Genetics and Evolution</i> , 2020, 79, 104150.	1.0	19

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2083	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
2084	Cophylogenetic relationships between <i>Dactylogyrus</i> (Monogenea) ectoparasites and endemic cyprinoids of the north-eastern European peri-Mediterranean region. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2020, 58, 1-21.	0.6	16
2085	New isolates of <i>Trichoderma</i> spp. as biocontrol and plant growth-promoting agents in the pathosystem <i>Pyrenophora teres</i> -barley in Argentina. <i>Biological Control</i> , 2020, 141, 104152.	1.4	29
2086	Breast milk-derived human milk oligosaccharides promote <i>Bifidobacterium</i> interactions within a single ecosystem. <i>ISME Journal</i> , 2020, 14, 635-648.	4.4	220
2087	Candidate foraging gene orthologs in a lower termite, <i>Reticulitermes flavipes</i> . <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2020, 334, 168-177.	0.6	4
2088	<i>Sarocladium</i> species associated with rice in Taiwan. <i>Mycological Progress</i> , 2020, 19, 67-80.	0.5	12
2089	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
2090	Characterization of the complete mitochondrial genome of <i>Cavisoma magnum</i> (Acanthocephala: Tj ETQq1 1 0.784314 rgBT /Over implications. <i>Infection, Genetics and Evolution</i> , 2020, 80, 104173.	1.0	7
2091	Ascidian caveolin induces membrane curvature and protects tissue integrity and morphology during embryogenesis. <i>FASEB Journal</i> , 2020, 34, 1345-1361.	0.2	23
2092	Molecular analysis of population and De Novo transcriptome sequencing of Thai medaka, <i>Oryzias minutillus</i> (Teleostei: Adrianichthyidae). <i>Heliyon</i> , 2020, 6, e03079.	1.4	1
2093	An overview of the Dactylosomatidae (Apicomplexa: Adeleorina: Dactylosomatidae), with the description of <i>Dactylosoma kermiti</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
2094	Molecular Phylogeny of Marine Gregarines (Apicomplexa) from the Sea of Japan and the Northwest Pacific Including the Description of Three Novel Species of <i>Selenidium</i> and <i>Trollidium akkeshiense</i> n. gen. n. sp.. <i>Protist</i> , 2020, 171, 125710.	0.6	8
2095	Phylogeny of <i>Diplazium</i> (Athriaceae) revisited: Resolving the backbone relationships based on plastid genomes and phylogenetic tree space analysis. <i>Molecular Phylogenetics and Evolution</i> , 2020, 143, 106699.	1.2	15
2096	Identification and molecular analysis of interaction sites in the MtSEO-F1 protein involved in forisome assembly. <i>International Journal of Biological Macromolecules</i> , 2020, 144, 603-614.	3.6	7
2097	Isolation and characterization of psychrophilic and psychrotolerant plant-growth promoting microorganisms from a high-altitude volcano crater in Mexico. <i>Microbiological Research</i> , 2020, 232, 126394.	2.5	49
2098	Integrative species delimitation of desmosomatid and nannoniscid isopods from the Kuril-Kamchatka trench, with description of a hadal species. <i>Progress in Oceanography</i> , 2020, 182, 102236.	1.5	15
2099	Evolutionary History of the Toll-Like Receptor Gene Family across Vertebrates. <i>Genome Biology and Evolution</i> , 2020, 12, 3615-3634.	1.1	74
2100	Two <i>Urosoma</i> species (Ciliophora, Hypotrichia): A multidisciplinary approach provides new insights into their ultrastructure and systematics. <i>European Journal of Protistology</i> , 2020, 72, 125661.	0.5	30

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2101	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
2102	Far away, so close! Integrative taxonomy reveals a new genus and species of land flatworm (Platyhelminthes: Geoplanidae) from southern South America. <i>Zoological Journal of the Linnean Society</i> , 2020, 189, 722-744.	1.0	8
2103	Complete mitochondrial genomes of two deep-sea pandalid shrimps, <i>Heterocarpus ensifer</i> and <i>Bitias brevis</i> : insights into the phylogenetic position of Pandalidae (Decapoda: Caridea). <i>Journal of Oceanology and Limnology</i> , 2020, 38, 816-825.	0.6	11
2104	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
2105	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
2106	Molecular phylogeny illuminates Amblyopinini (Coleoptera: Staphylinidae) rove beetles as a target for systematic and evolutionary research. <i>Systematic Entomology</i> , 2020, 45, 430-446.	1.7	9
2107	Evolutionary divergences mirror Pleistocene paleodrainages in a rapidly-evolving complex of oasis-dwelling jumping spiders (Salticidae, <i>Habronattus tarsalis</i>). <i>Molecular Phylogenetics and Evolution</i> , 2020, 144, 106696.	1.2	11
2108	Origin and Evolution of Carboxysome Positioning Systems in Cyanobacteria. <i>Molecular Biology and Evolution</i> , 2020, 37, 1434-1451.	3.5	60
2109	Novel hepac- and pegi-like viruses in native Australian wildlife and non-human primates. <i>Virus Evolution</i> , 2020, 6, veaa064.	2.2	21
2110	Blue genome: chromosome-scale genome reveals the evolutionary and molecular basis of indigo biosynthesis in <i>Strobilanthes cusia</i> . <i>Plant Journal</i> , 2020, 104, 864-879.	2.8	15
2111	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
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2114	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
2115	Mitogenomic architecture of the multivalent endemic black clam (<i>Villorita cyprinoides</i>) and its phylogenetic implications. <i>Scientific Reports</i> , 2020, 10, 15438.	1.6	2
2116	IMA Genome - F13. <i>IMA Fungus</i> , 2020, 11, 19.	1.7	13
2117	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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2128	Comparative genomics of rice false smut fungi <i>Ustilago indica</i> virens Uv-Gvt strain from India reveals genetic diversity and phylogenetic divergence. 3 Biotech, 2020, 10, 342.	1.1	10
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2134	Identification of Novel Astroviruses in the Gastrointestinal Tract of Domestic Cats. Viruses, 2020, 12, 1301.	1.5	8
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2136	Identification and Characterization of a Newly Isolated Chitinase-Producing Strain <i>Bacillus licheniformis</i> SSCL-10 for Chitin Degradation. Archaea, 2020, 2020, 1-9.	2.3	11

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2138	Genome Mining and Evaluation of the Biocontrol Potential of <i>Pseudomonas fluorescens</i> BRZ63, a New Endophyte of Oilseed Rape (<i>Brassica napus</i> L.) against Fungal Pathogens. <i>International Journal of Molecular Sciences</i> , 2020, 21, 8740.	1.8	37
2139	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
2140	<i>Lactarius brunneoaurantiacus</i> sp. nov. and <i>L. indoscrobiculatus</i> sp. nov. from India. <i>Nordic Journal of Botany</i> , 2020, 38, .	0.2	3
2141	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
2142	Multilocus Phylogeny Support the Nonbioluminescent Firefly <i>Chespirito</i> as a New Subfamily in the Lampyridae (Coleoptera: Elateroidea). <i>Insect Systematics and Diversity</i> , 2020, 4, .	0.7	16
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2147	Studies in <i>Gyromitra</i> I: the <i>Gyromitra gigas</i> species complex. <i>Mycological Progress</i> , 2020, 19, 1459-1473.	0.5	7
2148	Phylogenomic and Morphological Reevaluation of the Bee Tribes Biastini, Neolarrini, and Townsendiellini (Hymenoptera: Apidae) With Description of Three New Species of <i>Schwarzia</i> . <i>Insect Systematics and Diversity</i> , 2020, 4, .	0.7	9
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2150	The assessment of leading traits in the taxonomy of the <i>Bacillus cereus</i> group. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 2223-2242.	0.7	9
2151	Molecular Phylogenetic Analysis of 16S rRNA Sequences Identified Two Lineages of <i>Helicobacter pylori</i> Strains Detected from Different Regions in Sudan Suggestive of Differential Evolution. <i>International Journal of Microbiology</i> , 2020, 2020, 1-12.	0.9	11
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2153	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
2154	Anoxygenic photosynthesis and iron-sulfur metabolic potential of <i>Chlorobia</i> populations from seasonally anoxic Boreal Shield lakes. <i>ISME Journal</i> , 2020, 14, 2732-2747.	4.4	22

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2157	Genetic Diversity among Selected <i>Medicago sativa</i> Cultivars Using Inter-Retrotransposon-Amplified Polymorphism, Chloroplast DNA Barcodes and Morpho-Agronomic Trait Analyses. <i>Plants</i> , 2020, 9, 995.	1.6	11
2158	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
2159	Phylogenomic proof of Recurrent Demipolyploidization and Evolutionary Stalling of the "Triplod Bridge" in <i>Arundo</i> (Poaceae). <i>International Journal of Molecular Sciences</i> , 2020, 21, 5247.	1.8	5
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2161	<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
2162	Plastome Phylogenomic and Biogeographical Study on <i>Thuja</i> (<i>Cupressaceae</i>). <i>BioMed Research International</i> , 2020, 2020, 1-13.	0.9	5
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2164	Identification, molecular characterization and prevalence of a novel cytorhabdovirus infecting zucchini crops in Greece. <i>Virus Research</i> , 2020, 287, 198095.	1.1	7
2165	Plant growth promoting <i>Pseudomonas aeruginosa</i> from <i>Valeriana wallichii</i> displays antagonistic potential against three phytopathogenic fungi. <i>Molecular Biology Reports</i> , 2020, 47, 6015-6026.	1.0	43
2166	Systematic Redefinition of the <i>Hypotracha</i> (Alveolata, Ciliophora) Based on Combined Analyses of Morphological and Molecular Characters. <i>Protist</i> , 2020, 171, 125755.	0.6	25
2167	Characterization of the Complete Mitochondrial Genome of <i>Drabescus ineffectus</i> and <i>Roxasellana stellata</i> (Hemiptera: Cicadellidae: Deltocephalinae: Drabescini) and Their Phylogenetic Implications. <i>Insects</i> , 2020, 11, 534.	1.0	18
2168	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
2169	High altitude as a possible factor for dysbiosis of salivary microbiome in orthodontic patients. <i>Archives of Oral Biology</i> , 2020, 119, 104917.	0.8	3
2170	Chloroplast Genome Analysis of Two Medicinal <i>Coelogyne</i> spp. (<i>Orchidaceae</i>) Shed Light on the Genetic Information, Comparative Genomics, and Species Identification. <i>Plants</i> , 2020, 9, 1332.	1.6	7
2171	Genome biology of the paleotetraploid perennial biomass crop <i>Miscanthus</i> . <i>Nature Communications</i> , 2020, 11, 5442.	5.8	67
2172	Evolutionary genomics of mammalian lung cancer genes reveals signatures of positive selection in APC, RB1 and TP53. <i>Genomics</i> , 2020, 112, 4722-4731.	1.3	1

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2174	Carbapenems drive the collateral resistance to ceftaroline in cystic fibrosis patients with MRSA. <i>Communications Biology</i> , 2020, 3, 599.	2.0	9
2175	Chloroplast genome assembly of <i>Handroanthus impetiginosus</i> : comparative analysis and molecular evolution in Bignoniaceae. <i>Planta</i> , 2020, 252, 91.	1.6	24
2176	Formation and diversification of a paradigm biosynthetic gene cluster in plants. <i>Nature Communications</i> , 2020, 11, 5354.	5.8	50
2177	Reclassification of the Taxonomic Framework of Orders <i>Cellvibrionales</i> , <i>Oceanospirillales</i> , <i>Pseudomonadales</i> , and <i>Alteromonadales</i> in Class <i>Gammaproteobacteria</i> through Phylogenomic Tree Analysis. <i>MSystems</i> , 2020, 5, .	1.7	50
2178	The complete mitogenome and plastome of the haptophyte <i>Pavlova lutheri</i> NIVA-4/92. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2748-2749.	0.2	7
2179	Characterization and phylogenetic analysis of the mitochondrial genome of <i>Mileewa ponta</i> (Hemiptera: Cicadellidae: Mileewinae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2976-2977.	0.2	7
2180	<i>Jennwenomyces</i> , a new hyphomycete genus segregated from <i>Belemnospora</i> , producing versicolored phragmospores from percurrently extending conidiophores. <i>Mycological Progress</i> , 2020, 19, 869-883.	0.5	4
2181	<i>Farysia magdalena</i> sp. nov. and description of the anamorph of <i>Anthracoecystis heteropogoncola</i> from the Americas. <i>Mycological Progress</i> , 2020, 19, 921-934.	0.5	1
2182	Phylogenetic diversity of the lichenized algal genus <i>Trebouxia</i> (Trebouxiophyceae, Chlorophyta): a new lineage and novel insights from fungal-algal association patterns of Icelandic cetrarioid lichens (Parmeliaceae, Ascomycota). <i>Botanical Journal of the Linnean Society</i> , 2020, 194, 460-468.	0.8	17
2183	A first phylogenomic hypothesis for Eulophidae (Hymenoptera, Chalcidoidea). <i>Journal of Natural History</i> , 2020, 54, 597-609.	0.2	12
2184	Ancestral function of the phytochelatin synthase C-terminal domain in inhibition of heavy metal-mediated enzyme overactivation. <i>Journal of Experimental Botany</i> , 2020, 71, 6655-6669.	2.4	21
2185	Novel Gene Rearrangement and the Complete Mitochondrial Genome of <i>Cynoglossus monopus</i> : Insights into the Evolution of the Family Cynoglossidae (Pleuronectiformes). <i>International Journal of Molecular Sciences</i> , 2020, 21, 6895.	1.8	8
2186	Fragmented mitochondrial genomes evolved in opposite directions between closely related macaque louse <i>Pedicinus obtusus</i> and colobus louse <i>Pedicinus badii</i> . <i>Genomics</i> , 2020, 112, 4924-4933.	1.3	17
2187	Multiple DNA viruses identified in multimammate mouse (<i>Mastomys natalensis</i>) populations from across regions of sub-Saharan Africa. <i>Archives of Virology</i> , 2020, 165, 2291-2299.	0.9	3
2188	Mass mortality in freshwater mussels (<i>Actinonaias pectorosa</i>) in the Clinch River, USA, linked to a novel densovirus. <i>Scientific Reports</i> , 2020, 10, 14498.	1.6	41
2189	Genome study of Thermococcales reveals extensive genetic diversity and genetic evidence of thermophilic adaption. <i>Environmental Microbiology</i> , 2021, 23, 3599-3613.	1.8	4
2190	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

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2192	Structure and Expression of Bud Dormancy-Associated MADS-Box Genes (DAM) in European Plum. <i>Frontiers in Plant Science</i> , 2020, 11, 1288.	1.7	26
2193	Improved reference genome of the arboviral vector <i>Aedes albopictus</i> . <i>Genome Biology</i> , 2020, 21, 215.	3.8	65
2194	Mitogenome of <i>Tolypocladium guangdongense</i> . <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 9295-9308.	1.7	6
2195	Rare/cryptic <i>Aspergillus</i> species infections and importance of antifungal susceptibility testing. <i>Mycoses</i> , 2020, 63, 1283-1298.	1.8	10
2196	Depicting the RNA Virome of Hematophagous Arthropods from Belgrade, Serbia. <i>Viruses</i> , 2020, 12, 975.	1.5	19
2197	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
2198	Feeding specialization and longer generation time are associated with relatively larger brains in bees. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20200762.	1.2	12
2199	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
2200	Phylogenetic Assignment of the Fungicolous <i>Hypoxyton invadens</i> (Ascomycota, Xylariales) and Investigation of its Secondary Metabolites. <i>Microorganisms</i> , 2020, 8, 1397.	1.6	9
2201	The mitogenome of <i>Mileewa margheritae</i> (Hemiptera: Cicadellidae: Mileewinae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 3163-3164.	0.2	4
2202	Characterization of Two Complete Mitochondrial Genomes of <i>Ledrinae</i> (Hemiptera: Cicadellidae) and Phylogenetic Analysis. <i>Insects</i> , 2020, 11, 609.	1.0	14
2203	Phylogenetic placement and lectotypification of <i>Pseudotryblidium neesii</i> (Helotiales, Tj ETQq0 0.0,rgBT /Overlock 10	0.9	1
2204	Two new species of the genus <i>Russula</i> from western Himalaya with morphological details and phylogenetic estimations. <i>Nova Hedwigia</i> , 2020, 111, 115-130.	0.2	12
2205	Insights into the Metabolism and Evolution of the Genus <i>Acidiphilium</i> , a Typical Acidophile in Acid Mine Drainage. <i>MSystems</i> , 2020, 5, .	1.7	31
2206	First freshwater mussel-associated piscicolid leech from East Asia. <i>Scientific Reports</i> , 2020, 10, 19854.	1.6	6
2207	A highly contiguous genome assembly of <i>Brassica nigra</i> (BB) and revised nomenclature for the pseudochromosomes. <i>BMC Genomics</i> , 2020, 21, 887.	1.2	26
2208	Expression of Piwi Genes during the Regeneration of <i>Lineus sanguineus</i> (Nemertea, Pilidiophora,) Tj ETQq1 1 0.784314 rgBT /Overlock 1	1.0	5

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2210	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
2211	Using target enrichment sequencing to study the higher-level phylogeny of the largest lichen-forming fungi family: Parmeliaceae (Ascomycota). <i>IMA Fungus</i> , 2020, 11, 27.	1.7	7
2212	Phylogenetics and taxonomy of Telimenaceae (Phyllachorales) from Central America. <i>Mycological Progress</i> , 2020, 19, 1587-1599.	0.5	3
2213	A chromosome-scale genome assembly of a diploid alfalfa, the progenitor of autotetraploid alfalfa. <i>Horticulture Research</i> , 2020, 7, 194.	2.9	25
2214	New view on the organization and evolution of Palaeognathae mitogenomes poses the question on the ancestral gene rearrangement in Aves. <i>BMC Genomics</i> , 2020, 21, 874.	1.2	14
2215	Plant TDP1 (Tyrosyl-DNA Phosphodiesterase 1): A Phylogenetic Perspective and Gene Expression Data Mining. <i>Genes</i> , 2020, 11, 1465.	1.0	2
2216	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
2217	Driven progressive evolution of genome sequence complexity in Cyanobacteria. <i>Scientific Reports</i> , 2020, 10, 19073.	1.6	7
2218	Integrative systematics reveals the new land-snail genus <i>Taphrenalla</i> (Eupulmonata: Ariophantidae) with a description of nine new species from Thailand. <i>Contributions To Zoology</i> , 2020, 90, 21-69.	0.2	13
2219	A synoptic review of the family Dendronotidae (Mollusca: Nudibranchia): a multilevel organismal diversity approach. <i>Contributions To Zoology</i> , 2020, 90, 93-153.	0.2	19
2220	Comparative Genomic Analysis Provides Insights into the Phylogeny, Resistome, Virulome, and Host Adaptation in the Genus <i>Ewingella</i> . <i>Pathogens</i> , 2020, 9, 330.	1.2	7
2221	Sequencing and Functional Annotation of the Whole Genome of <i>Shiraia bambusicola</i> . <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 23-35.	0.8	8
2222	Delineation of a Subgroup of the Genus <i>Paraburkholderia</i> , Including <i>P. Atterae</i> DSM 17804T, <i>P. Hospita</i> DSM 17164T, and Four Soil-Isolated Fungiphiles, Reveals Remarkable Genomic and Ecological Features—Proposal for the Definition of a <i>P. Hospita</i> Species Cluster. <i>Genome Biology and Evolution</i> , 2020, 12, 325-344.	1.1	12
2223	The challenge of Coccidae (Hemiptera: Coccoidea) mitochondrial genomes: The case of <i>Saissetia coffeae</i> with novel truncated tRNAs and gene rearrangements. <i>International Journal of Biological Macromolecules</i> , 2020, 158, 854-864.	3.6	17
2224	Phylogenetic tree building in the genomic age. <i>Nature Reviews Genetics</i> , 2020, 21, 428-444.	7.7	226
2225	Genome data of shrimp acute hepatopancreatic necrosis disease causative <i>Vibrio parahaemolyticus</i> strains isolated from South Korea aquaculture farms. <i>Data in Brief</i> , 2020, 31, 105697.	0.5	2
2226	<i>Prosthenhystera gatti</i> n. sp. (Digenea: Callodistomidae), a gallbladder parasite of <i>Bryconamericus ika</i> a from the lower Iguazú River, described based on combined molecular and morphological evidence. <i>Journal of Helminthology</i> , 2020, 94, e151.	0.4	4

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2227	Precise phylogenetic analysis of microbial isolates and genomes from metagenomes using PhyloPhlAn 3.0. <i>Nature Communications</i> , 2020, 11, 2500.	5.8	368
2228	A PCR diagnostic assay for rapid detection of plant pathogenic pseudomonads. <i>Plant Pathology</i> , 2020, 69, 1311-1330.	1.2	6
2229	Parallel reductive genome evolution in <i>Desulfovibrio</i> ectosymbionts independently acquired by <i>Trichonympha</i> protists in the termite gut. <i>ISME Journal</i> , 2020, 14, 2288-2301.	4.4	10
2230	Coexpression Analysis Reveals Dynamic Modules Regulating the Growth and Development of Cirri in the Rattans (<i>Calamus simplicifolius</i> and <i>Daemonorops jenkinsiana</i>). <i>Frontiers in Genetics</i> , 2020, 11, 378.	1.1	4
2231	The Mitochondrial Genome of the Phytopathogenic Fungus <i>Bipolaris sorokiniana</i> and the Utility of Mitochondrial Genome to Infer Phylogeny of Dothideomycetes. <i>Frontiers in Microbiology</i> , 2020, 11, 863.	1.5	19
2232	The Protector within: Comparative Genomics of APSE Phages across Aphids Reveals Rampant Recombination and Diverse Toxin Arsenal. <i>Genome Biology and Evolution</i> , 2020, 12, 878-889.	1.1	22
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2240	<i>Leishmania</i> Encodes a Bacterium-like 2,4-Dienoyl-Coenzyme A Reductase That Is Required for Fatty Acid β -Oxidation and Intracellular Parasite Survival. <i>MBio</i> , 2020, 11, .	1.8	8
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2242	Mitochondrial DNA dataset suggest that the genus <i>Sphaerirostris</i> Golvan, 1956 is a synonym of the genus <i>Centrorhynchus</i> L��he, 1911. <i>Parasitology</i> , 2020, 147, 1149-1157.	0.7	8
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2247	Evolutionary analysis of genes coding for Cysteine-Rich Secretory Proteins (CRISPs) in mammals. <i>BMC Evolutionary Biology</i> , 2020, 20, 67.	3.2	7
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2253	<i>Streptococcus halichoeri</i> : Comparative Genomics of an Emerging Pathogen. <i>International Journal of Genomics</i> , 2020, 2020, 1-9.	0.8	7
2254	Estimating relative biomasses of organisms in microbiota using phylopeptidomics. <i>Microbiome</i> , 2020, 8, 30.	4.9	34
2255	Integrative description of two new <i>Cratena</i> species (Mollusca: Nudibranchia) from western India. <i>Zootaxa</i> , 2020, 4729, 359-370.	0.2	3
2256	Morphological Redescriptions and Molecular Phylogeny of Three <i>Stentor</i> Species (Ciliophora: Heterotrichea: Stentoridae) from Korea. <i>Zootaxa</i> , 2020, 4732, 435-452.	0.2	2
2257	Evolutionary divergence of function and expression of laccase genes in plants. <i>Journal of Genetics</i> , 2020, 99, 1.	0.4	21
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2284	The Afro-Oriental Genus <i>Yaepimus</i> Sasa et Suzuki (Diptera: Chironomidae: Chironomini): Phylogeny, New Species and Expanded Diagnoses. Diversity, 2020, 12, 31.	0.7	4
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2300	<i>Neofoleyellides boerewors</i> n. gen. n. sp. (Nematoda: Onchocercidae) parasitising common toads and mosquito vectors: morphology, life history, experimental transmission and host-vector interaction in situ. <i>International Journal for Parasitology</i> , 2020, 50, 177-194.	1.3	13
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2309	Identification of a Novel Papillomavirus Associated with Squamous Cell Carcinoma in a Domestic Cat. <i>Viruses</i> , 2020, 12, 124.	1.5	22
2310	The Genome of the Great Gerbil Reveals Species-Specific Duplication of an MHCII Gene. <i>Genome Biology and Evolution</i> , 2020, 12, 3832-3849.	1.1	5
2311	â€œLittle Red Jelliesâ€ in Monterey Bay, California (Cnidaria: Hydrozoa: Trachymedusae: <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 262 Td (</i>	1.2	6
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2320	Search for polyoma-, herpes-, and bornaviruses in squirrels of the family Sciuridae. <i>Virology Journal</i> , 2020, 17, 42.	1.4	11
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2322	Hayes Yard virus: a novel ephemerovirus isolated from a bull with severe clinical signs of bovine ephemeral fever is most closely related to Puchong virus. <i>Veterinary Research</i> , 2020, 51, 58.	1.1	5
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2324	Phylogenomic Species Delimitation, Taxonomy, and â€“Bird Guideâ€™ Identification for the Neotropical Ant Genus <i>Rasopone</i> (Hymenoptera: Formicidae). <i>Insect Systematics and Diversity</i> , 2020, 4, .	0.7	18
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2332	Identification and RNAi Profile of a Novel Iflavirus Infecting Senegalese <i>Aedes vexans arabiensis</i> Mosquitoes. <i>Viruses</i> , 2020, 12, 440.	1.5	16
2333	Molecular circumscription of new species of <i>Gyrocotyle</i> Diesing, 1850 (Cestoda) from deep-sea chimaeriform holocephalans in the North Atlantic. <i>Systematic Parasitology</i> , 2020, 97, 285-296.	0.5	2
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2336	First report of <i>Exserohilum</i> leaf spot: a unique halophilic pathogen in <i>Cucumis sativus</i> in the South Bengal area of India. <i>Australasian Plant Pathology</i> , 2020, 49, 257-266.	0.5	5
2337	Inter-individual variability in freshwater tolerance is related to transcript level differences in gill and posterior kidney of European sea bass. <i>Gene</i> , 2020, 741, 144547.	1.0	13
2338	A morphological and combined phylogenetic analysis of pirate spiders (Araneae, Mimetidae): evolutionary relationships, taxonomy and character evolution. <i>Invertebrate Systematics</i> , 2020, 34, 144.	0.5	9
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2342	Small and mighty: adaptation of superphylum Patescibacteria to groundwater environment drives their genome simplicity. <i>Microbiome</i> , 2020, 8, 51.	4.9	205
2343	Complete Mitogenomic Structure and Phylogenetic Implications of the Genus <i>Ostrinia</i> (Lepidoptera: Tj ETQq0 0 0 regBT /Overlock 10 Tf	1.0	20
2344	Characterization of the complete mitogenome of <i>Centrorhynchus clitorideus</i> (Meyer, 1931) (Palaeacanthocephala: Centrorhynchidae), the largest mitochondrial genome in Acanthocephala, and its phylogenetic implications. <i>Molecular and Biochemical Parasitology</i> , 2020, 237, 111274.	0.5	9
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2348	Phylogeny of Lithobiidae Newport, 1844, with emphasis on the megadiverse genus <i>Lithobius</i> Leach, 1814 (Myriapoda, Chilopoda). <i>Cladistics</i> , 2021, 37, 162-184.	1.5	5
2349	Do Alignment and Trimming Methods Matter for Phylogenomic (UCE) Analyses?. <i>Systematic Biology</i> , 2021, 70, 440-462.	2.7	30
2350	Lycopodium root meristem dynamics supports homology between shoots and roots in lycophytes. <i>New Phytologist</i> , 2021, 229, 460-468.	3.5	9
2351	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
2352	Evidence for the recognition of <i>Schoenus caespitans</i> as a separate species from <i>Schoenus apogon</i> . <i>New Zealand Journal of Botany</i> , 2021, 59, 217-228.	0.8	0

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2355	A chromosome-scale assembly of allotetraploid <i>Brassica juncea</i> (AABB) elucidates comparative architecture of the A and B genomes. <i>Plant Biotechnology Journal</i> , 2021, 19, 602-614.	4.1	62
2356	Evolution of coding sequence and gene expression of blowflies and botflies with contrasting feeding habits. <i>Genomics</i> , 2021, 113, 699-706.	1.3	3
2357	Mitogenomics of <i>Didelphis</i> (Mammalia; Didelphimorphia; Didelphidae) and insights into character evolution in the genus. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2021, 59, 498-509.	0.6	4
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2359	Assessing the Diversity of Benthic Sulfate-Reducing Microorganisms in Northwestern Gulf of Mexico by Illumina Sequencing of <i>dsrB</i> Gene. <i>Microbial Ecology</i> , 2021, 81, 908-921.	1.4	6
2360	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
2361	<i>Cryphonectria carpinicola</i> sp. nov. Associated with hornbeam decline in Europe. <i>Fungal Biology</i> , 2021, 125, 347-356.	1.1	8
2362	Exploring the impact of RNA editing on mitochondrial phylogenetic analyses in liverworts, an early land plant lineage. <i>Journal of Systematics and Evolution</i> , 2021, , .	1.6	6
2363	<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
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2365	How to Make a Rodent Giant: Genomic Basis and Tradeoffs of Gigantism in the Capybara, the World's Largest Rodent. <i>Molecular Biology and Evolution</i> , 2021, 38, 1715-1730.	3.5	16
2366	Genomic Analysis Enlightens Agaricales Lifestyle Evolution and Increasing Peroxidase Diversity. <i>Molecular Biology and Evolution</i> , 2021, 38, 1428-1446.	3.5	72
2367	Mitochondrial genes from 18 angiosperms fill sampling gaps for phylogenomic inferences of the early diversification of flowering plants. <i>Journal of Systematics and Evolution</i> , 2022, 60, 773-788.	1.6	16
2368	Total-evidence backbone phylogeny of Aleocharinae (Coleoptera: Staphylinidae). <i>Cladistics</i> , 2021, 37, 343-374.	1.5	9
2369	Phylogeny of <i>Orthotrichum</i> s.l. and <i>Ulota</i> s.l. (Orthotrichaceae, Bryophyta): Insights into stomatal evolution. <i>Journal of Systematics and Evolution</i> , 2022, 60, 876-900.	1.6	3
2370	Ionizing-radiation-resistant <i>Kocuria rhizophila</i> PT10 isolated from the Tunisian Sahara xerophyte <i>Panicum turgidum</i> : Polyphasic characterization and proteogenomic arsenal. <i>Genomics</i> , 2021, 113, 317-330.	1.3	7

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2372	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
2373	Colpodean ciliate phylogeny and reference alignments for phylogenetic placements. <i>European Journal of Protistology</i> , 2021, 77, 125747.	0.5	5
2374	A molecular phylogeny of historical and contemporary specimens of an understudied microinvertebrate group. <i>Ecology and Evolution</i> , 2021, 11, 309-320.	0.8	6
2375	Evolution of isoprene emission in Arecaceae (palms). <i>Evolutionary Applications</i> , 2021, 14, 902-914.	1.5	2
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2378	Phylogenomics of the lepidopteran endoparasitoid wasp subfamily Rogadinae (Hymenoptera: Tj ETQq1 1 0.784314, 1.7, 8	1.7	8
2379	A Total-Evidence Dated Phylogeny of Echinoidea Combining Phylogenomic and Paleontological Data. <i>Systematic Biology</i> , 2021, 70, 421-439.	2.7	33
2380	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
2381	Proteome specialization of anaerobic fungi during ruminal degradation of recalcitrant plant fiber. <i>ISME Journal</i> , 2021, 15, 421-434.	4.4	46
2382	Intracellular amorphous Ca-carbonate and magnetite biomineralization by a magnetotactic bacterium affiliated to the Alphaproteobacteria. <i>ISME Journal</i> , 2021, 15, 1-18.	4.4	52
2383	<i>Azolla</i> ferns testify: seed plants and ferns share a common ancestor for leucoanthocyanidin reductase enzymes. <i>New Phytologist</i> , 2021, 229, 1118-1132.	3.5	29
2385	Structural aspects of β -glucosidase of <i>Myceliophthora thermophila</i> (MtBgl3c) by homology modelling and molecular docking. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 5211-5228.	2.0	8
2386	Phylogenomics of the <i>Hyalella</i> amphipod species-flock of the Andean Altiplano. <i>Scientific Reports</i> , 2021, 11, 366.	1.6	7
2387	Diversity and phylogeny of <i>Paradiplozoon</i> species (Monogenea: Diplozoidae) parasitising endemic cyprinoids in the peri-Mediterranean area, with a description of three new <i>Paradiplozoon</i> species. <i>Parasitology Research</i> , 2021, 120, 481-496.	0.6	8
2388	An updated tribal classification of Lamiaceae based on plastome phylogenomics. <i>BMC Biology</i> , 2021, 19, 2.	1.7	126
2389	Genomic mechanisms of climate adaptation in polyploid bioenergy switchgrass. <i>Nature</i> , 2021, 590, 438-444.	13.7	144

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2392	Genome-wide signatures of mammalian skin covering evolution. <i>Science China Life Sciences</i> , 2021, 64, 1765-1780.	2.3	5
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2394	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
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2396	Discovery of a colossal slickhead (Alepocephaliformes: Alepocephalidae): an active-swimming top predator in the deep waters of Suruga Bay, Japan. <i>Scientific Reports</i> , 2021, 11, 2490.	1.6	6
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2398	Protein phylogenetics with mass spectrometry. A comparison of methods. <i>Analytical Methods</i> , 2021, 13, 1442-1454.	1.3	3
2399	Phylogenetic analyses of a new freshwater amphipod reveal polyphyly within the Holarctic family Crangonyctidae, with revision of the genus <i>Synurella</i> . <i>Zoological Journal of the Linnean Society</i> , 2022, 195, 1100-1115.	1.0	5
2400	Description of a new species of <i>Auriculostoma</i> (Digenea: Allocreadiidae) from <i>Characidium heirmostigmata</i> (Characiformes: Crenuchidae) from Argentina, using morphological and molecular data. <i>Journal of Helminthology</i> , 2021, 95, e19.	0.4	5
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2402	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
2404	Dynamic evolution of transposable elements, demographic history, and gene content of paleognathous birds. <i>Zoological Research</i> , 2021, 42, 51-61.	0.9	3
2405	Positive selection analysis reveals the deep-sea adaptation of a hadal sea cucumber (<i>Paelopatides</i> sp.) to the Mariana Trench. <i>Journal of Oceanology and Limnology</i> , 2021, 39, 266-281.	0.6	9
2406	Hepatic phaeohyphomycosis due to a novel dematiaceous fungus, <i>Pleurostoma hongkongense</i> sp. nov., and importance of antifungal susceptibility testing. <i>Emerging Microbes and Infections</i> , 2021, 10, 81-96.	3.0	7
2407	Draft Genome Sequences of <i>Thelohania contejeani</i> and <i>Cucumispora dikerogammari</i> , Pathogenic Microsporidia of Freshwater Crustaceans. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	6
2408	Comparative mitogenome phylogeography of two anteater genera (—Tamandua— and <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf traits</i> . <i>Zoological Research</i> , 2021, 42, 525-547.	0.9	6
2409	RNA-sequencing indicates high hemocyanin expression as a key strategy for cold adaptation in the Antarctic amphipod <i>Eusirus</i> cf. <i>giganteus</i> clade g3. <i>Biocell</i> , 2021, 45, 1611-1619.	0.4	5

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2411	MIINTyper: an outbreak-detection method for accurate and rapid SNP typing of clonal clusters with noisy long reads. <i>Biology Methods and Protocols</i> , 2021, 6, bpab008.	1.0	10
2412	Morphological and genomic evidence for a new species of <i>Corallorhiza</i> (Orchidaceae Epidendroideae) from SW China. <i>Plant Diversity</i> , 2021, 43, 409-419.	1.8	1
2413	Mitochondrial genomes of two eucotyliids as the first representatives from the superfamily Microphalloidea (Trematoda) and phylogenetic implications. <i>Parasites and Vectors</i> , 2021, 14, 48.	1.0	12
2414	Revisiting the phylogenetic predicament of the genus <i>Huia</i> (Amphibia: Ranidae) using molecular data and tadpole morphology. <i>Zoological Journal of the Linnean Society</i> , 2021, 193, 673-699.	1.0	5
2415	Homoplasy and morphological stasis revealed through multilocus phylogeny of new myrmecophilous species in Armadillidiidae (Isopoda: Oniscidea). <i>Zoological Journal of the Linnean Society</i> , 2022, 194, 1312-1340.	1.0	2
2416	<i>Hygrophorus</i> sect. <i>Olivaceoumbrini</i> : new boundaries, extended biogeography and unexpected diversity unravelled by transatlantic studies. <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2021, . .	1.6	3
2417	Genome and population evolution and environmental adaptation of <i>Glyptosternon maculatum</i> on the Qinghai-Tibet Plateau. <i>Zoological Research</i> , 2021, 42, 502-513.	0.9	7
2418	<i>Pseudooceanicola</i> algae 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
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2420	Redescription of the hermit crab <i>Diogenes pugilator</i> (Decapoda: Anomura) reveals the existence of a species complex in the Atlanto-Mediterranean transition zone, resulting in the resurrection of <i>D. curvimanus</i> and the description of a new species. <i>Zoological Journal of the Linnean Society</i> , 2022, 195, 1116-1146.	1.0	2
2421	Unexpected diversity in the sponge-associated shrimps. <i>Invertebrate Systematics</i> , 2021, 35, 361-393.	0.5	1
2422	Application of an immobilized microbial consortium for the treatment of pharmaceutical wastewater: Batch-wise and continuous studies. <i>Chinese Journal of Chemical Engineering</i> , 2021, 29, 391-400.	1.7	16
2423	Automated Phylogenetic Analysis Using Best Reciprocal BLAST. <i>Methods in Molecular Biology</i> , 2021, 2369, 41-63.	0.4	0
2424	The complete plastid genome of <i>Cotinus coggygria</i> and phylogenetic analysis of the Anacardiaceae. <i>Genetics and Molecular Biology</i> , 2021, 44, e20210006.	0.6	1
2425	Inferring the Phylogenetic Positions of Two Fig Wasp Subfamilies of Epichrysomallinae and Sycophaginae Using Transcriptomes and Mitochondrial Data. <i>Life</i> , 2021, 11, 40.	1.1	4
2426	Evolution of Tandem Repeats Is Mirroring Post-polyploid Cladogenesis in <i>Heliophila</i> (Brassicaceae). <i>Frontiers in Plant Science</i> , 2020, 11, 607893.	1.7	13
2428	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

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2430	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
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2432	Evolutionary and genomic comparisons of hybrid uninucleate and nonhybrid <i>Rhizoctonia</i> fungi. <i>Communications Biology</i> , 2021, 4, 201.	2.0	16
2433	Macrophages provide a transient muscle stem cell niche via NAMPT secretion. <i>Nature</i> , 2021, 591, 281-287.	13.7	111
2434	Draft Genome Sequences of Pelagimyophage Mosig EXVC030M and Pelagipodophage Lederberg EXVC029P, Isolated from Devil's Hole, Bermuda. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	5
2435	Pinpointing the PRDM9-PRDM7 Gene Duplication Event During Primate Divergence. <i>Frontiers in Genetics</i> , 2021, 12, 593725.	1.1	0
2437	Higher-level phylogenetic relationships of rove beetles (Coleoptera, Staphylinidae) inferred from mitochondrial genome sequences. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2021, 32, 98-105.	0.7	5
2438	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
2439	Molecular data on <i>Phyllodistomum macrocotyle</i> (Digenea: Gorgoderidae) from an intermediate host <i>Dreissena polymorpha</i> (Bivalvia: Dreissenidae) in the Northern Dvina River Basin, Northwest Russia. <i>Ecologica Montenegrina</i> , 0, 39, 69-75.	0.5	1
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2441	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
2442	Complete mitochondrial genome of <i>Mukaria splendida</i> Distant (Hemiptera: Cicadellidae: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 2622-623.	0.2	1
2443	Indel-K2P: a modified Kimura 2 Parameters (K2P) model to incorporate insertion and deletion (Indel) information in phylogenetic analysis. <i>Cyber-Physical Systems</i> , 2022, 8, 32-44.	1.6	21
2444	Complete Mitochondrial Genome of <i>Trichuristrichiura</i> from <i>Macaca sylvanus</i> and <i>Papio papio</i> . <i>Life</i> , 2021, 11, 126.	1.1	5
2445	Phylogenomics of peacock spiders and their kin (Salticidae: <i>Maratus</i>), with implications for the evolution of male courtship displays. <i>Biological Journal of the Linnean Society</i> , 2021, 132, 471-494.	0.7	5
2447	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
2448	Comparative Analyses of <i>Euonymus</i> Chloroplast Genomes: Genetic Structure, Screening for Loci With Suitable Polymorphism, Positive Selection Genes, and Phylogenetic Relationships Within Celastrineae. <i>Frontiers in Plant Science</i> , 2020, 11, 593984.	1.7	25

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2450	<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
2451	<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
2452	Phylogenomic Analysis of Ultraconserved Elements Resolves the Evolutionary and Biogeographic History of Segmented Trapdoor Spiders. <i>Systematic Biology</i> , 2021, 70, 1110-1122.	2.7	17
2453	Lineage-specific plastid degradation in subtribe Gentianinae (Gentianaceae). <i>Ecology and Evolution</i> , 2021, 11, 3286-3299.	0.8	21
2454	Complete mitochondrial genome of the whitefly <i>Aleyrodes shizuokensis</i> Kuwana (Hemiptera: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 0.2 1	0.2	1
2455	Chloroplast Genomes of Two Species of <i>Cypripedium</i> : Expanded Genome Size and Proliferation of AT-Biased Repeat Sequences. <i>Frontiers in Plant Science</i> , 2021, 12, 609729.	1.7	30
2456	Comparative Mitogenomic Analysis of Heptageniid Mayflies (Insecta: Ephemeroptera): Conserved Intergenic Spacer and tRNA Gene Duplication. <i>Insects</i> , 2021, 12, 170.	1.0	14
2457	Disentangling relationships among eastern Mediterranean Cymbalaria including description of a novel species from the southern Peloponnese (Greece). <i>Plant Systematics and Evolution</i> , 2021, 307, 1.	0.3	7
2458	Convergent evolution: A new subfamily for bipaliin-like Chilean land planarians (platyhelminthes). <i>Zoologica Scripta</i> , 2021, 50, 500-508.	0.7	9
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2460	Complete mitochondrial genome of the copepod <i>Sinergasilus undulates</i> (Copepoda: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 0.2 1	0.2	1
2461	A new species of <i>Pacifides</i> from the Western Pacific Coast and the first fully freshwater species of the maricolan planarian genus <i>Paucumara</i> (Platyhelminthes, Tricladida, Maricola). <i>Systematics and Biodiversity</i> , 2021, 19, 488-506.	0.5	2
2462	Unbiasing Genome-Based Analyses of Selection: An Example Using Iconic Shark Species. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	2
2463	Morphology and Phylogeny Reveal <i>Callistosporium subpetaloideum</i> sp. nov. (Callistosporiaceae) from China. <i>Current Microbiology</i> , 2021, 78, 2122-2129.	1.0	0
2464	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
2465	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
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2469	The genome of the stable fly, <i>Stomoxys calcitrans</i> , reveals potential mechanisms underlying reproduction, host interactions, and novel targets for pest control. <i>BMC Biology</i> , 2021, 19, 41.	1.7	19
2470	Primary Metabolism co-Opted for Defensive Chemical Production in the Carabid Beetle, <i>Harpalus pensylvanicus</i> . <i>Journal of Chemical Ecology</i> , 2021, 47, 334-349.	0.9	0
2471	There and Back Again from Monotypy: A New Species of the Casque-Headed <i>Corythomantis</i> Boulenger 1896 (Anura, Hylidae) from the Espinha�so Mountain Range, Brazil. <i>Herpetologica</i> , 2021, 77, .	0.2	0
2472	Interaction between matrix metalloproteinase-9 (MMP-9) and neutrophil gelatinase-associated lipocalin (NGAL): A recent evolutionary event in primates. <i>Developmental and Comparative Immunology</i> , 2021, 116, 103933.	1.0	3
2473	Evolution of Bird and Insect Flower Traits in <i>Fritillaria</i> L. (Liliaceae). <i>Frontiers in Plant Science</i> , 2021, 12, 656783.	1.7	6
2474	Integrating UCE Phylogenomics With Traditional Taxonomy Reveals a Trove of New World <i>Syscia</i> Species (Formicidae: Dorylinae). <i>Insect Systematics and Diversity</i> , 2021, 5, .	0.7	5
2475	Genomes of 12 fig wasps provide insights into the adaptation of pollinators to fig syconia. <i>Journal of Genetics and Genomics</i> , 2021, 48, 225-236.	1.7	6
2476	Characterization of the leafhopper mitogenome of <i>Milewa alara</i> (Hemiptera: Cicadellidae: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 422 T	0.2	3
2477	Predicting transcriptional responses to cold stress across plant species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	46
2478	The McdAB system positions ��carboxysomes in proteobacteria. <i>Molecular Microbiology</i> , 2021, 116, 277-297.	1.2	22
2479	Signal, bias, and the role of transcriptome assembly quality in phylogenomic inference. <i>Bmc Ecology and Evolution</i> , 2021, 21, 43.	0.7	8
2480	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
2482	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
2483	Crustacean diversity in the Puget Sound: reconciling species, phylogenetic, and functional diversity. <i>Marine Biodiversity</i> , 2021, 51, 1.	0.3	2
2484	Settling taxonomic and nomenclatural problems in brine shrimps, <i>Artemia</i> (Crustacea: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 422 T rules. <i>PeerJ</i> , 2021, 9, e10865.	0.9	22
2485	First complete mitogenomes of three mayflies in the genus <i>Afronurus</i> (Ephemeroptera: Heptageniidae) and their implications for phylogenetic reconstruction. <i>Biologia (Poland)</i> , 2021, 76, 2291-2302.	0.8	4
2486	Multi�country investigation of the diversity and associated microorganisms isolated from tick species from domestic animals, wildlife and vegetation in selected african countries. <i>Experimental and Applied Acarology</i> , 2021, 83, 427-448.	0.7	6

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2488	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. Genes, 2021, 12, 389.	1.0	5
2489	Redescription and molecular characterization of <i>Baruscapillaria spiculata</i> (Nematoda: Capillariidae) parasitizing the Neotropic cormorant <i>Phalacrocorax brasilianus</i> from two Argentinian lagoons. Parasitology Research, 2021, 120, 1637-1648.	0.6	3
2490	Insights Into the Evolutionary History of the Subfamily Orthotrichoideae (Orthotrichaceae,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T 5 Plant Science, 2021, 12, 629035.	1.7	12
2491	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. PeerJ, 2021, 9, e10867.	0.9	8
2492	The very early evolution of protein translocation across membranes. PLoS Computational Biology, 2021, 17, e1008623.	1.5	13
2493	The limits of Quediini at last (Staphylinidae: Staphylininae): a rove beetle mega-radiation resolved by comprehensive sampling and anchored phylogenomics. Systematic Entomology, 2021, 46, 396-421.	1.7	16
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2495	New molecular phylogenetic evidence for Indian endemic species of the tribe Merremieae, Convolvulaceae. Plant Biosystems, 2022, 156, 440-449.	0.8	7
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2497	Characterization of Two Complete Mitochondrial Genomes of <i>Atkinsoniella</i> (Hemiptera: Cicadellidae:) Tj ETQq0 0 0 rgBT /Overlock 10 T 5 1.8	1.8	11
2499	<i>Caproicibacterium amyolyticum</i> gen. nov., sp. nov., a novel member of the family Oscillospiraceae isolated from pit clay used for making Chinese strong aroma-type liquor. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	23
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2508	Impact of male trait exaggeration on sex-biased gene expression and genome architecture in a water strider. <i>BMC Biology</i> , 2021, 19, 89.	1.7	15
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2511	First detection of a novel "unknown host"™ flavivirus in a Malaysian rodent. <i>Access Microbiology</i> , 2021, 3, 000223.	0.2	1
2512	Characterization of the complete mitochondrial genomes of two <i>Ixodes</i> ticks, <i>I. nipponensis</i> and <i>I. Pholeoixodes</i> sp.. <i>Medical and Veterinary Entomology</i> , 2021, 35, 513-522.	0.7	5
2513	Komesuamide and odopenicillatamide, two linear lipopeptides from the marine cyanobacterium <i>Caldora penicillata</i> . <i>Tetrahedron</i> , 2021, 85, 131969.	1.0	2
2514	First Complete Mitochondrial Genome of a Tanaidacean Crustacean (<i>Arctotanais alascensis</i>). <i>Zoological Science</i> , 2021, 38, 267-272.	0.3	3
2515	Quest for the type species of the genus <i>Hepatozoon</i> – phylogenetic position of hemogregarines of rats and consequences for taxonomy. <i>Systematics and Biodiversity</i> , 2021, 19, 622-631.	0.5	11
2516	Endophytic fungus diversity in soybean plants submitted to conditions of elevated atmospheric CO ₂ and temperature. <i>Canadian Journal of Microbiology</i> , 2021, 67, 290-300.	0.8	4
2517	Interspecies Genomic Variation and Transcriptional Activeness of Secondary Metabolism-Related Genes in <i>Aspergillus</i> Section <i>Fumigati</i> . <i>Frontiers in Fungal Biology</i> , 2021, 2, .	0.9	5
2518	Diversity of the type I-U CRISPR-Cas system in <i>Bifidobacterium</i> . <i>Archives of Microbiology</i> , 2021, 203, 3235-3243.	1.0	3
2519	Phylogenomics of Ichneumoninae (Hymenoptera, Ichneumonidae) reveals pervasive morphological convergence and the shortcomings of previous classifications. <i>Systematic Entomology</i> , 2021, 46, 704-724.	1.7	20
2520	Plastid and nuclear phylogenomic incongruences and biogeographic implications of <i>Magnolia</i> s.l. (Magnoliaceae). <i>Journal of Systematics and Evolution</i> , 2022, 60, 1-15.	1.6	29
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2523	Complete Chloroplast Genome of <i>Clethra fargesii</i> Franch., an Original Sympetalous Plant from Central China: Comparative Analysis, Adaptive Evolution, and Phylogenetic Relationships. <i>Forests</i> , 2021, 12, 441.	0.9	22
2524	A chromosome-level reference genome of the hazelnut, <i>Corylus heterophylla</i> Fisch. <i>GigaScience</i> , 2021, 10, .	3.3	13

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2527	De novo assembly of a new <i>Olea europaea</i> genome accession using nanopore sequencing. <i>Horticulture Research</i> , 2021, 8, 64.	2.9	41
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2529	Integrative descriptions of two new species of <i>Dugesia</i> from Hainan Island, China (Platyhelminthes). <i>Trends in Parasitology</i> , 2021, 36, 101917.	0.5	9
2530	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
2532	The assembly of caprine Y chromosome sequence reveals a unique paternal phylogenetic pattern and improves our understanding of the origin of domestic goat. <i>Ecology and Evolution</i> , 2021, 11, 7779-7795.	0.8	6
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2537	A New Burrowing Frog of the <i>Odontophrynus americanus</i> Species Group (Anura, Odontophrynidae) from Subtropical Regions of Argentina, Brazil, and Paraguay. <i>Ichthyology and Herpetology</i> , 2021, 109, .	0.3	4
2538	The chloroplast genome evolution of Venus slipper (<i>Paphiopedilum</i>): IR expansion, SSC contraction, and highly rearranged SSC regions. <i>BMC Plant Biology</i> , 2021, 21, 248.	1.6	49
2539	Impacts of allopolyploidization and structural variation on intraspecific diversification in <i>Brassica rapa</i> . <i>Genome Biology</i> , 2021, 22, 166.	3.8	80
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2546	Crystal structure and molecular dynamics of human <sc>POLDIP2</sc>, a multifaceted adaptor protein in metabolism and genome stability. <i>Protein Science</i> , 2021, 30, 1196-1209.	3.1	6
2547	<i>Coxiella burnetii</i> and Related Tick Endosymbionts Evolved from Pathogenic Ancestors. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	27
2548	Early embryogenesis and organogenesis in the annelid <i>Owenia fusiformis</i> . <i>EvoDevo</i> , 2021, 12, 5.	1.3	42
2549	Genome Sequencing and Assembly Strategies and a Comparative Analysis of the Genomic Characteristics in Penaeid Shrimp Species. <i>Frontiers in Genetics</i> , 2021, 12, 658619.	1.1	14
2550	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
2551	The complete mitogenome of <i>Phymorhynchus</i> sp. (Neogastropoda, Conoidea, Raphitomidae) provides insights into the deep-sea adaptive evolution of Conoidea. <i>Ecology and Evolution</i> , 2021, 11, 7518-7531.	0.8	10
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2553	Molecular Evolution of DNA Topoisomerase III Beta (TOP3B) in Metazoa. <i>Journal of Molecular Evolution</i> , 2021, 89, 384-395.	0.8	5
2554	Characterization of Three Complete Mitogenomes of Flatidae (Hemiptera: Fulgoroidea) and Compositional Heterogeneity Analysis in the Planthoppers'™ Mitochondrial Phylogenomics. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5586.	1.8	4
2555	Complete chloroplast genomes of <i>Achnatherum inebrians</i> and comparative analyses with related species from Poaceae. <i>FEBS Open Bio</i> , 2021, 11, 1704-1718.	1.0	7
2556	Diversity and infectivity of the RNA virome among different cryptic species of an agriculturally important insect vector: whitefly <i>Bemisia tabaci</i> . <i>Npj Biofilms and Microbiomes</i> , 2021, 7, 43.	2.9	21
2558	The Chromosome-Level Genome of <i>Triphlophysa dalaica</i> (Cypriniformes: Cobitidae) Provides Insights into Its Survival in Extremely Alkaline Environment. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	7
2560	Media and strain studies for the scaled production of cis-enone resorcylic acid lactones as feedstocks for semisynthesis. <i>Journal of Antibiotics</i> , 2021, 74, 496-507.	1.0	7
2561	Morphological and complete mitogenomic characterisation of the acanthocephalan <i>Polymorphus minutus</i> infecting the duck <i>Anas platyrhynchos</i> . <i>Folia Parasitologica</i> , 2021, 68, .	0.7	7
2562	Multiple mitochondrial haplotypes within individual specimens may interfere with species identification and biodiversity estimation by <sc>DNA</sc> barcoding and metabarcoding in fig wasps. <i>Systematic Entomology</i> , 2021, 46, 887-899.	1.7	7
2563	The complete plastome sequence of <i>Pinellia peltata</i> Pei (Araceae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2112-2113.	0.2	3
2564	A Combined Morphological and Molecular Evolutionary Analysis of Karst-Environment Adaptation for the Genus <i>Urophysa</i> (Ranunculaceae). <i>Frontiers in Plant Science</i> , 2021, 12, 667988.	1.7	2

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2567	Five Mitochondrial Genomes of the Genus <i>Eysarcoris</i> Hahn, 1834 with Phylogenetic Implications for the Pentatominae (Hemiptera: Pentatomidae). <i>Insects</i> , 2021, 12, 597.	1.0	9
2568	The mitochondrial genomes of bryophytes. <i>Bryophyte Diversity and Evolution</i> , 2021, 43, .	1.0	4
2569	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
2570	Gene duplication and adaptive evolution of Toll-like receptor genes in birds. <i>Developmental and Comparative Immunology</i> , 2021, 119, 103990.	1.0	8
2572	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
2573	The complete mitochondrial genome of <i>Oestrus ovis</i> (Linnaeus, 1758) (Diptera: Oestridae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1847-1848.	0.2	3
2576	The complete chloroplast genome of <i>Ormosia nuda</i> (fabaceae), an endemic species in China. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2095-2096.	0.2	1
2577	A preliminary phylogeny and review of the genus <i>Tasmanitachoides</i> , with descriptions of two new species (Coleoptera, Carabidae, Bembidarenini). <i>ZooKeys</i> , 2021, 1044, 153-196.	0.5	3
2579	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
2580	The mitochondrial genome of the semi-slug <i>Omalonyx unguis</i> (Gastropoda: Succineidae) and the phylogenetic relationships within <i>Stylommatophora</i> . <i>PLoS ONE</i> , 2021, 16, e0253724.	1.1	5
2581	Mitochondrial phylogenomics reveal the origin and adaptive evolution of the deep-sea caridean shrimps (Decapoda: Caridea). <i>Journal of Oceanology and Limnology</i> , 2021, 39, 1948-1960.	0.6	3
2582	Characterization of the First Complete Mitochondrial Genome of Cyphonocerinae (Coleoptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 26	1.0	9
2583	A subterranean adaptive radiation of amphipods in Europe. <i>Nature Communications</i> , 2021, 12, 3688.	5.8	47
2584	Dynamic Molecular Evolution of Mammalian Homeobox Genes: Duplication, Loss, Divergence and Gene Conversion Sculpt PRD Class Repertoires. <i>Journal of Molecular Evolution</i> , 2021, 89, 396-414.	0.8	9
2585	Australian bush medicines harbour diverse microbial endophytes with broad spectrum antibacterial activity. <i>Journal of Applied Microbiology</i> , 2021, 131, 2244-2256.	1.4	1
2586	Unravelling unexplored diversity of cercosporoid fungi (Mycosphaerellaceae, Mycosphaerellales,) Tj ETQq0 0 0 rgBT /Overlock 4 Tf 50 1	0.8	4
2587	<i>Sechelleptus arborivagus</i> sp. nov., a new arboreal spirostreptid millipede (Diplopoda, Spirostreptidae) endemic to Mayotte Island (Comoros Archipelago), Indian Ocean. <i>European Journal of Taxonomy</i> , 0, 755, .	0.6	2

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2589	Phylogeny of the supertribe Nebriitae (Coleoptera, Carabidae) based on analyses of DNA sequence data. <i>ZooKeys</i> , 2021, 1044, 41-152.	0.5	6
2590	Integrative taxonomy and biogeographic affinities of the first freshwater sponge and mollusc association discovered in tropical Asia. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2021, 59, 1167-1189.	0.6	5
2591	Comparative genomics of the <i>Pseudomonas corrugata</i> subgroup reveals high species diversity and allows the description of <i>Pseudomonas ogarae</i> sp. nov.. <i>Microbial Genomics</i> , 2021, 7, .	1.0	19
2592	Differential Evolutionary History in Visual and Olfactory Floral Cues of the Bee-Pollinated Genus <i>Campanula</i> (Campanulaceae). <i>Plants</i> , 2021, 10, 1356.	1.6	2
2593	Using target capture to address conservation challenges: Population-level tracking of a globally-traded herbal medicine. <i>Molecular Ecology Resources</i> , 2022, 22, 212-224.	2.2	11
2594	A chromosome-level genome assembly of <i>Cairina moschata</i> and comparative genomic analyses. <i>BMC Genomics</i> , 2021, 22, 581.	1.2	4
2595	Genome and transcriptome analysis of the mealybug <i>Maconellicoccus hirsutus</i> : Correlation with its unique phenotypes. <i>Genomics</i> , 2021, 113, 2483-2494.	1.3	8
2596	Characterization and Molecular Identification of Poly Urethane Degrading Bacteria. <i>Journal of Pure and Applied Microbiology</i> , 2021, 15, 1291-1300.	0.3	0
2597	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. <i>Ecology and Evolution</i> , 2021, 11, 12114-12128.	0.8	3
2598	Evolutionary dynamics of sex-biased genes expressed in cricket brains and gonads. <i>Journal of Evolutionary Biology</i> , 2021, 34, 1188-1211.	0.8	14
2599	Virulence and antimicrobial resistance genes are enriched in the plasmidome of clinical <i>Escherichia coli</i> isolates compared with wastewater isolates from western Kenya. <i>Infection, Genetics and Evolution</i> , 2021, 91, 104784.	1.0	5
2600	A new freshwater leech species from Asian Swamp Eel stocks in China. <i>Parasitology Research</i> , 2021, 120, 2769-2778.	0.6	5
2601	The methylome of the model arbuscular mycorrhizal fungus, <i>Rhizophagus irregularis</i> , shares characteristics with early diverging fungi and <i>Dikarya</i> . <i>Communications Biology</i> , 2021, 4, 901.	2.0	17
2602	The complete mitochondrial genome of a non-biting midge <i>Polypedilum unifascium</i> (Tokunaga), <i>Tj ETQq000rgBT/Overlock 10 T</i>	0.2	10
2604	Phosphite Reduces the Predation Impact of <i>Poteroiochromonas malhamensis</i> on Cyanobacterial Culture. <i>Plants</i> , 2021, 10, 1361.	1.6	5
2605	Two Complete Mitochondrial Genomes of Mileewinae (Hemiptera: Cicadellidae) and a Phylogenetic Analysis. <i>Insects</i> , 2021, 12, 668.	1.0	10
2606	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

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2607	Antifungal Activity and Biosynthetic Potential of New <i>Streptomyces</i> sp. MW-W600-10 Strain Isolated from Coal Mine Water. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7441.	1.8	7
2608	Massive colonization of protein-coding exons by selfish genetic elements in <i>Paramecium</i> germline genomes. <i>PLoS Biology</i> , 2021, 19, e3001309.	2.6	30
2609	Comparative genomics of <i>Leishmania</i> isolates from Brazil confirms the presence of <i>Leishmania major</i> in the Americas. <i>International Journal for Parasitology</i> , 2021, 51, 1047-1057.	1.3	7
2610	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
2611	Phylogenomic analyses clarify the pattern of evolution of Adephaga (Coleoptera) and highlight phylogenetic artefacts due to model misspecification and excessive data trimming. <i>Systematic Entomology</i> , 2021, 46, 991-1018.	1.7	12
2612	A novel <i>Actinidia</i> cytorhabdovirus characterized using genomic and viral protein interaction features. <i>Molecular Plant Pathology</i> , 2021, 22, 1271-1287.	2.0	8
2613	Recycling of the major thylakoid lipid MGDG and its role in lipid homeostasis in <i>Chlamydomonas reinhardtii</i> . <i>Plant Physiology</i> , 2021, 187, 1341-1356.	2.3	11
2614	Phylogenomics of Opsin Genes in Diptera Reveals Lineage-Specific Events and Contrasting Evolutionary Dynamics in <i>Anopheles</i> and <i>Drosophila</i> . <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	16
2615	Evolution of Superoxide Dismutases and Catalases in Cyanobacteria: Occurrence of the Antioxidant Enzyme Genes before the Rise of Atmospheric Oxygen. <i>Journal of Molecular Evolution</i> , 2021, 89, 527-543.	0.8	8
2616	Hepatozoon in Eurasian red squirrels <i>Sciurus vulgaris</i> , its taxonomic identity, and phylogenetic placement. <i>Parasitology Research</i> , 2021, 120, 2989-2993.	0.6	3
2617	Integrative phylogenomics reveals a Permian origin of Adephaga beetles. <i>Systematic Entomology</i> , 2021, 46, 968-990.	1.7	15
2618	Whole-genome analysis of giraffe supports four distinct species. <i>Current Biology</i> , 2021, 31, 2929-2938.e5.	1.8	49
2619	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
2620	<i>Pythium intermedium</i> , a species complex consisting of three phylogenetic species found in cool-temperate forest ecosystems. <i>Fungal Biology</i> , 2021, 125, 1017-1025.	1.1	2
2621	Evolution of Transmissible Spongiform Encephalopathies and the Prion Protein Gene (PRNP) in Mammals. <i>Journal of Mammalian Evolution</i> , 2021, 28, 573-582.	1.0	1
2622	<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
2623	Draft Genome Assembly and Transcriptome Dataset for European Turnip (<i>Brassica rapa</i> L. ssp. <i>rapifera</i>), ECD4 Carrying Clubroot Resistance. <i>Frontiers in Genetics</i> , 2021, 12, 651298.	1.1	5
2624	Diversity, host specificity and biogeography in the Cladocorynidae (Hydrozoa, Capitata), with description of a new genus. <i>Cladistics</i> , 2022, 38, 13-37.	1.5	7

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2625	A second capsidless hadakavirus strain with 10 positive-sense single-stranded RNA genomic segments from <i>Fusarium nygamai</i> . <i>Archives of Virology</i> , 2021, 166, 2711-2722.	0.9	20
2626	Molecular Evolution of clock Genes in Vertebrates. <i>Journal of Molecular Evolution</i> , 2021, 89, 494-512.	0.8	2
2627	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
2628	Structural Features and Phylogenetic Implications of 11 New Mitogenomes of Typhlocybinae (Hemiptera: Cicadellidae). <i>Insects</i> , 2021, 12, 678.	1.0	11
2629	Phylogenetic placement of <i>Flacillula</i> Strand, 1932 with seven new species from Sri Lanka (Araneae: Salticidae). <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2021, 59, 1255-1272.	0.6	1
2630	Commentary: Unbiasing Genome-Based Analyses of Selection: An Example Using Iconic Shark Species. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	0
2631	<i>Caloplaca tephromelae</i> (Teloschistaceae), a new lichenicolous species from Tasmania. <i>Lichenologist</i> , 2021, 53, 317-325.	0.5	0
2632	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
2633	<i>Lactobacillus corticis</i> sp. nov., isolated from hardwood bark. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	9
2634	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
2635	Genomics and transcriptomics of epizoic Seisonidea (Rotifera, syn. Syndermata) reveal strain formation and gradual gene loss with growing ties to the host. <i>BMC Genomics</i> , 2021, 22, 604.	1.2	6
2636	Frequent tRNA gene translocation towards the boundaries with control regions contributes to the highly dynamic mitochondrial genome organization of the parasitic lice of mammals. <i>BMC Genomics</i> , 2021, 22, 598.	1.2	7
2637	Plastid genomes and phylogenomics of liverworts (Marchantiophyta): Conserved genome structure but highest relative plastid substitution rate in land plants. <i>Molecular Phylogenetics and Evolution</i> , 2021, 161, 107171.	1.2	12
2638	A broadly resolved molecular phylogeny of New Zealand cheilostome bryozoans as a framework for hypotheses of morphological evolution. <i>Molecular Phylogenetics and Evolution</i> , 2021, 161, 107172.	1.2	8
2640	EntroPhylo: An entropy-based tool to select phylogenetic informative regions and primer design. <i>Infection, Genetics and Evolution</i> , 2021, 92, 104857.	1.0	3
2641	Î±-Glucosidase and PTP-1B Inhibitors from <i>Malbranchea dendritica</i> . <i>ACS Omega</i> , 2021, 6, 22969-22981.	1.6	8
2642	Isolation and Total Synthesis of Kinenzoline, an Antitrypanosomal Linear Depsipeptide Isolated from a Marine <i>Salileptolyngbya</i> sp. Cyanobacterium. <i>Journal of Organic Chemistry</i> , 2021, 86, 12528-12536.	1.7	5
2643	Identification of a Novel Quinvirus in the Family Betaflexiviridae That Infects Winter Wheat. <i>Frontiers in Microbiology</i> , 2021, 12, 715545.	1.5	7

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2645	The complete mitochondrial genome of capillariid nematodes (<i>Eucoleus annulatus</i>): A novel gene arrangement and phylogenetic implications. <i>Veterinary Parasitology</i> , 2021, 296, 109476.	0.7	6
2646	Characterization of a microbial consortium with potential for biological degradation of cactus pear biomass for biofuel production. <i>Heliyon</i> , 2021, 7, e07854.	1.4	4
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2650	No species-level losses of s2m suggests critical role in replication of SARS-related coronaviruses. <i>Scientific Reports</i> , 2021, 11, 16145.	1.6	15
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2653	The worm affair: fidelity and environmental adaptation in symbiont species that co-occur in vestimentiferan tubeworms. <i>Environmental Microbiology Reports</i> , 2021, 13, 744-752.	1.0	3
2654	Virulence Traits and Population Genomics of the Black Yeast <i>Aureobasidium melanogenum</i> . <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 665.	1.5	8
2656	A new species of <i>Solaropsis</i> Beck, 1837 (Gastropoda: Stylommatophora: Solaropsidae) from the Brazilian Amazon. <i>Folia Malacologica</i> , 2021, 29, 178-185.	0.1	1
2658	Mitogenomic analysis of extant condor species provides insight into the molecular evolution of vultures. <i>Scientific Reports</i> , 2021, 11, 17109.	1.6	4
2660	Ciliate SSU-rDNA reference alignments and trees for phylogenetic placements of metabarcoding data. <i>Metabarcoding and Metagenomics</i> , 0, 5, .	0.0	6
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2662	Identification of Unique Peptides for SARS-CoV-2 Diagnostics and Vaccine Development by an In Silico Proteomics Approach. <i>Frontiers in Immunology</i> , 2021, 12, 725240.	2.2	12
2663	The potential for using shell proteins in gastropod systematics, assessed in patellogastropod limpets. <i>Zoological Journal of the Linnean Society</i> , 2022, 194, 1177-1193.	1.0	0
2664	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
2665	Due South: The evolutionary history of Sub-Antarctic and Antarctic Tritoniidae nudibranchs. <i>Molecular Phylogenetics and Evolution</i> , 2021, 162, 107209.	1.2	10

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2667	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
2668	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
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2674	Adrenergically induced translocation of red blood cell β -adrenergic sodium-proton exchangers has ecological relevance for hypoxic and hypercapnic white seabass. <i>American Journal of Physiology - Regulatory Integrative and Comparative Physiology</i> , 2021, 321, R655-R671.	0.9	4
2675	The Evolution of Alternative Buoyancy Mechanisms in Freshwater Fish Eggs. <i>Frontiers in Ecology and Evolution</i> , 2021, 9, .	1.1	6
2676	The role of vicariance and dispersal on the temporal range dynamics of forest vipers in the Neotropical region. <i>PLoS ONE</i> , 2021, 16, e0257519.	1.1	4
2677	Genome Analysis of <i>Acinetobacter lwoffii</i> Strains Isolated from Permafrost Soils Aged from 15 Thousand to 1.8 Million Years Revealed Their Close Relationships with Present-Day Environmental and Clinical Isolates. <i>Biology</i> , 2021, 10, 871.	1.3	5
2678	An endophytic fungus, <i>Penicillium simplicissimum</i> conjugated with C60 fullerene for its potential antimutagenic, anti-inflammatory, anticancer and photodegradation activities. <i>Environmental Technology (United Kingdom)</i> , 2023, 44, 817-831.	1.2	7
2679	Phenotypically exceptional <i>Echiniscus</i> species (Heterotardigrada: Echiniscidae) from Argentina (Neotropics). <i>Zoologischer Anzeiger</i> , 2021, 294, 210-228.	0.4	6
2680	The complete mitochondrial genome of <i>Cephenemyia stimulator</i> (Diptera: Oestridae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2941-2942.	0.2	1
2681	Insights into the diversity, distribution and phylogeny of three ergasilid copepods (Hexanauplia: Tj ETQq1 1 0.784314 rgBT /Overlock 10 125922.	0.7	13
2682	Two new psathyrelloid species of <i>Coprinopsis</i> (Agaricales, Psathyrellaceae) from China. <i>MycKeys</i> , 2021, 83, 85-103.	0.8	2
2683	Measuring Phylogenetic Information of Incomplete Sequence Data. <i>Systematic Biology</i> , 2021, , .	2.7	1

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2685	Little known <i>Curculigo brevifolia</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
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2691	Tackling the phylogenetic conundrum of Hydroidolina (Cnidaria: Medusozoa: Hydrozoa) by assessing competing tree topologies with targeted high-throughput sequencing. <i>PeerJ</i> , 2021, 9, e12104.	0.9	8
2692	Solving the Coral Species Delimitation Conundrum. <i>Systematic Biology</i> , 2022, 71, 461-475.	2.7	16
2693	The genome of the naturally evolved obesity-prone Ossabaw miniature pig. <i>IScience</i> , 2021, 24, 103081.	1.9	9
2694	<i>Disporella guada</i> sp. nov., an erect-ramose rectangulate cyclostome (Bryozoa, Stenolaemata) from the Caribbean Sea: convergent evolution in bryozoan colony morphology. <i>European Journal of Taxonomy</i> , 0, 773, .	0.6	0
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2696	Molecular systematics and taxonomic overview of the bird's nest fungi (Nidulariaceae). <i>Fungal Biology</i> , 2021, 125, 693-703.	1.1	10
2697	Frequent lineage-specific substitution rate changes support an episodic model for protein evolution. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	1
2698	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
2699	Two new species of <i>Dugesia</i> (Platyhelminthes, Tricladida, Dugesiidae) from the tropical monsoon forest in southern China. <i>ZooKeys</i> , 2021, 1059, 89-116.	0.5	5
2700	<i>Aggregata polibraxiona</i> n. sp. (Apicomplexa: Aggregatidae) from <i>Octopus bimaculatus</i> Verrill, 1883 (Mollusca: Cephalopoda) from the Gulf of California, Mexico. <i>European Journal of Protistology</i> , 2021, 81, 125825.	0.5	5
2701	Foodborne illness caused by muscarine-containing mushrooms and identification of mushroom remnants using phylogenetics and LC-MS/MS. <i>Food Control</i> , 2021, 128, 108182.	2.8	12
2702	Isolation, identification, and gene expression analysis of the main digestive enzymes during ontogeny of the Neotropical catfish <i>Pseudoplatystoma punctifer</i> (Castelnau, 1855). <i>Aquaculture</i> , 2021, 543, 737031.	1.7	6

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2704	Macroevolutionary analyses of ciliates associated with hosts support high diversification rates. <i>International Journal for Parasitology</i> , 2021, 51, 967-976.	1.3	1
2705	Geography-Driven Evolution of Potato Virus A Revealed by Genetic Diversity Analysis of the Complete Genome. <i>Frontiers in Microbiology</i> , 2021, 12, 738646.	1.5	0
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2707	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
2708	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
2709	Biogeography, reproductive biology and phylogenetic divergence within the Fungiidae (mushroom) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50</i>	1.2	7
2710	Characterization of the complete mitochondrial genomes of six horseflies (Diptera: Tabanidae). <i>Infection, Genetics and Evolution</i> , 2021, 95, 105054.	1.0	9
2711	Biodegradation of poultry feather waste by keratinase producing <i>Bacillus cereus</i> strain isolated from poultry farms waste disposal site. <i>Case Studies in Chemical and Environmental Engineering</i> , 2021, 4, 100114.	2.9	4
2712	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
2713	Complete genome analysis of a divergent isolate of narcissus yellow stripe virus from China. <i>Journal of Plant Pathology</i> , 2021, 103, 605-609.	0.6	0
2715	â€ˆ <i>Candidatus</i> Sarmatiella mevalonicaâ€™ endosymbiont of the ciliate <i>Paramecium</i> provides insights on evolutionary plasticity among <i>Rickettsiales</i> . <i>Environmental Microbiology</i> , 2021, 23, 1684-1701.	1.8	20
2716	Variations in the Mitochondrial Genome of a Goldfish-Like Hybrid [Koi Carp (â€™) Ã— Blunt Snout Bream (â€™)] Indicate Paternal Leakage. <i>Frontiers in Genetics</i> , 2020, 11, 613520.	1.1	0
2717	Genome sequencing and functional annotation of <i>Bacillus</i> sp. strain BS-Z15 isolated from cotton rhizosphere soil having antagonistic activity against <i>Verticillium dahliae</i> . <i>Archives of Microbiology</i> , 2021, 203, 1565-1575.	1.0	8
2718	<i>Crittendenia</i> gen. nov., a new lichenicolous lineage in the Agaricostilbomycetes (Pucciniomycotina), and a review of the biology, phylogeny and classification of lichenicolous heterobasidiomycetes. <i>Lichenologist</i> , 2021, 53, 103-116.	0.5	10
2719	Novel gene rearrangement in the mitochondrial genome of <i>Muraenesox cinereus</i> and the phylogenetic relationship of Anguilliformes. <i>Scientific Reports</i> , 2021, 11, 2411.	1.6	23
2720	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
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2723	Evolutionary relationships of <i>Metchnikovella dogieli</i> Paskerova et al., 2016 (Microsporidia: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 7) 525-534.	0.6	6
2724	New morphological and molecular data reveal an important underestimation of species diversity and indicate evolutionary patterns in European. <i>Invertebrate Systematics</i> , 2021, 35, 471-492.	0.5	5
2725	Role of an ancient light-harvesting protein of PSI in light absorption and photoprotection. <i>Nature Communications</i> , 2021, 12, 679.	5.8	28
2727	Gains and Losses in <i>Yersinia enterocolitica</i> subsp. <i>paleartica</i> Genomes. <i>Advances in Experimental Medicine and Biology</i> , 2012, 954, 23-29.	0.8	5
2728	Comparative Analyses of Extrachromosomal Bacterial Replicons, Identification of Chromids, and Experimental Evaluation of Their Indispensability. <i>Methods in Molecular Biology</i> , 2015, 1231, 15-29.	0.4	7
2729	Rho GTPases: Deciphering the Evolutionary History of a Complex Protein Family. <i>Methods in Molecular Biology</i> , 2012, 827, 13-34.	0.4	34
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2731	Exploring Molecular Evolution Reconstruction Using a Parallel Cloud Based Scientific Workflow. <i>Lecture Notes in Computer Science</i> , 2012, , 179-191.	1.0	15
2732	3 Phylogenomics for the Study of Fungal Biology. , 2014, , 61-79.		3
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2734	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
2735	Invasion and distribution of the redclaw crayfish, <i>Cherax quadricarinatus</i> , in Martinique. <i>Knowledge and Management of Aquatic Ecosystems</i> , 2020, , 50.	0.5	5
2736	Bioremediation of 2,4-Diaminotoluene in Aqueous Solution Enhanced by Lipopeptide Biosurfactant Production from Bacterial Strains. <i>Journal of Environmental Engineering, ASCE</i> , 2020, 146, 04020069.	0.7	4
2738	<i>Coxiella</i> Detection in Ticks from Wildlife and Livestock in Malaysia. <i>Vector-Borne and Zoonotic Diseases</i> , 2016, 16, 744-751.	0.6	33
2739	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
2740	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
2741	Comparative Genomics of Strictly Vertically Transmitted, Feminizing Microsporidia Endosymbionts of Amphipod Crustaceans. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	12

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2742	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
2743	Chromosomal genome of <i>Triplophysa bleekeri</i> provides insights into its evolution and environmental adaptation. <i>GigaScience</i> , 2020, 9, .	3.3	19
2744	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
2745	Extensive genetic diversity and host range of rodent-borne coronaviruses. <i>Virus Evolution</i> , 2020, 6, veaa078.	2.2	31
2746	<i>Algoriphagus machipongonensis</i> sp. nov., co-isolated with a colonial choanoflagellate. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013, 63, 163-168.	0.8	43
2747	<i>Bifidobacterium myosotis</i> sp. nov., <i>Bifidobacterium tissieri</i> sp. nov. and <i>Bifidobacterium hapali</i> sp. nov., isolated from faeces of baby common marmosets (<i>Callithrix jacchus</i> L.). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 255-265.	0.8	37
2748	Isolation and characterization of <i>Flexilinea flocculi</i> gen. nov., sp. nov., a filamentous, anaerobic bacterium belonging to the class Anaerolineae in the phylum Chloroflexi. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 988-996.	0.8	75
2749	<i>Bifidobacterium eulemuris</i> sp. nov., isolated from faeces of black lemurs (<i>Eulemur macaco</i>). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 1567-1576.	0.8	17
2750	<i>Lentimicrobium saccharophilum</i> gen. nov., sp. nov., a strictly anaerobic bacterium representing a new family in the phylum Bacteroidetes, and proposal of <i>Lentimicrobiaceae</i> fam. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 2635-2642.	0.8	177
2751	<i>Gordonia hongkongensis</i> sp. nov., isolated from blood culture and peritoneal dialysis effluent of patients in Hong Kong. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 3942-3950.	0.8	22
2752	Genome-based phylogeny and taxonomy of the "Enterobacteriales": 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.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 5575-5599.	0.8	792
2753	<i>Silvanigrellaceae</i> fam. nov. and <i>Silvanigrellales</i> ord. nov., reclassification of the order <i>Bdellovibrionales</i> in the class <i>Oligoflexia</i> , reclassification of the families <i>Bacteriovoracaceae</i> and <i>Halobacteriovoracaceae</i> in the new order <i>Bacteriovoracales</i> ord. nov., and reclassification of the family <i>Pseudobacteriovoracaceae</i> in the order <i>Oligoflexales</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 2555-2568.	0.8	76
2754	<i>Bifidobacterium callitrichidarum</i> sp. nov. from the faeces of the emperor tamarin (<i>Saguinus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 262 T	0.8	25
2755	<i>Bifidobacterium catulorum</i> sp. nov., a novel taxon from the faeces of the baby common marmoset (<i>Callithrix jacchus</i>). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 575-581.	0.8	27
2756	<i>Kandeliimicrobium roseum</i> gen. nov., sp. nov., a new member of the family <i>Rhodobacteraceae</i> isolated from mangrove rhizosphere soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 2158-2164.	0.8	10
2757	<i>Virgibacillus indicus</i> sp. nov. and <i>Virgibacillus profundi</i> sp. nov, two moderately halophilic bacteria isolated from marine sediment by using microfluidic streak plates. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 2015-2023.	0.8	17
2758	<i>Amycolatopsis antarctica</i> sp. nov., isolated from the surface of an Antarctic brown macroalga. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 2348-2356.	0.8	21
2759	<i>Petroclostridium xylanilyticum</i> gen. nov., sp. nov., a xylan-degrading bacterium isolated from an oilfield, and reclassification of clostridial cluster III members into four novel genera in a new <i>Hungateiclostridiaceae</i> fam. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 3197-3211.	0.8	182

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2761	Comparative genomics of <i>Parolsenella catena</i> and <i>Libanicoccus massiliensis</i> : Reclassification of <i>Libanicoccus massiliensis</i> as <i>Parolsenella massiliensis</i> comb. nov.. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 1123-1129.	0.8	11
2762	<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> . International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 1185-1194.	0.8	32
2763	Genome-based classification of two halotolerant extreme acidophiles, <i>Acidihalobacter prosperus</i> V6 (=DSM 14174 =JCM 32253) and ' <i>Acidihalobacter ferrooxidans</i> ' V8 (=DSM 14175 =JCM 32254) as two new species, <i>Acidihalobacter aeolianus</i> sp. nov. and <i>Acidihalobacter ferrooxydans</i> sp. nov., respectively. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 1557-1565.	0.8	25
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2766	Phylogenomic revision of the family <i>Streptosporangiaceae</i> , 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 <i>Streptosporangiaceae</i> . International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 2569-2579.	0.8	17
2767	<i>Lactobacillus buchneri</i> subsp. <i>silagei</i> subsp. nov., isolated from rice grain silage. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 3111-3116.	0.8	17
2768	<i>Gemmobacter serpentinus</i> sp. nov., isolated from conserved forages. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 4224-4232.	0.8	7
2769	<i>Dickeya poaceiphila</i> sp. nov., a plant-pathogenic bacterium isolated from sugar cane (<i>Saccharum</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 30	0.8	30
2770	<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
2771	Genome-based classification of <i>Acidihalobacter prosperus</i> F5 (=DSM 105917=JCM 32255) as <i>Acidihalobacter yilgarnensis</i> sp. nov.. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 6226-6234.	0.8	13
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2945	Exploring <i>Monacha cantiana</i> (Montagu, 1803) phylogeography: cryptic lineages and new insights into the origin of the English populations (Eupulmonata, Stylommatophora, Hygromiidae). ZooKeys, 2018, 765, 1-41.	0.5	7
2946	Sequence capture phylogenomics of eyeless Cicurina spiders from Texas caves, with emphasis on US federally-endangered species from Bexar County (Araneae, Hahniidae). ZooKeys, 2018, 769, 49-76.	0.5	23
2947	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.) Tj ETQq1 1 0.784314 rgBT /Overlock 10 TF	0.5	12
2948	Characterization of the complete mitochondrial genome of <i>Parabreviscolex niepini</i> Xi et al., 2018 (Cestoda, Caryophyllidea). ZooKeys, 2018, 783, 97-112.	0.5	4
2949	New species of bone-eating worm <i>Osedax</i> from the abyssal South Atlantic Ocean (Annelida.) Tj ETQq1 1 0.784314 rgBT /Overlock 10 TF	0.5	12
2950	Systematic re-structure and new species of Sphaerodoridae (Annelida) after morphological revision and molecular phylogenetic analyses of the North East Atlantic fauna. ZooKeys, 2019, 845, 1-97.	0.5	3
2951	Sitticine jumping spiders: phylogeny, classification, and chromosomes (Araneae, Salticidae, Sitticini). ZooKeys, 2020, 925, 1-54.	0.5	12
2952	A new Terrarana frog of genus <i>Pristimantis</i> from an unexplored cloud forest from the eastern Andes, Colombia. ZooKeys, 2020, 961, 129-156.	0.5	6
2953	Uncovering the shell game with barcodes: diversity of meiofaunal Caecidae snails (Truncatelloidea,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 TF	0.5	12
2954	Molecular phylogenetic analysis of a taxonomically unstable ranid from Sumatra, Indonesia, reveals a new genus with gastromyzophorous tadpoles and two new species. Zoosystematics and Evolution, 2018, 94, 163-193.	0.4	14
2955	A new species of <i>Dugesia</i> (Platyhelminthes, Tricladida, Dugesiidae) from China, with an account on the histochemical structure of its major nervous system. Zoosystematics and Evolution, 2020, 96, 431-447.	0.4	11
2956	Molecular phylogenetic analysis of Punctoidea (Gastropoda, Stylommatophora). Zoosystematics and Evolution, 2020, 96, 397-410.	0.4	11
2957	Pseudognaphalium aldunateoides de nuevo bajo Gnaphalium (Compositae: Gnaphalieae). Collectanea Botanica, 0, 37, 012.	0.2	3
2958	A new Felimare (Mollusca: Heterobranchia: Nudibranchia) of the Atlantic blue chromodorid chromatic group from Cape Verde. Scientia Marina, 2017, 81, 387.	0.3	1
2959	Following the Phoenician example: western Mediterranean colonization by Spirobranchus cf. tetraceros (Annelida: Serpulidae). Scientia Marina, 2020, 84, 83.	0.3	6
2960	Frequent Association of <i>Colletotrichum</i> Species with Citrus Fruit and Leaf Spot Disease Symptoms and their Genetic Diversity in Ethiopia. Journal of Plant Pathology & Microbiology, 2017, 08, .	0.3	4
2961	Amino Acid Biosynthesis and Proteolysis in Lactobacillus Bulgaricus; Revisited: A Genomic Comparison. Computational Molecular Bioscience, 2012, 02, 61-77.	0.6	7

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2963	Genetic Characterization of the Patois Serogroup (Genus <i>Orthobunyavirus</i> ; Family <i>Peribunyaviridae</i>) and Evidence That Estero Real Virus is a Member of the Genus <i>Orthonairovirus</i> . <i>American Journal of Tropical Medicine and Hygiene</i> , 2018, 99, 451-457.	0.6	6
2964	Molecular identification of dye degrading bacterial isolates and FT-IR analysis of degraded products. <i>Environmental Engineering Research</i> , 2020, 25, 561-570.	1.5	2
2965	Productivity-diversity relationships from chemolithoautotrophically based sulfidic karst systems. <i>International Journal of Speleology</i> , 2009, 38, 27-40.	0.4	67
2966	Diversity of cultured bacteria from the perennial ice block of Scarisoara Ice Cave, Romania. <i>International Journal of Speleology</i> , 2016, 45, 89-100.	0.4	20
2967	Polyphasic approach to a characteristic <i>Ulva</i> population from a limno-rheocrenic, mineral (chloride), Tj ETQq1 1 0.784314 rgBT /Overlock 0.4	0.4	3
2968	First record of the rare freshwater alga <i>Tetrasporopsis fuscescens</i> (Chrysomerophyceae,) Tj ETQq0 0 0 rgBT /Overlock 0.4 Tf 50 502 Td (0.4	5
2969	Incorporating molecular data in fungal systematics: a guide for aspiring researchers. <i>Current Research in Environmental and Applied Mycology</i> , 2013, 3, 1-32.	0.3	65
2970	Hypogeous gasteroid <i>Lactarius sulphosmus</i> sp. nov. and agaricoid <i>Russula vinosobrunneola</i> sp. nov. (<i>Russulaceae</i>) from China. <i>Mycosphere</i> , 2018, 9, 838-858.	1.9	7
2971	Phylogenetic analysis of uroporphyrinogen III synthase (UROS) gene. <i>Bioinformatics</i> , 2012, 8, 1265-1270.	0.2	1
2972	Loss and Gain of Group I Introns in the Mitochondrial Gene of the Scleractinia (Cnidaria; Anthozoa). <i>Zoological Studies</i> , 2017, 56, e9.	0.3	3
2973	Regenerative Capacity of the Upside-down Jellyfish. <i>Zoological Studies</i> , 2019, 58, e37.	0.3	11
2974	A bacterial sulfonolipid triggers multicellular development in the closest living relatives of animals. <i>ELife</i> , 2012, 1, e00013.	2.8	224
2975	Neural circuitry of a polycystin-mediated hydrodynamic startle response for predator avoidance. <i>ELife</i> , 2018, 7, .	2.8	44
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2977	Evolution of <i>Wolbachia</i> mutualism and reproductive parasitism: insight from two novel strains that co-infect cat fleas. <i>PeerJ</i> , 2020, 8, e10646.	0.9	43
2978	Phylogenetic analysis of higher-level relationships within Hydroidolina (Cnidaria: Hydrozoa) using mitochondrial genome data and insight into their mitochondrial transcription. <i>PeerJ</i> , 2015, 3, e1403.	0.9	43
2979	RNA-Seq of the Caribbean reef-building coral <i>Orbicella faveolata</i> (Scleractinia-Merulinidae) under bleaching and disease stress expands models of coral innate immunity. <i>PeerJ</i> , 2016, 4, e1616.	0.9	56

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2981	Candidate pathogenicity islands in the genome of <i>Candidatus</i> <i>Rickettsiella isopodorum</i> TM , an intracellular bacterium infecting terrestrial isopod crustaceans. PeerJ, 2016, 4, e2806.	0.9	13
2982	Arrival and diversification of mabuyine skinks (Squamata: Scincidae) in the Neotropics based on a fossil-calibrated timetree. PeerJ, 2017, 5, e3194.	0.9	10
2983	Accumulation and expression of multiple antibiotic resistance genes in <i>Arcobacter cryaerophilus</i> that thrives in sewage. PeerJ, 2017, 5, e3269.	0.9	29
2984	A laid-back trip through the Hennigian Forests. PeerJ, 2017, 5, e3578.	0.9	38
2985	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
2986	Out of Asia: mitochondrial evolutionary history of the globally introduced supralittoral isopod <i>Ligia exotica</i> . PeerJ, 2018, 6, e4337.	0.9	9
2987	Comparative genome analysis of 24 bovine-associated <i>Staphylococcus</i> isolates with special focus on the putative virulence genes. PeerJ, 2018, 6, e4560.	0.9	30
2988	The mitochondrial genomes of two walnut pests, <i>Gastrolina depressa depressa</i> and <i>G. depressa thoracica</i> (Coleoptera: Chrysomelidae), and phylogenetic analyses. PeerJ, 2018, 6, e4919.	0.9	11
2989	Genome analysis of the ubiquitous boxwood pathogen <i>Pseudonectria foliicola</i> . PeerJ, 2018, 6, e5401.	0.9	18
2990	Identification of an aquaculture poriferan ‘Pest with Potential’ and its phylogenetic implications. PeerJ, 2018, 6, e5586.	0.9	13
2991	Three, two, one! Revision of the long-bodied sphaerodorids (Sphaerodoridae, Annelida) and synonymization of <i>Ephesiella</i> , <i>Ephesiopsis</i> and <i>Sphaerodorum</i> . PeerJ, 2018, 6, e5783.	0.9	4
2992	Do longer sequences improve the accuracy of identification of forensically important Calliphoridae species?. PeerJ, 2018, 6, e5962.	0.9	10
2993	The complete chloroplast genomes of three Betulaceae species: implications for molecular phylogeny and historical biogeography. PeerJ, 2019, 7, e6320.	0.9	26
2994	Embracing heterogeneity: coalescing the Tree of Life and the future of phylogenomics. PeerJ, 2019, 7, e6399.	0.9	111
2995	Phylogenomic analysis and revised classification of atypoid mygalomorph spiders (Araneae, Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tj	0.9	62
2996	First genomic insights into members of a candidate bacterial phylum responsible for wastewater bulking. PeerJ, 2015, 3, e740.	0.9	157
2997	Sequencing and analyses on chloroplast genomes of <i>Tetrataenium candicans</i> and two allies give new insights on structural variants, DNA barcoding and phylogeny in Apiaceae subfamily Apioideae. PeerJ, 2019, 7, e8063.	0.9	18

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2999	The mitochondrial genome of <i>Apion squamigerum</i> (Coleoptera, Curculionoidea, Brentidae) and the phylogenetic implications. PeerJ, 2020, 8, e8386.	0.9	6
3000	Five new pseudocryptic land planarian species of <i>Cratera</i> (Platyhelminthes: Tricladida) unveiled through integrative taxonomy. PeerJ, 2020, 8, e9726.	0.9	7
3001	<i>Asperosporus subterraneus</i> , a new genus and species of sequestrate Agaricaceae found in Florida nursery production. Fungal Systematics and Evolution, 2021, 8, 91-100.	0.9	0
3003	Evolution and phylogeny of the deep-sea isopod families Desmosomatidae Sars, 1897 and Nannoniscidae Hansen, 1916A (Isopoda: Asellota). Organisms Diversity and Evolution, 2021, , 1-27.	0.7	7
3004	No hybrid snowcocks in the Altai—Hyper-variable markers can be problematic for phylogenetic inference. Ecology and Evolution, 2021, 11, 16354-16364.	0.8	1
3005	The mitochondrial genome of <i>Nemalécium lighti</i> (Hydrozoa, Leptothecata). Mitochondrial DNA Part B: Resources, 2021, 6, 3196-3198.	0.2	2
3006	The genome of <i>Shorea leprosula</i> (Dipterocarpaceae) highlights the ecological relevance of drought in aseasonal tropical rainforests. Communications Biology, 2021, 4, 1166.	2.0	13
3007	Discovery and Evolution of a Divergent Coronavirus in the Plateau Pika From China That Extends the Host Range of Alphacoronaviruses. Frontiers in Microbiology, 2021, 12, 755599.	1.5	9
3009	Phylogeny of <i>Crataegus</i> (Rosaceae) based on 257 nuclear loci and chloroplast genomes: evaluating the impact of hybridization. PeerJ, 2021, 9, e12418.	0.9	6
3010	Implications of divergence of methionine adenosyltransferase in archaea. FEBS Open Bio, 2022, 12, 130-145.	1.0	2
3011	New insights on <i>Pomphorhynchus sphaericus</i> Gil de Pertierra, Spatz et Doma, 1996 (Acanthocephala:). Tj ETQq1 1 0,784314 rgBT /Over	0,6	8
3012	Phylogenetic relationships and the evolution of host preferences in the largest clade of brood parasitic bees (Apidae: Nomadinae). Molecular Phylogenetics and Evolution, 2022, 166, 107326.	1.2	11
3013	Comparative genomics reveals molecular mechanisms underlying health and reproduction in cryptorchid mammals. BMC Genomics, 2021, 22, 763.	1.2	2
3014	Mitochondrial and karyotypic evidence reveals a lack of support for the genus <i>Nasuella</i> (Procyonidae.) Tj ETQq0 0 0,rgBT /Overlock 10 TF	0,4	2
3015	High-quality reference genome of <i>Fasciola gigantica</i> : Insights into the genomic signatures of transposon-mediated evolution and specific parasitic adaption in tropical regions. PLoS Neglected Tropical Diseases, 2021, 15, e0009750.	1.3	12
3016	Molecular characterization of superoxide dismutase and catalase genes, and the induction of antioxidant genes under the zinc oxide nanoparticle-induced oxidative stress in air-breathing magur catfish (<i>Clarias magur</i>). Fish Physiology and Biochemistry, 2021, 47, 1909-1932.	0.9	9
3017	A new tetra-segmented splipalmivirus with divided RdRP domains from <i>Cryphonectria naterciae</i> , a fungus found on chestnut and cork oak trees in Europe. Virus Research, 2022, 307, 198606.	1.1	16

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3019	The genome of the black cutworm <i>Agrotis ipsilon</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2021, 139, 103665.	1.2	8
3022	Methods to Study the Occurrence and the Evolution of Pseudogenes Through a Phylogenetic Approach. <i>Methods in Molecular Biology</i> , 2014, 1167, 87-99.	0.4	0
3023	Computational Biology:: The Fundamentals of Sequence-Based Techniques. , 2014, , 1-28.		0
3024	Systematics and phylogeography of <i>Acanthodactylus schreiberi</i> and its relationships with <i>Acanthodactylus boskianus</i> (Reptilia: Squamata: Lacertidae). <i>Zoological Journal of the Linnean Society</i> , 2014, 172, 720-739.	1.0	8
3025	Genome-Wide Detection of Selection and Other Evolutionary Forces. <i>Methods in Molecular Biology</i> , 2015, 1231, 271-287.	0.4	1
3028	Report of isolation of <i>Cryptobacterium curtum</i> from a pelvic abscess. <i>JMM Case Reports</i> , 2015, 2, .	1.3	0
3038	A simple method to test the reproducibility of the phylogenetic reconstructions: the molecular systematics of cyanobacteria as a case study. <i>Fottea</i> , 2016, 16, 209-217.	0.4	0
3040	Ä±nâ€™de Kanatlı± Hayvanlardan Ä°zole Edilen <i>Pasteurella multocida</i> SuÄ°YarÄ±nÄ±n MolekÄ¼ler Karakterizasyonu ve tonB Geni AÄŠÄ±sÄ±ndan Genetik Analizi. <i>Kafkas Universitesi Veteriner Fakultesi Dergisi</i> , 2017, , .	0.0	0
3041	First report of <i>Mycena clavata</i> (Fungi, Agaricales) in the Czech Republic including notes on its taxonomy, phylogenetic position and ecology.. <i>Czech Mycology</i> , 2017, 69, 1-14.	0.2	3
3042	Alignment and Mapping. , 2017, , 105-125.		0
3046	Revisiting the phylogeny of phylum Ctenophora: a molecular perspective. <i>F1000Research</i> , 0, 5, 2881.	0.8	0
3049	A new large tellinid species of the genus <i>Pharaonella</i> from the Ryukyu Archipelago, Japan (Mollusca.) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 74</i>	0.5	2
3062	<i>Chromobacterium pseudoviolaceum</i> KÄmpfer et al. 2009 is a later heterotypic synonym of <i>Chromobacterium violaceum</i> Bergonzini 1880. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 2967-2968.	0.8	6
3067	Isolation and Identification of <i>Listeria monocytogenes</i> from Fish Intestines and Phylogenetic Analysis. <i>International Journal of Current Microbiology and Applied Sciences</i> , 2018, 7, 1177-1187.	0.0	0
3069	First record of the box crab <i>Cryptosoma balguerii</i> (Desbonne in Desbonne and Schramm, 1867) (Brachyura: Calappidae) from SÄ±o Paulo, Brazil revealed by DNA markers. <i>Nauplius</i> , 0, 27, .	0.3	1
3070	Identification of Plant Growth Promoting Rhizobacteria as Biofertilizer for Salt Stress Environment. <i>International Journal of Current Microbiology and Applied Sciences</i> , 2019, 8, 2633-2645.	0.0	0
3074	<i>Usnea oreophila</i> (Parmeliaceae), a new saxicolous species from the mountains of Brazil. <i>Bryologist</i> , 2019, 122, 122.	0.1	3

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3081	Phylogenetics Study of <i>Salvia</i> L. spp. Collections from the Botanical Garden of Medicinal Plants of Wrocław Medical University. <i>Biodiversity Information Science and Standards</i> , 0, 3, .	0.0	0
3082	<i>Frischella japonica</i> sp. nov., an anaerobic member of the Orbales in the Gammaproteobacteria, isolated from the gut of the eastern honey bee, <i>Apis cerana japonica</i> Fabricius. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 71, .	0.8	7
3085	<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
3090	A Comparative Study on <i>Pseudomonas</i> and <i>Bacillus</i> L. asparaginases.. <i>Journal of Pure and Applied Microbiology</i> , 2019, 13, 1635-1644.	0.3	0
3093	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
3095	<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
3096	<i>Sphaerocarpaceae</i> (Marchantiophyta) new to China, with special references to a new species of <i>Sphaerocarpos</i> from Hengduan Mountains. <i>Bryologist</i> , 2019, 122, 586.	0.1	8
3100	10. Robust Inferences from Ambiguous Alignments. , 2019, , 209-270.		3
3103	Taxonomic Notes on <i>Pycnothelia</i> Dufour and <i>Gymnoderma</i> Nyl. (Cladoniaceae) in Madagascan Region. <i>Cryptogamie, Mycologie</i> , 2020, 41, 109.	0.2	1
3104	New morphological and molecular data for <i>Xystretrum solidum</i> (Gorgoderidae, Gorgoderinae) from <i>Sphoeroides testudineus</i> (Tetraodontiformes, Tetraodontidae) in Mexican waters. <i>ZooKeys</i> , 2020, 925, 141-161.	0.5	3
3110	<i>Halanonchus scintillatulus</i> sp. nov. from New Zealand and a review of the suborder Trefusiina (Nematoda: Enoplida). <i>European Journal of Taxonomy</i> , 2020, , .	0.6	1
3118	Genomewide analysis of sperm whale E2 ubiquitin conjugating enzyme genes. <i>Journal of Genetics</i> , 2021, 100, 1.	0.4	0
3119	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
3120	Genome and gene evolution of seahorse species revealed by the chromosome-level genome of <i>Hippocampus abdominalis</i> . <i>Molecular Ecology Resources</i> , 2022, 22, 1465-1477.	2.2	11
3121	Genotype I African swine fever viruses emerged in domestic pigs in China and caused chronic infection. <i>Emerging Microbes and Infections</i> , 2021, 10, 2183-2193.	3.0	113
3122	Pan-phylum genome-wide identification of sodium calcium exchangers reveal heterogeneous expansions and possible roles in nematode parasitism. <i>Gene</i> , 2022, 810, 146052.	1.0	2
3123	Morphology and molecular phylogeny of <i>Pauciconfibuloides amazonica</i> gen. n. sp. n. (Platyhelminthes.) <i>Tj ETQq1 1 0.784314 rgBT / Otel</i> <i>International</i> , 2021, 87, 102489.	0.6	1

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3124	A draft genome, resequencing, and metabolomes reveal the genetic background and molecular basis of the nutritional and medicinal properties of loquat (<i>Eriobotrya japonica</i> (Thunb.) Lindl). <i>Horticulture Research</i> , 2021, 8, 231.	2.9	14
3125	Detection of Pathogenic and Beneficial Microbes for Roselle Wilt Disease. <i>Frontiers in Microbiology</i> , 2021, 12, 756100.	1.5	2
3126	Connected across the ocean: taxonomy and biogeography of deep-water Nudibranchia from the Northwest Pacific reveal trans-Pacific links and two undescribed species. <i>Organisms Diversity and Evolution</i> , 2021, 21, 753-782.	0.7	6
3129	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> . <i>Journal of Eukaryotic Microbiology</i> , 2021, 68, e12832.	0.8	4
3130	Morphological and Molecular Evidence for the Occurrence of <i>Hodophilus variabilipes</i> (Clavariaceae). <i>Trends in Microbiology</i> , 2021, 29, 1012120.	0.3	0
3136	A Differentially Expressed Gene from a High Oil Producer Cultivar of Castor Bean (<i>Ricinus communis</i>) Is Involved in the Biosynthesis of Ricinoleic Acid. <i>American Journal of Plant Sciences</i> , 2020, 11, 393-412.	0.3	1
3137	Morphological and molecular characterization of <i>Haemoproteus coatneyi</i> and <i>Haemoproteus erythrogravidus</i> (Haemosporida: Haemoproteidae) in Passeriformes in Brazil's Atlantic Forest. <i>Brazilian Journal of Veterinary Parasitology</i> , 2020, 29, e011520.	0.2	1
3142	Diversity and toxicity of Pacific strains of the benthic dinoflagellate <i>Coolia</i> (Dinophyceae), with a look at the <i>Coolia canariensis</i> species complex. <i>Harmful Algae</i> , 2021, 109, 102120.	2.2	3
3143	Different gene rearrangements of the genus <i>Dardanus</i> (Anomura: Diogenidae) and insights into the phylogeny of Paguroidea. <i>Scientific Reports</i> , 2021, 11, 21833.	1.6	7
3144	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
3148	Two new species and six new records of <i>Buellia</i> s.l. (lichenized Ascomycota, Caliciaceae) from China. <i>Bryologist</i> , 2020, 123, .	0.1	2
3150	<i>Zehneria grandibracteata</i> (Cucurbitaceae), an overlooked new species from western Kenyan forests. <i>PhytoKeys</i> , 2020, 165, 85-98.	0.4	2
3155	Geographically structured genomic diversity of non-human primate-infecting <i>Treponema pallidum</i> subsp. <i>pertenue</i> . <i>Microbial Genomics</i> , 2020, 6, .	1.0	2
3157	Molecular assessment and transcriptome profiling of wild fish populations of <i>Oryzias mekongensis</i> and <i>O. songkhramensis</i> (Adrianichthyidae: Beloniformes) from Thailand. <i>PLoS ONE</i> , 2020, 15, e0242382.	1.1	0
3158	Taxonomic Study of <i>Hypotrachyna</i> Subg. <i>Everniastrum</i> (Hale Ex Sipman) Divakar, A.Crespo, Sipman, Elix & Lumbsch (Ascomycota) from China. <i>Cryptogamie, Mycologie</i> , 2020, 41, .	0.2	0
3159	New records of non-indigenous <i>Branchiommata</i> and <i>Parasabella</i> species (Sabellidae: Annelida) in South Australia highlight the continuing challenges for sabellid taxonomy. <i>Journal of Natural History</i> , 2020, 54, 2647-2673.	0.2	0
3160	A new species of the lichenised genus (Baeomycetaceae, Baeomycetales) from Tengger Desert of China. <i>Mycology</i> , 2018, , 107-118.	0.8	0
3161	<i>Polyozellus</i> vs. <i>Pseudotomentella</i> : generic delimitation with a multi-gene dataset. <i>Fungal Systematics and Evolution</i> , 2021, 8, 143-154.	0.9	0

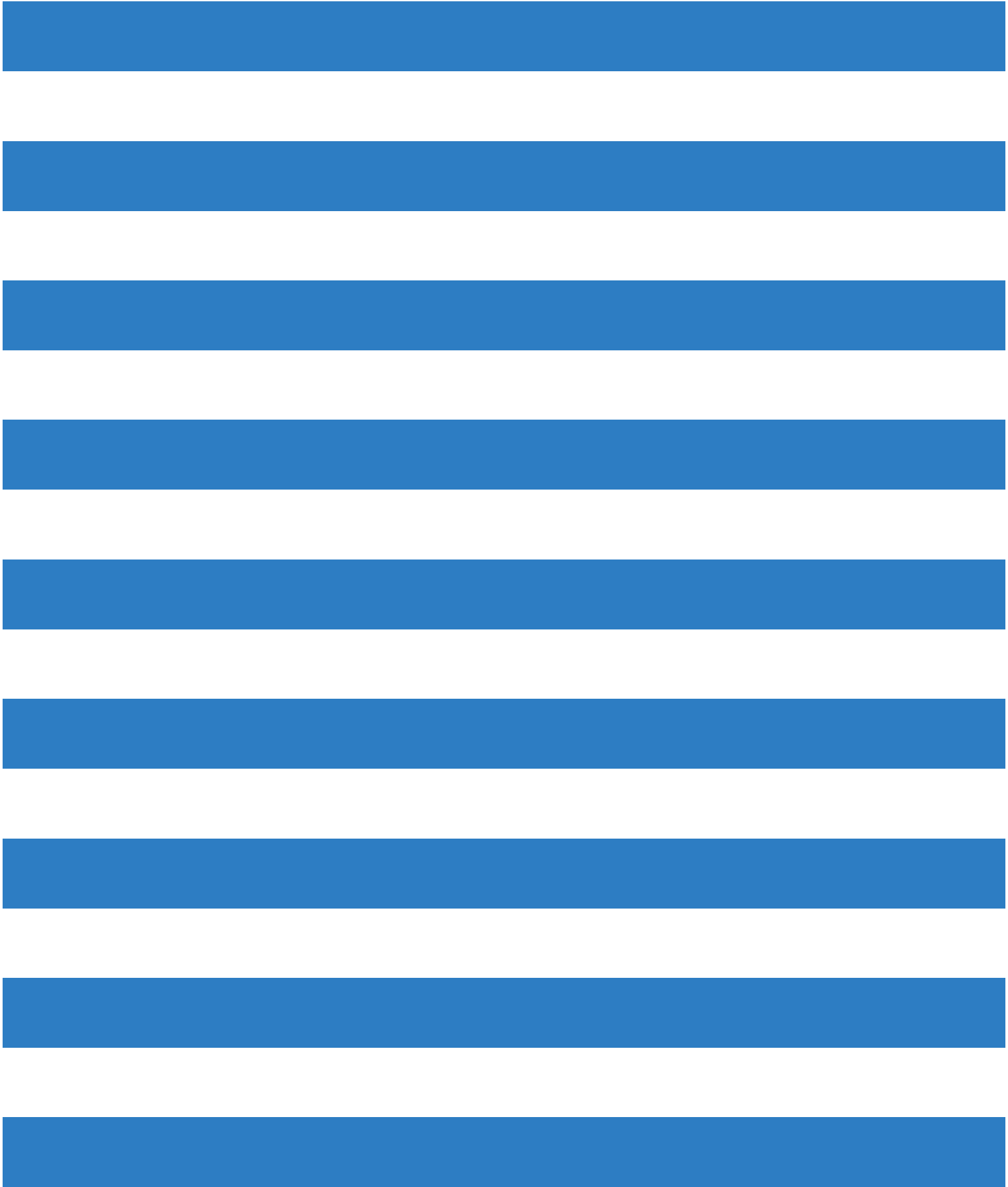
#	ARTICLE	IF	CITATIONS
3162	Global dispersal and diversification in ground beetles of the subfamily Carabinae. <i>Molecular Phylogenetics and Evolution</i> , 2022, 167, 107355.	1.2	9
3163	Conserved molecular signatures in the spike protein provide evidence indicating the origin of SARS-CoV-2 and a Pangolin-CoV (MP789) by recombination(s) between specific lineages of Sarbecoviruses. <i>PeerJ</i> , 2021, 9, e12434.	0.9	5
3164	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
3165	A Minimal yet Flexible Likelihood Framework to Assess Correlated Evolution. <i>Systematic Biology</i> , 2022, 71, 823-838.	2.7	4
3166	Genome analysis suggests the bacterial family Acetobacteraceae is a source of undiscovered specialized metabolites. <i>Antonie Van Leeuwenhoek</i> , 2022, 115, 41-58.	0.7	8
3167	Morphological and Molecular Characterization of Some Egyptian Six-Rowed Barley (<i>Hordeum vulgare</i>) Tj ETQq1 1 0,784314 rgBT /Overd	1.6	5
3168	Mitochondrial Genome of <i>Episesarma lafondii</i> (Brachyura: Sesamidae) and Comparison with Other Sesamid Crabs. <i>Journal of Ocean University of China</i> , 2021, 20, 1545-1556.	0.6	7
3170	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
3171	Resurrecting Enzymes by Ancestral Sequence Reconstruction. <i>Methods in Molecular Biology</i> , 2022, 2397, 111-136.	0.4	13
3173	Regulatory circuits involving bud dormancy factor PpeDAM6. <i>Horticulture Research</i> , 2021, 8, 261.	2.9	13
3174	Identification and pathogenicity of <i>Alternaria</i> species associated with leaf blotch disease and premature defoliation in French apple orchards. <i>PeerJ</i> , 2021, 9, e12496.	0.9	13
3175	Bacterial, archaeal, and fungal community structure and interrelationships of deep-sea shrimp intestine and the surrounding sediment. <i>Environmental Research</i> , 2022, 205, 112461.	3.7	5
3176	Nucleotide composition bias of rDNA sequences as a source of phylogenetic artifacts in Basidiomycota—a case of a new lineage of a uredinicolous <i>Ramularia</i> -like anamorph with affinities to <i>Ustilaginomycotina</i> . <i>Mycological Progress</i> , 2021, 20, 1553-1571.	0.5	3
3177	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
3178	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
3179	A molecular phylogeny of the circum-Antarctic Opiliones family <i>Neopilionidae</i> . <i>Invertebrate Systematics</i> , 2021, 35, 827-849.	0.5	3
3180	Epidemic of cutaneous fowlpox in a naïve population of chickens and turkeys in Austria: Detailed phylogenetic analysis indicates co-evolution of Fowlpox virus with reticuloendotheliosis virus. <i>Transboundary and Emerging Diseases</i> , 2022, , .	1.3	2
3181	<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

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3183	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
3184	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
3185	Genomic Characterization of <i>Parengyodontium torokii</i> sp. nov., a Biofilm-Forming Fungus Isolated from Mars 2020 Assembly Facility. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 66.	1.5	4
3186	Conservation genomics of federally endangered <i>Texella</i> harvester species (Arachnida, Opiliones). <i>Systematic Entomology and Biogeography</i> , 2022, 48, 101-110.	0.8	7
3187	Plastome structure, evolution, and phylogeny of <i>Selaginella</i> . <i>Molecular Phylogenetics and Evolution</i> , 2022, 169, 107410.	1.2	11
3188	Identification and sequencing of bacteria from crop field: Application of bacteria as agro-waste biosorbent for rapid pesticide removal. <i>Environmental Technology and Innovation</i> , 2022, 25, 102116.	3.0	7
3189	Description of <i>Gyrodactylus banmae</i> n. sp. (Monogenea, Gyrodactylidae) parasitic on zebrafish, <i>Danio rerio</i> . <i>Parasitology International</i> , 2022, 87, 102531.	0.6	2
3190	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
3191	Should we hail the Red King? Evolutionary consequences of a mutualistic lifestyle in genomes of lichenized ascomycetes. <i>Ecology and Evolution</i> , 2022, 12, e8471.	0.8	4
3192	First Phylogenomic Assessment of the Amphitropical New World Ant Genus <i>Dorymyrmex</i> (Hymenoptera: Formicidae), a Longstanding Taxonomic Puzzle. <i>Insect Systematics and Diversity</i> , 2022, 6, .	0.7	2
3193	Higher-level phylogeny of Chrysomelidae based on expanded sampling of mitogenomes. <i>PLoS ONE</i> , 2022, 17, e0258587.	1.1	2
3194	Characterization, Comparison of Four New Mitogenomes of Centrotinae (Hemiptera: Membracidae) and Phylogenetic Implications Supports New Synonymy. <i>Life</i> , 2022, 12, 61.	1.1	4
3195	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>SSRN Electronic Journal</i> , 0, .	0.4	0
3196	Higher classification of mealybugs (Hemiptera: Coccoomorpha) inferred from molecular phylogeny and their endosymbionts. <i>Systematic Entomology</i> , 2022, 47, 354-370.	1.7	10
3197	Comparative chloroplast genome analyses of cultivated spinach and two wild progenitors shed light on the phylogenetic relationships and variation. <i>Scientific Reports</i> , 2022, 12, 856.	1.6	7
3198	Evidence of positive selection on six spider developmental genes. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2022, 338, 314-322.	0.6	2
3199	Rapid alignment updating with Extensiphy. <i>Methods in Ecology and Evolution</i> , 2022, 13, 682-693.	2.2	0

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3201	Novel duplication remnant in the first complete mitogenome of <i>Hemitriakis japonica</i> and the unique phylogenetic position of family Triakidae. <i>Gene</i> , 2022, 820, 146232.	1.0	5
3202	The complete mitochondrial genome of a tropical midge <i>Chironomus kiiensis</i> Tokunaga, 1936 (Diptera: Chironomidae). <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 211-212.	0.2	4
3203	Complete genomic sequence of Hibiscus latent Fort Pierce virus in a new host, <i>Passiflora edulis</i> , in China. <i>Journal of Plant Pathology</i> , 2022, 104, 369-373.	0.6	3
3204	Chromosome restructuring and number change during the evolution of <i>Morus notabilis</i> and <i>Morus alba</i> . <i>Horticulture Research</i> , 2022, 9, .	2.9	16
3205	A new species of the genus <i>Coryphella</i> (Gastropoda: Nudibranchia) from the Kuril Islands. <i>Ruthenica</i> , 2022, 32, 41-48.	0.2	2
3206	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
3207	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
3208	Rapid radiation in a highly diverse marine environment. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	10
3209	New data on the mitochondrial genome of Nematocera (lower Diptera): features, structures and phylogenetic implications. <i>Zoological Journal of the Linnean Society</i> , 2023, 197, 229-245.	1.0	13
3210	Convergent evolution of a blood-red nectar pigment in vertebrate-pollinated flowers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	15
3212	Activation by cleavage of the epithelial Na ⁺ channel β and γ subunits independently coevolved with the vertebrate terrestrial migration. <i>ELife</i> , 2022, 11, .	2.8	5
3213	Chromosome-level genome assembly of <i>Zizania latifolia</i> provides insights into its seed shattering and phytocassane biosynthesis. <i>Communications Biology</i> , 2022, 5, 36.	2.0	11
3214	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
3215	Species Paraphyly and Social Parasitism: Phylogenomics, Morphology, and Geography Clarify the Evolution of the <i>Pseudomyrmex elongatulus</i> Group (Hymenoptera: Formicidae), a Mesoamerican Ant Clade. <i>Insect Systematics and Diversity</i> , 2022, 6, .	0.7	5
3217	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	1
3219	Comparative Analysis of the Complete Mitochondrial Genomes of Five Species of Ricaniidae (Hemiptera: Tj ETQq0 0.0 rgBT /Qverlock 10	1.3	5
3220	Genomes shed light on the evolution of <i>Begonia</i> , a mega-diverse genus. <i>New Phytologist</i> , 2022, 234, 295-310.	3.5	18

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3243	Comparison of chloroplast genomes of compound-leaved maples and phylogenetic inference with other <i>Acer</i> species. <i>Tree Genetics and Genomes</i> , 2022, 18, 1.	0.6	3
3244	First complete mitochondrial genomes of Otoretinae (Coleoptera, Lampyridae) with evolutionary insights into the gene rearrangement. <i>Genomics</i> , 2022, 114, 110305.	1.3	6
3245	Comparative and phylogenomic analyses of mitochondrial genomes in Coccinellidae (Coleoptera: Tj ETQq1 1 0.784314 rgBT ₃ Overlo	0.9	3
3246	Chromosome-level genome assembly, annotation, and phylogenomics of the gooseneck barnacle <i>Pollicipes pollicipes</i> . <i>GigaScience</i> , 2022, 11, .	3.3	8
3247	Evolutionary DÃ©jÃ Vu: Extreme Convergence in an Ant-Plant Association. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
3248	Chromosome-Scale <i>Cerasus Humilis</i> Genome Assembly Reveals Gene Family Evolution and Possible Genomic Basis of Calcium Accumulation in Fruits. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
3249	Evolutionary impacts of purine metabolism genes on mammalian oxidative stress adaptation. <i>Zoological Research</i> , 2022, 43, 241-254.	0.9	21
3250	A New Termitophilous Genus of Paederinae Rove Beetles (Coleoptera, Staphylinidae) from the Neotropics and Its Phylogenetic Position. <i>Neotropical Entomology</i> , 2022, 51, 282-291.	0.5	3
3251	Convergent consequences of parthenogenesis on stick insect genomes. <i>Science Advances</i> , 2022, 8, eabg3842.	4.7	27
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3255	A new endemic, <i>Pannaria oregonensis</i> , replaces two misapplied names in the Pacific Northwest of North America. <i>Bryologist</i> , 2022, 125, .	0.1	1
3256	DNA Barcoding versus Morphological Variability of <i>Pterostichus brevicornis brevicornis</i> (Kirby, 1837) (Coleoptera, Carabidae) in the Arctic and Subarctic. <i>Insects</i> , 2022, 13, 204.	1.0	5
3257	Comparative and Phylogenetic Analysis Based on the Chloroplast Genome of <i>Coleanthus subtilis</i> (Tratt.) Seidel, a Protected Rare Species of Monotypic Genus. <i>Frontiers in Plant Science</i> , 2022, 13, 828467.	1.7	13
3258	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
3260	Evolutionary Significance of NHX Family and NHX1 in Salinity Stress Adaptation in the Genus <i>Oryza</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 2092.	1.8	19
3261	The S100A7 nuclear interactors in autoimmune diseases: a coevolutionary study in mammals. <i>Immunogenetics</i> , 2022, , 1.	1.2	0
3262	Phylogenomics of paleoendemic lampshade spiders (Araneae, Hypochilidae, <i>Hypochilus</i>), with the description of a new species from montane California. <i>ZooKeys</i> , 2022, 1086, 163-204.	0.5	5

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3264	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
3265	Comprehensive identification of protein orthologs in the family Ascoviridae facilitates an understanding of phylogenomics, protein conservation, and phosphorylation. <i>Archives of Virology</i> , 2022, 167, 1075-1087.	0.9	0
3267	Origin and Evolution of Enzymes with MIO Prosthetic Group: Microbial Coevolution After the Mass Extinction Event. <i>Frontiers in Genetics</i> , 2022, 13, 851738.	1.1	0
3268	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
3269	A Novel and Ubiquitous Marine Methylophage Provides Insights into Viral-Host Coevolution and Possible Host-Range Expansion in Streamlined Marine Heterotrophic Bacteria. <i>Applied and Environmental Microbiology</i> , 2022, 88, e0025522.	1.4	2
3270	The Complete Mitochondrial Genome of the Chicken Body Louse, <i>Menacanthus cornutus</i> , and Evolutionary Patterns of Extensive Gene Rearrangements in the Mitochondrial Genomes of Amblycera (Psocodea: Phthiraptera). <i>Genes</i> , 2022, 13, 522.	1.0	2
3272	Mitogenomics provides new insights into the phylogenetic relationships and evolutionary history of deep-sea sea stars (Asteroidea). <i>Scientific Reports</i> , 2022, 12, 4656.	1.6	9
3273	Phylogeny and biogeography of the northern temperate genus <i>Dracocephalum</i> s.l. (Lamiaceae). <i>Cladistics</i> , 2022, 38, 429-451.	1.5	6
3274	Biogeography and Diversification of Bumblebees (Hymenoptera: Apidae), with Emphasis on Neotropical Species. <i>Diversity</i> , 2022, 14, 238.	0.7	7
3275	Genomes, repeatomes and interphase chromosome organization in the meadowfoam family (Limnanthaceae, Brassicales). <i>Plant Journal</i> , 2022, 110, 1462-1475.	2.8	2
3276	Dactylogyridae 2022: a meta-analysis of phylogenetic studies and generic diagnoses of parasitic flatworms using published genetic and morphological data. <i>International Journal for Parasitology</i> , 2022, 52, 427-457.	1.3	8
3277	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
3278	Taxonomy and Phylogeny of Two Tintinnid Ciliates of <i>Leprotintinnus</i> (Protista, Ciliophora). <i>Frontiers in Marine Science</i> , 2022, 9, .	1.2	1
3279	Unraveling the evolutionary history of the snakefly family Inocelliidae (Insecta: Raphidioptera) through integrative phylogenetics. <i>Cladistics</i> , 2022, 38, 515-537.	1.5	5
3280	Comparative analysis of four complete mitogenomes from hoverfly genus <i>Eristalinus</i> with phylogenetic implications. <i>Scientific Reports</i> , 2022, 12, 4164.	1.6	0
3281	Evolution analysis of <i>FRIZZY PANICLE</i> (<i>FZP</i>) orthologs explored the mutations in DNA coding sequences in the grass family (Poaceae). <i>PeerJ</i> , 2022, 10, e12880.	0.9	7
3283	The complete mitochondrial genome of <i>Ephemera serica</i> (Ephemeroptera: Ephemeridae) and phylogenetic analysis. <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 461-463.	0.2	1

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3285	Stasis and diversity in living fossils: Species delimitation and evolution of lingulid brachiopods. <i>Molecular Phylogenetics and Evolution</i> , 2022, 175, 107460.	1.2	5
3286	Co-expression network analyses of anthocyanin biosynthesis genes in <i>Ruellia</i> (Wild Petunias); Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 662	0.7	2
3287	Molecular phylogeny and speciation patterns in host-specific monogeneans (<i>Cichlidogyrus</i>), Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 662 <i>Journal for Parasitology</i> , 2022, , .	1.3	9
3288	Integrated metagenomics identifies a crucial role for trimethylamine-producing <i>Lachnoclostridium</i> in promoting atherosclerosis. <i>Npj Biofilms and Microbiomes</i> , 2022, 8, 11.	2.9	41
3289	<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
3290	Mitogenomic phylogenetics and population genetics of several taxa of agouties (<i>Dasyprocta</i> sp.), Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 662 1.	0.6	1
3291	Rapid evolution fuels transcriptional plasticity to ocean acidification. <i>Global Change Biology</i> , 2022, 28, 3007-3022.	4.2	23
3292	Genomic Fishing and Data Processing for Molecular Evolution Research. <i>Methods and Protocols</i> , 2022, 5, 26.	0.9	4
3293	<i>Agromyces archimandritae</i> sp. nov., isolated from the cockroach <i>Archimandrita tessellata</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	7
3294	Genomic and Experimental Analysis of the Insecticidal Factors Secreted by the Entomopathogenic Fungus <i>Beauveria pseudobassiana</i> RGM 2184. <i>Journal of Fungi</i> (Basel, Switzerland), 2022, 8, 253.	1.5	11
3296	Phylogeny of <i>Marsdenieae</i> (Apocynaceae, Asclepiadoideae) based on chloroplast and nuclear loci, with a conspectus of the genera. <i>Taxon</i> , 2022, 71, 833-875.	0.4	9
3297	The First Deep-Sea Stylasterid (Hydrozoa, Stylasteridae) of the Red Sea. <i>Diversity</i> , 2022, 14, 241.	0.7	5
3298	Sequence analysis of <i>Erianthus arundinaceus</i> chromosome 1 isolated by flow sorting after genomic in situ hybridization in suspension. <i>Crop Journal</i> , 2022, , .	2.3	0
3299	Phylogenomic analyses of echinoid diversification prompt a re-evaluation of their fossil record. <i>ELife</i> , 2022, 11, .	2.8	22
3300	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
3301	CIAlign: A highly customisable command line tool to clean, interpret and visualise multiple sequence alignments. <i>PeerJ</i> , 2022, 10, e12983.	0.9	32
3302	The evolution of huge Y chromosomes in <i>Coccinia grandis</i> and its sister, <i>Coccinia schimperi</i> . <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2022, 377, 20210294.	1.8	5

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3304	Phylogenomics of braconid wasps (Hymenoptera, Braconidae) sheds light on classification and the evolution of parasitoid life history traits. <i>Molecular Phylogenetics and Evolution</i> , 2022, 173, 107452.	1.2	21
3305	The new <i>Haemaphysalis longicornis</i> genome provides insights into its requisite biological traits. <i>Genomics</i> , 2022, 114, 110317.	1.3	9
3306	An improved <i>Raphanus sativus</i> cv. WK10039 genome localizes centromeres, uncovers variation of DNA methylation and resolves arrangement of the ancestral Brassica genome blocks in radish chromosomes. <i>Theoretical and Applied Genetics</i> , 2022, 135, 1731-1750.	1.8	6
3307	Phylogeography of the endangered orchids <i>Cypripedium japonicum</i> and <i>Cypripedium formosanum</i> in East Asia: Deep divergence at infraâ€and interspecific levels. <i>Taxon</i> , 2022, 71, 733-757.	0.4	4
3308	<i>Amanita</i> sect. Phalloideae: two interesting non-lethal species from West Africa. <i>Mycological Progress</i> , 2022, 21, 1.	0.5	5
3309	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
3310	Paleozoic origins of cheilostome bryozoans and their parental care inferred by a new genome-skimmed phylogeny. <i>Science Advances</i> , 2022, 8, eabm7452.	4.7	19
3311	New data in Porotheleaceae and Cyphellaceae: epitypification of <i>Prunulus scabripes</i> Murrill, the status of <i>Mycopan Redhead</i> , <i>Moncalvo</i> & <i>Vilgalys</i> and a new combination in <i>Pleurella</i> Horak emend.. <i>Mycological Progress</i> , 2022, 21, 1.	0.5	6
3312	Comparative Analysis of Four Complete Mitochondrial Genomes of Epinephelidae (Perciformes). <i>Genes</i> , 2022, 13, 660.	1.0	5
3313	Finding the needle in the haystack: a revision of <i>Crittendenia</i> , a surprisingly diverse lichenicolous genus of Agaricostilbomycetes, Pucciniomycotina. <i>Bryologist</i> , 2022, 125, .	0.1	5
3314	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
3315	Description of an Enigmatic Alveolate, <i>Platyproteum noduliferae</i> n. sp., and Reconstruction of its Flagellar Apparatus. <i>Protist</i> , 2022, 173, 125878.	0.6	1
3316	New Insight Into Visual Adaptation in the Mudskipper Cornea: From Morphology to the Cornea-Related COL8A2 Gene. <i>Frontiers in Ecology and Evolution</i> , 2022, 10, .	1.1	3
3317	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
3318	Phylogenomics and historical biogeography of the cleptoparasitic bee genus <i>Nomada</i> (Hymenoptera: Tj ETQq1 1 0,784314 rgBT /Overle	1.2	4
3319	Chromosome-scale <i>Cerasus humilis</i> genome assembly reveals gene family evolution and possible genomic basis of calcium accumulation in fruits. <i>Scientia Horticulturae</i> , 2022, 299, 111012.	1.7	5
3320	The first phylogenetic and species delimitation study of the nudibranch genus <i>Gymnodoris</i> reveals high species diversity (Gastropoda: Nudibranchia). <i>Molecular Phylogenetics and Evolution</i> , 2022, 171, 107470.	1.2	7

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3333	<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
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3588	The complete plastid genome of an Antarctic moss <i>Chorisodontium aciphyllum</i> (Hook. f. & amp;) Tj ETQq1 1 0,784314 rgBT / Overlock 10 Tf 50 262	0.2	0
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3680	Hidden Species Diversity was Explored in Two Genera of Catapyrenioid Lichens (Verrucariaceae,) Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.5	3

#	ARTICLE	IF	CITATIONS
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3684	Comparative genome anatomy reveals evolutionary insights into a unique amphitriploid fish. <i>Nature Ecology and Evolution</i> , 2022, 6, 1354-1366.	3.4	29
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3688	Out of the temperate zone: A phylogenomic test of the biogeographical conservatism hypothesis in a contrarian clade of ants. <i>Journal of Biogeography</i> , 2022, 49, 1640-1653.	1.4	7
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3690	A Chromosome-Level Genome Assembly of <i>Toona ciliata</i> (Meliaceae). <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	7
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3699	Morphology, Palynology and Molecular Phylogeny of <i>Barleria cristata</i> L. (Acanthaceae) Morphotypes from India. <i>Diversity</i> , 2022, 14, 677.	0.7	0

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3702	<i>Idaho</i> and <i>Subularia</i> : Hidden polyploid origins of two enigmatic genera of crucifers. <i>American Journal of Botany</i> , 0, , .	0.8	4
3703	ZW sex-chromosome evolution and contagious parthenogenesis in <i>Artemia</i> brine shrimp. <i>Genetics</i> , 2022, 222, .	1.2	5
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3712	Phylogenetic position of the enigmatic genus <i>Atherospio</i> and description of <i>Atherospio aestuarii</i> sp. nov. (Annelida: Spionidae) from Japan. <i>PeerJ</i> , 0, 10, e13909.	0.9	1
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3714	Genome Organization and Comparative Evolutionary Mitochondriomics of Brown Planthopper, <i>Nilaparvata lugens</i> Biotype 4 Using Next Generation Sequencing (NGS). <i>Life</i> , 2022, 12, 1289.	1.1	0
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3717	Comparative analysis of complete mitochondrial genomes of three <i>Trichoglossus</i> species (Psittaciformes: Psittacidae). <i>Molecular Biology Reports</i> , 0, , .	1.0	0
3718	Novel insertions in the mitochondrial maxicircle of <i>Trypanosoma musculi</i> , a mouse trypanosome. <i>Parasitology</i> , 2022, 149, 1546-1555.	0.7	0
3719	<i>Pseudocitrobacter corydidari</i> sp. nov., isolated from the Asian emerald cockroach <i>Corydarium magnifica</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	1

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3721	Molecular Phylogenetic Analysis of Salt-Tolerance-Related Genes in Root-Nodule Bacteria Species <i>Sinorhizobium meliloti</i> . <i>Agronomy</i> , 2022, 12, 1968.	1.3	3
3722	Comparative mitochondrial genome analysis of Sesamidae and its phylogenetic implications. <i>Acta Oceanologica Sinica</i> , 2022, 41, 62-73.	0.4	2
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3725	Evaluation of various distance computation methods for construction of haplotype-based phylogenies from large MLST datasets. <i>Molecular Phylogenetics and Evolution</i> , 2022, 177, 107608.	1.2	7
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3727	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
3728	Deeper diversity exploration: New Typhlotanaidae (Crustacea: Tanaidacea) from the Kuril-Kamchatka Trench area. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	3
3729	Functional genomics analysis reveals the evolutionary adaptation and demographic history of pygmy lorises. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	5
3730	<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. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	3
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3735	A Chromosome-Level Genome Assembly of the <i>Rhus</i> Gall Aphid <i>Schlechtendalia chinensis</i> ; Provides Insight into the Endogenization of <i>Parvovirus</i> -Like DNA Sequences. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
3736	Metagonia spiders of Galápagos: blind cave-dwellers and their epigeal relatives (Araneae, Pholcidae). <i>Invertebrate Systematics</i> , 2022, 36, 647.	0.5	4
3737	Clonality, inbreeding, and hybridization in two extremotolerant black yeasts. <i>GigaScience</i> , 2022, 11, .	3.3	9

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3739	An Integrated Method to Reconstruct Ancient Proteins. <i>Methods in Molecular Biology</i> , 2022, , 267-281.	0.4	0
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3743	Bioleaching of Heavy Metals by <i>Streptomyces avermitilis</i> "BBA4 Isolate from Coal Mine Soil of Tamil Nadu. <i>Current Microbiology</i> , 2022, 79, .	1.0	3
3744	The complete mitochondrial genome of <i>Parachilglanis hodgarti</i> and its phylogenetic position within Sisoridae. <i>Journal of Oceanology and Limnology</i> , 2023, 41, 267-279.	0.6	2
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3746	Unfolding the mitochondrial genome structure of green semilooper (<i>Chrysodeixis acuta</i> Walker): An emerging pest of onion (<i>Allium cepa</i> L.). <i>PLoS ONE</i> , 2022, 17, e0273635.	1.1	1
3747	Chromosome-scale genome assembly of <i>Camellia sinensis</i> combined with multi-omics provides insights into its responses to infestation with green leafhoppers. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	6
3748	A chromosome-scale genome assembly of <i>Quercus gilva</i> : Insights into the evolution of <i>Quercus</i> section <i>Cyclobalanopsis</i> (Fagaceae). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	8
3749	Comparative genomics reveals putative evidence for high-elevation adaptation in the American pika (<i>Ochotona princeps</i>). <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	2
3750	Genomic Sequencing and Phylogenomics of Cowpox Virus. <i>Viruses</i> , 2022, 14, 2134.	1.5	8
3751	Plastome sequences fail to resolve shallow level relationships within the rapidly radiated genus <i>Isodon</i> (Lamiaceae). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
3752	Phylogenetic position of the relict South American genus <i>Idiopyrgus</i> Pilsbry, 1911 (Gastropoda, Tj ETQq1 1 0.784314 rgBT /Overlock 98, 365-375.	0.4	3
3753	New Insights into Lichenization in Agaricomycetes Based on an Unusual New Basidiolichen Species of <i>Omphalina</i> s. str.. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 1033.	1.5	2
3754	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
3755	Description and complete mitochondrial genome of <i>Atkinsoniella zizhongii</i> sp. nov. (Hemiptera:) Tj ETQq0 0 0 rgBT /Overlock 10 T	0.9	2
3756	Complete Mitogenomes of Polypedates Tree Frogs Unveil Gene Rearrangement and Concerted Evolution within Rhacophoridae. <i>Animals</i> , 2022, 12, 2449.	1.0	1

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3761	Phylotranscriptomics reveal the spatio-temporal distribution and morphological evolution of <i>Macrozamia</i> , an Australian endemic genus of Cycadales. Annals of Botany, 2022, 130, 671-685.	1.4	5
3762	Phylotranscriptomics of liverworts: revisiting the backbone phylogeny and ancestral gene duplications. Annals of Botany, 2022, 130, 951-964.	1.4	7
3763	MAIA, Fc receptor-like 3, supersedes JUNO as IZUMO1 receptor during human fertilization. Science Advances, 2022, 8, .	4.7	10
3764	Genetic diversity of Ralstonia solanacearum causing vascular bacterial wilt under different agro-climatic regions of West Bengal, India. PLoS ONE, 2022, 17, e0274780.	1.1	2
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3768	The coral <i>Acropora loripes</i> genome reveals an alternative pathway for cysteine biosynthesis in animals. Science Advances, 2022, 8, .	4.7	10
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3770	Evolution of mitochondrial and nuclear genomes in Pennatulacea. Molecular Phylogenetics and Evolution, 2023, 178, 107630.	1.2	2
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3775	Large-scale phylogenetic analysis provides insights into the diversification and evolution of sessilid peritrich ciliates (Protista: Ciliophora). Journal of Eukaryotic Microbiology, 2023, 70, .	0.8	2
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3778	Omics data unveil early molecular response underlying limb regeneration in the Chinese mitten crab, <i>Eriocheir sinensis</i> . Science Advances, 2022, 8, .	4.7	9
3779	Adaptation and evolution of the sea anemone <i>Alvinactis</i> sp. to deep-sea hydrothermal vents: A comparison using transcriptomes. Ecology and Evolution, 2022, 12, .	0.8	2

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3780	The complete mitochondrial genome of sea slug <i>Phyllidia elegans</i> Bergh, 1869 (Nudibranchia). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf</i>	0.2	1
3781	The Complete Mitochondrial Genome of <i>Spirobolus bungii</i> (Diplopoda, Spirobolidae): The First Sequence for the Genus <i>Spirobolus</i> . <i>Genes</i> , 2022, 13, 1587.	1.0	3
3782	Disentangling a 40-year-old taxonomic puzzle: the phylogenetic position of <i>Mimulicalyx</i> (Lamiales). <i>Botanical Journal of the Linnean Society</i> , 2023, 201, 135-153.	0.8	3
3783	Molecular phylogeny and historical biogeography of marine palaemonid shrimps (Palaemonidae). <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf</i>	1.6	8
3784	Organellar genome comparisons of <i>Sargassum polycystum</i> and <i>S. plagiophyllum</i> (Fucales). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf</i>	1.2	582
3785	A new species of land planarian split off from <i>Luteostriata ernesti</i> (Leal-Zanchet &) <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf</i>	0.5	0
3786	<i>De novo</i> genome assembly of the medicinal plant <i>Gentiana macrophylla</i> provides insights into the genomic evolution and biosynthesis of iridoids. <i>DNA Research</i> , 2022, 29, .	1.5	10
3787	Morphology of ctenostome bryozoans: 6. <i>Amphibiobeania epiphylla</i> . <i>Journal of Morphology</i> , 2022, 283, 1505-1516.	0.6	2
3788	Large-scale genetic investigation of nematode diversity and their phylogenetic patterns in New Zealand's marine animals. <i>Parasitology</i> , 2022, 149, 1794-1809.	0.7	3
3789	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
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3792	Characterization of the complete mitochondrial genome of <i>Cryptotermes domesticus</i> (Blattodea: Kalotermitidae): Gnome description and phylogenetic implications. <i>Archives of Insect Biochemistry and Physiology</i> , 0, , .	0.6	1
3793	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
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3795	Characterization of the complete mitochondrial genome of the fluke of turdus, <i>Plagiorchis elegans</i> , and phylogenetic implications. <i>Experimental Parasitology</i> , 2022, 242, 108387.	0.5	2
3796	The <i>Capparis spinosa</i> var. <i>herbacea</i> genome provides the first genomic instrument for a diversity and evolution study of the Capparaceae family. <i>GigaScience</i> , 2022, 11, .	3.3	5
3797	Description of <i>Diegoglossidium maradonai</i> n. g. and n. sp. (Digenea: Alloglossidiidae) through an integrative taxonomy approach, with an amended diagnosis of the family. <i>Journal of Helminthology</i> , 2022, 96, .	0.4	0
3798	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

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3800	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
3801	Two New Species and Two New Records of the Lichen-Forming Fungal Genus <i>Peltula</i> (Ascomycota: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 347 16	1.3	0
3803	Genome report: chromosome-level draft assemblies of the snow leopard, African leopard, and tiger (<i>Panthera uncia</i> , <i>Panthera pardus pardus</i> , and <i>Panthera tigris</i>). <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	5
3804	A reference-grade genome assembly for <i>Astragalus mongholicus</i> and insights into the biosynthesis and high accumulation of triterpenoids and flavonoids in its roots. <i>Plant Communications</i> , 2023, 4, 100469.	3.6	8
3805	Comparative Genomic Insights into Chemoreceptor Diversity and Habitat Adaptation of Archaea. <i>Applied and Environmental Microbiology</i> , 0, , .	1.4	0
3806	Straw-Colored Fruit Bats (<i>Eidolon helvum</i>) and Their Bat Flies (<i>Cyclopodia greefi</i>) in Nigeria Host Viruses with Multifarious Modes of Transmission. <i>Vector-Borne and Zoonotic Diseases</i> , 2022, 22, 545-552.	0.6	2
3809	Evolutionary Divergence between <i>Toona ciliata</i> and <i>Toona sinensis</i> Assayed with Their Whole Genome Sequences. <i>Genes</i> , 2022, 13, 1799.	1.0	8
3811	Taxonomic revision of the Australian stick insect genus <i>Candovia</i> (Phasmida: Necroschiinae): insight from molecular systematics and species-delimitation approaches. <i>Zoological Journal of the Linnean Society</i> , 0, , .	1.0	1
3813	The complete mitochondrial genome of the woodwasp <i>Euxiphidria potanini</i> (Hymenoptera, Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 347 16	1.6	1
3814	Telomere-to-telomere genome assembly of bitter melon (<i>Momordica charantia</i> L. var.) <i>Horticulture Research</i> , 2023, 10, .	2.9	16
3815	Evaluation of the Antifungal Activity of Endophytic and Rhizospheric Bacteria against Grapevine Trunk Pathogens. <i>Microorganisms</i> , 2022, 10, 2035.	1.6	12
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3817	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
3818	Comprehensive Comparative Analysis and Development of Molecular Markers for <i>Dianthus</i> Species Based on Complete Chloroplast Genome Sequences. <i>International Journal of Molecular Sciences</i> , 2022, 23, 12567.	1.8	4
3819	Tempo and Mode of Floristic Exchanges between Hainan Island and Mainland Asia: A Case Study of the <i>Persea</i> Group (Lauraceae). <i>Forests</i> , 2022, 13, 1722.	0.9	0
3820	An Unwanted Association: The Threat to Papaya Crops by a Novel Potexvirus in Northwest Argentina. <i>Viruses</i> , 2022, 14, 2297.	1.5	4
3821	A Novel Mitochondrial Genome Fragmentation Pattern in the Buffalo Louse <i>Haematopinus tuberculatus</i> (Psocodea: Haematopiniidae). <i>International Journal of Molecular Sciences</i> , 2022, 23, 13092.	1.8	3

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3822	Gene family expansions in Antarctic winged midge as a strategy for adaptation to cold environments. <i>Scientific Reports</i> , 2022, 12, .	1.6	7
3823	Comparative analysis of the complete mitochondrial genomes of two species of Clupeiformes and the phylogenetic implications for Clupeiformes. <i>Journal of the Marine Biological Association of the United Kingdom</i> , 0, , 1-12.	0.4	0
3824	Characterization of Seventeen Complete Mitochondrial Genomes: Structural Features and Phylogenetic Implications of the Lepidopteran Insects. <i>Insects</i> , 2022, 13, 998.	1.0	4
3825	<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
3826	Plastome phylogenomic analysis reveals evolutionary divergences of Polypodiales suborder Dennstaedtiineae. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	3
3827	Genome mining reveals abiotic stress resistance genes in plant genomes acquired from microbes via HGT. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	4
3828	Genome-wide scan for potential CD4+ T-cell vaccine candidates in <i>Candida auris</i> by exploiting reverse vaccinology and evolutionary information. <i>Frontiers in Medicine</i> , 0, 9, .	1.2	3
3829	Chromosome-level genome assembly of <i>Nibea coibor</i> using PacBio HiFi reads and Hi-C technologies. <i>Scientific Data</i> , 2022, 9, .	2.4	3
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3835	The Characterization of Three Novel Insect-Specific Viruses Discovered in the Bean Bug, <i>Riptortus pedestris</i> . <i>Viruses</i> , 2022, 14, 2500.	1.5	2
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3837	Behavioral and genomic divergence between a generalist and a specialist fly. <i>Cell Reports</i> , 2022, 41, 111654.	2.9	5
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3842	Nematocyst sequestration within the family Fionidae (Gastropoda: Nudibranchia) considering ecological properties and evolution. <i>Frontiers in Zoology</i> , 2022, 19, .	0.9	1

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3844	Comparative genomic analyses reveal genetic characteristics and pathogenic factors of <i>Bacillus pumilus</i> HM-7. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	0
3845	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
3847	<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
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3849	Monogeneans and chubs: Ancient host-parasite system under the looking glass. <i>Molecular Phylogenetics and Evolution</i> , 2023, 179, 107667.	1.2	4
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3851	Complete Mitochondrial Genome Analysis of <i>Daphniopsis tibetana</i> (Branchiopoda: Diplostraca): New Insights into the Taxonomy of the Genus and Its Phylogenetic Implications for Branchiopoda. <i>Journal of Ocean University of China</i> , 2022, 21, 1622-1632.	0.6	2
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3855	Diversity and metabolic potentials of microbial communities associated with pollinator and cheater fig wasps in fig-fig wasp mutualism system. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	0
3856	<i>Onchobothrium malakhovi</i> n. sp. (Cestoda: Onchoproteocephalidea) ex <i>Bathyraja</i> (<i>Arctoraja</i>) <i>sexoculata</i> (Rajiformes: Arhynchobatidae) from Kuril Islands (Russia), with comments on the status of the genus <i>Onchobothrium</i> . <i>Parasitology International</i> , 2022, , 102709.	0.6	0
3857	Comparative mitochondrial genomic analysis provides new insights into the evolution of the subfamily Lamiinae (Coleoptera: Cerambycidae). <i>International Journal of Biological Macromolecules</i> , 2023, 225, 634-647.	3.6	5
3859	Bacterial diversity on stained glass windows. <i>International Biodeterioration and Biodegradation</i> , 2023, 177, 105529.	1.9	4
3860	Microscale dynamics of dark zone alterations in anthropized karstic cave shows abrupt microbial community switch. <i>Science of the Total Environment</i> , 2023, 862, 160824.	3.9	2
3861	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
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3864	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
3865	Complete Mitogenome and Phylogenetic Analyses of <i>Galerita orientalis</i> Schmidt-Goebel, 1846 (Insecta: Tj ETQq0 0.0 rgBT /Overlock 10	1.0	1
3866	Insights into cryptic speciation of quillworts in China. <i>Plant Diversity</i> , 2023, 45, 284-301.	1.8	1
3867	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
3868	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
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3870	Complete mitochondrial genome of <i>Cyclopelta obscura</i> (Lepelletier & Serville, 1825) (Hemiptera: Pentatomoidea: Dinidoridae) and phylogenetic analysis of Pentatomoidea species. <i>Archives of Insect Biochemistry and Physiology</i> , 0, , .	0.6	0
3871	Ultrastructure of <i>Diophrys appendiculata</i> and new systematic consideration of the euplotid family Uronychiidae (Protista, Ciliophora). <i>Marine Life Science and Technology</i> , 2022, 4, 551-568.	1.8	7
3872	The widely reported but poorly studied ciliate family Folliculinidae (Protozoa, Ciliophora,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 <i>Marine Life Science and Technology</i> , 2022, 4, 471-492.	1.8	7
3873	Chromosome-Level Genome Assembly of the Speckled Blue Grouper (<i>Epinephelus cyanopodus</i>) Provides Insight into Its Adaptive Evolution. <i>Biology</i> , 2022, 11, 1810.	1.3	1
3874	A Compositional Heterogeneity Analysis of Mitochondrial Phylogenomics in Chalcidoidea Involving Two Newly Sequenced Mitogenomes of Eupelminae (Hymenoptera: Chalcidoidea). <i>Genes</i> , 2022, 13, 2340.	1.0	1
3876	Integrative taxonomy of the subfamily Orbioninae (Crustacea: Isopoda) based on mitochondrial and nuclear data with evidence that supports Epicaridea as a suborder. <i>Molecular Phylogenetics and Evolution</i> , 2023, 180, 107681.	1.2	2
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3878	Fine-Mapping and Comparative Genomic Analysis Reveal the Gene Composition at the <i>S</i> and <i>Z</i> Self-incompatibility Loci in Grasses. <i>Molecular Biology and Evolution</i> , 2023, 40, .	3.5	3
3879	The chromosome-level genome assembly of goldstripe ponyfish (<i>Karalla daura</i>) reveals its similarity to Chinese sillago on contracted immune gene families. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	0
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3884	Screening of plant growth-promoting attributes bearing endogenous bacteria from abiotic stress resisting high altitude plants. <i>Journal of Agriculture and Food Research</i> , 2023, 11, 100489.	1.2	1
3885	Codonoblepharontaeae, a New Major Lineage among Orthotrichoideae (Orthotrichaceae, Bryophyta). <i>Plants</i> , 2022, 11, 3557.	1.6	1
3888	An RNA Virome Analysis of the Pink-Winged Grasshopper <i>Atractomorpha sinensis</i> . <i>Insects</i> , 2023, 14, 9.	1.0	2
3889	Phylogeny and systematics of Sphaeriusidae (Coleoptera: Myxophaga): minute living fossils with underestimated past and present day diversity. <i>Systematic Entomology</i> , 2023, 48, 233-249.	1.7	4
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3891	Genetic Determinants of Antagonistic Interactions and the Response of New Endophytic Strain <i>Serratia quinivorans</i> KP32 to Fungal Phytopathogens. <i>International Journal of Molecular Sciences</i> , 2022, 23, 15561.	1.8	3
3892	Morphological Characteristics and Comparative Chloroplast Genome Analyses between Red and White Flower Phenotypes of <i>Pyracantha fortuneana</i> (Maxim.) Li (Rosaceae), with Implications for Taxonomy and Phylogeny. <i>Genes</i> , 2022, 13, 2404.	1.0	3
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3895	The complete plastome of <i>Cynanchum rostellatum</i> (Apocynaceae), an indigenous plant in Korea. <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 2035-2039.	0.2	1
3896	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
3897	A novel genotype of avian hepatitis E virus identified in chickens and common pheasants (<i>Phasianus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 156 1		
3898	<i>Azospirillum Endophyticum</i> sp. nov., an Endophyte of <i>Paris Polyphylla</i> Smith var. <i>Yunnanensis</i> . <i>Current Microbiology</i> , 2023, 80, .	1.0	0
3899	The complete mitochondrial genome of <i>Coccotorus beijingensis</i> Lin et Li, 1990 (Coleoptera,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 187 7 <i>Journal</i> , 0, 10, .	0.4	0
3900	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
3901	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
3902	Chromosome-scale genome assembly of <i>Eustoma grandiflorum</i> , the first complete genome sequence in the genus <i>Eustoma</i> . <i>G3: Genes, Genomes, Genetics</i> , 2023, 13, .	0.8	2

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3925	Comparative mitogenomics and phylogenetic analyses of the genus <i>Menida</i> (Hemiptera, Heteroptera). <i>Tj ETQq1 1 0.784314 rgBT / 0.5</i>	0.5	1
3926	A novel gyrovirus is abundant in yellow-eyed penguin (<i>Megadyptes antipodes</i>) chicks with a fatal respiratory disease. <i>Virology</i> , 2023, 579, 75-83.	1.1	4
3927	An Integrative Approach for the Identification of Native and Exotic Lymnaeids from Brazil. <i>Malacologia</i> , 2022, 65, .	0.2	1
3928	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
3929	The Cladoniaceae (Lecanorales, Ascomycota) from Bulgaria. <i>Herzogia</i> , 2022, 35, .	0.1	0
3930	Chromosome-level assembly of triploid genome of Sichuan pepper (<i>Zanthoxylum armatum</i>). <i>Horticultural Plant Journal</i> , 2024, 10, 437-449.	2.3	2
3931	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
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3935	Re-discovery and novel contributions to morphology and multigene phylogeny of <i>Protospirella mazurica</i> (Raabe, 1968) Aescht, 2001 (Ciliophora: Pleuronematida), an obligate symbiont of the river nerite <i>Theodoxus fluviatilis</i> Linnaeus, 1758 (Mollusca: Gastropoda). <i>European Journal of Protistology</i> , 2023, 88, 125956.	0.5	1
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3937	Evolution of TOP1 and TOP1MT Topoisomerases in Chordata. <i>Journal of Molecular Evolution</i> , 2023, 91, 192-203.	0.8	1
3938	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
3939	New insights into the distribution, ecology, and systematic position of the rare water mite <i>Rutripalpus limicola</i> Sokolow, 1934 (Acari: Rutripalpidae). <i>Acarologia</i> , 2023, 63, 106-121.	0.2	0
3941	The complete mitochondrial genome of <i>Cuspidaria undata</i> (Bivalvia, Anomalodesmata). <i>Tj ETQq0 0 0 rgBT / Overlock 10 Tf 50 102</i>	0.2	0
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3945	STRESS AND IMMUNITY OF NODULE BACTERIA <i>SINORHIZOBIUM MELILOTI</i> : LOCALIZATION, POLYMORPHISM AND PHYLOGENY OF GENETIC DETERMINANTS. , 2022, , .		0
3946	High Throughput Reproducible Literate Phylogenetic Analysis. , 2022, , .		0
3947	Bioremediation of hexavalent chromium by transformation of <i>Escherichia coli</i> DH5 α with chromate reductase (ChrR) genes of <i>Pseudomonas putida</i> isolated from tannery effluent. <i>Journal of Applied Microbiology</i> , 2023, 134, .	1.4	0
3949	Evolutionary History and Taxonomic Reclassification of the Critically Endangered Daggernose Shark, a Species Endemic to the Western Atlantic. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2023, 2023, 1-16.	0.6	3
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3951	Genomes of the human filarial parasites <i>Mansonella perstans</i> and <i>Mansonella ozzardi</i> . <i>Frontiers in Tropical Diseases</i> , 0, 4, .	0.5	8
3952	Infection of <i>Corbicula</i> clams by trematode cercariae in Myanmar. <i>Ecologica Montenegrina</i> , 0, 62, 1-11.	0.5	0
3953	Potential negative effect of long-term exposure to nitrofurans on bacteria isolated from wastewater. <i>Science of the Total Environment</i> , 2023, 872, 162199.	3.9	3
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3958	Molecular evolution of the hemoglobin gene family across vertebrates. <i>Genetica</i> , 0, , .	0.5	0
3959	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
3960	The <i>Populus koreana</i> genome provides insights into the biosynthesis of plant aroma. <i>Industrial Crops and Products</i> , 2023, 197, 116453.	2.5	1
3964	An Efficient and User-Friendly Software for PCR Primer Design for Detection of Highly Variable Bacteria. <i>Lecture Notes in Computer Science</i> , 2022, , 138-147.	1.0	0
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3967	Annelid functional genomics reveal the origins of bilaterian life cycles. <i>Nature</i> , 2023, 615, 105-110.	13.7	34
3968	Morphological and Molecular Identification of <i>Dactylogyrus gobiocypris</i> (Monogenea: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 667 Td (Da 2023, 12, 206.	1.2	2
3969	Deciphering complex reticulate evolution of Asian <i>Buddleja</i> (<i>Scrophulariaceae</i>): insights into the taxonomy and speciation of polyploid taxa in the Sino-Himalayan region. <i>Annals of Botany</i> , 2023, 132, 15-28.	1.4	3
3970	Characterization of the Plastid Genome of the Vulnerable Endemic <i>Indosasa lipoensis</i> and Phylogenetic Analysis. <i>Diversity</i> , 2023, 15, 197.	0.7	3
3971	Cytogenetics, Typification, Molecular Phylogeny and Biogeography of <i>Bentinckia</i> (<i>Arecoideae</i> , Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 667 Td (Da 2023, 12, 206.	1.3	1
3972	Comparative chloroplast genome analyses of diverse <i>Phoebe</i> (<i>Lauraceae</i>) species endemic to China provide insight into their phylogeographical origin. <i>PeerJ</i> , 0, 11, e14573.	0.9	11
3973	Mitochondrial Genome of <i>Spotted Numbfish</i> <i>Narcine timlei</i> (Bloch & Schneider, 1801) and Phylogenetic Relationships among Order <i>Torpediniformes</i> . <i>Journal of Applied Ichthyology</i> , 2023, 2023, 1-8.	0.3	1
3974	Plastome Phylogeny and Taxonomy of <i>Cinnamomum guizhouense</i> (<i>Lauraceae</i>). <i>Forests</i> , 2023, 14, 310.	0.9	0
3975	<i>Aristophania vespae</i> gen. nov., sp. nov., isolated from wasps, is related to <i>Bombella</i> and <i>Oecophyllibacter</i> , isolated from bees and ants. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2023, 73, .	0.8	1
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