

MUSCLE: multiple sequence alignment with high accuracy

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Citation Report

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1795	Phylogenetic analysis of the minute brown scavenger beetles (Coleoptera: Latridiidae), and recognition of a new beetle family, Akalyptoischiidae fam.n. (Coleoptera: Cucujoidea). <i>Systematic Entomology</i> , 2010, 35, 753-763.	1.7	20
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1810	Revised classification of former genus <i>Phoxinellus</i> using nuclear DNA sequences. <i>Biochemical Systematics and Ecology</i> , 2010, 38, 1069-1073.	0.6	7
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1841	Clonal origin of emerging populations of <i>Ehrlichia ruminantium</i> in Burkina Faso. <i>Infection, Genetics and Evolution</i> , 2010, 10, 903-912.	1.0	19
1842	A protein sequence meta-functional signature for calcium binding residue prediction. <i>Pattern Recognition Letters</i> , 2010, 31, 2103-2112.	2.6	16
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1851	Evolutionary inferences based on ITS rDNA and actin sequences reveal extensive diversity of the common lichen alga <i>Asterochloris</i> (Trebouxiophyceae, Chlorophyta). <i>Molecular Phylogenetics and Evolution</i> , 2010, 54, 36-46.	1.2	112
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1866	A molecular phylogenetic framework for the Muricidae, a diverse family of carnivorous gastropods. <i>Molecular Phylogenetics and Evolution</i> , 2010, 56, 1025-1039.	1.2	71
1867	An expanded phylogeny of treefrogs (Hylidae) based on nuclear and mitochondrial sequence data. <i>Molecular Phylogenetics and Evolution</i> , 2010, 55, 871-882.	1.2	138
1868	Species boundaries and cryptic lineage diversity in a Philippine forest skink complex (Reptilia; <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 65</i> )	1.2	47
1869	Of Least Concern? Systematics of a cryptic species complex: <i>Limnectes kuhlii</i> (Amphibia: Anura): <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 65</i>	1.2	69
1870	Incorporating molecular phylogenetics with larval morphology while mitigating the effects of substitution saturation on phylogeny estimation: A new hypothesis of relationships for the flatfish family Pleuronectidae (Percomorpha: Pleuronectiformes). <i>Molecular Phylogenetics and Evolution</i> , 2010, 56, 586-600.	1.2	20
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1877	Phylogeography and historical demography of <i>Polypedates leucomystax</i> in the islands of Indonesia and the Philippines: Evidence for recent human-mediated range expansion?. <i>Molecular Phylogenetics and Evolution</i> , 2010, 57, 598-619.	1.2	64
1878	Including secondary structure, fossils and molecular dating in the centipede tree of life. <i>Molecular Phylogenetics and Evolution</i> , 2010, 57, 301-313.	1.2	90
1879	Molecular phylogeny of Enchytraeidae (Annelida, Clitellata). <i>Molecular Phylogenetics and Evolution</i> , 2010, 57, 849-858.	1.2	71
1880	Phylogenetic position of the enigmatic <i>Lepidogalaxias salamandroides</i> with comment on the orders of lower euteleostean fishes. <i>Molecular Phylogenetics and Evolution</i> , 2010, 57, 932-936.	1.2	56

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1882	Genetic variation and phylogeny of the cosmopolitan marine genus <i>Tubificoides</i> (Annelida: Clitellata:). <i>Tj ETQq1 1 0.784314 rgBT /Overlock</i>	1.2	92
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1884	Phylogeny and biogeography of the Asian trogons (Aves: Trogoniformes) inferred from nuclear and mitochondrial DNA sequences. <i>Molecular Phylogenetics and Evolution</i> , 2010, 57, 1219-1225.	1.2	21
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1887	The phylogenetic placement of <i>Hollandichthys Eigenmann 1909</i> (Teleostei: Characidae) and related genera. <i>Molecular Phylogenetics and Evolution</i> , 2010, 57, 1347-1352.	1.2	18
1888	Computational approaches for protein function prediction: A combined strategy from multiple sequence alignment to molecular docking-based virtual screening. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2010, 1804, 1695-1712.	1.1	97
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1892	Mitogen-activated protein kinase 4 of <i>Leishmania</i> parasite as a therapeutic target. <i>European Journal of Medicinal Chemistry</i> , 2010, 45, 5662-5670.	2.6	12
1893	Structure of <i>Staphylococcus aureus</i> adenylosuccinate lyase ( <i>PurB</i> ) and assessment of its potential as a target for structure-based inhibitor discovery. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 881-888.	2.5	17
1894	Crystallization and preliminary X-ray analysis of <i>L</i> -azetidine-2-carboxylate hydrolase from <i>Pseudomonas</i> sp. strain A2C. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 801-804.	0.7	6
1895	Structure of uracil-DNA glycosylase from <i>Mycobacterium tuberculosis</i> : insights into interactions with ligands. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 887-892.	0.7	8
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1916	Sequence fingerprint and structural analysis of the SCOR enzyme A3DFK9 from <i>Clostridium thermocellum</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 603-613.	1.5	1

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1919	Homology modelling of <i>Drosophila</i> cytochrome P450 enzymes associated with insecticide resistance. <i>Pest Management Science</i> , 2010, 66, 1106-1115.	1.7	52
1920	Characterization of <i>drCol 15a1b</i> : A Novel Component of the Stem Cell Niche in the Zebrafish Retina. <i>Stem Cells</i> , 2010, 28, 1399-1411.	1.4	16
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1924	Detecting Gene Duplications in the Human Lineage. <i>Annals of Human Genetics</i> , 2010, 74, 555-565.	0.3	6
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1926	Evidence for the involvement of <i>GLOBOSA</i> -like gene duplications and expression divergence in the evolution of floral morphology in the Zingiberales. <i>New Phytologist</i> , 2010, 187, 521-541.	3.5	50
1927	Phylogenetic and ecological analyses of soil and sporocarp DNA sequences reveal high diversity and strong habitat partitioning in the boreal ectomycorrhizal genus <i>Russula</i> (Russulales). <i>Journal of Ecology</i> , 2010, 98, 1075-1083.	1.7	337
1928	Production of ectomycorrhizal mycelium peaks during canopy closure in Norway spruce forests. <i>New Phytologist</i> , 2010, 187, 1124-1134.	3.5	156
1929	Phylogenetic patterns differ for native and exotic plant communities across a richness gradient in Northern California. <i>Diversity and Distributions</i> , 2010, 16, 892-901.	1.9	56
1930	Ratios between Alpha-, Beta- and Gamma-proteobacteria in tap water determined by the ProteoQuant assay. <i>Letters in Applied Microbiology</i> , 2010, 50, 1-6.	1.0	13
1931	Mapping the Druggable Allosteric Space of G-Protein Coupled Receptors: a Fragment-Based Molecular Dynamics Approach. <i>Chemical Biology and Drug Design</i> , 2010, 76, 201-217.	1.5	106
1932	Sequence similarities between Raspberry leaf mottle virus, Raspberry leaf spot virus and the closterovirus Raspberry mottle virus. <i>Annals of Applied Biology</i> , 2010, 156, 439-448.	1.3	16
1933	Induced systemic resistance against three foliar diseases of <i>Agrostis stolonifera</i> by (2 <i>R</i> ,3 <i>R</i> )-butanediol or an isoparaffin mixture. <i>Annals of Applied Biology</i> , 2010, 157, 179-189.	1.3	68
1934	Genome-Wide Analysis of <i>WOX</i> Gene Family in Rice, Sorghum, Maize, <i>Arabidopsis</i> and Poplar. <i>Journal of Integrative Plant Biology</i> , 2010, 52, 1016-1026.	4.1	134

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1936	THE SPECIATION HISTORY OF THE <i>PHYSCOMITRIUM-PHYSCOMITRELLA</i> SPECIES COMPLEX. <i>Evolution; International Journal of Organic Evolution</i> , 2010, 64, 217-231.	1.1	59
1937	DIVERSIFICATION AND PERSISTENCE AT THE ARID-MONSOONAL INTERFACE: AUSTRALIA-WIDE BIOGEOGRAPHY OF THE BYNOE'S GECKO ( <i>HETERONOTIA BINOEI</i> ; <i>GEKKONIDAE</i> ). <i>Evolution; International Journal of Organic Evolution</i> , 2010, 64, no-no.	1.1	96
1938	NUCLEAR AND MITOCHONDRIAL SEQUENCE DATA REVEAL AND CONCEAL DIFFERENT DEMOGRAPHIC HISTORIES AND POPULATION GENETIC PROCESSES IN CARIBBEAN REEF FISHES. <i>Evolution; International Journal of Organic Evolution</i> , 2010, 64, 3380-3397.	1.1	65
1939	Biogeography of thermophilic cyanobacteria: insights from the Zerka Ma'in hot springs (Jordan). <i>FEMS Microbiology Ecology</i> , 2010, 72, 103-113.	1.3	55
1940	Ultramafic soils from New Caledonia structure <i>Pisolithus albus</i> in ecotype. <i>FEMS Microbiology Ecology</i> , 2010, 72, 238-249.	1.3	36
1941	Multidrug efflux pumps: The structures of prokaryotic ATP-binding cassette transporter efflux pumps and implications for our understanding of eukaryotic glycoproteins and homologues. <i>FEBS Journal</i> , 2010, 277, 550-563.	2.2	54
1942	Purification of three aminotransferases from <i>Hydrogenobacter thermophilus</i> novel types of alanine or glycine aminotransferase. <i>FEBS Journal</i> , 2010, 277, 1876-1885.	2.2	9
1943	Expression profile of PIN, AUX/LAX and PGP auxin transporter gene families in <i>Sorghum bicolor</i> under phytohormone and abiotic stress. <i>FEBS Journal</i> , 2010, 277, 2954-2969.	2.2	139
1944	A conserved primary salt tolerance mechanism mediated by HKT transporters: a mechanism for sodium exclusion and maintenance of high K <sup>+</sup> /Na <sup>+</sup> ratio in leaves during salinity stress. <i>Plant, Cell and Environment</i> , 2010, 33, 552-565.	2.8	455
1945	Comparison of induced resistance activated by benzothiadiazole, (2R,3R)-butanediol and an isoparaffin mixture against anthracnose of <i>Nicotiana benthamiana</i> . <i>Plant Pathology</i> , 2010, 59, 643-653.	1.2	77
1946	Biological and molecular diagnosis of seedborne viruses in cowpea germplasm of geographically diverse sub-Saharan origins. <i>Plant Pathology</i> , 2010, 59, 773-784.	1.2	26
1947	Evolutionary conservation, diversity and specificity of LTR retrotransposons in flowering plants: insights from genome-wide analysis and multi-specific comparison. <i>Plant Journal</i> , 2010, 63, 584-598.	2.8	153
1948	Tomato MAPKKK1 is a positive regulator of cell-death signaling networks associated with plant immunity. <i>Plant Journal</i> , 2010, 64, 379-391.	2.8	92
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1950	Extensive intraspecific genetic diversity of a freshwater crayfish in a biodiversity hotspot. <i>Freshwater Biology</i> , 2010, 55, 1861-1873.	1.2	34
1951	A coleopteran triosephosphate isomerase: X-ray structure and phylogenetic impact of insect sequences. <i>Insect Molecular Biology</i> , 2010, 19, 35-48.	1.0	7
1952	Anterior development in the parthenogenetic and viviparous form of the pea aphid, <i>Acyrtosiphon pisum</i> : <i>hunchback</i> and <i>orthodenticle</i> expression. <i>Insect Molecular Biology</i> , 2010, 19, 75-85.	1.0	26

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1954	The draft genome sequence of <i>Arsenophonus nasoniae</i> , sonâ€killer bacterium of <i>Nasonia vitripennis</i> , reveals genes associated with virulence and symbiosis. <i>Insect Molecular Biology</i> , 2010, 19, 59-73.	1.0	46
1955	Organization, evolution and transcriptional profile of hexamerin genes of the parasitic wasp <i>Nasonia vitripennis</i> (Hymenoptera: Pteromalidae). <i>Insect Molecular Biology</i> , 2010, 19, 137-146.	1.0	20
1956	Analysis of <i>Rickettsia typhi</i> -infected and uninfected cat flea ( <i>Ctenocephalides felis</i> ) midgut cDNA libraries: deciphering molecular pathways involved in host response to <i>R. typhi</i> infection. <i>Insect Molecular Biology</i> , 2010, 19, 229-241.	1.0	30
1957	Proposed new nomenclature for <i>Bos taurus</i> cytochromes P450 involved in xenobiotic drug metabolism. <i>Journal of Veterinary Pharmacology and Therapeutics</i> , 2010, 33, 528-536.	0.6	15
1958	An integrative approach to species discovery in odonates: from characterâ€based DNA barcoding to ecology. <i>Molecular Ecology</i> , 2010, 19, 3881-3893.	2.0	76
1959	The discordance of diversification: evolution in the tropicalâ€montane frogs of the Eastern Arc Mountains of Tanzania. <i>Molecular Ecology</i> , 2010, 19, 4046-4060.	2.0	58
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1961	A bacterial elongation factor G homologue exclusively functions in ribosome recycling in the spirochaete <i>Borrelia burgdorferi</i> . <i>Molecular Microbiology</i> , 2010, 75, 1445-1454.	1.2	24
1962	Specificity of localization and phosphotransfer in the CheA proteins of <i>Rhodobacter sphaeroides</i> . <i>Molecular Microbiology</i> , 2010, 76, 318-330.	1.2	23
1963	Distinct roles for Caf1, Ccr4, Edc3 and CutA in the coâ€ordination of transcript deadenylation, decapping and Pâ€body formation in <i>Aspergillus nidulans</i> . <i>Molecular Microbiology</i> , 2010, 76, 503-516.	1.2	26
1964	A split active site couples cap recognition by Dcp2 to activation. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 1096-1101.	3.6	51
1965	Genetic variability at the PARK16 locus. <i>European Journal of Human Genetics</i> , 2010, 18, 1356-1359.	1.4	85
1966	Dis3-like 1: a novel exoribonuclease associated with the human exosome. <i>EMBO Journal</i> , 2010, 29, 2358-2367.	3.5	134
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1969	Bacteriophage predation regulates microbial abundance and diversity in a full-scale bioreactor treating industrial wastewater. <i>ISME Journal</i> , 2010, 4, 327-336.	4.4	138
1970	Hydrography shapes bacterial biogeography of the deep Arctic Ocean. <i>ISME Journal</i> , 2010, 4, 564-576.	4.4	179

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1973	Natural allelic variation underlying a major fitness trade-off in <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2010, 465, 632-636.	13.7	378
1974	Sequence space and the ongoing expansion of the protein universe. <i>Nature</i> , 2010, 465, 922-926.	13.7	184
1975	HIF-1 antagonizes p53-mediated apoptosis through a secreted neuronal tyrosinase. <i>Nature</i> , 2010, 465, 577-583.	13.7	179
1976	Viruses in the faecal microbiota of monozygotic twins and their mothers. <i>Nature</i> , 2010, 466, 334-338.	13.7	1,054
1977	Genomic and functional adaptation in surface ocean planktonic prokaryotes. <i>Nature</i> , 2010, 468, 60-66.	13.7	280
1978	<i>Populus</i> CEN/TFL1 regulates first onset of flowering, axillary meristem identity and dormancy release in <i>Populus</i> . <i>Plant Journal</i> , 2010, 62, 674-688.	2.8	197
1979	Increasing the accuracy of global alignment of amino acid sequences by constructing a set of alignment candidates. <i>Biophysics (Russian Federation)</i> , 2010, 55, 891-900.	0.2	0
1980	Origins of <i>Allium ampeloprasum</i> horticultural groups and a molecular phylogeny of the section <i>Allium</i> ( <i>Allium</i> : <i>Alliaceae</i> ). <i>Molecular Phylogenetics and Evolution</i> , 2010, 54, 488-497.	1.2	64
1981	The long way to diversity – Phylogeny and evolution of the Heterobranchia (Mollusca: Gastropoda). <i>Molecular Phylogenetics and Evolution</i> , 2010, 55, 60-76.	1.2	98
1982	Hennig's orphans revisited: Testing morphological hypotheses in the Opomyzoidea (Diptera: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	1.2	17
1983	Circumantarctic distribution in Southern Ocean benthos? A genetic test using the genus <i>Macroscapha</i> (Crustacea, Ostracoda) as a model. <i>Molecular Phylogenetics and Evolution</i> , 2010, 55, 1055-1069.	1.2	63
1984	Phylogeny and biogeography of Philippine bent-toed geckos (Gekkonidae: <i>Cyrtodactylus</i> ) contradict a prevailing model of Pleistocene diversification. <i>Molecular Phylogenetics and Evolution</i> , 2010, 55, 699-710.	1.2	108
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1987	Molecular phylogeny and node time estimation of bioluminescent Lantern Sharks (Elasmobranchii: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.2	69
1988	The first molecular phylogeny of cladobranchian opisthobranchs (Mollusca, Gastropoda,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	1.2	83

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1991	Alignment of, and phylogenetic inference from, random sequences: The susceptibility of alternative alignment methods to creating artifactual resolution and support. <i>Molecular Phylogenetics and Evolution</i> , 2010, 57, 1004-1016.	1.2	21
1992	Discordant mitochondrial and nuclear gene phylogenies in emydid turtles: implications for speciation and conservation. <i>Biological Journal of the Linnean Society</i> , 0, 99, 445-461.	0.7	117
1993	Failure to cospeciate: an unsorted tale of millipedes and mites. <i>Biological Journal of the Linnean Society</i> , 0, 101, 272-287.	0.7	4
1994	Broad-scale amplification of <i>matK</i> for DNA barcoding plants, a technical note. <i>Botanical Journal of the Linnean Society</i> , 0, 164, 1-9.	0.8	139
1995	Biogeography and phylogenetic relations within the Dinaric subgenus <i>Monolistra</i> ( <i>Microlistra</i> ) (Crustacea: Isopoda: Sphaeromatidae), with a description of two new species. <i>Zoological Journal of the Linnean Society</i> , 2010, 159, 1-21.	1.0	8
1996	Molecular phylogeny in endemic weevils: revision of the genera of Macaronesian <i>Cryptorhynchinae</i> (Coleoptera: Curculionidae). <i>Zoological Journal of the Linnean Society</i> , 2010, 160, 40-87.	1.0	14
1997	Identification and characterization of new <i>LuxR/LuxI</i> -type quorum sensing systems from metagenomic libraries. <i>Environmental Microbiology</i> , 2010, 12, 105-117.	1.8	51
1998	Microbial community dynamics in a seasonally anoxic fjord: Saanich Inlet, British Columbia. <i>Environmental Microbiology</i> , 2010, 12, 172-191.	1.8	198
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2000	A novel hybrid kinase is essential for regulating the $\sigma^B$ -mediated stress response of <i>Bacillus cereus</i> . <i>Environmental Microbiology</i> , 2010, 12, 730-745.	1.8	30
2001	Streptomycetes contributing to atmospheric molecular hydrogen soil uptake are widespread and encode a putative high-affinity [NiFe]-hydrogenase. <i>Environmental Microbiology</i> , 2010, 12, 821-829.	1.8	131
2002	Effect of the herbicide glyphosate on glyphosate-tolerant maize rhizobacterial communities: a comparison with pre-emergence applied herbicide consisting of a combination of acetochlor and terbuthylazine. <i>Environmental Microbiology</i> , 2010, 12, 1021-1030.	1.8	57
2003	Selenium controls transcription of paralogous formate dehydrogenase genes in the termite gut acetogen, <i>Treponema primitia</i> . <i>Environmental Microbiology</i> , 2010, 12, 2245-2258.	1.8	30
2004	Ironing out the wrinkles in the rare biosphere through improved OTU clustering. <i>Environmental Microbiology</i> , 2010, 12, 1889-1898.	1.8	1,226
2005	Amino acid signatures of salinity on an environmental scale with a focus on the Dead Sea. <i>Environmental Microbiology</i> , 2010, 12, 2613-2623.	1.8	45
2006	The genome of the Gram-positive metal- and sulfate-reducing bacterium <i>Desulfotomaculum reducens</i> strain M1. <i>Environmental Microbiology</i> , 2010, 12, 2738-2754.	1.8	60



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2008	Phylogenetics and evolution of Capitata (Cnidaria: Hydrozoa), and the systematics of Corynidae. Zoologica Scripta, 2010, 39, 290-304.	0.7	271
2009	Molecular phylogeny of Nearctic species of <i>Rhynchelmis</i> (Annelida). Zoologica Scripta, 2010, 39, 378-393.	0.7	20
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2033	Validation of Coevolving Residue Algorithms via Pipeline Sensitivity Analysis: ELSC and OMES and ZNMI, Oh My!. <i>PLoS ONE</i> , 2010, 5, e10779.	1.1	31
2034	Evolution of DNA Replication Protein Complexes in Eukaryotes and Archaea. <i>PLoS ONE</i> , 2010, 5, e10866.	1.1	30
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2038	Increased Genetic Diversity of HIV-1 Circulating in Hong Kong. <i>PLoS ONE</i> , 2010, 5, e12198.	1.1	22
2039	Identification and Characterization of an Unusual Class I Myosin Involved in Vesicle Traffic in <i>Trypanosoma brucei</i> . <i>PLoS ONE</i> , 2010, 5, e12282.	1.1	20
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2044	Metagenomic Comparison of Two <i>Thiomicrospira</i> Lineages Inhabiting Contrasting Deep-Sea Hydrothermal Environments. <i>PLoS ONE</i> , 2010, 5, e13530.	1.1	49
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2047	On the Mechanism of Chloroquine Resistance in <i>Plasmodium falciparum</i> . <i>PLoS ONE</i> , 2010, 5, e14064.	1.1	67
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2049	A Complete Analysis of HA and NA Genes of Influenza A Viruses. <i>PLoS ONE</i> , 2010, 5, e14454.	1.1	38
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2053	Nme Gene Family Evolutionary History Reveals Pre-Metazoan Origins and High Conservation between Humans and the Sea Anemone, <i>Nematostella vectensis</i> . <i>PLoS ONE</i> , 2010, 5, e15506.	1.1	29
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2055	Molecular studies of the Brazilian infectious bronchitis virus isolates. <i>Brazilian Journal of Poultry Science</i> , 2010, 12, 107-110.	0.3	3
2056	Architecture of Y-Family DNA Polymerases Relevant to Translesion DNA Synthesis as Revealed in Structural and Molecular Modeling Studies. <i>Journal of Nucleic Acids</i> , 2010, 2010, 1-20.	0.8	12
2057	Positive Selection Differs between Protein Secondary Structure Elements in <i>Drosophila</i> . <i>Genome Biology and Evolution</i> , 2010, 2, 166-179.	1.1	33
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2477	<i>Penicillium araraquense</i> sp. nov., <i>Penicillium elleniae</i> sp. nov., <i>Penicillium penarojense</i> sp. nov., <i>Penicillium vanderhammenii</i> sp. nov. and <i>Penicillium wotroi</i> sp. nov., isolated from leaf litter. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2011, 61, 1462-1475.	0.8	44

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2481	Phylogeography of <i>Ostreopsis</i> along West Pacific Coast, with Special Reference to a Novel Clade from Japan. <i>PLoS ONE</i> , 2011, 6, e27983.	1.1	92
2483	Multilocus Sequence Typing of Pathogens. , 2011, , 503-521.		5
2484	The evolutionary and biogeographic history of the armoured harvestmen “Laniatores phylogeny based on ten molecular markers, with the description of two new families of Opiliones (Arachnida). <i>Invertebrate Systematics</i> , 2011, 25, 106.	0.5	110
2485	A diversity of Antibiotic-resistant <i>Staphylococcus</i> spp. in a Public Transportation System. <i>Osong Public Health and Research Perspectives</i> , 2011, 2, 202-209.	0.7	16
2486	Gains, Losses and Changes of Function after Gene Duplication: Study of the Metallothionein Family. <i>PLoS ONE</i> , 2011, 6, e18487.	1.1	67
2487	<i>MED12</i> , the <i>Mediator Complex Subunit 12</i> Gene, Is Mutated at High Frequency in Uterine Leiomyomas. <i>Science</i> , 2011, 334, 252-255.	6.0	547
2488	A New Gekko from Sibuyan Island, Central Philippines. <i>Herpetologica</i> , 2011, 67, 460-476.	0.2	13
2489	Colonization of roots of cultivated <i>Solanum lycopersicum</i> by dark septate and other ascomycetous endophytes. <i>Mycologia</i> , 2011, 103, 710-721.	0.8	43
2490	Origin and Diversification of Major Clades in Parmelioid Lichens (Parmeliaceae, Ascomycota) during the Paleogene Inferred by Bayesian Analysis. <i>PLoS ONE</i> , 2011, 6, e28161.	1.1	86
2491	Phylogeny of Gobiidae and identification of gobiid lineages. <i>Systematics and Biodiversity</i> , 2011, 9, 329-347.	0.5	121
2492	New Abundant Microbial Groups in Aquatic Hypersaline Environments. <i>Scientific Reports</i> , 2011, 1, 135.	1.6	288
2493	Regulation by Ca <sup>2+</sup> -Signaling Pathways of Adenylyl Cyclases. <i>Cold Spring Harbor Perspectives in Biology</i> , 2011, 3, a004143-a004143.	2.3	156
2494	Systematics of the spider genus <i>Neoleptoneta</i> Brignoli, 1972 (Araneae:Leptonetidae) with a discussion of the morphology and relationships for the North American Leptonetidae. <i>Invertebrate Systematics</i> , 2011, 25, 334.	0.5	17
2495	Selection of organisms for the co-evolution-based study of protein interactions. <i>BMC Bioinformatics</i> , 2011, 12, 363.	1.2	13
2496	The spatial scale of genetic subdivision in populations of <i>Ifremeria nautilei</i> , a hydrothermal-vent gastropod from the southwest Pacific. <i>BMC Evolutionary Biology</i> , 2011, 11, 372.	3.2	46
2497	Expression level, cellular compartment and metabolic network position all influence the average selective constraint on mammalian enzymes. <i>BMC Evolutionary Biology</i> , 2011, 11, 89.	3.2	34
2498	Diversity of metalloproteinases in <i>Bothrops neuwiedi</i> snake venom transcripts: evidences for recombination between different classes of SVMPs. <i>BMC Genetics</i> , 2011, 12, 94.	2.7	34

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2508	DNA barcoding: a new tool for palm taxonomists?. <i>Annals of Botany</i> , 2011, 108, 1445-1451.	1.4	49
2509	Relaxed selection is a precursor to the evolution of phenotypic plasticity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 15936-15941.	3.3	148
2510	A novel immunity system for bacterial nucleic acid degrading toxins and its recruitment in various eukaryotic and DNA viral systems. <i>Nucleic Acids Research</i> , 2011, 39, 4532-4552.	6.5	184
2511	The Evolutionary History of YAP and the Hippo/YAP Pathway. <i>Molecular Biology and Evolution</i> , 2011, 28, 2403-2417.	3.5	134
2512	Phylogeographic origin of <i>Helicobacter pylori</i> is a determinant of gastric cancer risk. <i>Gut</i> , 2011, 60, 1189-1195.	6.1	120
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2514	T-Coffee: a web server for the multiple sequence alignment of protein and RNA sequences using structural information and homology extension. <i>Nucleic Acids Research</i> , 2011, 39, W13-W17.	6.5	982
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2516	Morphological and Molecular Analysis of <i>Fusarium lateritium</i> , the Cause of Gray Necrosis of Hazelnut Fruit in Italy. <i>Phytopathology</i> , 2011, 101, 679-686.	1.1	37

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2519	A Bioinformatics Pipeline for Sequence-Based Analyses of Fungal Biodiversity. <i>Methods in Molecular Biology</i> , 2011, 722, 141-155.	0.4	22
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2521	Bacterial genome chimaerism and the origin of mitochondria. <i>Canadian Journal of Microbiology</i> , 2011, 57, 49-61.	0.8	35
2522	An olfactory receptor for food-derived odours promotes male courtship in <i>Drosophila</i> . <i>Nature</i> , 2011, 478, 236-240.	13.7	345
2523	Design of multiple sequence alignment algorithms on parallel, distributed memory supercomputers. , 2011, 2011, 924-7.		9
2524	PAAA: A Progressive Iterative Alignment Algorithm Based on Anchors. <i>Lecture Notes in Computer Science</i> , 2011, , 296-305.	1.0	2
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2526	Discovery of a Cytokinin Deaminase. <i>ACS Chemical Biology</i> , 2011, 6, 1036-1040.	1.6	15
2527	Cloning and characterization of <i>mariner</i> -like elements in the soybean aphid, <i>Aphis glycines</i> Matsumura. <i>Bulletin of Entomological Research</i> , 2011, 101, 697-704.	0.5	8
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2532	Comparative genomics of the social amoebae <i>Dictyostelium discoideum</i> and <i>Dictyostelium purpureum</i> . <i>Genome Biology</i> , 2011, 12, R20.	13.9	141
2533	Use of the Chloroplast Gene <i>ycf1</i> for the Genetic Differentiation of Pine Nuts Obtained from Consumers Experiencing Dysgeusia. <i>Journal of Agricultural and Food Chemistry</i> , 2011, 59, 10995-11002.	2.4	22
2534	Screening for potential probiotic bacteria to reduce prevalence of WSSV and IHNV in whiteleg shrimp ( <i>Litopenaeus vannamei</i> ) under experimental conditions. <i>Aquaculture</i> , 2011, 322-323, 16-22.	1.7	56
2535	The crystal structure of rice ( <i>Oryza sativa</i> L.) Os4BGlu12, an oligosaccharide and tuberonic acid glucoside-hydrolyzing Î <sup>2</sup> -glucosidase with significant thioglucosylhydrolase activity. <i>Archives of Biochemistry and Biophysics</i> , 2011, 510, 62-72.	1.4	28

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2537	Exome Sequencing of Ion Channel Genes Reveals Complex Profiles Confounding Personal Risk Assessment in Epilepsy. <i>Cell</i> , 2011, 145, 1036-1048.	13.5	274
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2543	Characterization of the gilthead seabream ( <i>Sparus aurata</i> L.) transferrin gene: Genomic structure, constitutive expression and SNP variation. <i>Fish and Shellfish Immunology</i> , 2011, 31, 548-56.	1.6	14
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2555	Molecular evolution of bacterial indoleamine 2,3-dioxygenase. <i>Gene</i> , 2011, 485, 22-31.	1.0	14
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2559	Linker and/or transmembrane regions of influenza A/Group-1, A/Group-2, and type B virus hemagglutinins are packed differently within trimers. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2011, 1808, 1843-1854.	1.4	38
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2561	Structural modeling of RNase P RNA of the hyperthermophilic archaeon <i>Pyrococcus horikoshii</i> OT3. <i>Biochemical and Biophysical Research Communications</i> , 2011, 414, 517-522.	1.0	13
2562	A novel fungal family of oligopeptide transporters identified by functional metatranscriptomics of soil eukaryotes. <i>ISME Journal</i> , 2011, 5, 1871-1880.	4.4	74
2563	Fungal and algal gene expression in early developmental stages of lichen-symbiosis. <i>Mycologia</i> , 2011, 103, 291-306.	0.8	65
2564	Recent advances in the transcriptional regulation of the flavonoid biosynthetic pathway. <i>Journal of Experimental Botany</i> , 2011, 62, 2465-2483.	2.4	990
2565	Divergence Time Estimation Using Fossils as Terminal Taxa and the Origins of Lissamphibia. <i>Systematic Biology</i> , 2011, 60, 466-481.	2.7	354
2566	Intrinsic disorder in S100 proteins. <i>Molecular BioSystems</i> , 2011, 7, 2164.	2.9	28
2567	PATRIC: the Comprehensive Bacterial Bioinformatics Resource with a Focus on Human Pathogenic Species. <i>Infection and Immunity</i> , 2011, 79, 4286-4298.	1.0	252
2568	Integrating High-Throughput Pyrosequencing and Quantitative Real-Time PCR to Analyze Complex Microbial Communities. <i>Methods in Molecular Biology</i> , 2011, 733, 107-128.	0.4	22
2569	The <i>Selaginella</i> Genome Identifies Genetic Changes Associated with the Evolution of Vascular Plants. <i>Science</i> , 2011, 332, 960-963.	6.0	794
2570	Systematics and redescription of the European meiofaunal slug <i>Microhedyle glandulifera</i> (Kowalevsky, 1901) (Heterobranchia: Acochlidia): evidence from molecules and morphology. <i>Journal of Molluscan Studies</i> , 2011, 77, 388-400.	0.4	12
2571	Differentiation of <i>Candida parapsilosis</i> , <i>C. orthopsilosis</i> , and <i>C. metapsilosis</i> by specific PCR amplification of the RPS0 intron. <i>International Journal of Medical Microbiology</i> , 2011, 301, 531-535.	1.5	15

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2573	Improved molecular methods to characterise <i>Serpula lacrymans</i> and other Basidiomycetes involved in wood decay. <i>Journal of Microbiological Methods</i> , 2011, 84, 208-215.	0.7	16
2574	Asian corn borer pheromone binding protein 3, a candidate for evolving specificity to the 12-tetradecenyl acetate sex pheromone. <i>Insect Biochemistry and Molecular Biology</i> , 2011, 41, 141-149.	1.2	42
2575	Four potato ( <i>Solanum tuberosum</i> ) ABCG transporters and their expression in response to abiotic factors and <i>Phytophthora infestans</i> infection. <i>Journal of Plant Physiology</i> , 2011, 168, 2225-2233.	1.6	28
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2577	Temporal Regulation of Gene Expression of the <i>Thermus thermophilus</i> Bacteriophage P23-45. <i>Journal of Molecular Biology</i> , 2011, 405, 125-142.	2.0	33
2578	iWRAP: An Interface Threading Approach with Application to Prediction of Cancer-Related Protein-Protein Interactions. <i>Journal of Molecular Biology</i> , 2011, 405, 1295-1310.	2.0	56
2579	The Alternating-Access Mechanism of MFS Transporters Arises from Inverted-Topology Repeats. <i>Journal of Molecular Biology</i> , 2011, 407, 698-715.	2.0	169
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2582	Allotetraploid origin and divergence in Eleusine ( <i>Chloridoideae</i> , <i>Poaceae</i> ): evidence from low-copy nuclear gene phylogenies and a plastid gene chronogram. <i>Annals of Botany</i> , 2011, 108, 1287-1298.	1.4	30
2583	Influence of sequence variability on bactericidal activity sera induced by Factor H binding protein variant 1.1. <i>Vaccine</i> , 2011, 29, 1072-1081.	1.7	47
2584	Highly pathogenic avian influenza virus H5N1 from Egypt escapes vaccine-induced immunity but confers clinical protection against a heterologous clade 2.2.1 Egyptian isolate. <i>Vaccine</i> , 2011, 29, 5567-5573.	1.7	92
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2587	The ‘‘original’’ Hepatitis B virus of Eastern chimpanzees ( <i>Pan troglodytes schweinfurthii</i> ). <i>Virus Research</i> , 2011, 155, 372-375.	1.1	5
2588	Population differentiation and selective constraints in <i>Pelargonium</i> line pattern virus. <i>Virus Research</i> , 2011, 155, 274-282.	1.1	6
2589	Genetic characterization of K13965, a strain of Oak Vale virus from Western Australia. <i>Virus Research</i> , 2011, 160, 206-213.	1.1	23



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2604	A comparative review of short and long neuropeptide F signaling in invertebrates: Any similarities to vertebrate neuropeptide Y signaling?. <i>Peptides</i> , 2011, 32, 1335-1355.	1.2	271
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2610	Taxonomic and functional prokaryote diversity in mildly arsenic-contaminated sediments. <i>Research in Microbiology</i> , 2011, 162, 877-887.	1.0	51
2611	Polarity and the diversity of growth mechanisms in bacteria. <i>Seminars in Cell and Developmental Biology</i> , 2011, 22, 790-798.	2.3	55
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2613	UniProt Knowledgebase: a hub of integrated protein data. <i>Database: the Journal of Biological Databases and Curation</i> , 2011, 2011, bar009-bar009.	1.4	1,271
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3588	Real-time captioning by groups of non-experts. , 2012, , .		151
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3843	Kinetic and phylogenetic analysis of plant polyamine uptake transporters. <i>Planta</i> , 2012, 236, 1261-1273.	1.6	41
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3960	Species-level phylogeny of <i>Satanâ€™s perchesâ€™</i> based on discordant gene trees ( <i>Teleostei</i> : <i>Cichlidae</i> ): Tj ETQq1 1 0.784314 rgBT 1.2 20	1.2	20
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3997	Rapid and accurate identification of genomic species from the <i>Acinetobacter baumannii</i> (Ab) group by MALDI-TOF MS. <i>Clinical Microbiology and Infection</i> , 2012, 18, 1097-1103.	2.8	90
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4020	Presence and distribution of the endosymbiont <i>Wolbachia</i> among <i>Solenopsis</i> spp. (Hymenoptera: Tj ETQq1 1 0.784314 rgBT /Overlock 287-296.	1.5	30
4021	Natural occurrence of <i>Zoophthora radicans</i> (Entomophthorales: Entomophthoraceae) on <i>Thaumastocoris peregrinus</i> (Heteroptera: Thaumastocoridae), an invasive pest recently found in Brazil. <i>Journal of Invertebrate Pathology</i> , 2012, 110, 401-404.	1.5	26
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4073	Impact of seminal cytomegalovirus replication on HIV-1 dynamics between blood and semen. <i>Journal of Medical Virology</i> , 2012, 84, 1703-1709.	2.5	19
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4140	Related bifunctional restriction endonuclease-methyltransferase triplets: TspDTI, Tth111II/TthHB27I and TsoI with distinct specificities. <i>BMC Molecular Biology</i> , 2012, 13, 13.	3.0	20
4141	Clustered metallothionein genes are co-regulated in rice and ectopic expression of OsMT1e-P confers multiple abiotic stress tolerance in tobacco via ROS scavenging. <i>BMC Plant Biology</i> , 2012, 12, 107.	1.6	131
4142	Frequency of <i>Chlamydia trachomatis</i> in <i>Ureaplasma</i> -positive healthy women attending their first prenatal visit in a community hospital in Sapporo, Japan. <i>BMC Infectious Diseases</i> , 2012, 12, 82.	1.3	26

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4144	Evolutionarily consistent families in SCOP: sequence, structure and function. <i>BMC Structural Biology</i> , 2012, 12, 27.	2.3	14
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4146	The pupylation pathway and its role in mycobacteria. <i>BMC Biology</i> , 2012, 10, 95.	1.7	54
4147	Hidden evolutionary complexity of Nucleo-Cytoplasmic Large DNA viruses of eukaryotes. <i>Virology Journal</i> , 2012, 9, 161.	1.4	155
4148	Genetic diversity and recombination analysis of sweepoviruses from Brazil. <i>Virology Journal</i> , 2012, 9, 241.	1.4	38
4149	Subtype- and antigenic site-specific differences in biophysical influences on evolution of influenza virus hemagglutinin. <i>Virology Journal</i> , 2012, 9, 91.	1.4	43
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4151	Stop codons in bacteria are not selectively equivalent. <i>Biology Direct</i> , 2012, 7, 30.	1.9	34
4152	Proteorhodopsin genes in giant viruses. <i>Biology Direct</i> , 2012, 7, 34.	1.9	102
4153	Updated clusters of orthologous genes for Archaea: a complex ancestor of the Archaea and the byways of horizontal gene transfer. <i>Biology Direct</i> , 2012, 7, 46.	1.9	142
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4155	Evolutionary constraints and expression analysis of gene duplications in <i>Rhodobacter sphaeroides</i> 2.4.1. <i>BMC Research Notes</i> , 2012, 5, 192.	0.6	8
4156	Rapid phylogenetic and functional classification of short genomic fragments with signature peptides. <i>BMC Research Notes</i> , 2012, 5, 460.	0.6	24
4157	Mutual information and variants for protein domain-domain contact prediction. <i>BMC Research Notes</i> , 2012, 5, 472.	0.6	5
4158	In silico approach to predict candidate R proteins and to define their domain architecture. <i>BMC Research Notes</i> , 2012, 5, 678.	0.6	41
4159	Assessment of the genetic relationship between <i>Dictyocaulus</i> species from <i>Bos taurus</i> and <i>Cervus elaphus</i> using complete mitochondrial genomic datasets. <i>Parasites and Vectors</i> , 2012, 5, 241.	1.0	36
4160	New species of <i>Ehrlichia</i> isolated from <i>Rhipicephalus (Boophilus) microplus</i> shows an ortholog of the <i>E. canis</i> major immunogenic glycoprotein gp36 with a new sequence of tandem repeats. <i>Parasites and Vectors</i> , 2012, 5, 291.	1.0	53

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4172	Molecular phylogeny and dating of Asteliaceae (Asparagales): <i>Astelia</i> s.l. evolution provides insight into the Oligocene history of New Zealand. <i>Molecular Phylogenetics and Evolution</i> , 2012, 65, 102-115.	1.2	19
4173	Cross-neutralization of influenza A viruses mediated by a single antibody loop. <i>Nature</i> , 2012, 489, 526-532.	13.7	434
4174	<i>Trichuris</i> sp. and <i>Strongyloides</i> sp. Infections in a Free-Ranging Baboon Colony. <i>Journal of Parasitology</i> , 2012, 98, 205-208.	0.3	14
4175	Phylum XXVI. Actinobacteria phyl. nov., 2012, , 33-2028.		58
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4186	Identification of Homologous Gene Sequences by PCR with Degenerate Primers. <i>Methods in Molecular Biology</i> , 2012, 772, 245-256.	0.4	11
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4194	<i>Wickerhamomyces xylosica</i> sp. nov. and <i>Candida phayaonensis</i> sp. nov., two xylose-assimilating yeast species from soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2012, 62, 2786-2792.	0.8	20
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4211	Membrane-associated nanomotors for macromolecular transport. <i>Current Opinion in Biotechnology</i> , 2012, 23, 537-544.	3.3	23
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4216	Global alignment of molecular sequences via ancestral state reconstruction. <i>Stochastic Processes and Their Applications</i> , 2012, 122, 3852-3874.	0.4	10
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4434	CONTOR—A new knowledge-based fold recognition potential, based on side chain orientation and contacts between residue terminal groups. Protein Science, 2012, 21, 134-141.	3.1	3
4435	A novel method for protein-protein interaction site prediction using phylogenetic substitution models. Proteins: Structure, Function and Bioinformatics, 2012, 80, 126-141.	1.5	27
4436	Prescont: Predicting protein-protein interfaces utilizing four residue properties. Proteins: Structure, Function and Bioinformatics, 2012, 80, 154-168.	1.5	41
4437	Solution structure of gp17 from the <i>Siphoviridae</i> bacteriophage SPP1: Insights into its role in virion assembly. Proteins: Structure, Function and Bioinformatics, 2012, 80, 319-326.	1.5	15
4438	Camps 2.0: Exploring the sequence and structure space of prokaryotic, eukaryotic, and viral membrane proteins. Proteins: Structure, Function and Bioinformatics, 2012, 80, 839-857.	1.5	13
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4440	Evolutionary information hidden in a single protein structure. Proteins: Structure, Function and Bioinformatics, 2012, 80, 1647-1657.	1.5	38
4441	Multi-ZerD: Multiple protein docking for asymmetric complexes. Proteins: Structure, Function and Bioinformatics, 2012, 80, 1818-1833.	1.5	71
4442	Phylogenetic placement of <i>Geastrum melanocephalum</i> and polyphyly of <i>Geastrum triplex</i> . Mycoscience, 2012, 53, 411-426.	0.3	36
4443	Raspberry leaf blotch virus, a putative new member of the genus Emaravirus, encodes a novel genomic RNA. Journal of General Virology, 2012, 93, 430-437.	1.3	85
4444	Computational Challenges in Characterization of Bacteria and Bacteria-Host Interactions Based on Genomic Data. Journal of Computer Science and Technology, 2012, 27, 225-239.	0.9	9
4445	Genetical Genomics for Evolutionary Studies. Methods in Molecular Biology, 2012, 856, 469-485.	0.4	2
4446	Phylogenetic placement of lichenicolous <i>Phoma</i> species in the Phaeosphaeriaceae (Pleosporales). Tj ETQq1 1 0.784314 rgBT /Overloc 4.7 50		
4447	Structure-Based Design, Synthesis, and Characterization of Dual Hotspot Small-Molecule HIV-1 Entry Inhibitors. Journal of Medicinal Chemistry, 2012, 55, 4382-4396.	2.9	90
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4449	Origins and Genetic Legacy of Neolithic Farmers and Hunter-Gatherers in Europe. Science, 2012, 336, 466-469.	6.0	507
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4453	Molecular phylogenetics: principles and practice. <i>Nature Reviews Genetics</i> , 2012, 13, 303-314.	7.7	572
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4455	Evolution of increased complexity in a molecular machine. <i>Nature</i> , 2012, 481, 360-364.	13.7	181
4456	Multigene phylogeny and taxonomy of the genus <i>Melanconielliella</i> (Diaporthales). <i>Fungal Diversity</i> , 2012, 57, 1-44.	4.7	63
4457	Evolution of coding and non-coding genes in HOX clusters of a marsupial. <i>BMC Genomics</i> , 2012, 13, 251.	1.2	47
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4461	Viral clones from the GOS expedition with an unusual photosystem-I gene cassette organization. <i>ISME Journal</i> , 2012, 6, 1617-1620.	4.4	14
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4463	Evolution of CRISPs Associated with Toxicoforan-Reptilian Venom and Mammalian Reproduction. <i>Molecular Biology and Evolution</i> , 2012, 29, 1807-1822.	3.5	89
4464	Dramatic Expansion and Developmental Expression Diversification of the <i>Methuselah</i> Gene Family During Recent <i>Drosophila</i> Evolution. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2012, 318, 368-387.	0.6	30
4465	An oocyte-preferential histone mRNA stem-loop-binding protein like is expressed in several mammalian species. <i>Molecular Reproduction and Development</i> , 2012, 79, 380-391.	1.0	9
4466	Expression and phylogeny of candidate genes for sex differentiation in a primitive fish species, the Siberian sturgeon, <i>Acipenser baerii</i> . <i>Molecular Reproduction and Development</i> , 2012, 79, 504-516.	1.0	45
4467	Population-based resequencing revealed an ancestral winter group of cultivated flax: implication for flax domestication processes. <i>Ecology and Evolution</i> , 2012, 2, 622-635.	0.8	11
4468	Genome-wide and molecular evolution analysis of the <i>P</i> oplar <i>KT</i> / <i>HAK</i> / <i>KUP</i> potassium transporter gene family. <i>Ecology and Evolution</i> , 2012, 2, 1996-2004.	0.8	48



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4470	Locus-specific view of flax domestication history. <i>Ecology and Evolution</i> , 2012, 2, 139-152.	0.8	53
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4473	The origins and evolution of ubiquitination sites. <i>Molecular BioSystems</i> , 2012, 8, 1865.	2.9	23
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4476	Molecular Phylogenetics, Molecular Evolution, and Patterns of Clade Support in <i>Lithospermum</i> ( <i>Boraginaceae</i> ) and Related Taxa. <i>Systematic Botany</i> , 2012, 37, .	0.2	8
4477	Phylogeny of the dragonfly genus <i>Sympetrum</i> ( <i>Odonata</i> : <i>Libellulidae</i> ). <i>Organisms Diversity and Evolution</i> , 2012, 12, 281-295.	0.7	11
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4479	More than 1000 ultraconserved elements provide evidence that turtles are the sister group of archosaurs. <i>Biology Letters</i> , 2012, 8, 783-786.	1.0	331
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4482	Relaxed Clocks and Inferences of Heterogeneous Patterns of Nucleotide Substitution and Divergence Time Estimates across Whales and Dolphins ( <i>Mammalia</i> : <i>Cetacea</i> ). <i>Molecular Biology and Evolution</i> , 2012, 29, 721-736.	3.5	115
4483	Developmental and evolutionary diversity of plant MADS-domain factors: insights from recent studies. <i>Development (Cambridge)</i> , 2012, 139, 3081-3098.	1.2	462
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4488	Genome sequence of foxtail millet ( <i>Setaria italica</i> ) provides insights into grass evolution and biofuel potential. <i>Nature Biotechnology</i> , 2012, 30, 549-554.	9.4	636
4489	Toward Genetics-Based Virus Taxonomy: Comparative Analysis of a Genetics-Based Classification and the Taxonomy of Picornaviruses. <i>Journal of Virology</i> , 2012, 86, 3905-3915.	1.5	52
4490	Independent evolution of striated muscles in cnidarians and bilaterians. <i>Nature</i> , 2012, 487, 231-234.	13.7	221
4491	Analysis of High-Throughput Ancient DNA Sequencing Data. <i>Methods in Molecular Biology</i> , 2012, 840, 197-228.	0.4	177
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4493	PhyLAT: a phylogenetic local alignment tool. <i>Bioinformatics</i> , 2012, 28, 1336-1344.	1.8	5
4494	Genome Research in the Cloud. <i>OMICS A Journal of Integrative Biology</i> , 2012, 16, 422-428.	1.0	15
4495	Phylogeny and Biogeography of the Core Babblers (Aves: Timaliidae). <i>Systematic Biology</i> , 2012, 61, 631-651.	2.7	124
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4497	A new species of <i>Gehyra</i> Gray, 1834 (Squamata, Gekkonidae) from the Loyalty Islands and Vanuatu, and phylogenetic relationships in the genus <i>Gehyra</i> in Melanesia. <i>Zoosystema</i> , 2012, 34, 203-221.	0.2	9
4498	A field guide to eukaryotic circular single-stranded DNA viruses: insights gained from metagenomics. <i>Archives of Virology</i> , 2012, 157, 1851-1871.	0.9	254
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4500	The poetry of reproduction: the role of LEAFY in <i>Arabidopsis thaliana</i> flower formation. <i>International Journal of Developmental Biology</i> , 2012, 56, 207-221.	0.3	77
4501	Phylogenomic analysis of transcriptome data elucidates occurrence of a paleopolyploid event and the origin of bimodal karyotypes in Agavoideae (Asparagaceae). <i>American Journal of Botany</i> , 2012, 99, 397-406.	0.8	94
4502	The phylogeny of halichondrid demosponges: past and present re-visited with DNA-barcoding data. <i>Organisms Diversity and Evolution</i> , 2012, 12, 57-70.	0.7	30
4503	Fungi associated with Asphondylia (Diptera: Cecidomyiidae) galls on <i>Sarcocornia quinqueflora</i> and <i>Tecticornia arbuscula</i> (Chenopodiaceae). <i>Fungal Diversity</i> , 2012, 55, 143-154.	4.7	12
4504	The phylogenetic relationships of the Andean swamp rat genus <i>Neotomys</i> (Rodentia, Cricetidae). <i>Tj ETQq1 1 0.784314 rgBT /Overlock 1.1 20</i>	1.1	20

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4507	Genomic organization and comparative chromosome mapping of the U1 snRNA gene in cichlid fish, with an emphasis in <i>Oreochromis niloticus</i> . <i>Chromosome Research</i> , 2012, 20, 279-292.	1.0	49
4508	Low genetic diversity and evidence of population structure among subspecies of <i>Nerodia harteri</i> , a threatened water snake endemic to Texas. <i>Conservation Genetics</i> , 2012, 13, 977-986.	0.8	11
4509	Thermal stability of chicken brain $\alpha$ -spectrin repeat 17: a spectroscopic study. <i>Journal of Biomolecular NMR</i> , 2012, 53, 71-83.	1.6	7
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4513	Phylogeny and evolutionary history of the silkworm. <i>Science China Life Sciences</i> , 2012, 55, 483-496.	2.3	71
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4515	Differential gene expression in <i>Alternaria gaisen</i> exposed to dark and light. <i>Mycological Progress</i> , 2012, 11, 373-382.	0.5	19
4516	<i>Genea mexicana</i> , sp. nov., and <i>Geopora toluca</i> , sp. nov., new hypogeous Pyronemataceae from Mexico, and the taxonomy of <i>Geopora</i> reevaluated. <i>Mycological Progress</i> , 2012, 11, 711-724.	0.5	12
4517	TBC: A clustering algorithm based on prokaryotic taxonomy. <i>Journal of Microbiology</i> , 2012, 50, 181-185.	1.3	26
4518	Expression of multiple tfb genes in different <i>Halobacterium salinarum</i> strains and interaction of TFB with transcriptional activator GvpE. <i>Archives of Microbiology</i> , 2012, 194, 269-279.	1.0	24
4519	Microbial biodiversity in a Malaysian oil field and a systematic comparison with oil reservoirs worldwide. <i>Archives of Microbiology</i> , 2012, 194, 513-523.	1.0	49
4520	Cryptic hammerhead shark lineage occurrence in the western South Atlantic revealed by DNA analysis. <i>Marine Biology</i> , 2012, 159, 829-836.	0.7	22
4521	Detection and Identification of Species-Specific Bacteria Associated with Synanthropic Mites. <i>Microbial Ecology</i> , 2012, 63, 919-928.	1.4	65
4522	Highly divergent dimorphic alleles of the proteasome subunit beta type-8 (PSMB8) gene of the bichir <i>Polypterus senegalus</i> : implication for evolution of the PSMB8 gene of jawed vertebrates. <i>Immunogenetics</i> , 2012, 64, 447-453.	1.2	5

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4527	Genome-wide analysis and expression profiling of the DREB transcription factor gene family in <i>Malus</i> under abiotic stress. <i>Molecular Genetics and Genomics</i> , 2012, 287, 423-436.	1.0	112
4528	Assessing the monophyly of polyploid <i>Gossypium</i> species. <i>Plant Systematics and Evolution</i> , 2012, 298, 1177-1183.	0.3	44
4529	Plasmid pP62BP1 isolated from an Arctic <i>Psychrobacter</i> sp. strain carries two highly homologous type II restriction-modification systems and a putative organic sulfate metabolism operon. <i>Extremophiles</i> , 2012, 16, 363-376.	0.9	8
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4533	<i>Vuilleminia erastii</i> sp. nov. (Corticiales), an amphi-Beringian species and revision of the occurrence of <i>Vuilleminia comedens</i> in North America. <i>Mycoscience</i> , 2012, 53, 290-299.	0.3	4
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4536	Divergent evolution of oxidosqualene cyclases in plants. <i>New Phytologist</i> , 2012, 193, 1022-1038.	3.5	122
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4538	No evidence of cross-species transmission of mouse retroviruses to animal workers exposed to mice. <i>Transfusion</i> , 2012, 52, 317-325.	0.8	3
4539	<i>PROROCENTRUM BIMACULATUM</i> SP. NOV. (DINOPHYCEAE, PROROCENTRALES), A NEW BENTHIC DINOFLAGELLATE SPECIES FROM KUWAIT (ARABIAN GULF). <i>Journal of Phycology</i> , 2012, 48, 211-221.	1.0	12
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4542	Physiological implications of genomic state in parthenogenetic lizards of reciprocal hybrid origin. <i>Journal of Evolutionary Biology</i> , 2012, 25, 252-263.	0.8	10
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4544	Tudor domain-containing proteins of <i>Drosophila melanogaster</i> . <i>Development Growth and Differentiation</i> , 2012, 54, 32-43.	0.6	22
4545	Two distinct RNA-dependent RNA polymerases are required for initiation and amplification of RNA silencing in the basal fungus <i>Mucor circinelloides</i> . <i>Molecular Microbiology</i> , 2012, 83, 379-394.	1.2	67
4546	The GtaR protein negatively regulates transcription of the <i>gtaRl</i> operon and modulates gene transfer agent (RcGTA) expression in <i>Rhodobacter capsulatus</i> . <i>Molecular Microbiology</i> , 2012, 83, 759-774.	1.2	55
4547	Separate structural and functional domains of Tn4430 transposase contribute to target immunity. <i>Molecular Microbiology</i> , 2012, 83, 805-820.	1.2	25
4548	Phylogenetic structure illuminates the mechanistic role of environmental heterogeneity in community organization. <i>Journal of Animal Ecology</i> , 2012, 81, 455-462.	1.3	34
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4550	Evaluating aggressiveness and host range of <i>Alternaria dauci</i> in a controlled environment. <i>Plant Pathology</i> , 2012, 61, 63-75.	1.2	41
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4552	Phylogenetics and biogeography of the Balkan sand gobies™ (Teleostei: Gobiidae): vulnerable species in need of taxonomic revision. <i>Biological Journal of the Linnean Society</i> , 2012, 105, 73-91.	0.7	35
4553	THE PROMISCUOUS AND THE CHASTE: FREQUENT ALLOPOLYPLOID SPECIATION AND ITS GENOMIC CONSEQUENCES IN AMERICAN DAISIES (MELAMPODIUM, SECT. MELAMPODIUM; ASTERACEAE). <i>Evolution; International Journal of Organic Evolution</i> , 2012, 66, 211-228.	1.1	44
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4555	Phylogenetic and functional diversity of Bacteria and Archaea in a unique stratified lagoon, the Clipperton atoll (N Pacific). <i>FEMS Microbiology Ecology</i> , 2012, 79, 203-217.	1.3	25
4556	Pasteuria endospores from <i>Heterodera cajani</i> (Nematoda: Heteroderidae) exhibit inverted attachment and altered germination in cross-infection studies with <i>Globodera pallida</i> (Nematoda: Heteroderidae). <i>FEMS Microbiology Ecology</i> , 2012, 79, 675-684.	1.3	22
4557	Comparative analysis of cyanobacteria in the rhizosphere and as endosymbionts of cycads in drought-affected soils. <i>FEMS Microbiology Ecology</i> , 2012, 80, 204-215.	1.3	25
4558	<i>Methanoculleus</i> spp. as a biomarker of methanogenic activity in swine manure storage tanks. <i>FEMS Microbiology Ecology</i> , 2012, 80, 427-440.	1.3	36

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4560	Phylogenetic Position of the Adeleorinid Coccidia (Myzozoa, Apicomplexa, Coccidia, Eucoccidiorida,) Tj ETQq1 1 0.784314 rgBT /Overbo 59, 171-180.	0.8	111
4561	Structural basis for specificity of TGF $\beta$ family receptor small molecule inhibitors. <i>Cellular Signalling</i> , 2012, 24, 476-483.	1.7	50
4562	<i>Dermacentor variabilis</i> : Characterization and modeling of macrophage migration inhibitory factor with phylogenetic comparisons to other ticks, insects and parasitic nematodes. <i>Experimental Parasitology</i> , 2012, 130, 232-238.	0.5	10
4563	Analysis of a calcium-binding EF-hand protein family in <i>Fasciola gigantica</i> . <i>Experimental Parasitology</i> , 2012, 130, 364-373.	0.5	26
4564	Genetic and molecular characterization reveals a unique nucleobase cation symporter 1 in <i>Arabidopsis</i> . <i>FEBS Letters</i> , 2012, 586, 1370-1378.	1.3	37
4565	Structural and functional consequences of mutating a proteobacteria-specific surface residue in the catalytic domain of <i>Escherichia coli</i> GluRS. <i>FEBS Letters</i> , 2012, 586, 1724-1730.	1.3	4
4566	The genome of wine yeast <i>Dekkera bruxellensis</i> provides a tool to explore its food-related properties. <i>International Journal of Food Microbiology</i> , 2012, 157, 202-209.	2.1	102
4567	Identification of biotypes and secondary endosymbionts of <i>Bemisia tabaci</i> in Korea and relationships with the occurrence of TYLCV disease. <i>Journal of Asia-Pacific Entomology</i> , 2012, 15, 186-191.	0.4	38
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4569	A <i>Rhipicephalus</i> ( <i>Boophilus</i> ) <i>microplus</i> cathepsin with dual peptidase and antimicrobial activity. <i>International Journal for Parasitology</i> , 2012, 42, 635-645.	1.3	20
4570	From cryptogene to gene? ND8 editing domain reduction in insect trypanosomatids. <i>European Journal of Protistology</i> , 2012, 48, 185-193.	0.5	25
4571	Four years of experimental climate change modifies the microbial drivers of N <sub>2</sub> O fluxes in an upland grassland ecosystem. <i>Global Change Biology</i> , 2012, 18, 2520-2531.	4.2	100
4572	Raaln, a transcript enriched in the honey bee brain, is a remnant of genomic rearrangement in hymenoptera. <i>Insect Molecular Biology</i> , 2012, 21, 305-318.	1.0	5
4573	The historical biogeography of <i>Scabiosa</i> ( <i>Dipsacaceae</i> ): implications for Old World plant disjunctions. <i>Journal of Biogeography</i> , 2012, 39, 1086-1100.	1.4	49
4574	Did geckos ride the Palawan raft to the Philippines?. <i>Journal of Biogeography</i> , 2012, 39, 1217-1234.	1.4	69
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4578	CYTOLOGICAL AND PHYLOGENETIC DIVERSITY IN FRESHWATER <i>ESOPTRODINIUM</i> / <i>BERNARDINIUM</i> SPECIES (DINOPHYCEAE) <sup>1</sup> . Journal of Phycology, 2012, 48, 793-807.	1.0	10
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4581	A <i>S</i> -adenosylmethionine methyltransferase-like domain within the essential, Fe <sup>2+</sup> -containing yeast protein Dre2. FEBS Journal, 2012, 279, 2108-2119.	2.2	25
4582	Influenza Research Database: an integrated bioinformatics resource for influenza research and surveillance. Influenza and Other Respiratory Viruses, 2012, 6, 404-416.	1.5	270
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4590	EXPLOSIVE RADIATION OF A BACTERIAL SPECIES GROUP. Evolution; International Journal of Organic Evolution, 2012, 66, 2577-2586.	1.1	35
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4593	Lichen myco- and photobiont diversity and their relationships at the edge of life (McMurdo Dry) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 10 1.3 66	1.3	66
4594	Molecular data do not support the current division of <i>Orthotrichum</i> (Bryophyta) species with immersed stomata. Journal of Systematics and Evolution, 2012, 50, 12-24.	1.6	26

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4621	Indel information eliminates trivial sequence alignment in maximum likelihood phylogenetic analysis. <i>Cladistics</i> , 2012, 28, 514-528.	1.5	11
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4701	Evolution of petaloid sepals independent of shifts in B-class MADS box gene expression. <i>Development Genes and Evolution</i> , 2012, 222, 19-28.	0.4	15
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#	ARTICLE	IF	CITATIONS
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4704	Matita, a new retroelement from peanut: characterization and evolutionary context in the light of the <i>Arachis</i> A-B genome divergence. <i>Molecular Genetics and Genomics</i> , 2012, 287, 21-38.	1.0	43
4705	Successful COG8 and PDF overlap is mediated by alterations in splicing and polyadenylation signals. <i>Human Genetics</i> , 2012, 131, 265-274.	1.8	4
4706	Reclassification of <i>Thermoproteus neutrophilus</i> Stetter and Zillig 1989 as <i>Pyrobaculum neutrophilum</i> comb. nov. based on phylogenetic analysis. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013, 63, 751-754.	0.8	21
4707	Occurrence of <i>Metarhizium</i> spp. in Central Brazilian soils. <i>Journal of Basic Microbiology</i> , 2013, 53, 251-259.	1.8	61
4708	The metagenome of the marine anammox bacterium <i>Candidatus Scalindua profunda</i> ™ illustrates the versatility of this globally important nitrogen cycle bacterium. <i>Environmental Microbiology</i> , 2013, 15, 1275-1289.	1.8	246
4709	An ABC transporter and an outer membrane lipoprotein participate in posttranslational activation of type VI secretion in <i>Pseudomonas aeruginosa</i> . <i>Environmental Microbiology</i> , 2013, 15, 471-486.	1.8	84
4710	Mitochondrial <i>scpD</i> loop analysis reveals low diversity in <i>scpM</i> angalica pigs and their relationship to historical specimens. <i>Journal of Animal Breeding and Genetics</i> , 2013, 130, 312-320.	0.8	10
4711	Genetic identification of members of the <i>Bemisia tabaci</i> cryptic species complex from South Africa reveals native and introduced haplotypes. <i>Journal of Applied Entomology</i> , 2013, 137, 122-135.	0.8	54
4712	Morphological and molecular diversity of <i>Colletotrichum</i> spp. causing pepper spot and anthracnose of lychee ( <i>Litchi chinensis</i> ) in Australia. <i>Plant Pathology</i> , 2013, 62, 279-288.	1.2	26
4713	Multiple <i>Alternaria</i> species groups are associated with leaf blotch and fruit spot diseases of apple in Australia. <i>Plant Pathology</i> , 2013, 62, 289-297.	1.2	59
4714	Distribution of <i>Bemisia tabaci</i> (Homoptera: Aleyrodidae) biotypes and their associated symbiotic bacteria on host plants in West Africa. <i>Insect Conservation and Diversity</i> , 2013, 6, 411-421.	1.4	66
4715	Pholcid spider molecular systematics revisited, with new insights into the biogeography and the evolution of the group. <i>Cladistics</i> , 2013, 29, 132-146.	1.5	52
4716	Impact of rotavirus vaccine on rotavirus genotypes and caliciviruses circulating in French cattle. <i>Vaccine</i> , 2013, 31, 2433-2440.	1.7	15
4717	Identification of diverse full-length endogenous betaretroviruses in megabats and microbats. <i>Retrovirology</i> , 2013, 10, 35.	0.9	45
4718	Characterization of Farmington virus, a novel virus from birds that is distantly related to members of the family Rhabdoviridae. <i>Virology Journal</i> , 2013, 10, 219.	1.4	14
4719	Virophages, polintons, and transpovirons: a complex evolutionary network of diverse selfish genetic elements with different reproduction strategies. <i>Virology Journal</i> , 2013, 10, 158.	1.4	99
4720	Mimiviridae: clusters of orthologous genes, reconstruction of gene repertoire evolution and proposed expansion of the giant virus family. <i>Virology Journal</i> , 2013, 10, 106.	1.4	97

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4722	Draft genome of the mountain pine beetle, <i>Dendroctonus ponderosae</i> Hopkins, a major forest pest. <i>Genome Biology</i> , 2013, 14, R27.	13.9	260
4723	Transcriptome analyses of primitively eusocial wasps reveal novel insights into the evolution of sociality and the origin of alternative phenotypes. <i>Genome Biology</i> , 2013, 14, R20.	13.9	139
4724	Two novel PIWI families: roles in inter-genomic conflicts in bacteria and Mediator-dependent modulation of transcription in eukaryotes. <i>Biology Direct</i> , 2013, 8, 13.	1.9	45
4725	Insights into archaeal evolution and symbiosis from the genomes of a nanoarchaeon and its inferred crenarchaeal host from Obsidian Pool, Yellowstone National Park. <i>Biology Direct</i> , 2013, 8, 9.	1.9	102
4726	Deep transcriptome-sequencing and proteome analysis of the hydrothermal vent annelid <i>Alvinella pompejana</i> identifies the CvP-bias as a robust measure of eukaryotic thermostability. <i>Biology Direct</i> , 2013, 8, 2.	1.9	47
4727	In silico analysis of the fucosylation-associated genome of the human blood fluke <i>Schistosoma mansoni</i> : cloning and characterization of the enzymes involved in GDP-L-fucose synthesis and Golgi import. <i>Parasites and Vectors</i> , 2013, 6, 201.	1.0	6
4728	A multi-locus approach to barcoding in the <i>Anopheles strodei</i> subgroup (Diptera: Culicidae). <i>Parasites and Vectors</i> , 2013, 6, 111.	1.0	62
4729	Highly diverse chromoviruses of <i>Beta vulgaris</i> are classified by chromodomains and chromosomal integration. <i>Mobile DNA</i> , 2013, 4, 8.	1.3	36
4730	Monitoring the antigenic evolution of human influenza A viruses to understand how and when viruses escape from existing immunity. <i>BMC Research Notes</i> , 2013, 6, 227.	0.6	4
4731	Multilocus phylogeography of the European ground squirrel: cryptic interglacial refugia of continental climate in Europe. <i>Molecular Ecology</i> , 2013, 22, 4256-4269.	2.0	33
4732	Genetic variation within the cosmopolitan aquatic fungus <i>Lignicola laevis</i> (Microascales). <i>Trends in Microbiology</i> , 2013, 21, 107-110.	0.7	10
4733	The Orthosiinae Revisited (Apocynaceae, Asclepiadoideae, Asclepiadeae). <i>Annals of the Missouri Botanical Garden</i> , 2013, 99, 44-81.	1.3	11
4734	Evolutionary analysis of TLR9 genes reveals the positive selection of extant teleosts in Perciformes. <i>Fish and Shellfish Immunology</i> , 2013, 35, 448-457.	1.6	21
4735	The unique pseudanthium of <i>Actinodium</i> (Myrtaceae) - morphological reinvestigation and possible regulation by CYCLOIDEA-like genes. <i>EvoDevo</i> , 2013, 4, 8.	1.3	16
4736	Novel algorithm for phylogenetic analysis of proteins: application to analysis of the evolution of H5N1 influenza viruses. <i>Journal of Mathematical Chemistry</i> , 2013, 51, 2238-2255.	0.7	10
4737	Plot protein: visualization of mutations. <i>Journal of Clinical Bioinformatics</i> , 2013, 3, 14.	1.2	16
4738	Does Computational Biology Help us to Understand the Molecular Phylogenetics and Evolution of Cluster of Differentiation (CD) Proteins?. <i>Protein Journal</i> , 2013, 32, 143-154.	0.7	2

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4740	Evolution of RNA interference proteins dicer and argonaute in Basidiomycota. <i>Mycologia</i> , 2013, 105, 1489-1498.	0.8	42
4741	A multi-locus molecular timescale for the origin and diversification of eels (Order: Anguilliformes). <i>Molecular Phylogenetics and Evolution</i> , 2013, 69, 884-894.	1.2	43
4742	Molecular and phylogenetic characterization of honey bee viruses, <i>Nosema</i> microsporidia, protozoan parasites, and parasitic mites in China. <i>Ecology and Evolution</i> , 2013, 3, 298-311.	0.8	70
4743	Solution NMR structure of the helicase associated domain BVU_0683(627-691) from <i>Bacteroides vulgatus</i> provides first structural coverage for protein domain family PF03457 and indicates domain binding to DNA. <i>Journal of Structural and Functional Genomics</i> , 2013, 14, 19-24.	1.2	0
4744	The OitaAG and OitaSTK genes of the orchid <i>Orchis italica</i> : a comparative analysis with other C- and D-class MADS-box genes. <i>Molecular Biology Reports</i> , 2013, 40, 3523-3535.	1.0	35
4745	Uniquely Localized Intra-Molecular Amino Acid Concentrations at the Glycolytic Enzyme Catalytic/Active Centers of Archaea, Bacteria and Eukaryota are Associated with Their Proposed Temporal Appearances on Earth. <i>Origins of Life and Evolution of Biospheres</i> , 2013, 43, 161-187.	0.8	2
4746	Exploring the genome of the salt-marsh <i>Spartina maritima</i> (Poaceae, Chloridoideae) through BAC end sequence analysis. <i>Plant Molecular Biology</i> , 2013, 83, 591-606.	2.0	11
4747	Identification of two additional members of the tRNA isopentenyltransferase family in <i>Physcomitrella patens</i> . <i>Plant Molecular Biology</i> , 2013, 82, 417-426.	2.0	12
4748	The <i>Arabidopsis thaliana</i> ortholog of a purported maize cholinesterase gene encodes a GDSL-lipase. <i>Plant Molecular Biology</i> , 2013, 81, 565-576.	2.0	14
4749	Identification, Phylogeny, and Expression Analysis of Pto-like Genes in Pepper. <i>Plant Molecular Biology Reporter</i> , 2013, 31, 901-916.	1.0	2
4750	Phylogenetic Analyses of Teleki Grapevine Rootstocks Using Three Chloroplast DNA Markers. <i>Plant Molecular Biology Reporter</i> , 2013, 31, 371-386.	1.0	12
4751	Evolution of the ABPA Subunit of Androgen-Binding Protein Expressed in the Submaxillary Glands in New and Old World Rodent Taxa. <i>Journal of Molecular Evolution</i> , 2013, 76, 324-331.	0.8	7
4752	Mosaic Evolution of Silk Genes in <i>Aliatypus</i> Trapdoor Spiders (Mygalomorphae, Antrodiaetidae). <i>Journal of Molecular Evolution</i> , 2013, 76, 216-227.	0.8	1
4753	Vector Affinity and Diversity of <i>Geosmithia</i> Fungi Living on Subcortical Insects Inhabiting Pinaceae Species in Central and Northeastern Europe. <i>Microbial Ecology</i> , 2013, 66, 682-700.	1.4	39
4754	Structure and Community Composition of Sprout-Like Bacterial Aggregates in a Dinaric Karst Subterranean Stream. <i>Microbial Ecology</i> , 2013, 66, 5-18.	1.4	32
4755	Deep Sequencing of <i>Myxilla</i> ( <i>Ectyomyxilla</i> ) <i>methanophila</i> , an Epibiotic Sponge on Cold-Seep Tubeworms, Reveals Methylophilic, Thiotrophic, and Putative Hydrocarbon-Degrading Microbial Associations. <i>Microbial Ecology</i> , 2013, 65, 450-461.	1.4	25
4756	Bacterial Consortium of <i>Millepora dichotoma</i> Exhibiting Unusual Multifocal Lesion Event in the Gulf of Eilat, Red Sea. <i>Microbial Ecology</i> , 2013, 65, 50-59.	1.4	10



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4757	Phylogeny of <i>Entoloma</i> s.l. subgenus <i>Pouzarella</i> , with descriptions of five new species from China. <i>Fungal Diversity</i> , 2013, 58, 227-243.	4.7	20
4758	A divergence dating analysis of turtles using fossil calibrations: an example of best practices. <i>Journal of Paleontology</i> , 2013, 87, 612-634.	0.5	128
4759	Piscine reovirus encodes a cytotoxic, non-fusogenic, integral membrane protein and previously unrecognized virion outer-capsid proteins. <i>Journal of General Virology</i> , 2013, 94, 1039-1050.	1.3	44
4760	Nod factor perception protein carries weight in biotic interactions. <i>Trends in Plant Science</i> , 2013, 18, 566-574.	4.3	53
4761	A genome-wide pairwise-identity-based proposal for the classification of viruses in the genus <i>Mastrevirus</i> (family <i>Geminiviridae</i> ). <i>Archives of Virology</i> , 2013, 158, 1411-1424.	0.9	216
4763	Ancient invasion of an extinct gammaretrovirus in cetaceans. <i>Virology</i> , 2013, 441, 66-69.	1.1	5
4764	Previously unknown and highly divergent ssDNA viruses populate the oceans. <i>ISME Journal</i> , 2013, 7, 2169-2177.	4.4	160
4765	<i>Plant Defensin type 1</i> ( <i>PDF1</i> ): protein promiscuity and expression variation within the <i>Arabidopsis</i> genus shed light on zinc tolerance acquisition in <i>Arabidopsis halleri</i> . <i>New Phytologist</i> , 2013, 200, 820-833.	3.5	50
4766	Hagfish phylogeny and taxonomy, with description of the new genus <i>Rubicundus</i> (Craniata). <i>Trends in Microbiology</i> , 2013, 21, 25-30.	0.6	25
4767	Are flatfishes (Pleuronectiformes) monophyletic?. <i>Molecular Phylogenetics and Evolution</i> , 2013, 69, 664-673.	1.2	43
4768	Accelerated Evolutionary Rate of the Myoglobin Gene in Long-Diving Whales. <i>Journal of Molecular Evolution</i> , 2013, 76, 380-387.	0.8	23
4769	Phylogeny and systematic position of <i>Mesoptychia</i> (Lindb.) A. Evans. <i>Plant Systematics and Evolution</i> , 2013, 299, 1243-1251.	0.3	11
4770	A new multi-locus timescale reveals the evolutionary basis of diversity patterns in triggerfishes and filefishes (Balistidae, Monacanthidae; Tetraodontiformes). <i>Molecular Phylogenetics and Evolution</i> , 2013, 69, 165-176.	1.2	39
4771	A new phylogeny of tetraodontiform fishes (Tetraodontiformes, Acanthomorpha) based on 22 loci. <i>Molecular Phylogenetics and Evolution</i> , 2013, 69, 177-187.	1.2	39
4772	A multi-locus timetree of surgeonfishes (Acanthuridae, Percomorpha), with revised family taxonomy. <i>Molecular Phylogenetics and Evolution</i> , 2013, 68, 150-160.	1.2	56
4773	FUNGALOXPHOS: An integrated database for oxidative phosphorylation in fungi. <i>Mitochondrion</i> , 2013, 13, 357-359.	1.6	3
4774	Microbial communities on deteriorated artistic tiles from Pena National Palace (Sintra, Portugal). <i>International Biodeterioration and Biodegradation</i> , 2013, 84, 322-332.	1.9	42
4775	Real-time RT-PCR assay to differentiate clades of H5N1 avian influenza viruses circulating in Vietnam. <i>Journal of Virological Methods</i> , 2013, 193, 452-458.	1.0	12

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4777	Community structure of Diplostomum spp. (Digenea: Diplostomidae) in eyes of fish: Main determinants and potential interspecific interactions. International Journal for Parasitology, 2013, 43, 929-939.	1.3	24
4778	Evolution of cave <i>Axiobolus</i> and <i>Sphaerobolus</i> ( <i>Sphaerobolus</i> calibregmatidae, <i>Axiobolus</i> nnelida). Zoologica Scripta, 2013, 42, 623-636.	0.7	23
4779	Structural and functional characterization of a plant S-nitrosoglutathione reductase from Solanum lycopersicum. Biochimie, 2013, 95, 889-902.	1.3	76
4780	A novel <i>hAT</i> element in <i>Bombyx mori</i> and <i>Rhodnius prolixus</i> : its relationship with miniature inverted repeat transposable elements (MITEs) and horizontal transfer. Insect Molecular Biology, 2013, 22, 584-596.	1.0	15
4781	Molecular epidemiology of influenza A (H5N1) viruses, Bangladesh, 2007-2011. Preventive Veterinary Medicine, 2013, 111, 314-318.	0.7	8
4782	Acetylation with Structural Mapping Reveals the Significance of Lysine Acetylation in <i>Thermus thermophilus</i> . Journal of Proteome Research, 2013, 12, 3952-3968.	1.8	97
4783	Protists in Arctic drift and fast sea ice. Journal of Phycology, 2013, 49, 229-240.	1.0	65
4784	The Eyes Have It: Long-Distance Dispersal by an Intraorbital Leech Parasite of Birds. Journal of Parasitology, 2013, 99, 1137-1139.	0.3	12
4785	Complex dynamic of dengue virus serotypes 2 and 3 in Cambodia following series of climate disasters. Infection, Genetics and Evolution, 2013, 15, 77-86.	1.0	11
4786	Biomining active cellulases from a mining bioremediation system. Journal of Biotechnology, 2013, 167, 462-471.	1.9	35
4787	Phylogenetic and structural analysis of major surface proteins hemagglutinin and neuraminidase of novel avian influenza virus A H7N9 from chinese patient. Chemical Research in Chinese Universities, 2013, 29, 934-940.	1.3	5
4788	A molecular phylogenetic assessment of the genus <i>Gyromitra</i> in North America. Mycologia, 2013, 105, 1306-1314.	0.8	12
4789	Detection and molecular characterisation of <i>Pyrenopeziza brassicae</i> isolates resistant to methyl benzimidazole carbamates. Pest Management Science, 2013, 69, 1040-1048.	1.7	29
4790	Correcting widespread misidentifications of the highly abundant and commercially important sardine species <i>Sardinella lemuru</i> , Bleeker, 1853 in the Philippines. Journal of Applied Ichthyology, 2013, 29, 881-885.	0.3	15
4791	The bee tree of life: a supermatrix approach to apoid phylogeny and biogeography. BMC Evolutionary Biology, 2013, 13, 138.	3.2	134
4792	Impacts of inundation and drought on eukaryote biodiversity in semi-arid floodplain soils. Molecular Ecology, 2013, 22, 1746-1758.	2.0	54
4793	The rise of potentially toxin producing cyanobacteria in Lake Naivasha, Great African Rift Valley, Kenya. Harmful Algae, 2013, 27, 42-51.	2.2	22

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4795	Into the deep: A phylogenetic approach to the bivalve subclass Protobranchia. <i>Molecular Phylogenetics and Evolution</i> , 2013, 69, 188-204.	1.2	77
4796	Multifactorial diversity sustains microbial community stability. <i>ISME Journal</i> , 2013, 7, 2126-2136.	4.4	176
4797	Spatial spread and demographic expansion of Lyme borreliosis spirochaetes in Eurasia. <i>Infection, Genetics and Evolution</i> , 2013, 14, 147-155.	1.0	43
4798	Ecological Differentiation of Cryptic Species within an Asexual Protist Morphospecies: A Case Study of Filamentous Green Alga <i>Klebsormidium</i> (Streptophyta). <i>Journal of Eukaryotic Microbiology</i> , 2013, 60, 350-362.	0.8	78
4799	Phylogenetic position and revised classification of <i>Acacia</i> s.l. (Fabaceae: Mimosoideae) in Africa, including new combinations in <i>Vachellia</i> and <i>Senegalia</i> . <i>Botanical Journal of the Linnean Society</i> , 2013, 172, 500-523.	0.8	218
4800	Multiple dispersal out of Anatolia: biogeography and evolution of oriental green lizards. <i>Biological Journal of the Linnean Society</i> , 2013, 110, 398-408.	0.7	57
4801	Predicting function from sequence in a large multifunctional toxin family. <i>Toxicon</i> , 2013, 72, 113-125.	0.8	14
4802	Gene Loss and Adaptation to Hominids Underlie the Ancient Origin of HIV-1. <i>Cell Host and Microbe</i> , 2013, 14, 85-92.	5.1	93
4803	Avihepadnavirus diversity in parrots is comparable to that found amongst all other avian species. <i>Virology</i> , 2013, 438, 98-105.	1.1	14
4804	Characterization of bud emergence 46 (BEM46) protein: Sequence, structural, phylogenetic and subcellular localization analyses. <i>Biochemical and Biophysical Research Communications</i> , 2013, 438, 526-532.	1.0	10
4805	Bucephalidae (Platyhelminthes: Digenea) of <i>Plectropomus</i> (Serranidae: Epinephelinae) in the tropical Pacific. <i>Parasitology Research</i> , 2013, 112, 2561-2584.	0.6	15
4806	The species of <i>Cortinarius</i> , section <i>Bovini</i> , associated with conifers in northern Europe. <i>Mycologia</i> , 2013, 105, 977-993.	0.8	21
4807	Morphological and molecular data for Australian <i>Hebeloma</i> species do not support the generic status of <i>Anamika</i> . <i>Mycologia</i> , 2013, 105, 1043-1058.	0.8	14
4808	Sequence and evolutionary analysis of ribosomal DNA from Huanglongbing (HLB) isolates of Western India. <i>Phytoparasitica</i> , 2013, 41, 295-305.	0.6	11
4809	PoPLAR: Portal for Petascale Lifescience Applications and Research. <i>BMC Bioinformatics</i> , 2013, 14, S3.	1.2	8
4810	bioNerDS: exploring bioinformatics database and software use through literature mining. <i>BMC Bioinformatics</i> , 2013, 14, 194.	1.2	23
4811	Disk-based k-mer counting on a PC. <i>BMC Bioinformatics</i> , 2013, 14, 160.	1.2	61

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4813	Phylogenetic relationships of the Gorgoderidae (Platyhelminthes: Trematoda), including the proposal of a new subfamily (Degeneriinae n. subfam.). <i>Parasitology Research</i> , 2013, 112, 3063-3074.	0.6	48
4814	Evolution of protein indels in plants, animals and fungi. <i>BMC Evolutionary Biology</i> , 2013, 13, 140.	3.2	58
4815	Parasitic plants have increased rates of molecular evolution across all three genomes. <i>BMC Evolutionary Biology</i> , 2013, 13, 126.	3.2	120
4816	Hypervariable antigen genes in malaria have ancient roots. <i>BMC Evolutionary Biology</i> , 2013, 13, 110.	3.2	47
4817	The role of retrotransposons in gene family expansions: insights from the mouse Abpgene family. <i>BMC Evolutionary Biology</i> , 2013, 13, 107.	3.2	20
4818	Complete chloroplast genome of the genus <i>Cymbidium</i> : lights into the species identification, phylogenetic implications and population genetic analyses. <i>BMC Evolutionary Biology</i> , 2013, 13, 84.	3.2	262
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4820	High lability of sexual system over 250 million years of evolution in morphologically conservative tadpole shrimps. <i>BMC Evolutionary Biology</i> , 2013, 13, 30.	3.2	21
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4822	Multiscale modeling of the causal functional roles of nsSNPs in a genome-wide association study: application to hypoxia. <i>BMC Genomics</i> , 2013, 14, S9.	1.2	6
4823	Identification of G protein-coupled receptor signaling pathway proteins in marine diatoms using comparative genomics. <i>BMC Genomics</i> , 2013, 14, 503.	1.2	20
4824	Evidence of antimicrobial resistance-conferring genetic elements among pneumococci isolated prior to 1974. <i>BMC Genomics</i> , 2013, 14, 500.	1.2	40
4825	Cytosine methylation is a conserved epigenetic feature found throughout the phylum Platyhelminthes. <i>BMC Genomics</i> , 2013, 14, 462.	1.2	35
4826	The complete mitochondrial genome of <i>Solemya velum</i> (Mollusca: Bivalvia) and its relationships with Conchifera. <i>BMC Genomics</i> , 2013, 14, 409.	1.2	53
4827	Genomic basis of ecological niche divergence among cryptic sister species of non-biting midges. <i>BMC Genomics</i> , 2013, 14, 384.	1.2	25
4828	Unsupervised genome-wide recognition of local relationship patterns. <i>BMC Genomics</i> , 2013, 14, 347.	1.2	59
4829	Frequent loss of lineages and deficient duplications accounted for low copy number of disease resistance genes in Cucurbitaceae. <i>BMC Genomics</i> , 2013, 14, 335.	1.2	74

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4831	A burst of ABC genes in the genome of the polyphagous spider mite <i>Tetranychus urticae</i> . <i>BMC Genomics</i> , 2013, 14, 317.	1.2	118
4832	Reevaluation of the evolutionary events within <i>recA/RAD51</i> phylogeny. <i>BMC Genomics</i> , 2013, 14, 240.	1.2	24
4833	Tyrosine pathway regulation is host-mediated in the pea aphid symbiosis during late embryonic and early larval development. <i>BMC Genomics</i> , 2013, 14, 235.	1.2	51
4834	RNAseq versus genome-predicted transcriptomes: a large population of novel transcripts identified in an Illumina-454 Hydra transcriptome. <i>BMC Genomics</i> , 2013, 14, 204.	1.2	61
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4837	Tandem repeats derived from centromeric retrotransposons. <i>BMC Genomics</i> , 2013, 14, 142.	1.2	86
4838	Comparative transcriptomics of early dipteran development. <i>BMC Genomics</i> , 2013, 14, 123.	1.2	41
4839	Genomic reconstruction of transcriptional regulatory networks in lactic acid bacteria. <i>BMC Genomics</i> , 2013, 14, 94.	1.2	38
4840	Identification of the <i>Hevea brasiliensis</i> AP2/ERF superfamily by RNA sequencing. <i>BMC Genomics</i> , 2013, 14, 30.	1.2	73
4841	Comparative genome analysis of <i>Spiroplasma melliferum</i> IPMB4A, a honeybee-associated bacterium. <i>BMC Genomics</i> , 2013, 14, 22.	1.2	118
4842	Different evolutionary histories of two cation/proton exchanger gene families in plants. <i>BMC Plant Biology</i> , 2013, 13, 97.	1.6	28
4843	Functional genomics of a generalist parasitic plant: Laser microdissection of host-parasite interface reveals host-specific patterns of parasite gene expression. <i>BMC Plant Biology</i> , 2013, 13, 9.	1.6	61
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4845	A member of the <i>Plasmodium falciparum</i> PHIST family binds to the erythrocyte cytoskeleton component band 4.1. <i>Malaria Journal</i> , 2013, 12, 160.	0.8	34
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4847	Phylogenetic analysis of the mitochondrial genomes and nuclear rRNA genes of ticks reveals a deep phylogenetic structure within the genus <i>Haemaphysalis</i> and further elucidates the polyphyly of the genus <i>Amblyomma</i> with respect to <i>Amblyomma sphegodonti</i> and <i>Amblyomma elaphense</i> . <i>Ticks and Tick-borne Diseases</i> , 2013, 4, 265-274.	1.1	85

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4850	Bacterial and archaeal globins – A revised perspective. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 1789-1800.	1.1	93
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4852	Three new species of <i>Pristionchus</i> (Nematoda: Diplogastridae) show morphological divergence through evolutionary intermediates of a novel feeding-structure polymorphism. <i>Zoological Journal of the Linnean Society</i> , 2013, 168, 671-698.	1.0	25
4853	Experimental plant communities develop phylogenetically overdispersed abundance distributions during assembly. <i>Ecology</i> , 2013, 94, 465-477.	1.5	38
4855	Evolutionary Divergence and Convergence in Shape and Size Within African Antelope Proximal Phalanges. <i>Journal of Mammalian Evolution</i> , 2013, 20, 239-248.	1.0	34
4856	Monosaccharide analysis of succulent leaf tissue in <i>Aloe</i> . <i>Phytochemistry</i> , 2013, 93, 79-87.	1.4	29
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4859	Phylogeography in the northern Andes: Complex history and cryptic diversity in a cloud forest frog, <i>Pristimantis w-nigrum</i> (Craugastoridae). <i>Molecular Phylogenetics and Evolution</i> , 2013, 69, 417-429.	1.2	24
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4861	PhyloPhlAn is a new method for improved phylogenetic and taxonomic placement of microbes. <i>Nature Communications</i> , 2013, 4, 2304.	5.8	797
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4869	Isolation of <i>Pseudobutyrvibrio ruminis</i> and <i>Pseudobutyrvibrio xylanivorans</i> from rumen of Creole goats fed native forage diet. <i>Folia Microbiologica</i> , 2013, 58, 367-373.	1.1	23
4870	Inference of global HIV-1 sequence patterns and preliminary feature analysis. <i>Virologica Sinica</i> , 2013, 28, 228-238.	1.2	1
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4883	Two new species of sequestrate <i>Agaricus</i> (section <i>Minores</i> ) from Australia. <i>Mycological Progress</i> , 2013, 12, 699-707.	0.5	19
4884	Interpreting the Omics "era" Data. <i>Smart Innovation, Systems and Technologies</i> , 2013, , 79-100.	0.5	7
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4925	Testing monophyly without well-supported gene trees: Evidence from multi-locus nuclear data conflicts with existing taxonomy in the snake tribe Thamnophiini. <i>Molecular Phylogenetics and Evolution</i> , 2013, 68, 425-431.	1.2	15
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4943	<scp>ProA</scp>, a transcriptional regulator of fungal fruiting body development, regulates leaf hyphal network development in the <i><scp>E</scp>pichloÃ« festucae</i>â€™<i><scp>L</scp>olium perenne</i> symbiosis. <i>Molecular Microbiology</i> , 2013, 90, 551-568.	1.2	49
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4988	Inhibitory signalling to the Arp2/3 complex steers cell migration. <i>Nature</i> , 2013, 503, 281-284.	13.7	208
4989	First record of <i>Pentaphragmatium</i> ( <i>Pentaphragmatales</i> ) Tj ETQq1 1 0.784314 rgBT / Overlock 10 Tf 50 312 T ( <i>Pentaphragmatium</i> var. <i>aciculiferum</i> ). <i>Phycological Research</i> , 2013, 61, 256-267.	0.8	7
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5029	Cyanobacterial Polyketide Synthase Docking Domains: A Tool for Engineering Natural Product Biosynthesis. <i>Chemistry and Biology</i> , 2013, 20, 1340-1351.	6.2	100
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5040	Genotyping and phylogenetic analysis of <i>Acanthamoeba</i> isolates associated with keratitis. <i>Parasitology Research</i> , 2013, 112, 3807-3816.	0.6	53
5041	TreeParser-Aided Klee Diagrams Display Taxonomic Clusters in DNA Barcode and Nuclear Gene Datasets. <i>Scientific Reports</i> , 2013, 3, 2635.	1.6	10
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5061	Morphological and genetic evidence for early Holocene cattle management in northeastern China. <i>Nature Communications</i> , 2013, 4, 2755.	5.8	82
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5066	Genome-wide identification and expression analysis of MAPK and MAPKK gene family in <i>Malus domestica</i> . <i>Gene</i> , 2013, 531, 377-387.	1.0	92
5067	Complete mitochondrial genomes of the Japanese pink coral ( <i>Corallium elatius</i> ) and the Mediterranean red coral ( <i>Corallium rubrum</i> ): a reevaluation of the phylogeny of the family Coralliidae based on molecular data. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2013, 8, 209-219.	0.4	15
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5076	Pandoraviruses are highly derived phycodnaviruses. <i>Biology Direct</i> , 2013, 8, 25.	1.9	64
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5079	Gene discovery, evolutionary affinity and molecular detection of <i>Oxyspirura petrowi</i> , an eye worm parasite of game birds. <i>BMC Microbiology</i> , 2013, 13, 233.	1.3	17
5080	Genome-wide identification and analysis of membrane-bound O-acyltransferase (MBOAT) gene family in plants. <i>Planta</i> , 2013, 238, 907-922.	1.6	14
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5082	Comparative genomics of emerging pathogens in the <i>Candida glabrata</i> clade. <i>BMC Genomics</i> , 2013, 14, 623.	1.2	174
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5090	Endonuclease-containing Penelope retrotransposons in the bdelloid rotifer <i>Adineta vaga</i> exhibit unusual structural features and play a role in expansion of host gene families. <i>Mobile DNA</i> , 2013, 4, 19.	1.3	18
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5101	Phylogenetic analysis of threatened and range-restricted limestone specialists in the land snail genus <i>Anguispira</i> . <i>Conservation Genetics</i> , 2013, 14, 671-682.	0.8	5
5102	The evolution, impact and properties of exonic splice enhancers. <i>Genome Biology</i> , 2013, 14, R143.	13.9	77
5103	The drug:H <sup>+</sup> antiporters of family 2 (DHA2), siderophore transporters (ARN) and glutathione:H <sup>+</sup> antiporters (GEX) have a common evolutionary origin in hemiascomycete yeasts. <i>BMC Genomics</i> , 2013, 14, 901.	1.2	36
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5109	Polysaccharides utilization in human gut bacterium <i>Bacteroides thetaiotaomicron</i> : comparative genomics reconstruction of metabolic and regulatory networks. <i>BMC Genomics</i> , 2013, 14, 873.	1.2	122
5110	Characterization of cytokinin signaling and homeostasis gene families in two hardwood tree species: <i>Populus trichocarpa</i> and <i>Prunus persica</i> . <i>BMC Genomics</i> , 2013, 14, 885.	1.2	38
5111	Phylogenetic and transcriptional analysis of an expanded bZIP transcription factor family in <i>Phytophthora sojae</i> . <i>BMC Genomics</i> , 2013, 14, 839.	1.2	30
5112	Molecular and serological evidence for the circulation of the tick symbiont <i>Midichloria</i> ( <i>Rickettsiales</i> : <i>Midichloriaceae</i> ) in different mammalian species. <i>Parasites and Vectors</i> , 2013, 6, 350.	1.0	53
5113	Stringent DDI-based Prediction of <i>H. sapiens</i> - <i>M. tuberculosis</i> H37Rv Protein-Protein Interactions. <i>BMC Systems Biology</i> , 2013, 7, S6.	3.0	34
5114	PREAL: prediction of allergenic protein by maximum Relevance Minimum Redundancy (mRMR) feature selection. <i>BMC Systems Biology</i> , 2013, 7, S9.	3.0	38
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5135	Bayesian phylogeographic inferences reveal contrasting colonization dynamics among European groundwater isopods. <i>Molecular Ecology</i> , 2013, 22, 5685-5699.	2.0	37
5136	Optimal operational conditions for biohydrogen production from sugar refinery wastewater in an ASBR. <i>International Journal of Hydrogen Energy</i> , 2013, 38, 13895-13906.	3.8	36
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5247	-MSA â€” A GPU-based, fast and accurate algorithm for multiple sequence alignment. <i>Journal of Parallel and Distributed Computing</i> , 2013, 73, 32-41.	2.7	44
5248	<i>Cortinarius</i> section <i>Sanguinei</i> in North America. <i>Mycologia</i> , 2013, 105, 344-356.	0.8	14

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5250	Diversity of sequences encoded by the Gsp-1 genes in wheat and other grass species. <i>Journal of Cereal Science</i> , 2013, 57, 1-9.	1.8	15
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5254	Using Supermatrices for Phylogenetic Inquiry: An Example Using the Sedges. <i>Systematic Biology</i> , 2013, 62, 205-219.	2.7	99
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5261	Tribe Eritrichieae (Boraginaceae s.str.) in West Asia: a molecular phylogenetic perspective. <i>Plant Systematics and Evolution</i> , 2013, 299, 197-208.	0.3	13
5262	Isoflavone synthase (IFS) gene phylogeny in <i>Trifolium</i> species associated with plant isoflavone contents. <i>Plant Systematics and Evolution</i> , 2013, 299, 357-367.	0.3	5
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5280	<i>Babesia divergens</i> and <i>Neospora caninum</i> apical membrane antigen 1 structures reveal selectivity and plasticity in apicomplexan parasite host cell invasion. Protein Science, 2013, 22, 114-127.	3.1	35
5281	Prediction of phenotypes of missense mutations in human proteins from biological assemblies. Proteins: Structure, Function and Bioinformatics, 2013, 81, 199-213.	1.5	20
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5283	A variety of melanised root-associated fungi from the Sydney basin form endophytic associations with <i>Trifolium subterraneum</i> . Fungal Ecology, 2013, 6, 70-82.	0.7	12
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5287	Role of antisense RNAs in evolution of yeast regulatory complexity. <i>Genomics</i> , 2013, 102, 484-490.	1.3	10
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5295	Origin and evolution of medium chain alcohol dehydrogenases. <i>Chemico-Biological Interactions</i> , 2013, 202, 91-96.	1.7	30
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5304	What can naturally occurring mutations tell us about Cav1.x channel function?. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2013, 1828, 1598-1607.	1.4	27
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5316	<i>Laccaria</i> (Agaricomycetes, Basidiomycota) from Tibet (Xizang Autonomous Region, China). <i>Mycoscience</i> , 2013, 54, 406-419.	0.3	28
5317	Bacteria diversity and arsenic mobilization in rock biofilm from an ancient gold and arsenic mine. <i>Science of the Total Environment</i> , 2013, 461-462, 330-340.	3.9	34
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5319	Molecular Modeling and Molecular Dynamics Simulations of Recombinase Rad51. <i>Biophysical Journal</i> , 2013, 104, 1556-1565.	0.2	6
5320	Gonadotrophin-releasing hormone in winter flounder ( <i>Pseudopleuronectes americanus</i> ): Molecular characterization, distribution and effects of fasting. <i>General and Comparative Endocrinology</i> , 2013, 184, 9-21.	0.8	17

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5323	Evolution of leaf anatomy and photosynthetic pathways in Portulacaceae. <i>American Journal of Botany</i> , 2013, 100, 2388-2402.	0.8	48
5324	Identification of a possible respiratory arsenate reductase in <i>Denitrovibrio acetiphilus</i> , a member of the phylum Deferribacteres. <i>Archives of Microbiology</i> , 2013, 195, 661-670.	1.0	11
5325	Molecular Systematics of the Calliphoridae (Diptera: Oestroidea): Evidence From One Mitochondrial and Three Nuclear Genes. <i>Journal of Medical Entomology</i> , 2013, 50, 15-23.	0.9	51
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5327	Development of Real-Time Polymerase Chain Reaction Assay for Detection of <i>Ornithobacterium rhinotracheale</i> in Poultry. <i>Avian Diseases</i> , 2013, 57, 663-666.	0.4	13
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5333	Description of a Riboflavin Biosynthetic Gene Variant Prevalent in the Phylum Proteobacteria. <i>Journal of Bacteriology</i> , 2013, 195, 5479-5486.	1.0	25
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5341	Phylogeny and evolution of porcine parvovirus. <i>Virus Research</i> , 2013, 178, 392-397.	1.1	29
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5343	A comprehensive analysis of the <i>Manduca sexta</i> immunotranscriptome. <i>Developmental and Comparative Immunology</i> , 2013, 39, 388-398.	1.0	52
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5353	Molecular evidence for dietary selectivity and pest suppression potential in an epigeal spider community in winter wheat. <i>Biological Control</i> , 2013, 65, 72-86.	1.4	64
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5355	Genetic diversity, population structure, and demographic history of exploited sea urchin populations ( <i>Tripleneustes gratilla</i> ) in the Philippines. <i>Journal of Experimental Marine Biology and Ecology</i> , 2013, 449, 284-293.	0.7	14
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5359	From PPRM to caul: The evolution of membrane rupture in mammals. <i>Applied &amp; Translational Genomics</i> , 2013, 2, 70-77.	2.1	3
5360	Understanding the general packing rearrangements required for successful template based modeling of protein structure from a CASP experiment. <i>Computational Biology and Chemistry</i> , 2013, 42, 40-48.	1.1	0
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5365	Molecular phylogeny of <i>Cissus</i> L. of Vitaceae (the grape family) and evolution of its pantropical intercontinental disjunctions. <i>Molecular Phylogenetics and Evolution</i> , 2013, 66, 43-53.	1.2	71
5366	Intraspecific variation and emendation of <i>Hannaella kunmingensis</i> . <i>Mycological Progress</i> , 2013, 12, 157-165.	0.5	6
5367	<i>Dissulfuribacter thermophilus</i> gen. nov., sp. nov., a thermophilic, autotrophic, sulfur-disproportionating, deeply branching deltaproteobacterium from a deep-sea hydrothermal vent. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013, 63, 1967-1971.	0.8	46
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5371	Allelic variation at a single gene increases food value in a drought-tolerant staple cereal. <i>Nature Communications</i> , 2013, 4, 1483.	5.8	41
5372	Differential requirements for mRNA folding partially explain why highly expressed proteins evolve slowly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E678-86.	3.3	110
5373	Sequencing and characterization of the complete mitochondrial genomes of three <i>Pneumocystis</i> species provide new insights into divergence between human and rodent <i>Pneumocystis</i> . <i>FASEB Journal</i> , 2013, 27, 1962-1972.	0.2	40
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5376	Mouse cytomegalovirus egress protein pM50 interacts with cellular endophilin-A2. <i>Cellular Microbiology</i> , 2013, 15, 335-351.	1.1	23
5377	Microbial methane turnover at <i>Marmara</i> cold seeps: a combined 16S rRNA and lipid biomarker investigation. <i>Geobiology</i> , 2013, 11, 55-71.	1.1	29
5378	Contrasting global-scale evolutionary radiations: phylogeny, diversification, and morphological evolution in the major clades of iguanian lizards. <i>Biological Journal of the Linnean Society</i> , 2013, 108, 127-143.	0.7	30
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5380	Molecular phylogenetics and biogeography of Neotropical Paepalanthoideae with emphasis on Brazilian Paepalanthus (Eriocaulaceae). <i>Botanical Journal of the Linnean Society</i> , 2013, 171, 225-243.	0.8	60
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5383	New approaches for unravelling reassortment pathways. <i>BMC Evolutionary Biology</i> , 2013, 13, 1.	3.2	278
5384	Consistent mutational paths predict eukaryotic thermostability. <i>BMC Evolutionary Biology</i> , 2013, 13, 7.	3.2	60
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5386	Delimiting species in recent radiations with low levels of morphological divergence: A case study in Australian <i>Gehyra</i> geckos. <i>Molecular Phylogenetics and Evolution</i> , 2013, 68, 135-143.	1.2	33
5387	Genomes of marine cyanopodoviruses reveal multiple origins of diversity. <i>Environmental Microbiology</i> , 2013, 15, 1356-1376.	1.8	99
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5389	Discovery of STL polyomavirus, a polyomavirus of ancestral recombinant origin that encodes a unique T antigen by alternative splicing. <i>Virology</i> , 2013, 436, 295-303.	1.1	145
5390	Structure of the MutL C-terminal domain reveals how Mlh1 contributes to Pms1 endonuclease site. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 461-468.	3.6	103
5391	GEOGRAPHIC AND TAXONOMIC DISPARITIES IN SPECIES DIVERSITY: DISPERSAL AND DIVERSIFICATION RATES ACROSS WALLACE'S LINE. <i>Evolution; International Journal of Organic Evolution</i> , 2013, 67, 2058-2071.	1.1	42
5392	Using DNA barcoding to link cystacanths and adults of the acanthocephalan <i>Polyomorphus brevis</i> in central Mexico. <i>Molecular Ecology Resources</i> , 2013, 13, 1116-1124.	2.2	39

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5394	Proposal for a new class within the phylum Proteobacteria , <i>Acidithiobacillia</i> classis nov., with the type order <i>Acidithiobacillales</i> , and emended description of the class <i>Gammaproteobacteria</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013, 63, 2901-2906.	0.8	129
5395	The discovery of a natural whale fall in the Antarctic deep sea. <i>Deep-Sea Research Part II: Topical Studies in Oceanography</i> , 2013, 92, 87-96.	0.6	54
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5398	A Revised Timescale for Human Evolution Based on Ancient Mitochondrial Genomes. <i>Current Biology</i> , 2013, 23, 553-559.	1.8	540
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5402	The determinants of the molecular substitution process in turtles. <i>Journal of Evolutionary Biology</i> , 2013, 26, 38-50.	0.8	53
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5404	Genetic variation in Norwegian piscine myocarditis virus in Atlantic salmon, <i>Salmo salar</i> L. <i>Journal of Fish Diseases</i> , 2013, 36, 129-139.	0.9	21
5405	The ITS region of groundwater amphipods: length, secondary structure and phylogenetic information content in Crangonyctoids and Niphargids. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2013, 51, 19-28.	0.6	6
5406	Genetic identity of free-living <i>Symbiodinium</i> obtained over a broad latitudinal range in the Japanese coast. <i>Phycological Research</i> , 2013, 61, 68-80.	0.8	56
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5408	A mutation "hot spot" in the Schmallenberg virus M segment. <i>Journal of General Virology</i> , 2013, 94, 1161-1167.	1.3	43
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5417	Using Analyses of Amino Acid Coevolution to Understand Protein Structure and Function. <i>Methods in Enzymology</i> , 2013, 523, 191-212.	0.4	13
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5422	A narrowly endemic photosynthetic orchid is non-specific in its mycorrhizal associations. <i>Molecular Ecology</i> , 2013, 22, 2341-2354.	2.0	58
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5428	Comparative Analysis of 126 Cyanobacterial Genomes Reveals Evidence of Functional Diversity Among Homologs of the Redox-Regulated CP12 Protein. <i>Plant Physiology</i> , 2013, 161, 824-835.	2.3	47

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5434	Intricate patterns of phylogenetic relationships in the olive family as inferred from multi-locus plastid and nuclear DNA sequence analyses: A close-up on <i>Chionanthus</i> and <i>Noronhia</i> (Oleaceae). <i>Molecular Phylogenetics and Evolution</i> , 2013, 67, 367-378.	1.2	37
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5437	phyloGenerator: an automated phylogeny generation tool for ecologists. <i>Methods in Ecology and Evolution</i> , 2013, 4, 692-698.	2.2	85
5438	Phylogenetic analyses of termite post-embryonic sequences illuminate caste and developmental pathway evolution. <i>Evolution &amp; Development</i> , 2013, 15, 146-157.	1.1	21
5439	Phylogeny and taxonomy of the "manna lichens". <i>Mycological Progress</i> , 2013, 12, 231-269.	0.5	41
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5451	Alternate pathways for NADH oxidation in <i>Thermus thermophilus</i> using type 2 NADH dehydrogenases. <i>Biological Chemistry</i> , 2013, 394, 667-676.	1.2	7
5452	<i>Rhizobium calliandrae</i> sp. nov., <i>Rhizobium mayense</i> sp. nov. and <i>Rhizobium jaguaris</i> sp. nov., rhizobial species nodulating the medicinal legume <i>Calliandra grandiflora</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013, 63, 3423-3429.	0.8	60
5453	Indigenous <i>Vibrio cholerae</i> strains from a non-endemic region are pathogenic. <i>Open Biology</i> , 2013, 3, 120181.	1.5	35
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5456	Reverse vaccinology in the 21st century: improvements over the original design. <i>Annals of the New York Academy of Sciences</i> , 2013, 1285, 115-132.	1.8	77
5457	Molecular phylogeny of thorny catfishes (Siluriformes: Doradidae). <i>Molecular Phylogenetics and Evolution</i> , 2013, 67, 560-577.	1.2	32
5458	Spatiotemporal reconstruction of the <i>Aquilegia</i> rapid radiation through nextâ€œgeneration sequencing of rapidly evolving cpDNA regions. <i>New Phytologist</i> , 2013, 198, 579-592.	3.5	86
5459	Phylogeny of Tetillidae (Porifera, Demospongiae, Spirophorida) based on three molecular markers. <i>Molecular Phylogenetics and Evolution</i> , 2013, 67, 509-519.	1.2	29
5460	Small phytoplankton in Arctic seas: vulnerability to climate change. <i>Biodiversity</i> , 2013, 14, 2-18.	0.5	31
5461	Molecular systematics of <i>Allium</i> subgenus <i>Amerallium</i> (Amaryllidaceae) in North America. <i>American Journal of Botany</i> , 2013, 100, 701-711.	0.8	40
5462	<i>Penicillium subrubescens</i> , a new species efficiently producing inulinase. <i>Antonie Van Leeuwenhoek</i> , 2013, 103, 1343-1357.	0.7	39
5463	CCAAT-box binding transcription factors in plants: Y so many?. <i>Trends in Plant Science</i> , 2013, 18, 157-166.	4.3	265
5464	The systematic position of <i>Ergasticus</i> (Decapoda, Brachyura) and allied genera, a molecular and morphological approach. <i>Zoologica Scripta</i> , 2013, 42, 427-439.	0.7	24

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5466	A New Freshwater Amoeba: <i>Cochliopodium pentatrifurcatum</i> n. sp. (Amoebozoa, Amorphea). <i>Journal of Eukaryotic Microbiology</i> , 2013, 60, 342-349.	0.8	24
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5472	Crystal structure of a eukaryotic phosphate transporter. <i>Nature</i> , 2013, 496, 533-536.	13.7	202
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5474	<i>Bacillus cytotoxicus</i> sp. nov. is a novel thermotolerant species of the <i>Bacillus cereus</i> Group occasionally associated with food poisoning. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013, 63, 31-40.	0.8	303
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5476	Molecular Identification of A Hitchhiking Frog. <i>Northwestern Naturalist</i> , 2013, 94, 81-84.	0.5	0
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5478	Genome mining for methanobactins. <i>BMC Biology</i> , 2013, 11, 17.	1.7	64
5479	Composition and interrelationships of a large Neotropical freshwater fish group, the subfamily Cheirodontinae (Characiformes: Characidae): A case study based on mitochondrial and nuclear DNA sequences. <i>Molecular Phylogenetics and Evolution</i> , 2013, 68, 23-34.	1.2	18
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5481	Restricted variation in plant barcoding markers limits identification in closely related bryophyte species. <i>Molecular Ecology Resources</i> , 2013, 13, 1047-1057.	2.2	40
5482	The Family Narnaviridae. <i>Advances in Virus Research</i> , 2013, 86, 149-176.	0.9	246



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5487	Testing three pipelines for 18S rDNA-based metabarcoding of soil faunal diversity. Science China Life Sciences, 2013, 56, 73-81.	2.3	24
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5498	Molecular epidemiology of bovine papillomatosis and the identification of a putative new virus type in Brazilian cattle. Veterinary Journal, 2013, 197, 368-373.	0.6	34
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5500	Diversity, host switching and evolution of <i>Plasmodium vivax</i> infecting African great apes. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 8123-8128.	3.3	82

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5502	Assembly-free metagenomic analysis reveals new metabolic capabilities in surface ocean bacterioplankton. <i>Environmental Microbiology Reports</i> , 2013, 5, 686-696.	1.0	8
5503	Two new Antarctic <i>Ophryotrocha</i> (Annelida: Dorvilleidae) described from shallow-water whale bones. <i>Polar Biology</i> , 2013, 36, 1031-1045.	0.5	29
5504	Nonhybrid, finished microbial genome assemblies from long-read SMRT sequencing data. <i>Nature Methods</i> , 2013, 10, 563-569.	9.0	4,029
5505	Selective tryptophan determination using tryptophan oxidases involved in bis-indole antibiotic biosynthesis. <i>Analytical Biochemistry</i> , 2013, 438, 124-132.	1.1	25
5506	Population genomics of post-vaccine changes in pneumococcal epidemiology. <i>Nature Genetics</i> , 2013, 45, 656-663.	9.4	364
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5509	Minipig and beagle animal model genomes aid species selection in pharmaceutical discovery and development. <i>Toxicology and Applied Pharmacology</i> , 2013, 270, 149-157.	1.3	61
5510	The architecture of <i>T. brucei</i> tubulin-binding cofactor B and implications for function. <i>FEBS Journal</i> , 2013, 280, 3270-3280.	2.2	6
5511	Endophytic fungi harbored in <i>Cannabis sativa</i> L.: diversity and potential as biocontrol agents against host plant-specific phytopathogens. <i>Fungal Diversity</i> , 2013, 60, 137-151.	4.7	151
5512	Endophytes versus biotrophic and necrotrophic pathogens are fungal lifestyles evolutionarily stable traits?. <i>Fungal Diversity</i> , 2013, 60, 125-135.	4.7	175
5513	Demographic Inference Reveals African and European Admixture in the North American <i>Drosophila melanogaster</i> Population. <i>Genetics</i> , 2013, 193, 291-301.	1.2	139
5514	Molecular Phylogeny of Echiuran Worms (Phylum: Annelida) Reveals Evolutionary Pattern of Feeding Mode and Sexual Dimorphism. <i>PLoS ONE</i> , 2013, 8, e56809.	1.1	27
5515	Diversification of the monoterpene synthase gene family (TPSb) in <i>Protium</i> , a highly diverse genus of tropical trees. <i>Molecular Phylogenetics and Evolution</i> , 2013, 68, 432-442.	1.2	13
5516	Understanding the formation of ancient intertropical disjunct distributions using Asian and Neotropical hinged-teeth snakes ( <i>Sibynophis</i> and <i>Scaphiodontophis</i> : Serpentes: Colubridae). <i>Molecular Phylogenetics and Evolution</i> , 2013, 66, 254-261.	1.2	31
5517	Successful establishment and global dispersal of genotype VI avian paramyxovirus serotype 1 after cross species transmission. <i>Infection, Genetics and Evolution</i> , 2013, 17, 260-268.	1.0	23
5518	Arbuscular mycorrhizal fungi associated with a single agronomic plant host across the landscape: The structure of an assemblage. <i>Soil Biology and Biochemistry</i> , 2013, 64, 181-190.	4.2	17

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5520	Dynamics of ammonia-oxidizing Archaea and Bacteria in contrasted freshwater ecosystems. <i>Research in Microbiology</i> , 2013, 164, 360-370.	1.0	47
5521	Diversity of human small intestinal <i>Streptococcus</i> and <i>Veillonella</i> populations. <i>FEMS Microbiology Ecology</i> , 2013, 85, 376-388.	1.3	121
5522	Gene invasion in distant eukaryotic lineages: discovery of mutually exclusive genetic elements reveals marine biodiversity. <i>ISME Journal</i> , 2013, 7, 1764-1774.	4.4	27
5523	Genome of the red alga <i>Porphyridium purpureum</i> . <i>Nature Communications</i> , 2013, 4, 1941.	5.8	204
5524	Phylogeny of the <i>Bouteloua curtispindula</i> Complex (Poaceae: Chloridoideae) Based on Nuclear Ribosomal and Plastid DNA Sequences from Diploid Taxa. <i>Systematic Botany</i> , 2013, 38, 379-389.	0.2	11
5525	Novel <i>Rhizobium</i> lineages isolated from root nodules of the common bean ( <i>Phaseolus vulgaris</i> L.) in Andean and Mesoamerican areas. <i>Research in Microbiology</i> , 2013, 164, 740-748.	1.0	78
5526	From Messinian crisis to Mediterranean climate: A temporal gap of diversification recovered from multiple plant phylogenies. <i>Perspectives in Plant Ecology, Evolution and Systematics</i> , 2013, 15, 130-137.	1.1	51
5527	Morphology, ultrastructure and phylogeny of <i>Takayama xiamenensis</i> sp. nov. (Gymnodinales). <i>Trends in Microbiology</i> , 2013, 21, 107-118.	0.5	18
5528	<i>Psammomonas australis</i> gen. et sp. nov. (Raphidophyceae), a new dimorphic, sand-dwelling alga. <i>Phycologia</i> , 2013, 52, 57-64.	0.6	14
5529	Morphology and phylogeny of <i>Scrippsiella enormis</i> sp. nov. and <i>S. cf. spinifera</i> (Peridinales, Dinophyceae) from the China Sea. <i>Phycologia</i> , 2013, 52, 182-190.	0.6	8
5530	Deep sequencing of non-ribosomal peptide synthetases and polyketide synthases from the microbiomes of Australian marine sponges. <i>ISME Journal</i> , 2013, 7, 1842-1851.	4.4	53
5531	Rapid identification of acetic acid bacteria using MALDI-TOF mass spectrometry fingerprinting. <i>Systematic and Applied Microbiology</i> , 2013, 36, 75-81.	1.2	42
5532	Diversity of Beet curly top Iran virus isolated from different hosts in Iran. <i>Virus Genes</i> , 2013, 46, 571-575.	0.7	29
5533	Unrecognized fine-scale recombination can mimic the effects of adaptive radiation. <i>Gene</i> , 2013, 518, 483-488.	1.0	4
5534	Tracking the molecular epidemiology of Brazilian Infectious bursal disease virus (IBDV) isolates. <i>Infection, Genetics and Evolution</i> , 2013, 13, 18-26.	1.0	24
5535	Comparative Genomics of a Plant-Pathogenic Fungus, <i>Pyrenophora tritici-repentis</i> , Reveals Transduplication and the Impact of Repeat Elements on Pathogenicity and Population Divergence. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 41-63.	0.8	167
5536	Partial venom gland transcriptome of a <i>Drosophila</i> parasitoid wasp, <i>Leptopilina heterotoma</i> , reveals novel and shared bioactive profiles with stinging Hymenoptera. <i>Gene</i> , 2013, 526, 195-204.	1.0	54

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5538	Regulation of protein-protein binding by coupling between phosphorylation and intrinsic disorder: analysis of human protein complexes. <i>Molecular BioSystems</i> , 2013, 9, 1620.	2.9	60
5539	Sequence microheterogeneity of parvalbumin, the major fish allergen. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 1607-1614.	1.1	8
5540	Origins of amyloid- $\beta$ . <i>BMC Genomics</i> , 2013, 14, 290.	1.2	66
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5542	Topographic diversity of fungal and bacterial communities in human skin. <i>Nature</i> , 2013, 498, 367-370.	13.7	950
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5545	Involvement of the Wnt/ $\beta$ -catenin pathway in neurectoderm architecture in <i>Platynereis dumerilii</i> . <i>Nature Communications</i> , 2013, 4, 1915.	5.8	40
5546	Testing the use of ITS rDNA and protein-coding genes in the generic and species delimitation of the lichen genus <i>Usnea</i> (Parmeliaceae, Ascomycota). <i>Molecular Phylogenetics and Evolution</i> , 2013, 68, 357-372.	1.2	32
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5549	Phylogeny and Classification of Automolus Foliage-gleaners and Allies (Furnariidae). <i>Condor</i> , 2013, 115, 375-385.	0.7	14
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5551	Natural variation in the sequence of PSY1 and frequency of favorable polymorphisms among tropical and temperate maize germplasm. <i>Theoretical and Applied Genetics</i> , 2013, 126, 923-935.	1.8	53
5552	Multilocus phylogeny and Bayesian estimates of species boundaries reveal hidden evolutionary relationships and cryptic diversity in Southeast Asian monitor lizards. <i>Molecular Ecology</i> , 2013, 22, 3495-3510.	2.0	40
5553	Evolutionary history of x-tox genes in three lepidopteran species: Origin, evolution of primary and secondary structure and alternative splicing, generating a repertoire of immune-related proteins. <i>Insect Biochemistry and Molecular Biology</i> , 2013, 43, 54-64.	1.2	7
5554	Evolution of the vertebrate bone matrix: An expression analysis of the network forming collagen paralogues in amphibian osteoblasts. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2013, 320, 375-384.	0.6	12

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5556	Genetic diversity in cultured and wild marine cyanomyoviruses reveals phosphorus stress as a strong selective agent. <i>ISME Journal</i> , 2013, 7, 1827-1841.	4.4	67
5557	Variable Unisexuales and Uniform Bisexuales: Morphology, Genetics, and Biogeography of the <i>Nactus pelagicus</i> Complex on Tanna Island, Vanuatu. <i>Herpetologica</i> , 2013, 69, 199-213.	0.2	3
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5560	A Practical Approach to Reconstruct Evolutionary History of Animal Sialyltransferases and Gain Insights into the Sequence-Function Relationships of Golgi-Glycosyltransferases. <i>Methods in Molecular Biology</i> , 2013, 1022, 73-97.	0.4	9
5561	Multilocus phylogeny of the avian family Alaudidae (larks) reveals complex morphological evolution, non-monophyletic genera and hidden species diversity. <i>Molecular Phylogenetics and Evolution</i> , 2013, 69, 1043-1056.	1.2	60
5562	<i>Rhizobium freirei</i> sp. nov., a symbiont of <i>Phaseolus vulgaris</i> that is very effective at fixing nitrogen. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013, 63, 4167-4173.	0.8	91
5563	An Introduction to Sequence Similarity (‘‘Homology’’) Searching. <i>Current Protocols in Bioinformatics</i> , 2013, 42, Unit3.1.	25.8	565
5564	New insights in the long-debated evolutionary history of Triuridaceae (Pandanales). <i>Molecular Phylogenetics and Evolution</i> , 2013, 69, 994-1004.	1.2	40
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5566	Influence of oxic/anoxic fluctuations on ammonia oxidizers and nitrification potential in a wet tropical soil. <i>FEMS Microbiology Ecology</i> , 2013, 85, 179-194.	1.3	62
5567	Extensive lysine acetylation occurs in evolutionarily conserved metabolic pathways and parasite-specific functions during <i>Plasmodium falciparum</i> intraerythrocytic development. <i>Molecular Microbiology</i> , 2013, 89, 660-675.	1.2	86
5568	Historical biogeography and cryptic diversity in the Callichthyinae (Siluriformes, Callichthyidae). <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2013, 51, 308-315.	0.6	18
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5572	Isolation, identification and characterization of a novel high level Î²-glucosidase-producing <i>Lichtheimia ramosa</i> strain. <i>Biocatalysis and Agricultural Biotechnology</i> , 2013, 2, 377-384.	1.5	29

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5574	Computational analysis of xanthine dehydrogenase enzyme from different source organisms. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2013, 2, 185-189.	1.2	6
5575	Morphology, phylogeny and toxin profiles of <i>Gymnodinium inusitatum</i> sp. nov., <i>Gymnodinium catenatum</i> and <i>Gymnodinium microreticulatum</i> (Dinophyceae) from the Yellow Sea, China. <i>Harmful Algae</i> , 2013, 28, 97-107.	2.2	33
5576	Genetic diversity and lineage dynamic of dengue virus serotype 1 (DENV-1) in Cambodia. <i>Infection, Genetics and Evolution</i> , 2013, 15, 59-68.	1.0	26
5577	Molecular phylogeny of broken-back shrimps (genus <i>Lysmata</i> and allies): A test of the "Tomlinson-Chiselin" hypothesis explaining the evolution of hermaphroditism. <i>Molecular Phylogenetics and Evolution</i> , 2013, 69, 46-62.	1.2	47
5578	Intra-host evolutionary rates in HIV-1C env and gag during primary infection. <i>Infection, Genetics and Evolution</i> , 2013, 19, 361-368.	1.0	31
5579	Morphology and molecular taxonomy of <i>Evlachovaea</i> -like fungi, and the status of this unusual conidial genus. <i>Fungal Biology</i> , 2013, 117, 1-12.	1.1	16
5580	Genomic and Proteomic Dissection of the Ubiquitous Plant Pathogen, <i>Armillaria mellea</i> : Toward a New Infection Model System. <i>Journal of Proteome Research</i> , 2013, 12, 2552-2570.	1.8	85
5581	Evidence for Acquisition of Copper Resistance Genes from Different Sources in Citrus-Associated Xanthomonads. <i>Phytopathology</i> , 2013, 103, 409-418.	1.1	73
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5584	The characterization of the <i>Plebotomus papatasi</i> transcriptome. <i>Insect Molecular Biology</i> , 2013, 22, 211-232.	1.0	20
5585	Stochastic faunal exchanges drive diversification in widespread Wallacean and Pacific island lizards (Squamata: Scincidae: <i>Lamprolepis smaragdina</i> ). <i>Journal of Biogeography</i> , 2013, 40, 507-520.	1.4	35
5586	Global population divergence of the sea star <i>Hippasteria phrygiana</i> corresponds to the onset of the last glacial period of the Pleistocene. <i>Marine Biology</i> , 2013, 160, 1285-1296.	0.7	18
5587	Thermospermine levels are controlled by an auxin-dependent feedback loop mechanism in <i>Populus</i> xylem. <i>Plant Journal</i> , 2013, 75, 685-698.	2.8	57
5588	Phylogenetic relationships of <i>Hamadryas</i> ( <i>Nymphalidae</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 Cladistics, 2013, 29, 629-642.	1.5	9
5589	Elongation factor-1 $\beta$ , a putative single-copy nuclear gene, has divergent sets of paralogs in an arachnid. <i>Molecular Phylogenetics and Evolution</i> , 2013, 68, 471-481.	1.2	12
5590	Characterization of a novel flavivirus isolated from <i>Culex</i> (Melanoconion) ocosa mosquitoes from Iquitos, Peru. <i>Journal of General Virology</i> , 2013, 94, 1266-1272.	1.3	32

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5593	Metagenomic analysis of an anaerobic alkane-degrading microbial culture: potential hydrocarbon-activating pathways and inferred roles of community members. <i>Genome</i> , 2013, 56, 599-611.	0.9	82
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5595	Reshaping Antibody Diversity. <i>Cell</i> , 2013, 153, 1379-1393.	13.5	179
5596	The potential of distance-based thresholds and character-based <sc>DNA</sc> barcoding for defining problematic taxonomic entities by <sc>CO</sc> 1 and <sc>ND</sc> 1. <i>Molecular Ecology Resources</i> , 2013, 13, 1069-1081.	2.2	36
5597	Snowdrops falling slowly into place: An improved phylogeny for <i>Galanthus</i> (Amaryllidaceae). <i>Molecular Phylogenetics and Evolution</i> , 2013, 69, 205-217.	1.2	17
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5599	Molecular phylogenetics and phylogeographic structure of <i>Sumichrasti</i> 's harvest mouse ( <i>Reithrodontomys sumichrasti</i> : Cricetidae) based on mitochondrial and nuclear DNA sequences. <i>Molecular Phylogenetics and Evolution</i> , 2013, 68, 282-292.	1.2	22
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5603	A genome-wide analysis of the RNA helicase gene family in <i>Solanum lycopersicum</i> . <i>Gene</i> , 2013, 513, 128-140.	1.0	26
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5605	Evolutionary analyses of gap junction protein families. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2013, 1828, 4-14.	1.4	109
5606	The Read-Across Hypothesis and Environmental Risk Assessment of Pharmaceuticals. <i>Environmental Science &amp; Technology</i> , 2013, 47, 11384-11395.	4.6	187
5607	Uncovering symbiont-driven genetic diversity across <sc>N</sc>orth <sc>A</sc>merican pea aphids. <i>Molecular Ecology</i> , 2013, 22, 2045-2059.	2.0	174
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5610	The <i>Herbaspirillum seropedicae</i> SmR1 Fnr orthologs controls the cytochrome composition of the electron transport chain. <i>Scientific Reports</i> , 2013, 3, 2544.	1.6	17
5611	CHROMATOGATE: A TOOL FOR DETECTING BASE MIS-CALLS IN MULTIPLE SEQUENCE ALIGNMENTS BY SEMI-AUTOMATIC CHROMATOGRAM INSPECTION. <i>Computational and Structural Biotechnology Journal</i> , 2013, 6, e201303001.	1.9	9
5612	Tetracycline Resistance and Class 1 Integron Genes Associated with Indoor and Outdoor Aerosols. <i>Environmental Science &amp; Technology</i> , 2013, 47, 4046-4052.	4.6	101
5613	Evolutionary rate patterns of genes involved in the <i>Drosophila</i> Toll and Imd signaling pathway. <i>BMC Evolutionary Biology</i> , 2013, 13, 245.	3.2	23
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5615	The scale and evolutionary significance of horizontal gene transfer in the choanoflagellate <i>Monosiga brevicollis</i> . <i>BMC Genomics</i> , 2013, 14, 729.	1.2	26
5616	Analysis of western lowland gorilla ( <i>Gorilla gorilla gorilla</i> ) specific Alu repeats. <i>Mobile DNA</i> , 2013, 4, 26.	1.3	13
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5618	Role of Glycoside Phosphorylases in Mannose Foraging by Human Gut Bacteria. <i>Journal of Biological Chemistry</i> , 2013, 288, 32370-32383.	1.6	50
5619	Integrative taxonomy identifies a new species of <i>Phyllodistomum</i> (Digenea: Gorgoderidae) from the twospot livebearer, <i>Heterandria bimaculata</i> (Teleostei: Poeciliidae), in Central Veracruz, Mexico. <i>Parasitology Research</i> , 2013, 112, 4137-4150.	0.6	24
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5621	Isolation and characterization of purple acid phosphatase gene during seedling development in mungbean. <i>Biologia Plantarum</i> , 2013, 57, 267-273.	1.9	2
5622	Infectivity and the phylogenetic relationship of a mastrevirus causing chickpea stunt disease in India. <i>European Journal of Plant Pathology</i> , 2013, 135, 429-438.	0.8	19
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5627	Mobile Elements in a Single-Filament Orange Guaymas Basin Beggiatoa ( <i>Candidatus Maribeggiatoa</i> ) sp. Draft Genome: Evidence for Genetic Exchange with Cyanobacteria. <i>Applied and Environmental Microbiology</i> , 2013, 79, 3974-3985.	1.4	33
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5630	Building Phylogenetic Trees from Molecular Data with MEGA. <i>Molecular Biology and Evolution</i> , 2013, 30, 1229-1235.	3.5	1,096
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5632	Genetic Diversity of the Photobiont of the Bipolar Lichen-Forming Ascomycete <i>Xanthomendoza borealis</i> . <i>Herzogia</i> , 2013, 26, 307-322.	0.1	7
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5634	Purifying selection in porcine reproductive and respiratory syndrome virus ORF5a protein influences variation in envelope glycoprotein 5 glycosylation. <i>Infection, Genetics and Evolution</i> , 2013, 20, 362-368.	1.0	14
5635	Exonic Deletions in <i>AUTS2</i> Cause a Syndromic Form of Intellectual Disability and Suggest a Critical Role for the C Terminus. <i>American Journal of Human Genetics</i> , 2013, 92, 210-220.	2.6	135
5636	Molecular characterization of the vitellogenin receptor from the tick, <i>Amblyomma hebraeum</i> (Acari: Tj ETQq1 1 0.784314 rgBT /Overl	1.2	32
5637	Diversification and dispersal of the Hawaiian <i>Drosophilidae</i> : The evolution of <i>Scaptomyza</i> . <i>Molecular Phylogenetics and Evolution</i> , 2013, 69, 95-108.	1.2	45
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5641	Near intron pairs and the metazoan tree. <i>Molecular Phylogenetics and Evolution</i> , 2013, 66, 811-823.	1.2	11
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5644	Discordant Genetic Diversity and Geographic Patterns Between <i>Crassicutis cichlasomae</i> (Digenea: Tj ETQq1 1 0.784314 rgBT /Overl Middle-America. <i>Journal of Parasitology</i> , 2013, 99, 978-988.	0.3	14
5645	Dramatic phenotypic plasticity within species of <i>Siphonutabilus</i> n. g. (Digenea: Cryptogonimidae) from Indo-Pacific caesionines (Perciformes: Lutjanidae). <i>Systematic Parasitology</i> , 2013, 86, 101-112.	0.5	22
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6356	<strong>A new species of Pachycerianthus</strong> (Cnidaria, Anthozoa.) Tj ETQq1 1 0,784314 rgBT /Overlock 10 Tf 50 587	0.2	7
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6381	Molecular and cytogenetic analyses of cryptic species within the <i>Synbranchus marmoratus</i> Bloch, 1795 (Synbranchiformes: Synbranchidae) grouping: species delimitations, karyotypic evolution and intraspecific diversification. <i>Neotropical Ichthyology</i> , 2014, 12, 903-911.	0.5	8
6382	Synthesis and degradation of poly(ADP-ribose) in plants. <i>Frontiers in Bioscience - Landmark</i> , 2014, 19, 1436.	3.0	7
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6397	<p><strong>One or two species? On the case of <em>Hyperolius</em> <em>discodactylus</em> Ahl, 1931 and H. alticola Ahl, 1931 (Anura:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 417 Td (Hyperolius</strong>	0.5	417
6398	Resolution of deep angiosperm phylogeny using conserved nuclear genes and estimates of early divergence times. Nature Communications, 2014, 5, 4956.	5.8	330
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6421	The Loss of Topography in the Microbial Communities of the Upper Respiratory Tract in the Elderly. <i>Annals of the American Thoracic Society</i> , 2014, 11, 513-521.	1.5	163
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6463	Human paternal and maternal demographic histories: insights from high-resolution Y chromosome and mtDNA sequences. <i>Investigative Genetics</i> , 2014, 5, 13.	3.3	145
6464	Using phylogenetically-informed annotation (PIA) to search for light-interacting genes in transcriptomes from non-model organisms. <i>BMC Bioinformatics</i> , 2014, 15, 350.	1.2	62
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6467	Genomewide identification and expression analysis of the ARF gene family in apple. <i>Journal of Genetics</i> , 2014, 93, 785-797.	0.4	40
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6470	The influence of secondary structure, selection and recombination on rubella virus nucleotide substitution rate estimates. <i>Virology Journal</i> , 2014, 11, 166.	1.4	3
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6474	Genome sequencing of <i>Sporisorium scitamineum</i> provides insights into the pathogenic mechanisms of sugarcane smut. <i>BMC Genomics</i> , 2014, 15, 996.	1.2	112
6475	Evolutionary history of Methyltransferase 1 genes in hexaploid wheat. <i>BMC Genomics</i> , 2014, 15, 922.	1.2	12
6476	Genome of the house fly, <i>Musca domestica</i> L., a global vector of diseases with adaptations to a septic environment. <i>Genome Biology</i> , 2014, 15, 466.	3.8	252
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6478	Multi-tissue transcriptomics of the black widow spider reveals expansions, co-options, and functional processes of the silk gland gene toolkit. <i>BMC Genomics</i> , 2014, 15, 365.	1.2	70
6479	<strong>Two new species of the tooth-carp <em>Aphanius</em> (Teleostei) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 5</strong> <em>Aphanius</em> species <strong></strong>. <i>Zootaxa</i> , 2014, 3786, 246.	0.2	43

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6880	Differential expression of endogenous plant cell wall degrading enzyme genes in the stick insect (Phasmatodea) midgut. <i>BMC Genomics</i> , 2014, 15, 917.	1.2	42
6881	Transcriptomic characterization of the immunogenetic repertoires of heteromyid rodents. <i>BMC Genomics</i> , 2014, 15, 929.	1.2	2
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6895	The heat sensitive factor (HSF) of <i>Yersinia ruckeri</i> produced by an alkyl sulphatase involved in sodium dodecyl sulphate (SDS) degradation but not in virulence. <i>BMC Microbiology</i> , 2014, 14, 221.	1.3	7

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6921	Diversity and Variability of NOD-Like Receptors in Fungi. <i>Genome Biology and Evolution</i> , 2014, 6, 3137-3158.	1.1	83
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6983	Presence of <i>Wolbachia</i> in Three Hymenopteran Species: <i>Diprion pini</i> (Hymenoptera: Diprionidae), <i>Neodiprion sertifer</i> (Hymenoptera: Diprionidae), and <i>Dahlbominus fuscipennis</i> (Hymenoptera: Tj ETQq1 1 0.784314.rgBT /Overlock 10		
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6988	A New Quantum Cuckoo Search Algorithm for Multiple Sequence Alignment. <i>Journal of Intelligent Systems</i> , 2014, 23, 261-275.	1.2	10
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7132	Genome of the human hookworm <i>Necator americanus</i> . <i>Nature Genetics</i> , 2014, 46, 261-269.	9.4	166
7133	Expression of abiotic stress inducible ETHE1-like protein from rice is higher in roots and is regulated by calcium. <i>Physiologia Plantarum</i> , 2014, 152, 1-16.	2.6	33
7134	A preliminary molecular phylogenetic assessment of the lichen moths (<sc>L</sc>epidoptera:) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T 5 chemical sequestration. <i>Systematic Entomology</i> , 2014, 39, 286-303.	1.7	25
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7136	Molecular Phylogeny and SNP Variation of Polar Bears ( <i>Ursus maritimus</i> ), Brown Bears ( <i>U. arctos</i> ), and Black Bears ( <i>U. americanus</i> ) Derived from Genome Sequences. <i>Journal of Heredity</i> , 2014, 105, 312-323.	1.0	20
7137	The Analysis of Eight Transcriptomes from All Poriferan Classes Reveals Surprising Genetic Complexity in Sponges. <i>Molecular Biology and Evolution</i> , 2014, 31, 1102-1120.	3.5	211
7138	A multi-locus molecular phylogeny for Australiaâ€™s iconic Jacky Dragon ( <i>Agamidae: Amphibolurus</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T 5 Molecular Phylogenetics and Evolution, 2014, 71, 149-156.	1.2	17
7139	Lichenicolous fungi of the genus <i>Abrothallus</i> (Dothideomycetes: Abrothallales ordo nov.) are sister to the predominantly aquatic Janhulales. <i>Fungal Diversity</i> , 2014, 64, 295-304.	4.7	23
7140	The complete mitochondrial genome sequence of the world's largest fish, the whale shark ( <i>Rhincodon typus</i> ), and its comparison with those of related shark species. <i>Gene</i> , 2014, 539, 44-49.	1.0	34
7141	A synchronized global sweep of the internal genes of modern avian influenza virus. <i>Nature</i> , 2014, 508, 254-257.	13.7	206
7142	Deep intraspecific divergences in the medically relevant fat-tailed scorpions ( <i>Androctonus</i> ,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T 5	0.9	20
7143	Phylogeography and diversity of the terrestrial isopod <i>Spherillo grossus</i> (Oniscidea: Armadillidae) on the Australian East Coast. <i>Zoological Journal of the Linnean Society</i> , 2014, 170, 297-309.	1.0	9
7144	Computational Approaches and Resources in Single Amino Acid Substitutions Analysis Toward Clinical Research. <i>Advances in Protein Chemistry and Structural Biology</i> , 2014, 94, 365-423.	1.0	22
7145	Chlorite dismutases â€ a heme enzyme family for use in bioremediation and generation of molecular oxygen. <i>Biotechnology Journal</i> , 2014, 9, 461-473.	1.8	55
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7147	Afro-Eurasia and the Americas present barriers to gene flow for the cosmopolitan neustonic nudibranch <i>Glaucus atlanticus</i> . <i>Marine Biology</i> , 2014, 161, 899-910.	0.7	24
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7150	THE COMPLEX EVOLUTIONARY HISTORY OF SEEING RED: MOLECULAR PHYLOGENY AND THE EVOLUTION OF AN ADAPTIVE VISUAL SYSTEM IN DEEP-SEA DRAGONFISHES (STOMIIFORMES: STOMIIDAE). <i>Evolution; International Journal of Organic Evolution</i> , 2014, 68, 996-1013.	1.1	27
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7153	Evolution of tryptophan biosynthetic pathway in microbial genomes: a comparative genetic study. <i>Systems and Synthetic Biology</i> , 2014, 8, 59-72.	1.0	25
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7155	Low genetic diversity and functional constraint in loci encoding <i>Plasmodium vivax</i> P12 and P38 proteins in the Colombian population. <i>Malaria Journal</i> , 2014, 13, 58.	0.8	28
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7161	Comparative genomics of <i>Cylindrospermopsis raciborskii</i> strains with differential toxicities. <i>BMC Genomics</i> , 2014, 15, 83.	1.2	64
7162	The Effects of Stabilizing and Directional Selection on Phenotypic and Genotypic Variation in a Population of RNA Enzymes. <i>Journal of Molecular Evolution</i> , 2014, 78, 101-108.	0.8	12
7163	On the Origin and Evolution of Plant Brassinosteroid Receptor Kinases. <i>Journal of Molecular Evolution</i> , 2014, 78, 118-129.	0.8	28
7164	The Use (and Misuse) of Phylogenetic Trees in Comparative Behavioral Analyses. <i>International Journal of Primatology</i> , 2014, 35, 32-54.	0.9	8
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7173	Genomic surveys and expression analysis of bZIP gene family in castor bean ( <i>Ricinus communis</i> L.). <i>Planta</i> , 2014, 239, 299-312.	1.6	90
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7176	Subdivision of arthropod cap-n-collar expression domains is restricted to Mandibulata. <i>EvoDevo</i> , 2014, 5, 3.	1.3	17
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7178	Genomics of <i>C</i> compositae crops: reference transcriptome assemblies and evidence of hybridization with wild relatives. <i>Molecular Ecology Resources</i> , 2014, 14, 166-177.	2.2	45
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7180	A genome-wide analysis of the expansin genes in <i>Malus domestica</i> . <i>Molecular Genetics and Genomics</i> , 2014, 289, 225-236.	1.0	39
7181	Application of Evolutionary Based in Silico Methods to Predict the Impact of Single Amino Acid Substitutions in Vitelliform Macular Dystrophy. <i>Advances in Protein Chemistry and Structural Biology</i> , 2014, 94, 177-267.	1.0	10
7182	XMRV low level of expression in human cells delays superinfection interference and allows proviral copies to accumulate. <i>Virology</i> , 2014, 456-457, 28-38.	1.1	2
7183	Multiple reassortment events among highly pathogenic avian influenza A(H5N1) viruses detected in Bangladesh. <i>Virology</i> , 2014, 450-451, 297-307.	1.1	35
7184	Distribution, abundance and diversity of <i>Gambierdiscus</i> spp. from a ciguatera-endemic area in Marakei, Republic of Kiribati. <i>Harmful Algae</i> , 2014, 34, 56-68.	2.2	56

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7187	PhyloFlu, a DNA Microarray for Determining the Phylogenetic Origin of Influenza A Virus Gene Segments and the Genomic Fingerprint of Viral Strains. <i>Journal of Clinical Microbiology</i> , 2014, 52, 803-813.	1.8	7
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7189	Structural studies, homology modeling and molecular docking of novel non-competitive antagonists of GluK1/GluK2 receptors. <i>Bioorganic and Medicinal Chemistry</i> , 2014, 22, 787-795.	1.4	14
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7191	Alterations in the predicted regulatory and coding regions of the sterol 14 $\alpha$ -demethylase gene (<i><sc>CYP51</sc></i>) confer decreased azole sensitivity in the oilseed rape pathogen <i><sc>P</sc>yrenopeziza brassicae</i>. <i>Molecular Plant Pathology</i> , 2014, 15, 513-522.	2.0	51
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7193	Channelrhodopsins: A bioinformatics perspective. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2014, 1837, 643-655.	0.5	11
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7195	Two new species of Cortinarius, subgenus Telamonia, sections Colymbadini and Uracei, from Europe. <i>Mycological Progress</i> , 2014, 13, 867-879.	0.5	13
7196	Global distribution and origin of target site insecticide resistance mutations in Tetranychus urticae. <i>Insect Biochemistry and Molecular Biology</i> , 2014, 48, 17-28.	1.2	67
7197	Horizontal gene transfer and the rock record: comparative genomics of phylogenetically distant bacteria that induce wrinkle structure formation in modern sediments. <i>Geobiology</i> , 2014, 12, 119-132.	1.1	30
7198	Characterization of a new picornavirus isolated from the freshwater fish Lepomis macrochirus. <i>Journal of General Virology</i> , 2014, 95, 601-613.	1.3	32
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7204	Misidentification of <i>Aspergillus nomius</i> and <i>Aspergillus tamaris</i> as <i>Aspergillus flavus</i> : Characterization by Internal Transcribed Spacer, $\beta$ -Tubulin, and Calmodulin Gene Sequencing, Metabolic Fingerprinting, and Matrix-Assisted Laser Desorption Ionization–Time of Flight Mass Spectrometry. <i>Journal of Clinical Microbiology</i> , 2014, 52, 1153-1160.	1.8	71
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7210	Group <i>VilE</i> thylene <i>R</i> esponse <i>F</i> actor diversification and regulation in four species from flood-prone environments. <i>Plant, Cell and Environment</i> , 2014, 37, 2421-2432.	2.8	58
7211	Antigenic Mapping of the Hemagglutinin of an H9N2 Avian Influenza Virus Reveals Novel Critical Amino Acid Positions in Antigenic Sites. <i>Journal of Virology</i> , 2014, 88, 3898-3901.	1.5	45
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7214	Single acquisition of protelomerase gave rise to speciation of a large and diverse clade within the <i>Agrobacterium/Rhizobium</i> supercluster characterized by the presence of a linear chromid. <i>Molecular Phylogenetics and Evolution</i> , 2014, 73, 202-207.	1.2	44
7215	Identification of amino acids in mitochondrially encoded proteins that correlate with lifespan. <i>Experimental Gerontology</i> , 2014, 56, 53-58.	1.2	2
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7222	Quantitative evaluation of the host-colonizing capabilities of the enteric bacterium <i>Pantoea</i> using plant and insect hosts. <i>Microbiology (United Kingdom)</i> , 2014, 160, 602-615.	0.7	59
7223	Genomic Features of a Bumble Bee Symbiont Reflect Its Host Environment. <i>Applied and Environmental Microbiology</i> , 2014, 80, 3793-3803.	1.4	53
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7225	<i>CladispaBaly</i> : revision, biology and reassignment of the genus to the tribe Spilophorini (Coleoptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.7	2
7226	The influence of the complex topography and dynamic history of the montane Neotropics on the evolutionary differentiation of a cloud forest bird ( <i>Premnoplex brunnescens</i> , Furnariidae). <i>Journal of Biogeography</i> , 2014, 41, 1533-1546.	1.4	55
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7233	A multigene phylogenetic synthesis for the class Lecanoromycetes (Ascomycota): 1307 fungi representing 1139 infrageneric taxa, 317 genera and 66 families. <i>Molecular Phylogenetics and Evolution</i> , 2014, 79, 132-168.	1.2	248
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7235	Bacterial origin of a diverse family of UDP-glycosyltransferase genes in the <i>Tetranychus urticae</i> genome. <i>Insect Biochemistry and Molecular Biology</i> , 2014, 50, 43-57.	1.2	59
7236	A New Two-Pored <i>Amphisbaena</i> Linnaeus, 1758, from Western Amazonia, Brazil ( <i>Amphisbaenia</i> ): Tj ETQq1 1 0.784314 rgBT /Over	0.5	29
7237	Origin and Evolution of B Chromosomes in the Cichlid Fish <i>Astatotilapia latifasciata</i> Based on Integrated Genomic Analyses. <i>Molecular Biology and Evolution</i> , 2014, 31, 2061-2072.	3.5	112
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7240	Evolution of symbiosis with <i>Lingula</i> (Brachiopoda) in the bivalve superfamily Galeommatoidea (Heterodonta), with description of a new species of <i>Koreamya</i> . <i>Journal of Molluscan Studies</i> , 2014, 80, 148-160.	0.4	13
7241	Molecular and ultrastructural analysis of forisome subunits reveals the principles of forisome assembly. <i>Annals of Botany</i> , 2014, 113, 1121-1137.	1.4	16
7242	EKPD: a hierarchical database of eukaryotic protein kinases and protein phosphatases. <i>Nucleic Acids Research</i> , 2014, 42, D496-D502.	6.5	52
7243	Ectomycorrhizal <i>Cortinarius</i> species participate in enzymatic oxidation of humus in northern forest ecosystems. <i>New Phytologist</i> , 2014, 203, 245-256.	3.5	256
7244	Taxonomic evaluation of <i>Streptomyces albus</i> and related species using multilocus sequence analysis and proposals to emend the description of <i>Streptomyces albus</i> and describe <i>Streptomyces pathocidini</i> sp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2014, 64, 894-900.	0.8	88
7245	Prevalence of phylogenetic clustering at multiple scales in an African rain forest tree community. <i>Journal of Ecology</i> , 2014, 102, 1008-1016.	1.9	33
7246	Comparative analysis reveals that polyploidy does not decelerate diversification in fish. <i>Journal of Evolutionary Biology</i> , 2014, 27, 391-403.	0.8	31
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7248	Sulfur Oxidation Genes in Diverse Deep-Sea Viruses. <i>Science</i> , 2014, 344, 757-760.	6.0	223
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7251	Evolutionary basis of mitonuclear discordance between sister species of mole salamanders ( <i>Ambystoma</i> sp.). <i>Molecular Ecology</i> , 2014, 23, 2811-2824.	2.0	21
7252	TGL-mediated lipolysis in <i>Manduca sexta</i> fat body: Possible roles for lipoamide-dehydrogenase (LipDH) and high-density lipophorin (HDLp). <i>Insect Biochemistry and Molecular Biology</i> , 2014, 45, 58-68.	1.2	7
7253	<i>Kudoa thunni</i> from Blackfin Tuna ( <i>Thunnus atlanticus</i> ) Harvested Off the Island of St. Kitts, West Indies. <i>Journal of Parasitology</i> , 2014, 100, 110-116.	0.3	11
7254	A review of the currently recognised opecoelid cercariae, including the identification and emergence ecology of <i>Cercaria capricornia</i> XII (Digenea: Opecoelidae) from <i>Nassarius olivaceus</i> (Gastropoda: Tj ETQq1 1 0.78431 4 rgBT7/Overlo		
7255	<i>Rhodobacter capsulatus</i> ... <i>DprA</i> is essential for <i>RecA</i> -mediated gene transfer agent ( <i>RcGTA</i> ) recipient capability regulated by quorum-sensing and the <i>CtrA</i> response regulator. <i>Molecular Microbiology</i> , 2014, 92, 1260-1278.	1.2	52
7256	<i>Liberibacter crescens</i> gen. nov., sp. nov., the first cultured member of the genus <i>Liberibacter</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2014, 64, 2461-2466.	0.8	81

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7258	The phylogeography of Eurasian <i>Fraxinus</i> species reveals ancient transcontinental reticulation. <i>Molecular Phylogenetics and Evolution</i> , 2014, 77, 223-237.	1.2	15
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7521	Hybridization effects and genetic diversity of the common and black-tufted marmoset ( <i>Callithrix jacchus</i> ) and <i>Callithrix penicillata</i> mitochondrial control region. <i>American Journal of Physical Anthropology</i> , 2014, 155, 522-536.	2.1	33
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7562	Mitogenomic analyses propose positive selection in mitochondrial genes for high-altitude adaptation in galliform birds. <i>Mitochondrion</i> , 2014, 18, 70-75.	1.6	70
7563	Bioinformatics: Concepts, Methods, and Data. , 2014, , 259-287.		9

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7922	Mitogenomic data resolve basal relationships among passeriform and passeridan birds. <i>Molecular Phylogenetics and Evolution</i> , 2014, 79, 313-324.	1.2	30
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7961	The Complete Genome Sequence of <i>Candidatus</i> Liberibacter americanus <sup>TM</sup> , Associated with Citrus Huanglongbing. <i>Molecular Plant-Microbe Interactions</i> , 2014, 27, 163-176.	1.4	97
7962	The Phylogenetic Relationship of <i>Tectaria brauniana</i> and <i>Tectaria nicotianifolia</i> , and the Recognition of <i>Hypoderris</i> (Tectariaceae). <i>Systematic Botany</i> , 2014, 39, 384-395.	0.2	27
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7973	Thyroid hormone and retinoid X receptor function and expression during sea lamprey ( <i>Petromyzon</i> ) Tj ETQq1 1 0.784314 rgBT /Overlo	0.8	16
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7992	Identifying subset errors in multiple sequence alignments. <i>Journal of Biomolecular Structure and Dynamics</i> , 2014, 32, 364-371.	2.0	4
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8004	A Practical Guide to Phylogenetics for Nonexperts. <i>Journal of Visualized Experiments</i> , 2014, , e50975.	0.2	6
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8017	Molecular phylogeny reveals the true colours of Myeloconidaceae (Ascomycota: Ostropales). <i>Australian Systematic Botany</i> , 2014, 27, 38.	0.3	13
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8022	Chordopoxvirus protein F12 implicated in enveloped virion morphogenesis is an inactivated DNA polymerase. <i>Biology Direct</i> , 2014, 9, 22.	1.9	7
8023	MSARC: Multiple sequence alignment by residue clustering. <i>Algorithms for Molecular Biology</i> , 2014, 9, 12.	0.3	9
8024	Complete genome sequence of <i>Planctomyces brasiliensis</i> type strain (DSM 5305T), phylogenomic analysis and reclassification of Planctomycetes including the descriptions of <i>Gimesia</i> gen. nov., <i>Planctopirus</i> gen. nov. and <i>Rubinisphaera</i> gen. nov. and emended descriptions of the order Planctomycetales and the family Planctomycetaceae. <i>Standards in Genomic Sciences</i> , 2014, 9, 10.	1.5	76
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8026	Conserved microRNA editing in mammalian evolution, development and disease. <i>Genome Biology</i> , 2014, 15, R83.	13.9	70
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8030	Characterization of Basidiomycetes Associated with Wood Rot of Citrus in Southern Italy. <i>Phytopathology</i> , 2014, 104, 851-858.	1.1	13
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8034	Integrins of the Starlet Sea Anemone <i>Nematostella vectensis</i> . <i>Biological Bulletin</i> , 2014, 227, 211-220.	0.7	14
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8041	Genes encoding meningococcal vaccine antigens are present in nonpathogenic bacteria found in the human microbiome. <i>Bios</i> , 2014, 85, 142-150.	0.0	1
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8333	Taxonomy, morphology, and genetic variation of <i>Nitella flexilis</i> var. <i>bifurcata</i> (Charales, Characeae) from Japan. <i>Phycological Research</i> , 2015, 63, 159-166.	0.8	2
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8343	Transcriptional coordination of physiological responses in <i>Nannochloropsis oceanica</i> <i>CCMP</i> 1779 under light/dark cycles. <i>Plant Journal</i> , 2015, 83, 1097-1113.	2.8	69

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8358	Integrative taxonomy reveals six new species related to the Mediterranean corn stalk borer <i>Sesamia nonagrioides</i> (Lefebvre) (Lepidoptera, Noctuidae, Sesamiina). <i>Zoological Journal of the Linnean Society</i> , 2015, 175, 244-270.	1.0	28
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8600	<i>Laimaphelenchus hyrcanus</i> n. sp. (Nematoda: Aphelenchoididae), a new species from northern Iran. <i>Zootaxa</i> , 2015, 3915, 591-600.	0.2	16
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8605	First record of <i>Mollisquama</i> sp. (Chondrichthyes: Squaliformes: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 66 &Mollisquama &parini & Dolganov &. <i>Zootaxa</i> , 2015, 3948, 587.	0.2	10
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8911	A rapid diagnostic approach to identify poisonous plants using DNA barcoding data. <i>Plant Biosystems</i> , 2015, 149, 537-545.	0.8	8
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8989	Evolution of plant virus movement proteins from the 30K superfamily and of their homologs integrated in plant genomes. <i>Virology</i> , 2015, 476, 304-315.	1.1	65
8990	Brazilian potato virus Y isolates identified as members of a new clade facilitate the reconstruction of evolutionary traits within this species. <i>Plant Pathology</i> , 2015, 64, 799-807.	1.2	9
8991	Studying Genome Heterogeneity within the Arbuscular Mycorrhizal Fungal Cytoplasm. <i>Genome Biology and Evolution</i> , 2015, 7, 505-521.	1.1	30
8992	Phylogenetic skew: an index of community diversity. <i>Molecular Ecology</i> , 2015, 24, 759-770.	2.0	8
8993	Revision and phylogeny of <i>Syrphetodes</i> (Coleoptera: Urodidae): implications for biogeography, alpinization and conservation. <i>Systematic Entomology</i> , 2015, 40, 143-168.	1.7	11
8994	Diverse bacterial communities are recruited on spores of different arbuscular mycorrhizal fungal isolates. <i>Biology and Fertility of Soils</i> , 2015, 51, 379-389.	2.3	111

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8996	The roles of history and ecology in chloroplast phylogeographic patterns of the bird-dispersed plant parasite <i>Phoradendron californicum</i> (Viscaceae) in the Sonoran Desert. <i>American Journal of Botany</i> , 2015, 102, 149-164.	0.8	25
8997	Comparative genomic analysis of evolutionarily conserved but functionally uncharacterized membrane proteins in archaea: Prediction of novel components of secretion, membrane remodeling and glycosylation systems. <i>Biochimie</i> , 2015, 118, 302-312.	1.3	11
8998	Effect of salinity on nitrification efficiency and structure of ammonia-oxidizing bacterial communities in a submerged fixed bed bioreactor. <i>Chemical Engineering Journal</i> , 2015, 266, 233-240.	6.6	74
8999	Kernel-based logistic regression model for protein sequence without vectorialization. <i>Biostatistics</i> , 2015, 16, 480-492.	0.9	3
9000	Integrated genome sequence and linkage map of physic nut ( <i>Jatropha curcas</i> L.), a biodiesel plant. <i>Plant Journal</i> , 2015, 81, 810-821.	2.8	149
9001	NAD kinase controls animal NADP biosynthesis and is modulated via evolutionarily divergent calmodulin-dependent mechanisms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 1386-1391.	3.3	49
9002	Emergence and Evolution of H10 Subtype Influenza Viruses in Poultry in China. <i>Journal of Virology</i> , 2015, 89, 3534-3541.	1.5	61
9003	Molecular contributions to species boundaries in dicyemid parasites from eastern Pacific cephalopods. <i>Marine Biology Research</i> , 2015, 11, 414-422.	0.3	4
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9008	Genome data from a sixteenth century pig illuminate modern breed relationships. <i>Heredity</i> , 2015, 114, 175-184.	1.2	39
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9010	Identification of a novel carbohydrate esterase from <i>Bjerkandera adusta</i> : Structural and function predictions through bioinformatics analysis and molecular modeling. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 533-546.	1.5	6
9011	RRDistMaps: a UCSF Chimera tool for viewing and comparing protein distance maps. <i>Bioinformatics</i> , 2015, 31, 1484-1486.	1.8	52
9012	The Role of Palmitoylation for Protein Recruitment to the Inner Membrane Complex of the Malaria Parasite. <i>Journal of Biological Chemistry</i> , 2015, 290, 1712-1728.	1.6	66

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9016	Diversity of Lake Ladoga (Russia) bacterial plankton inferred from 16S rRNA gene pyrosequencing: An emphasis on picocyanobacteria. <i>Journal of Great Lakes Research</i> , 2015, 41, 180-191.	0.8	8
9017	Description and phylogenetic position of <i>Amphora aliformis</i> (Bacillariophyta), a new species from Tokyo Bay. <i>Phycologia</i> , 2015, 54, 78-86.	0.6	4
9018	Distinct composition signatures of archaeal and bacterial phylotypes in the Wanda Glacier forefield, Antarctic Peninsula. <i>FEMS Microbiology Ecology</i> , 2015, 91, 1-10.	1.3	55
9019	Evolution of sexual traits influencing vectorial capacity in anopheline mosquitoes. <i>Science</i> , 2015, 347, 985-988.	6.0	68
9020	Eumetazoan Cryptochrome Phylogeny and Evolution. <i>Genome Biology and Evolution</i> , 2015, 7, 601-619.	1.1	35
9021	Seasonal dynamics of active SAR11 ecotypes in the oligotrophic Northwest Mediterranean Sea. <i>ISME Journal</i> , 2015, 9, 347-360.	4.4	93
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9024	<i>Rickettsia buchneri</i> sp. nov., a rickettsial endosymbiont of the blacklegged tick <i>Ixodes scapularis</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 965-970.	0.8	104
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9028	Two linked pairs of Arabidopsis TNL resistance genes independently confer recognition of bacterial effector AvrRps4. <i>Nature Communications</i> , 2015, 6, 6338.	5.8	147
9029	Phylogenetic relationships and chemical evolution of the genera <i>Stenus</i> and <i>Dianous</i> (Coleoptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.6	8
9030	<i>Streptomyces lunaelactis</i> sp. nov., a novel ferroverdin A-producing <i>Streptomyces</i> species isolated from a moonmilk speleothem. <i>Antonie Van Leeuwenhoek</i> , 2015, 107, 519-531.	0.7	38

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9038	The genome and transcriptome of the zoonotic hookworm <i>Ancylostoma ceylanicum</i> identify infection-specific gene families. <i>Nature Genetics</i> , 2015, 47, 416-422.	9.4	91
9039	Functional analysis of C1 family cysteine peptidases in the larval gut of <i>DÇenebrio molitor</i> and <i>Tribolium castaneum</i> . <i>BMC Genomics</i> , 2015, 16, 75.	1.2	39
9040	Phylogeny and Biogeography of North American and Asian <i>Pedicularis</i> (Orobanchaceae). <i>Systematic Botany</i> , 2015, 40, 229-258.	0.2	20
9041	Is Sequence Alignment an Art or a Science?. <i>Systematic Botany</i> , 2015, 40, 14-26.	0.2	25
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9044	Genome-wide comparative analysis of ABC systems in the <i>Bdellovibrio</i> -and-like organisms. <i>Gene</i> , 2015, 562, 132-137.	1.0	5
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9047	<i>Fusarium sambucinum</i> <i>astA</i> gene expressed during potato infection is a functional orthologue of <i>Aspergillus nidulans</i> <i>astA</i> . <i>Fungal Biology</i> , 2015, 119, 509-517.	1.1	4
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9050	High Gene Family Turnover Rates and Gene Space Adaptation in the Compact Genome of the Carnivorous Plant <i>Utricularia gibba</i> . <i>Molecular Biology and Evolution</i> , 2015, 32, 1284-1295.	3.5	53
9051	Coordinated Rates of Evolution between Interacting Plastid and Nuclear Genes in Geraniaceae. <i>Plant Cell</i> , 2015, 27, 563-573.	3.1	57
9052	Age and origin of Australian <i>Bennelongia</i> (Crustacea, Ostracoda). <i>Hydrobiologia</i> , 2015, 750, 125-146.	1.0	8
9053	Molecular phylogeny of Arcoidea with emphasis on Arcidae species (Bivalvia: Pteriomorphia) along the coast of China: Challenges to current classification of arcoids. <i>Molecular Phylogenetics and Evolution</i> , 2015, 85, 189-196.	1.2	9
9054	Host specificity, pathogenicity, and mixed infections of trypanoplasms from freshwater fishes. <i>Parasitology Research</i> , 2015, 114, 1071-1078.	0.6	11
9055	How does molecular-assisted identification affect our estimation of $\hat{I}^1$ , $\hat{I}^2$ and $\hat{I}^3$ biodiversity? An example from understory red seaweeds (Rhodophyta) of <i>Laminaria</i> kelp forests in Brittany, France. <i>Genetica</i> , 2015, 143, 207-223.	0.5	8
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9057	Compensatory Mutations Occur Within the Electrostatic Interaction Range of Deleterious Mutations in Protein Structure. <i>Journal of Molecular Evolution</i> , 2015, 80, 10-12.	0.8	4
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9059	Characterization of <i>Alkaliphilus hydrothermalis</i> sp. nov., a novel alkaliphilic anaerobic bacterium, isolated from a carbonaceous chimney of the Prony hydrothermal field, New Caledonia. <i>Extremophiles</i> , 2015, 19, 183-188.	0.9	40
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9064	Agronomically important thrips: development of species-specific primers in multiplex PCR and microarray assay using internal transcribed spacer 1 (ITS1) sequences for identification. <i>Bulletin of Entomological Research</i> , 2015, 105, 52-59.	0.5	18
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9067	Phylogeny of <i>Hedysarum</i> and tribe Hedysareae (Leguminosae: Papilionoideae) inferred from sequence data of ITS, <i>matK</i> , <i>trnL</i> and <i>rbcL</i> and <i>psbA</i> . <i>Taxon</i> , 2015, 64, 49-64.	0.4	37
9068	Sioxanthin, a novel glycosylated carotenoid, reveals an unusual subclustered biosynthetic pathway. <i>Environmental Microbiology</i> , 2015, 17, 2158-2171.	1.8	49
9069	Detection and Isolation of Sindbis Virus from Mosquitoes Captured During an Outbreak in Sweden, 2013. <i>Vector-Borne and Zoonotic Diseases</i> , 2015, 15, 133-140.	0.6	27
9070	Geographical distribution and genetic diversity of <i>Gymnogobius</i> sp. "Chokai-endemic species" (Perciformes: Gobiidae). <i>Ichthyological Research</i> , 2015, 62, 156-162.	0.5	8
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9073	Next-generation sequencing sheds light on the natural history of hepatitis C infection in patients who fail treatment. <i>Hepatology</i> , 2015, 61, 88-97.	3.6	36
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9076	Biochemical and functional characterizations of tyrosine phosphatases from pathogenic and nonpathogenic mycobacteria: indication of phenyl cyclopropyl methyl-/phenyl butenyl azoles as tyrosine phosphatase inhibitors. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 7539-7548.	1.7	9
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9080	Novel phenotype associated with a mutation in the <i>KCNA1</i> (Kv1.1) gene. <i>Frontiers in Physiology</i> , 2014, 5, 525.	1.3	42
9081	Strand-specific RNA sequencing in <i>Plasmodium falciparum</i> malaria identifies developmentally regulated long non-coding RNA and circular RNA. <i>BMC Genomics</i> , 2015, 16, 454.	1.2	160
9082	Fungal Communities Respond to Long-Term CO <sub>2</sub> Elevation by Community Reassembly. <i>Applied and Environmental Microbiology</i> , 2015, 81, 2445-2454.	1.4	48
9083	Wild waterfowl migration and domestic duck density shape the epidemiology of highly pathogenic H5N8 influenza in the Republic of Korea. <i>Infection, Genetics and Evolution</i> , 2015, 34, 267-277.	1.0	76
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9086	Methods for virus classification and the challenge of incorporating metagenomic sequence data. <i>Journal of General Virology</i> , 2015, 96, 1193-1206.	1.3	72
9087	Multiple introductions of the eastern fox squirrel ( <i>Sciurus niger</i> ) in California. <i>Mitochondrial DNA</i> , 2015, 26, 583-592.	0.6	7
9088	The absence of protein Y4yS affects negatively the abundance of T3SS <i>Mesorhizobium loti</i> secretin, RhcC2, in bacterial membranes. <i>Frontiers in Plant Science</i> , 2015, 6, 12.	1.7	19
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9092	Cu(II) pollution affects fecundity of the mangrove degrader community, the <i>Labyrinthulomycetes</i> . <i>Botanica Marina</i> , 2015, 58, 129-138.	0.6	6
9093	Discovery of a polyomavirus in European badgers ( <i>Meles meles</i> ) and the evolution of host range in the family <i>Polyomaviridae</i> . <i>Journal of General Virology</i> , 2015, 96, 1411-1422.	1.3	12
9094	Taxonomic re-examination of several Japanese <i>Stemphylium</i> strains based on morphological and molecular phylogenetic analyses. <i>Journal of General Plant Pathology</i> , 2015, 81, 358-367.	0.6	21
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9099	Evolutionary history of the Azteca-like mariner transposons and their host ants. <i>Die Naturwissenschaften</i> , 2015, 102, 44.	0.6	7
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9101	A corpora allata farnesyl diphosphate synthase in mosquitoes displaying a metal ion dependent substrate specificity. <i>Insect Biochemistry and Molecular Biology</i> , 2015, 64, 44-50.	1.2	16
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9104	Molecular Epidemiology and Evolution of Influenza Viruses Circulating within European Swine between 2009 and 2013. <i>Journal of Virology</i> , 2015, 89, 9920-9931.	1.5	148
9105	The barber's pole worm CAP protein superfamily – A basis for fundamental discovery and biotechnology advances. <i>Biotechnology Advances</i> , 2015, 33, 1744-1754.	6.0	16
9106	Î-Carbonic Anhydrases: Structure, Distribution, and Potential Roles. , 2015, , 337-349.		2
9107	Novel sulfated phosphoglycolipids from <i>Natronomonas moolapensis</i> . <i>Chemistry and Physics of Lipids</i> , 2015, 191, 8-15.	1.5	3
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9110	Geographical sequence variation in the <i>Leishmania major</i> virulence factor P46. <i>Infection, Genetics and Evolution</i> , 2015, 30, 195-205.	1.0	13
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9114	Assembly and variation analyses of <i>Clarias batrachus</i> mitogenome retrieved from WGS data and its phylogenetic relationship with other catfishes. <i>Meta Gene</i> , 2015, 5, 105-114.	0.3	9
9115	Novel and Recently Evolved MicroRNA Clusters Regulate Expansive <i>F-BOX</i> Gene Networks through Phased Small Interfering RNAs in Wild Diploid Strawberry. <i>Plant Physiology</i> , 2015, 169, 594-610.	2.3	73
9116	Distinct <i>SagA</i> from Hospital-Associated Clade A1 <i>Enterococcus faecium</i> Strains Contributes to Biofilm Formation. <i>Applied and Environmental Microbiology</i> , 2015, 81, 6873-6882.	1.4	35
9117	<i>Microplitis demolitor</i> Bracovirus Proviral Loci and Clustered Replication Genes Exhibit Distinct DNA Amplification Patterns during Replication. <i>Journal of Virology</i> , 2015, 89, 9511-9523.	1.5	32
9118	Diversity of viral photosystem-I <i>psaA</i> genes. <i>ISME Journal</i> , 2015, 9, 1892-1898.	4.4	10
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9530	Old Drugs To Treat Resistant Bugs: Methicillin-Resistant <i>Staphylococcus aureus</i> Isolates with <i>mecC</i> Are Susceptible to a Combination of Penicillin and Clavulanic Acid. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 7396-7404.	1.4	32
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9937	<i>Tulostoma ahmadii</i> sp. nov. and <i>T. squamosum</i> from Pakistan. <i>Turkish Journal of Botany</i> , 2016, 40, 218-225.	0.5	12
9938	First confirmed report on <i>Fusarium sporotrichioides</i> on <i>Pinus ponderosa</i> var. <i>jeffreyi</i> in Slovakia. <i>Plant Protection Science</i> , 2016, 52, 250-253.	0.7	6
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9948	First Report of Outbreaks of the Fall Armyworm <i>Spodoptera frugiperda</i> (J E Smith) (Lepidoptera,) Tj ETQq1 1 0.784314 rgBT /Overlock 1	1.1	931
9949	<i>Yorkie</i> Facilitates Organ Growth and Metamorphosis in <i>Bombyx</i> . <i>International Journal of Biological Sciences</i> , 2016, 12, 917-930.	2.6	15
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10005	Assessing the Gene Content of the Megagenome: Sugar Pine ( <i>Pinus lambertiana</i> ). <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 3787-3802.	0.8	51

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10043	Characterization of Non-coding DNA Satellites Associated with Sweepviruses (Genus Begomovirus,) Tj ETQq1 1 0.784314 rgBT /Ove <i>Microbiology</i> , 2016, 7, 162.	1.5	102
10044	In silico Analysis Revealed High-risk Single Nucleotide Polymorphisms in Human Pentraxin-3 Gene and their Impact on Innate Immune Response against Microbial Pathogens. <i>Frontiers in Microbiology</i> , 2016, 7, 192.	1.5	18
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10187	CATO: The Clone Alignment Tool. PLoS ONE, 2016, 11, e0159586.	1.1	0
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10193	Development of a Bioinformatics Framework for the Detection of Gene Conversion and the Analysis of Combinatorial Diversity in Immunoglobulin Heavy Chains in Four Cattle Breeds. PLoS ONE, 2016, 11, e0164567.	1.1	9
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10195	RAP2.4a Is Transported through the Phloem to Regulate Cold and Heat Tolerance in Papaya Tree ( <i>Carica</i> ) Tj ETQq1 1 0.784314,rgBT /Ov 1.1 27	1.1	27
10196	Metabarcoding of Fecal Samples to Determine Herbivore Diets: A Case Study of the Endangered Pacific Pocket Mouse. PLoS ONE, 2016, 11, e0165366.	1.1	49
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10203	Revealing the Micro-scale Signature of Endemic Zoonotic Disease Transmission in an African Urban Setting. PLoS Pathogens, 2016, 12, e1005525.	2.1	65

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10212	CYP96T1 of <i>Narcissus</i> sp. aff. <i>pseudonarcissus</i> Catalyzes Formation of the Para-Para' C-C Phenol Couple in the Amaryllidaceae Alkaloids. <i>Frontiers in Plant Science</i> , 2016, 7, 225.	1.7	56
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10216	Genetic Adaptation of Giant Lobelias ( <i>Lobelia aberdarica</i> and <i>Lobelia telekii</i> ) to Different Altitudes in East African Mountains. <i>Frontiers in Plant Science</i> , 2016, 7, 488.	1.7	9
10217	Identification and Overexpression of a Knotted1-Like Transcription Factor in Switchgrass ( <i>Panicum</i> ) Tj ETQq1 1 0.784314 rgBT/Overl	1.7	39
10218	In Search of Enzymes with a Role in 3â€², 5â€²-Cyclic Guanosine Monophosphate Metabolism in Plants. <i>Frontiers in Plant Science</i> , 2016, 7, 576.	1.7	48
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10223	Conservation and Expression Patterns Divergence of Ascorbic Acid d-mannose/l-galactose Pathway Genes in <i>Brassica rapa</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 778.	1.7	14
10224	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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10226	Assessment of Potential Risks of Dietary RNAi to a Soil Micro-arthropod, <i>Sinella curviseta</i> Brook (Collembola: Entomobryidae). <i>Frontiers in Plant Science</i> , 2016, 7, 1028.	1.7	37
10227	Molecular Evolution and Association of Natural Variation in <i>ZmARF31</i> with Low Phosphorus Tolerance in Maize. <i>Frontiers in Plant Science</i> , 2016, 7, 1076.	1.7	12
10228	Molecular Characterization of the 14-3-3 Gene Family in <i>Brachypodium distachyon</i> L. Reveals High Evolutionary Conservation and Diverse Responses to Abiotic Stresses. <i>Frontiers in Plant Science</i> , 2016, 7, 1099.	1.7	43
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10230	De novo Assembly of Leaf Transcriptome in the Medicinal Plant <i>Andrographis paniculata</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 1203.	1.7	40
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10232	Insights into the Genetic Relationships and Breeding Patterns of the African Tea Germplasm Based on nSSR Markers and cpDNA Sequences. <i>Frontiers in Plant Science</i> , 2016, 7, 1244.	1.7	39
10233	The Maize Divergent spindle-1 ( <i>dv1</i> ) Gene Encodes a Kinesin-14A Motor Protein Required for Meiotic Spindle Pole Organization. <i>Frontiers in Plant Science</i> , 2016, 7, 1277.	1.7	26
10234	Genomic Dissection and Expression Profiling Revealed Functional Divergence in <i>Triticum aestivum</i> Leucine Rich Repeat Receptor Like Kinases (TaLRRKs). <i>Frontiers in Plant Science</i> , 2016, 7, 1374.	1.7	68
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10236	Genome-Wide Identification and Evolution Analysis of Trehalose-6-Phosphate Synthase Gene Family in <i>Nelumbo nucifera</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 1445.	1.7	20
10237	Comparative Analysis of DNA Methyltransferase Gene Family in Fungi: A Focus on Basidiomycota. <i>Frontiers in Plant Science</i> , 2016, 7, 1556.	1.7	12
10238	Genome-Wide Identification of Dicer-Like, Argonaute, and RNA-Dependent RNA Polymerase Gene Families in <i>Brassica</i> Species and Functional Analyses of Their <i>Arabidopsis</i> Homologs in Resistance to <i>Sclerotinia sclerotiorum</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 1614.	1.7	56
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10241	Ca <sup>2+</sup> /Cation Antiporters (CaCA): Identification, Characterization and Expression Profiling in Bread Wheat ( <i>Triticum aestivum</i> L.). <i>Frontiers in Plant Science</i> , 2016, 7, 1775.	1.7	43
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10247	Splice Sites Seldom Slide: Intron Evolution in Oomycetes. <i>Genome Biology and Evolution</i> , 2016, 8, 2340-2350.	1.1	14
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10252	Isolation and characterization of <i>Dehalobacter</i> sp. strain UNSWDHB capable of chloroform and chlorinated ethane respiration. <i>Environmental Microbiology</i> , 2016, 18, 3092-3105.	1.8	48
10253	A multiproxy approach to evaluate biocidal treatments on biodeteriorated majolica glazed tiles. <i>Environmental Microbiology</i> , 2016, 18, 4794-4816.	1.8	33
10254	Genomic characterization of symbiotic mycoplasmas from the stomach of deep-sea isopod <i>bathynomus</i> sp. <i>Environmental Microbiology</i> , 2016, 18, 2646-2659.	1.8	49
10255	Population genomics of the symbiotic plasmids of sympatric nitrogen-fixing <i>Rhizobium</i> species associated with <i>Phaseolus vulgaris</i> . <i>Environmental Microbiology</i> , 2016, 18, 2660-2676.	1.8	72
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10260	Target genes of Dpp/BMP signaling pathway revealed by transcriptome profiling in the early <i>D. melanogaster</i> embryo. <i>Gene</i> , 2016, 591, 191-200.	1.0	6
10261	Complete genome sequence of bacteriophage P2559Y, a marine phage that infects <i>Croceibacter atlanticus</i> HTCC2559. <i>Marine Genomics</i> , 2016, 29, 35-38.	0.4	20
10262	Phylogenetic conservatism and climate factors shape flowering phenology in alpine meadows. <i>Oecologia</i> , 2016, 182, 419-428.	0.9	20
10263	Description and Phylogeny of <i>Urostyla grandis wiackowskii</i> subsp. nov. (Ciliophora). <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 T</i> 247-261.	0.8	18
10264	Environmental switching during biofilm development in a cold seep system and functional determinants of species sorting. <i>Molecular Ecology</i> , 2016, 25, 1958-1971.	2.0	5
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10266	Biosystematic studies on the genus <i>Heloniopsis</i> (Melanthiaceae) I. Phylogeny inferred from plastid DNA sequences and taxonomic implications. <i>Nordic Journal of Botany</i> , 2016, 34, 584-595.	0.2	2
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10269	Tan spot of pyrethrum is caused by a <i>Didymella</i> species complex. <i>Plant Pathology</i> , 2016, 65, 1170-1184.	1.2	18
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10271	Biosynthesis of the leucine derived $\hat{1}$ , $\hat{2}$ and $\hat{3}$ hydroxynitrile glucosides in barley ( <i>Hordeum vulgare</i> ). <i>Tj ETQq1 1 0.784314</i>	2.8	35
10272	When troglomorphism dupes taxonomists: morphology and molecules reveal the first pyramidopid harvestman (Arachnida, Opiliones, Pyramidopidae) from the New World. <i>Zoological Journal of the Linnean Society</i> , 2016, 177, 602-620.	1.0	24
10273	The genus <i>Cyclops</i> (Copepoda, Cyclopoida) in Europe. <i>Zoologica Scripta</i> , 2016, 45, 671-682.	0.7	14
10274	Growth of high-elevation <i>Cryptococcus</i> sp. during extreme freeze-thaw cycles. <i>Extremophiles</i> , 2016, 20, 579-588.	0.9	17
10275	Ectopic Expression of <i>BnaC.CP20.1</i> Results in Premature Tapetal Programmed Cell Death in <i>Arabidopsis</i> . <i>Plant and Cell Physiology</i> , 2016, 57, 1972-1984.	1.5	22

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10278	Becoming pure: identifying generational classes of admixed individuals within lesser and greater scaup populations. <i>Molecular Ecology</i> , 2016, 25, 661-674.	2.0	37
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10282	Hybrid Structure of a Dynamic Single-Chain Carboxylase from <i>Deinococcus radiodurans</i> . <i>Structure</i> , 2016, 24, 1227-1236.	1.6	3
10283	Speciation dynamics and biogeography of Neotropical spiral gingers (Costaceae). <i>Molecular Phylogenetics and Evolution</i> , 2016, 103, 55-63.	1.2	19
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10285	Genetic dissection of chlorate respiration in <i>Pseudomonas stutzeri</i> reveals syntrophic (per)chlorate reduction. <i>Environmental Microbiology</i> , 2016, 18, 3342-3354.	1.8	31
10286	Functional interactions of archaea, bacteria and viruses in a hypersaline endolithic community. <i>Environmental Microbiology</i> , 2016, 18, 2064-2077.	1.8	107
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10289	Morphology, Ontogeny, and Molecular Phylogeny of Two Freshwater Species of <i>Deviata</i> (Ciliophora, Hypotrichia) from Southern China. <i>Journal of Eukaryotic Microbiology</i> , 2016, 63, 771-785.	0.8	16
10290	Evolution and protein interactions of AP2 proteins in Brassicaceae: Evidence linking development and environmental responses. <i>Journal of Integrative Plant Biology</i> , 2016, 58, 549-563.	4.1	16
10291	Host resistances to <i>Aphanomyces trifolii</i> root rot of subterranean clover: first opportunity to successfully manage this severe pasture disease. <i>Plant Pathology</i> , 2016, 65, 901-913.	1.2	11
10292	Evolutionary history of a secondary terrestrial Australian diving beetle (Coleoptera, Dytiscidae) reveals a lineage of high morphological and ecological plasticity. <i>Systematic Entomology</i> , 2016, 41, 650-657.	1.7	15
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10295	Naturally Occurring Isoleucyl-tRNA Synthetase without tRNA-dependent Pre-transfer Editing. Journal of Biological Chemistry, 2016, 291, 8618-8631.	1.6	14
10296	A taxonomic and phylogenetic study of the <i>Golovinomyces biocellatus</i> complex (Erysiphales). Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 667 1.	0.5	30
10297	Genetic population structure and relatedness in the narrow-striped mongoose ( <i>Mungotictis</i> ). Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 667 3734-3749.	0.8	5
10298	HistoneDB 2.0: a histone database with variants—an integrated resource to explore histones and their variants. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw014.	1.4	99
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10302	Reduction of Tubulin Expression in <i>Angomonas deanei</i> by RNAi Modifies the Ultrastructure of the Trypanosomatid Protozoan and Impairs Division of Its Endosymbiotic Bacterium. Journal of Eukaryotic Microbiology, 2016, 63, 794-803.	0.8	6
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10305	A barley <i>SKP1</i> -like protein controls abundance of the susceptibility factor <i>RACB</i> and influences the interaction of barley with the barley powdery mildew fungus. Molecular Plant Pathology, 2016, 17, 184-195.	2.0	20
10306	Genetic variation and evolutionary forces shaping <i>Cucumber vein yellowing virus</i> populations: risk of emergence of virulent isolates in Europe. Plant Pathology, 2016, 65, 847-856.	1.2	10
10307	The genome of black raspberry ( <i>Rubus occidentalis</i> ). Plant Journal, 2016, 87, 535-547.	2.8	111
10308	An unprecedented new genus and family of Tetractinellida (Porifera, Demospongiae) from New Zealand's Colville Ridge, with a new type of mitochondrial group I intron. Zoological Journal of the Linnean Society, 2016, 177, 335-352.	1.0	15
10309	New considerations on the phylogeny of cyrtophorian ciliates (Protozoa, Ciliophora): expanded sampling to understand their evolutionary relationships. Zoologica Scripta, 2016, 45, 334-348.	0.7	25
10310	Potential Mechanisms for Microbial Energy Acquisition in Oxic Deep-Sea Sediments. Applied and Environmental Microbiology, 2016, 82, 4232-4243.	1.4	51
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10313	A Latitudinal Diversity Gradient in Terrestrial Bacteria of the Genus <i>Streptomyces</i> . <i>MBio</i> , 2016, 7, e02200-15.	1.8	98
10314	Novel Highly Pathogenic Avian A(H5N2) and A(H5N8) Influenza Viruses of Clade 2.3.4.4 from North America Have Limited Capacity for Replication and Transmission in Mammals. <i>MSphere</i> , 2016, 1, .	1.3	56
10315	Mutations in Encephalomyocarditis Virus 3A Protein Uncouple the Dependency of Genome Replication on Host Factors Phosphatidylinositol 4-Kinase III $\beta$ and Oxysterol-Binding Protein. <i>MSphere</i> , 2016, 1, .	1.3	18
10316	Functional diversification of sea urchin ABCC1 (MRP1) by alternative splicing. <i>American Journal of Physiology - Cell Physiology</i> , 2016, 310, C911-C920.	2.1	7
10317	Complete sequence of a double-stranded RNA from the phytopathogenic fungus <i>Erysiphe cichoracearum</i> that might represent a novel endornavirus. <i>Archives of Virology</i> , 2016, 161, 2343-2346.	0.9	9
10318	Pathogenicity and genetic characterization of a duck Tembusu virus associated with egg-dropping in Muscovy ducks. <i>Virus Research</i> , 2016, 223, 52-56.	1.1	16
10319	Differential Expression of Genes Involved in Host Recognition, Attachment, and Degradation in the Mycoparasite <i>Tolypocladium ophioglossoides</i> . <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 731-741.	0.8	21
10320	Four New Species in <i>Habenaria</i> (Orchidaceae) from the Espinha�so Range, Brazil. <i>Systematic Botany</i> , 2016, 41, 275-292.	0.2	7
10321	<i>Zornia melanocarpa</i> (Leguminosae, Papilionoideae, Dalbergieae), a New Species from Serra do Espinha�so, Brazil, and its Phylogenetic Position in the Genus. <i>Systematic Botany</i> , 2016, 41, 298-306.	0.2	3
10322	Evolutionary patterns and physicochemical properties explain macroinvertebrate sensitivity to heavy metals. <i>Ecological Applications</i> , 2016, 26, 1249-1259.	1.8	23
10323	Functional metagenomic selection of ribulose 1, 5-bisphosphate carboxylase/oxygenase from uncultivated bacteria. <i>Environmental Microbiology</i> , 2016, 18, 1187-1199.	1.8	26
10324	Genomic evidence for distinct carbon substrate preferences and ecological niches of <i>Bathyarchaeota</i> in estuarine sediments. <i>Environmental Microbiology</i> , 2016, 18, 1200-1211.	1.8	195
10325	Single TRAM domain RNA-binding proteins in <i>Archaea</i> : functional insight from Ctr3 from the Antarctic methanogen <i>Methanococcus burtonii</i> . <i>Environmental Microbiology</i> , 2016, 18, 2810-2824.	1.8	21
10326	Targeted gene enrichment and high-throughput sequencing for environmental biomonitoring: a case study using freshwater macroinvertebrates. <i>Molecular Ecology Resources</i> , 2016, 16, 1240-1254.	2.2	92
10327	Mitochondrial DNA variation of domestic sheep ( <i>Ovis aries</i> ) in Kenya. <i>Animal Genetics</i> , 2016, 47, 377-381.	0.6	19
10328	Phylogenetics and evolution of the <i>Tillandsia utriculata</i> complex (Bromeliaceae, Tillandsioideae) inferred from three plastid DNA markers and the ETS of the nuclear ribosomal DNA. <i>Botanical Journal of the Linnean Society</i> , 2016, 181, 362-390.	0.8	29
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10331	Phylogenetic signal in diatom ecology: perspectives for aquatic ecosystems biomonitoring. <i>Ecological Applications</i> , 2016, 26, 861-872.	1.8	37
10332	Maltase protein of <i>Ogataea (Hansenula) polymorpha</i> is a counterpart to the resurrected ancestor protein ancMALS of yeast maltases and isomaltases. <i>Yeast</i> , 2016, 33, 415-432.	0.8	17
10333	cDNA sequences of two arylphorin subunits of an insect biliprotein: phylogenetic differences and gene duplications during evolution of hexamerins-implications for hexamer formation. , 2016, 326, 136-148.		3
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10335	Preventing species invasion: A role for integrative taxonomy?. <i>Integrative Zoology</i> , 2016, 11, 214-228.	1.3	27
10336	Molecular phylogenetics of Australian weevils (Coleoptera: Tj ETQq0 0 0 rgBT /Overlock independent analyses. <i>Austral Entomology</i> , 2016, 55, 217-233.	10 Tf 50 507 Td 0.8	38
10337	Narrow water barriers prevent multiple colonizations and limit gene flow among California Channel Island wild buckwheats ( <i>Eriogonum</i> : Polygonaceae). <i>Botanical Journal of the Linnean Society</i> , 2016, 181, 246-268.	0.8	7
10338	Emergence and accumulation of novel pathogens suppress an invasive species. <i>Ecology Letters</i> , 2016, 19, 469-477.	3.0	99
10339	Separate histories in both sides of the Mediterranean: phylogeny and niche evolution of ocellated lizards. <i>Journal of Biogeography</i> , 2016, 43, 1242-1253.	1.4	32
10340	Evolutionary History of the Enzymes Involved in the Calvin-Benson Cycle in Euglenids. <i>Journal of Eukaryotic Microbiology</i> , 2016, 63, 326-339.	0.8	16
10341	On the use of high-throughput sequencing for the study of cyanobacterial diversity in Antarctic aquatic mats. <i>Journal of Phycology</i> , 2016, 52, 356-368.	1.0	36
10342	Characterization of equine cytochrome P450: role of CYP3A in the metabolism of diazepam. <i>Journal of Veterinary Pharmacology and Therapeutics</i> , 2016, 39, 478-487.	0.6	7
10343	Speciation, phenotypic plasticity, or ontogeny, the case of the genus <i>Galkinius</i> (Pyrgomatidae, Cirripedia, Crustacea). <i>Zoological Journal of the Linnean Society</i> , 2016, 176, 305-322.	1.0	6
10344	DNA sequencing reveals unexpected Recent diversity and an ancient dichotomy in the American marsupial genus <i>Marmosops</i> (Didelphidae: Thylamyini). <i>Zoological Journal of the Linnean Society</i> , 2016, 176, 914-940.	1.0	41
10345	<i>Wolbachia</i> endosymbionts distort DNA barcoding in the parasitoid wasp genus <i>Diplazon</i> (Hymenoptera: Ichneumonidae). <i>Zoological Journal of the Linnean Society</i> , 2016, 177, 541-557.	1.0	47
10346	Reassessment of the evolutionary relationships within the dog-faced bats, genus <i>Cynomops</i> (Chiroptera: Molossidae). <i>Zoologica Scripta</i> , 2016, 45, 465-480.	0.7	21
10347	Characterization of a Strain of <i>Fukuyoa paulensis</i> (Dinophyceae) from the Western Mediterranean Sea. <i>Journal of Eukaryotic Microbiology</i> , 2016, 63, 481-497.	0.8	58

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10349	Capturing the diversity of the human gut microbiota through culture-enriched molecular profiling. <i>Genome Medicine</i> , 2016, 8, 72.	3.6	150
10350	Discovery of an expanded set of avian leukosis subgroup E proviruses in chickens using Vermillion, a novel sequence capture and analysis pipeline. <i>Poultry Science</i> , 2016, 95, 2250-2258.	1.5	11
10351	Recapitulating Cross-Species Transmission of Simian Immunodeficiency Virus SIVcpz to Humans by Using Humanized BLT Mice. <i>Journal of Virology</i> , 2016, 90, 7728-7739.	1.5	31
10352	Phylogenetic Relationships in <i>Calyptanthus</i> (Myrtaceae) with Particular Emphasis on its Monophyly Relative to <i>Myrcia</i> s. l.. <i>Systematic Botany</i> , 2016, 41, 378-386.	0.2	22
10353	A New Southern Caribbean Species of Angel Shark (Chondrichthyes, Squaliformes, Squatinidae), Including Phylogeny and Tempo of Diversification of American Species. <i>Copeia</i> , 2016, 104, 577-585.	1.4	12
10354	The Mitochondrial Genome of the Potato Psyllid, <i>Bactericera cockerelli</i> Sulc., and Differences Among Potato Psyllid Populations of the United States. <i>Southwestern Entomologist</i> , 2016, 41, 347-360.	0.1	4
10355	Structural Change in Microbiota by a Probiotic Cocktail Enhances the Gut Barrier and Reduces Cancer via TLR2 Signaling in a Rat Model of Colon Cancer. <i>Digestive Diseases and Sciences</i> , 2016, 61, 2908-2920.	1.1	121
10356	Salinity stress increases lipid, secondary metabolites and enzyme activity in <i>Amphora subtropica</i> and <i>Dunaliella</i> sp. for biodiesel production. <i>Bioresource Technology</i> , 2016, 218, 816-825.	4.8	97
10357	A reexamination of <i>Allopsalliota</i> indicates synonymy with <i>Micropsalliota</i> (Agariceae, Agaricaceae.) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 102	0.3	5
10358	CLAUSA is a MYB Transcription Factor that Promotes Leaf Differentiation by Attenuating Cytokinin Signaling. <i>Plant Cell</i> , 2016, 28, tpc.00211.2016.	3.1	40
10359	<i>Trichinella spiralis</i> : Adaptation and parasitism. <i>Veterinary Parasitology</i> , 2016, 231, 8-21.	0.7	14
10360	Genome-Wide Identification of Regulatory Sequences Undergoing Accelerated Evolution in the Human Genome. <i>Molecular Biology and Evolution</i> , 2016, 33, 2565-2575.	3.5	64
10361	A revisited phylogeography of <i>Nautilus pompilius</i> . <i>Ecology and Evolution</i> , 2016, 6, 4924-4935.	0.8	18
10362	The distribution, diversity and function of predominant Thermoproteales in high-temperature environments of Yellowstone National Park. <i>Environmental Microbiology</i> , 2016, 18, 4755-4769.	1.8	24
10363	Phylogenetics of <i>Iriarteeae</i> (Arecaceae), cross-Andean disjunctions and convergence of clustered infructescence morphology in <i>Wettinia</i> . <i>Botanical Journal of the Linnean Society</i> , 2016, 182, 272-286.	0.8	18
10364	Recent assembly of the global herbaceous flora: evidence from the paper daisies (Asteraceae:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 102	3.5	97
10365	Characteristics of the draft genome of <i>Candidatus</i> <i>Arsenophonus nilaparvatae</i> , a facultative endosymbiont of <i>Nilaparvata lugens</i> . <i>Insect Science</i> , 2016, 23, 478-486.	1.5	25

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10367	The complete mitochondrial genome of <i>Choristoneura longicellana</i> (Lepidoptera: Tortricidae) and phylogenetic analysis of Lepidoptera. <i>Gene</i> , 2016, 591, 161-176.	1.0	40
10368	De novo discovery of neuropeptides in the genomes of parasitic flatworms using a novel comparative approach. <i>International Journal for Parasitology</i> , 2016, 46, 709-721.	1.3	45
10369	Structure, Diversity, and Evolution of a New Family of Soluble Carotenoid-Binding Proteins in Cyanobacteria. <i>Molecular Plant</i> , 2016, 9, 1379-1394.	3.9	83
10370	Increasing genetic diversity of Zika virus in the Latin American outbreak. <i>Emerging Microbes and Infections</i> , 2016, 5, 1-3.	3.0	28
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10372	Inflated organelle genomes and a circular-mapping mtDNA probably existed at the origin of coloniality in volvocine green algae. <i>European Journal of Phycology</i> , 2016, 51, 369-377.	0.9	20
10373	Prevalence of Transmitted HIV Drug Resistance Among Recently Infected Persons in San Diego, CA 1996-2013. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2016, 71, 228-236.	0.9	47
10374	A homolog of Blade-On-Petiole 1 and 2 (BOP1/2) controls internode length and homeotic changes of the barley inflorescence. <i>Plant Physiology</i> , 2016, 171, pp.00124.2016.	2.3	41
10375	ECDYSTEROID AND CHITINASE FLUCTUATIONS IN THE WESTERN TARNISHED PLANT BUG ( <i>Lygus</i> Tj ETQq1 1 0.784314 rgBT /Overlo Physiology, 2016, 92, 108-126.	0.6	3
10376	Expanding the modular ester fermentative pathways for combinatorial biosynthesis of esters from volatile organic acids. <i>Biotechnology and Bioengineering</i> , 2016, 113, 1764-1776.	1.7	51
10377	Additions to <i>Sporormiaceae</i> : Introducing Two Novel Genera, <i>Sparticola</i> and <i>Forliomyces</i> , from <i>Spartium</i> . <i>Cryptogamie, Mycologie</i> , 2016, 37, 75-97.	0.2	22
10378	<i>Saccharomyces eubayanus</i> and <i>Saccharomyces arboricola</i> reside in North Island native New Zealand forests. <i>Environmental Microbiology</i> , 2016, 18, 1137-1147.	1.8	64
10379	Cultivating microbial dark matter in benzene-degrading methanogenic consortia. <i>Environmental Microbiology</i> , 2016, 18, 2923-2936.	1.8	54
10380	Genomic resources for identification of the minimal $N_2$ -fixing symbiotic genome. <i>Environmental Microbiology</i> , 2016, 18, 2534-2547.	1.8	36
10381	De novo assembly and characterization of leaf and floral transcriptomes of the hybridizing bromeliad species ( <i>Pitcairnia</i> spp.) adapted to Neotropical Inselbergs. <i>Molecular Ecology Resources</i> , 2016, 16, 1012-1022.	2.2	37
10382	GLPS: a toolkit for fast and accurate analyses of genotyping-by-sequencing data without a reference genome. <i>Molecular Ecology Resources</i> , 2016, 16, 979-990.	2.2	20
10383	Phylogenetic inference and peristome evolution in haplolepidous mosses, focusing on Pseudoditrichaceae and Ditrichaceae s. l. <i>Botanical Journal of the Linnean Society</i> , 2016, 181, 139-155.	0.8	46

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10385	Sperm competition and the coevolution of pre- and postcopulatory traits: Weapons evolve faster than testes among onthophagine dung beetles. <i>Evolution; International Journal of Organic Evolution</i> , 2016, 70, 998-1008.	1.1	17
10386	Dispensability of the [4Fe-4S] cluster in novel homologues of adenine glycosylase MutY. <i>FEBS Journal</i> , 2016, 283, 521-540.	2.2	18
10387	Exploring complex pheromone biosynthetic processes in the bumblebee male labial gland by RNA sequencing. <i>Insect Molecular Biology</i> , 2016, 25, 295-314.	1.0	12
10388	Evidence for horizontal transfer of a recently active <i>Academ</i> transposon. <i>Insect Molecular Biology</i> , 2016, 25, 338-346.	1.0	7
10389	RNA interference-mediated knockdown of the Halloween gene <i>Spookiest</i> (CYP307B1) impedes adult eclosion in the western tarnished plant bug, <i>Lygus hesperus</i> . <i>Insect Molecular Biology</i> , 2016, 25, 550-565.	1.0	13
10390	Spatiotemporal diversification of a low-vagility Neotropical vertebrate clade (short-tailed opossums, <i>Tj ETQq0 0 0 rgBT /Overlock 10</i>	1.4	36
10391	Biogeographical history and coalescent species delimitation of Pacific island skinks (Squamata: <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10</i>	1.4	16
10392	<i>Tetrahymena australis</i> (Protozoa, Ciliophora): A Well-Known But “Non-Existing” Taxon – Consideration of Its Identification, Definition and Systematic Position. <i>Journal of Eukaryotic Microbiology</i> , 2016, 63, 760-770.	0.8	17
10393	Combining geometric morphometrics with molecular genetics to investigate a putative hybrid complex: a case study with barbels <i>Barbus</i> spp. (Teleostei: Cyprinidae). <i>Journal of Fish Biology</i> , 2016, 88, 1038-1055.	0.7	21
10394	Cichlids of the Banc d'Arguin National Park, Mauritania: insight into the diversity of the genus <i>Coptodon</i> . <i>Journal of Fish Biology</i> , 2016, 88, 1369-1393.	0.7	9
10395	Comparison of <i>Edwardsiella ictaluri</i> isolates from different hosts and geographic origins. <i>Journal of Fish Diseases</i> , 2016, 39, 947-969.	0.9	41
10396	Using nuclear genes to reconstruct angiosperm phylogeny at the species level: A case study with Brassicaceae species. <i>Journal of Systematics and Evolution</i> , 2016, 54, 438-452.	1.6	13
10397	Evolution of the leucine-rich repeat receptor-like protein kinase gene family: Ancestral copy number and functional divergence of <i>BAM1</i> and <i>BAM2</i> in Brassicaceae. <i>Journal of Systematics and Evolution</i> , 2016, 54, 204-218.	1.6	7
10398	Phylogenomics at the tips: inferring lineages and their demographic history in a tropical lizard, <i>Carlia amax</i> . <i>Molecular Ecology</i> , 2016, 25, 1367-1380.	2.0	46
10399	Characterization of pollen and bacterial community composition in brood provisions of a small carpenter bee. <i>Molecular Ecology</i> , 2016, 25, 2302-2311.	2.0	97
10400	Comparative and Transcriptome Analyses Uncover Key Aspects of Coding- and Long Noncoding RNAs in Flatworm Mitochondrial Genomes. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 1191-1200.	0.8	30
10401	<i>Petrocodon retroflexus</i> sp. nov. (Gesneriaceae) from a karst cave in Guizhou, China. <i>Nordic Journal of Botany</i> , 2016, 34, 159-164.	0.2	9



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10403	Overexpression of <i>SbMyb60</i> impacts phenylpropanoid biosynthesis and alters secondary cell wall composition in <i>Sorghum bicolor</i> . <i>Plant Journal</i> , 2016, 85, 378-395.	2.8	119
10404	Phylogenetic relationships of <i>Simpsonichthys</i> subgenera (Cyprinodontiformes, Rivulidae), including a proposal for a new genus. <i>Zoologica Scripta</i> , 2016, 45, 394-406.	0.7	4
10405	Stripes, jewels and spines: further investigations into the evolution of defensive strategies in a chemically defended gecko radiation ( <i>Strophurus</i> , Diplodactylidae). <i>Zoologica Scripta</i> , 2016, 45, 481-493.	0.7	13
10406	Trace Metal Acquisition by Marine Heterotrophic Bacterioplankton with Contrasting Trophic Strategies. <i>Applied and Environmental Microbiology</i> , 2016, 82, 1613-1624.	1.4	51
10407	DNA barcoding and surveillance sampling strategies for <i>Culicoides</i> biting midges (Diptera: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 36)	1.0	36
10408	Extensive horizontal gene transfers between plant pathogenic fungi. <i>BMC Biology</i> , 2016, 14, 41.	1.7	64
10409	Unique Loss of the PYHIN Gene Family in Bats Amongst Mammals: Implications for Inflammasome Sensing. <i>Scientific Reports</i> , 2016, 6, 21722.	1.6	113
10410	Reinstatement of <i>Varanus douarrha</i> Lesson, 1830 as a valid species with comments on the zoogeography of monitor lizards (Squamata : Varanidae) in the Bismarck Archipelago, Papua New Guinea. <i>Australian Journal of Zoology</i> , 2016, 64, 434.	0.6	5
10411	Divergence of RNA polymerase $\hat{\pm}$ subunits in angiosperm plastid genomes is mediated by genomic rearrangement. <i>Scientific Reports</i> , 2016, 6, 24595.	1.6	47
10412	The mitochondrial genome of <i>Murina huttoni rubella</i> (Chiroptera: Vespertilionidae) from China. <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 438-440.	0.2	4
10413	Primer design and in silico analysis using CLUSTALW and MUSCLE for L-arabinose isomerase ( <i>araA</i> ) gene detection in thermophilic bacteria. <i>AIP Conference Proceedings</i> , 2016, , .	0.3	5
10414	Endosperm Carotenoid Concentrations in Wheat are Better Correlated with PSY1 Transcript Levels than Enzyme Activities. <i>Crop Science</i> , 2016, 56, 3173-3184.	0.8	5
10415	Complete Genome Sequencing and Comparative Genomic Analysis of the Thermotolerant Acetic Acid Bacterium, <i>Acetobacter pasteurianus</i> SKU1108, Provide a New Insight into Thermotolerance. <i>Microbes and Environments</i> , 2016, 31, 395-400.	0.7	13
10416	Translational termination without a stop codon. <i>Science</i> , 2016, 354, 1437-1440.	6.0	72
10417	The Amaranth Genome: Genome, Transcriptome, and Physical Map Assembly. <i>Plant Genome</i> , 2016, 9, plantgenome2015.07.0062.	1.6	115
10418	The Rice Pentatricopeptide Repeat Gene TCD10 is Needed for Chloroplast Development under Cold Stress. <i>Rice</i> , 2016, 9, 67.	1.7	62
10419	Identification and characterization of histone lysine methylation modifiers in <i>Fragaria vesca</i> . <i>Scientific Reports</i> , 2016, 6, 23581.	1.6	28

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10421	<i>Deinococcus rubellus</i> sp. nov., bacteria isolated from the muscle of antarctic fish. <i>Journal of Microbiology</i> , 2016, 54, 796-801.	1.3	1
10422	<i>Bacillus piscis</i> sp. nov., a novel bacterium isolated from the muscle of the antarctic fish <i>Dissostichus mawsoni</i> . <i>Journal of Microbiology</i> , 2016, 54, 809-813.	1.3	4
10423	m6A modulates neuronal functions and sex determination in <i>Drosophila</i> . <i>Nature</i> , 2016, 540, 242-247.	13.7	453
10424	High-Throughput Sequencing Identifies Novel Viruses in Nectarine: Insights to the Etiology of Stem-Pitting Disease. <i>Phytopathology</i> , 2016, 106, 519-527.	1.1	71
10425	Genesis, Evolution and Prevalence of H5N6 Avian Influenza Viruses in China. <i>Cell Host and Microbe</i> , 2016, 20, 810-821.	5.1	257
10426	Improvement of mitochondrial DNA haplotyping in Japanese flounder populations using the sequences of control region and ND2 gene. <i>Nippon Suisan Gakkaishi</i> , 2016, 82, 712-719.	0.0	3
10427	Repression of RNA polymerase by the archaeo-viral regulator ORF145/RIP. <i>Nature Communications</i> , 2016, 7, 13595.	5.8	20
10428	Dynamic pre-BCR homodimers fine-tune autonomous survival signals in B cell precursor acute lymphoblastic leukemia. <i>Science Signaling</i> , 2016, 9, ra116.	1.6	15
10429	Heme pathway evolution in kinetoplastid protists. <i>BMC Evolutionary Biology</i> , 2016, 16, 109.	3.2	19
10430	Assessing genotype-phenotype associations in three dorsal colour morphs in the meadow spittlebug <i>Philaenus spumarius</i> (L.) (Hemiptera: Aphrophoridae) using genomic and transcriptomic resources. <i>BMC Genetics</i> , 2016, 17, 144.	2.7	14
10431	Analysis of Quasispecies of Avian Leukosis Virus Subgroup J Using Sanger and High-throughput Sequencing. <i>Virology Journal</i> , 2016, 13, 112.	1.4	4
10432	Comparative genomics provides new insights into the diversity, physiology, and sexuality of the only industrially exploited tremellomycete: <i>Phaffia rhodozyma</i> . <i>BMC Genomics</i> , 2016, 17, 901.	1.2	35
10433	<i>Salmonella</i> Degrades the Host Glycocalyx Leading to Altered Infection and Glycan Remodeling. <i>Scientific Reports</i> , 2016, 6, 29525.	1.6	66
10434	Discovery of a free-living nematode phylogenetically related to vertebrate parasites of the genus <i>Strongyloides</i> (Nematoda : Strongyloidoidea): morphological, anatomical and molecular characterisation. <i>Invertebrate Systematics</i> , 2016, 30, 387.	0.5	5
10435	Mass spectrometry analysis and transcriptome sequencing reveal glowing squid crystal proteins are in the same superfamily as firefly luciferase. <i>Scientific Reports</i> , 2016, 6, 27638.	1.6	18
10436	The Evolution of the FT/TFL1 Genes in Amaranthaceae and Their Expression Patterns in the Course of Vegetative Growth and Flowering in <i>Chenopodium rubrum</i> . <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 3065-3076.	0.8	15
10437	Efficient parallel UPGMA algorithm based on multiple GPUs. , 2016, , .		2

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10439	Prevalence and Molecular Characterization of Enterotoxin-Producing Strains of <i>Staphylococcus Aureus</i> Isolated from Serbian Dairy Cows. <i>Acta Veterinaria</i> , 2016, 66, 466-477.	0.2	5
10440	Identification of <i>Tobacco streak virus</i> in Cranberry and the Association of TSV with Berry Scarring. <i>Plant Disease</i> , 2016, 100, 696-703.	0.7	5
10441	Archaeal <i>Haloarcula californiae</i> Icosahedral Virus 1 Highlights Conserved Elements in Icosahedral Membrane-Containing DNA Viruses from Extreme Environments. <i>MBio</i> , 2016, 7, .	1.8	16
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10582	A molecular phylogeny and classification of the Cynodonteae (Poaceae: Chloridoideae) with four new genera: <i>Orthacanthus</i> , <i>Triplasiella</i> , <i>Tripogonella</i> , and <i>Zaqiqah</i> ; three new subtribes: <i>Dactylocteniinae</i> , <i>Orininae</i> , and <i>Zaqiqahinae</i> ; and a subgeneric classification of <i>Distichlis</i> . <i>Taxon</i> , 2016, 65, 1263-1287.	0.4	33

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10583	Gene Ages, Nomenclatures, and Functional Diversification of the Methuselah/Methuselah-Like GPCR Family in <i>Drosophila</i> and <i>Tribolium</i> . <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2016, 326, 453-463.	0.6	12
10584	Functional Analysis of the Chloroplast Division Complex Using <i>Schizosaccharomyces pombe</i> as a Heterologous Expression System. <i>Microscopy and Microanalysis</i> , 2016, 22, 275-289.	0.2	17
10585	Evolutionary and developmental analysis reveals KANK genes were co-opted for vertebrate vascular development. <i>Scientific Reports</i> , 2016, 6, 27816.	1.6	18
10586	Viral deep sequencing needs an adaptive approach: IRMA, the iterative refinement meta-assembler. <i>BMC Genomics</i> , 2016, 17, 708.	1.2	134
10587	A molecular phylogeny of the <i>Laelia</i> alliance (Orchidaceae) and a reassessment of <i>Laelia</i> and <i>Schomburgkia</i> . <i>Taxon</i> , 2016, 65, 1249-1262.	0.4	14
10588	Bacterial and protist community changes during a phytoplankton bloom. <i>Limnology and Oceanography</i> , 2016, 61, 198-213.	1.6	22
10589	Identification and characterization of toll-like receptors (TLRs) in the Chinese tree shrew ( <i>Tupaia</i> ) Tj ETQq0 0 0 rgBT/Overlock, 10 Tf 50 5	1.0	22
10590	Assessment of the contribution of cocoa-derived strains of <i>Acetobacter ghanensis</i> and <i>Acetobacter senegalensis</i> to the cocoa bean fermentation process through a genomic approach. <i>Food Microbiology</i> , 2016, 58, 68-78.	2.1	22
10591	Importance and controls of anaerobic ammonium oxidation influenced by riverbed geology. <i>Nature Geoscience</i> , 2016, 9, 357-360.	5.4	76
10592	Occurrence and molecular characterization of Tomato common mosaic virus (ToCmMV) in tomato fields in Espírito Santo state, Brazil. <i>Tropical Plant Pathology</i> , 2016, 41, 62-66.	0.8	24
10593	Gradual neofunctionalization in the convergent evolution of trichomonad lactate and malate dehydrogenases. <i>Protein Science</i> , 2016, 25, 1319-1331.	3.1	27
10594	Animal inference on human mitochondrial diseases. <i>Computational Biology and Chemistry</i> , 2016, 62, 17-28.	1.1	0
10595	The evolutionary history of the E2F and DEL genes in Viridiplantae. <i>Molecular Phylogenetics and Evolution</i> , 2016, 99, 225-234.	1.2	3
10596	Mitochondrial ROS regulate thermogenic energy expenditure and sulfenylation of UCP1. <i>Nature</i> , 2016, 532, 112-116.	13.7	341
10597	Tomato fruit carotenoid biosynthesis is adjusted to actual ripening progression by a light-dependent mechanism. <i>Plant Journal</i> , 2016, 85, 107-119.	2.8	149
10598	Phylogenetic analysis and tissue distribution of elasmobranch glucose transporters and their response to feeding. <i>Biology Open</i> , 2016, 5, 256-261.	0.6	10
10599	Structural and functional characterization of a small chitin-active lytic polysaccharide monooxygenase domain of a multi-modular chitinase from <i>Jonesia denitrificans</i> . <i>FEBS Letters</i> , 2016, 590, 34-42.	1.3	31
10600	Species differentiation in the genus <i>Chara</i> (Charophyceae): considerable phenotypic plasticity occurs within homogenous genetic groups. <i>European Journal of Phycology</i> , 2016, 51, 282-293.	0.9	32

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10601	Genome size and ploidy influence angiosperm species' biomass under nitrogen and phosphorus limitation. <i>New Phytologist</i> , 2016, 210, 1195-1206.	3.5	117
10602	Little Polymorphism at the K13 Propeller Locus in Worldwide <i>Plasmodium falciparum</i> Populations Prior to the Introduction of Artemisinin Combination Therapies. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 3340-3347.	1.4	18
10603	Both Epistasis and Diversifying Selection Drive the Structural Evolution of the Ebola Virus Glycoprotein Mucin-Like Domain. <i>Journal of Virology</i> , 2016, 90, 5475-5484.	1.5	18
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10605	Molecular phylogenetic analysis of <i>Rhizobium sulae</i> isolated from Algerian <i>Hedysarum flexuosum</i> . <i>Antonie Van Leeuwenhoek</i> , 2016, 109, 897-906.	0.7	6
10606	<i>Erysiphe aucubae</i> sp. nov., a new powdery mildew species on <i>Aucuba japonica</i> from Japan. <i>Mycoscience</i> , 2016, 57, 251-254.	0.3	4
10607	<i>Burkholderia novacaledonica</i> sp. nov. and <i>B. ultramafica</i> sp. nov. isolated from roots of <i>Costularia</i> spp. pioneer plants of ultramafic soils in New Caledonia. <i>Systematic and Applied Microbiology</i> , 2016, 39, 151-159.	1.2	24
10608	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
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10612	Multitasking of the piRNA Silencing Machinery: Targeting Transposable Elements and Foreign Genes in the Bdelloid Rotifer <i>Adineta vaga</i> . <i>Genetics</i> , 2016, 203, 255-268.	1.2	13
10613	Decoupled genomic elements and the evolution of partner quality in nitrogen-fixing rhizobia. <i>Ecology and Evolution</i> , 2016, 6, 1317-1327.	0.8	14
10614	Clade-specific positive selection on a developmental gene: BRANCHLESS TRICHOME and the evolution of stellate trichomes in <i>Physaria</i> (Brassicaceae). <i>Molecular Phylogenetics and Evolution</i> , 2016, 100, 31-40.	1.2	9
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10616	Predicting pathogenic single nucleotide variants through a comprehensive analysis on multiple level features. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2016, 156, 224-230.	1.8	0
10617	High-quality genome sequence and description of <i>Chryseobacterium senegalense</i> sp. nov.. <i>New Microbes and New Infections</i> , 2016, 10, 93-100.	0.8	4
10618	Isolation and molecular characterization of porcine epidemic diarrhea viruses collected in Japan in 2014. <i>Archives of Virology</i> , 2016, 161, 2189-2195.	0.9	15

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10620	The tertiary structures of porcine AhR and ARNT proteins and molecular interactions within the TCDD/AhR/ARNT complex. <i>Journal of Molecular Graphics and Modelling</i> , 2016, 67, 119-126.	1.3	1
10621	First record of <i>Atherigona reversura</i> Villeneuve (Diptera: Muscidae) feeding on Bermudagrass ( <i>Cynodon dactylon</i> ) in Brazil. <i>Revista Brasileira De Entomologia</i> , 2016, 60, 270-274.	0.1	5
10622	Structural Divergence of the Group I Intron Binding Surface in Fungal Mitochondrial Tyrosyl-tRNA Synthetases That Function in RNA Splicing. <i>Journal of Biological Chemistry</i> , 2016, 291, 11911-11927.	1.6	3
10623	Stage-specific Proteomes from <i>Onchocerca ochengi</i> , Sister Species of the Human River Blindness Parasite, Uncover Adaptations to a Nodular Lifestyle. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2554-2575.	2.5	23
10624	Advanced Genetic Methodologies in Tracking Evolution and Spread of Chikungunya Virus. <i>Methods in Molecular Biology</i> , 2016, 1426, 21-37.	0.4	0
10625	Evolution of reproductive traits in <i>Cataglyphis</i> desert ants: mating frequency, queen number, and thelytoky. <i>Behavioral Ecology and Sociobiology</i> , 2016, 70, 1367-1379.	0.6	27
10626	Data on the evolutionary history of the V(D)J recombination-activating protein 1 (RAG1) coupled with sequence and variant analyses. <i>Data in Brief</i> , 2016, 8, 87-92.	0.5	1
10627	A molecular phylogenetic study of pheretimoid species (Megascolecidae) in Mindanao and associated islands, Philippines. <i>European Journal of Soil Biology</i> , 2016, 73, 119-125.	1.4	11
10628	Molecular characterization of <i>Theileria orientalis</i> from cattle in Ethiopia. <i>Ticks and Tick-borne Diseases</i> , 2016, 7, 742-747.	1.1	28
10629	Testing for Independence between Evolutionary Processes. <i>Systematic Biology</i> , 2016, 65, 812-823.	2.7	13
10630	Australian spiny mountain crayfish and their temnocephalan ectosymbionts: an ancient association on the edge of coextinction?. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016, 283, 20160585.	1.2	13
10631	Biosynthesis of a broad-spectrum nicotianamine-like metallophore in <i>Staphylococcus aureus</i> . <i>Science</i> , 2016, 352, 1105-1109.	6.0	168
10632	Phylogenetic placement and generic re-circumscriptions of the multilocular genera <i>Arenifera</i> , <i>Octopoma</i> and <i>Schlechteranthus</i> (Aizoaceae: Ruschieae): Evidence from anatomical, morphological and plastid DNA data. <i>Taxon</i> , 2016, 65, 249-261.	0.4	9
10633	Phylogeographic and population genetic analyses reveal multiple species of <i>Boa</i> and independent origins of insular dwarfism. <i>Molecular Phylogenetics and Evolution</i> , 2016, 102, 104-116.	1.2	47
10634	Comparative Transcriptomic Approaches Exploring Contamination Stress Tolerance in <i>Salix</i> sp. Reveal the Importance for a Metaorganismal de Novo Assembly Approach for Nonmodel Plants. <i>Plant Physiology</i> , 2016, 171, 3-24.	2.3	20
10635	New species of xerocomoid boletes (Boletaceae) from Himalayan India based on morphological and molecular evidence. <i>Mycologia</i> , 2016, 108, 753-764.	0.8	11
10636	Exclusive expression of the Rab11 effector SH3TC2 in Schwann cells links integrin- $\beta$ 6 and myelin maintenance to Charcot-Marie-Tooth disease type 4C. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2016, 1862, 1279-1290.	1.8	16

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10638	Mole ghrelin: cDNA cloning, gene expression, and diverse molecular forms in <i>Mogera imaizumii</i> . <i>General and Comparative Endocrinology</i> , 2016, 232, 199-210.	0.8	2
10639	Staying well connected – Lithistid sponges on seamounts. <i>Journal of the Marine Biological Association of the United Kingdom</i> , 2016, 96, 437-451.	0.4	8
10640	MtDNA diversity of the Indonesian giant barrel sponge <i>Xestospongia testudinaria</i> (Porifera: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 Biological Association of the United Kingdom, 2016, 96, 323-332.	0.4	15
10641	Redescription and biology of <i>Diopatra neapolitana</i> (Annelida: Onuphidae), a protandric hermaphrodite with external spermaducal papillae. <i>Estuarine, Coastal and Shelf Science</i> , 2016, 174, 1-17.	0.9	16
10642	Islands in the desert: Species delimitation and evolutionary history of <i>Pseudotetracha</i> tiger beetles (Coleoptera: Cicindelidae: Megacephalini) from Australian salt lakes. <i>Molecular Phylogenetics and Evolution</i> , 2016, 101, 279-285.	1.2	18
10643	Depth-dependent and seasonal variability in archaeal community structure in the subarctic and subtropical western North Pacific. <i>Journal of Oceanography</i> , 2016, 72, 427-438.	0.7	8
10644	Forensic timber identification: a case study of a CITES listed species, <i>Gonystylus bancanus</i> (Thymelaeaceae). <i>Forensic Science International: Genetics</i> , 2016, 23, 197-209.	1.6	33
10645	Species limits, interspecific hybridization and phylogeny in the cryptic land snail complex <i>Pyramidula</i> : The power of RADseq data. <i>Molecular Phylogenetics and Evolution</i> , 2016, 101, 267-278.	1.2	53
10646	Signaling from maize organ primordia via FASCIATED EAR3 regulates stem cell proliferation and yield traits. <i>Nature Genetics</i> , 2016, 48, 785-791.	9.4	180
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10648	Culturing and Characterization of Gut Symbiont <i>Burkholderia</i> spp. from the Southern Chinch Bug, <i>Blissus insularis</i> (Hemiptera: Blissidae). <i>Applied and Environmental Microbiology</i> , 2016, 82, 3319-3330.	1.4	12
10649	Evolutionary modularity and morphological integration in the haptoral anchor structures of <i>Ligophorus</i> spp. (Monogenea: Dactylogyridae). <i>Parasitology Research</i> , 2016, 115, 3519-3533.	0.6	5
10650	Bioinformatics for the synthetic biology of natural products: integrating across the Design–Build–Test cycle. <i>Natural Product Reports</i> , 2016, 33, 925-932.	5.2	58
10651	Biological synthesis of fluorescent nanoparticles by cadmium and tellurite resistant Antarctic bacteria: exploring novel natural nanofactories. <i>Microbial Cell Factories</i> , 2016, 15, 76.	1.9	76
10652	Sequencing and characterization of leaf transcriptomes of six diploid <i>Nicotiana</i> species. <i>Journal of Biological Research</i> , 2016, 23, 6.	2.2	13
10653	Molecular Systematics of the Neotropical Diving Beetle Genus <i>Rugosus</i> Garcia, 2001 (Coleoptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 <i>Rugosus</i> spp. (Coleoptera: Dytiscidae). <i>Systematic Entomology and Biogeography</i> , 2016, 42, 1-15.	0.1	2
10654	Antibiotic and metal resistance of cultivable bacteria in the Antarctic sea urchin. <i>Antarctic Science</i> , 2016, 28, 261-268.	0.5	23

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10655	Three new species of <i>Atla</i> from calcareous rocks ( <i>Verrucariaceae</i> , lichenized) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 742 Td</i>	0.5	7
10656	The lysidyl aminoacyl transfer RNA synthetase intron, a new marker for demosponge phylogeographics – case study on <i>Neopetrosia</i> . <i>Journal of the Marine Biological Association of the United Kingdom</i> , 2016, 96, 333-339.	0.4	0
10657	Subaerial biofilms on granitic historic buildings: microbial diversity and development of phototrophic multi-species cultures. <i>Biofouling</i> , 2016, 32, 657-669.	0.8	49
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10659	Characterization of the Cadherin–Catenin Complex of the Sea Anemone <i>Nematostella vectensis</i> and Implications for the Evolution of Metazoan Cell–Cell Adhesion. <i>Molecular Biology and Evolution</i> , 2016, 33, 2016-2029.	3.5	22
10660	Nondegenerative Evolution in Ancient Heritable Bacterial Endosymbionts of Fungi. <i>Molecular Biology and Evolution</i> , 2016, 33, 2216-2231.	3.5	14
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10662	Protein architecture and core residues in unwound $\alpha$ -helices provide insights to the transport function of plant AtCHX17. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2016, 1858, 1983-1998.	1.4	16
10663	Uptake of radioiodide by <i>Paenibacillus</i> sp., <i>Pseudomonas</i> sp., <i>Burkholderia</i> sp. and <i>Rhodococcus</i> sp. isolated from a boreal nutrient-poor bog. <i>Journal of Environmental Sciences</i> , 2016, 44, 26-37.	3.2	13
10664	Genome of Plant Maca ( <i>Lepidium meyenii</i> ) Illuminates Genomic Basis for High-Altitude Adaptation in the Central Andes. <i>Molecular Plant</i> , 2016, 9, 1066-1077.	3.9	69
10665	<i>Cantharellus chicagoensis</i> sp. nov. is supported by molecular and morphological analysis as a new yellow chanterelle in midwestern United States. <i>Mycologia</i> , 2016, 108, 765-772.	0.8	25
10666	Genomic insights into the carbohydrate catabolism of <i>Cairneyella variabilis</i> gen. nov. sp. nov., the first reports from a genome of an ericoid mycorrhizal fungus from the southern hemisphere. <i>Mycorrhiza</i> , 2016, 26, 345-352.	1.3	18
10667	Diversity of group A rotavirus genes detected in the Triângulo Mineiro region, Minas Gerais, Brazil. <i>Brazilian Journal of Microbiology</i> , 2016, 47, 731-740.	0.8	8
10668	Spot the difference: Two cryptic species of <i>Gyrodactylus</i> von Nordmann, 1832 (Platyhelminthes) <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 742 Td</i>	0.6	19
10669	Two Bacterial Genera, <i>Sodalis</i> and <i>Rickettsia</i> , Associated with the Seal Louse <i>Proechinophthirus fluctus</i> (Phthiraptera: Anoplura). <i>Applied and Environmental Microbiology</i> , 2016, 82, 3185-3197.	1.4	63
10670	F <sub>420</sub> H <sub>2</sub> Is Required for Phthiocerol Dimycocerosate Synthesis in Mycobacteria. <i>Journal of Bacteriology</i> , 2016, 198, 2020-2028.	1.0	15
10671	Phylogenomic analysis identifies a sodium-translocating decarboxylating oxidoreductase in thermotogae. <i>Biochemistry (Moscow)</i> , 2016, 81, 481-490.	0.7	2
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10674	Phosphorylation of spore coat proteins by a family of atypical protein kinases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E3482-91.	3.3	56
10675	Environmental factors shaping cultured free-living amoebae and their associated bacterial community within drinking water network. <i>Water Research</i> , 2016, 100, 382-392.	5.3	60
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10677	A novel method for identifying polymorphic transposable elements via scanning of high-throughput short reads. <i>DNA Research</i> , 2016, 23, 241-251.	1.5	18
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10679	Temperature priming and memory in soil filamentous fungi. <i>Fungal Ecology</i> , 2016, 21, 10-15.	0.7	47
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10681	Term-seq reveals abundant ribo-regulation of antibiotics resistance in bacteria. <i>Science</i> , 2016, 352, aad9822.	6.0	294
10682	Sexual differences in prevalence of a new species of trypanosome infecting tÃngara frogs. <i>International Journal for Parasitology: Parasites and Wildlife</i> , 2016, 5, 40-47.	0.6	39
10683	Ribosomal DNA analysis of tsetse and non-tsetse transmitted Ethiopian <i>Trypanosoma vivax</i> strains in view of improved molecular diagnosis. <i>Veterinary Parasitology</i> , 2016, 220, 15-22.	0.7	10
10684	Asymmetric Functional Conversion of Eubacterial Light-driven Ion Pumps. <i>Journal of Biological Chemistry</i> , 2016, 291, 9883-9893.	1.6	48
10685	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
10686	Clades of Photosynthetic Bacteria Belonging to the Genus <i>Rhodospseudomonas</i> Show Marked Diversity in Light-Harvesting Antenna Complex Gene Composition and Expression. <i>MSystems</i> , 2016, 1, .	1.7	9
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10688	Automatic detection of rate change in large data sets with an unsupervised approach: the case of influenza viruses. <i>Genome</i> , 2016, 59, 253-262.	0.9	2
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10696	Phylogenomic analysis of <i>Candidatus</i> <i>Thiomargarita</i> species: free-living representatives from a <i>Tenericutes</i> clade found in methane seeps. ISME Journal, 2016, 10, 2679-2692.	4.4	88
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10698	No evidence for larger brains in cooperatively breeding cichlid fishes. Canadian Journal of Zoology, 2016, 94, 373-378.	0.4	14
10699	<strong>A new species of dwarf gecko in the genus <em>Lygodactylus</em> (squamata): Tj ETQq0.0.0 rgBT /Overlock 10	0.2	4
10700	Cenoses of phototrophic algae of ultrasaline lakes in the Kulunda steppe (Altai krai, Russian) Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.3	8
10701	Bivalve-specific gene expansion in the pearl oyster genome: implications of adaptation to a sessile lifestyle. Zoological Letters, 2016, 2, 3.	0.7	133
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10706	A new artificial bee colony algorithm to solve the multiple sequence alignment problem. International Journal of Data Mining and Bioinformatics, 2016, 14, 332.	0.1	24
10707	Annotated mitochondrial genome assemblies for two sand lances (genus: <i>Ammodytes</i> ) from the northwest Atlantic. Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2016, 27, 4607-4608.	0.7	2
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10854	Different roads lead to Rome: Integrative taxonomic approaches lead to the discovery of two new lizard lineages in the <i>Liolaemus montanus</i> group (Squamata: Liolaemidae). <i>Biological Journal of the Linnean Society</i> , 2016, , .	0.7	8
10855	Fatty acid production of tropical thraustochytrids from Malaysian mangroves. <i>Botanica Marina</i> , 2016, 59, 321-338.	0.6	17
10856	Characterization of new transposable element sub-families from white clover ( <i>Trifolium repens</i> ) using PCR amplification. <i>Genetica</i> , 2016, 144, 577-589.	0.5	1
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10985	Two novel <i>Fusarium</i> species that cause canker disease of prickly ash ( <i>Zanthoxylum</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 108, 668-681.	0.8	32
10986	Genomics and expression analysis of DHHC-cysteine-rich domain S-acyl transferase protein family in apple. <i>Genes and Genomics</i> , 2016, 38, 671-684.	0.5	0
10987	Novel miniature inverted-repeat transposable elements derived from novel CACTA transposons were discovered in the genome of the ant <i>Camponotus floridanus</i> . <i>Genes and Genomics</i> , 2016, 38, 1189-1199.	0.5	4
10988	Phylogeography and ecological niche modelling in <i>Eugenia uniflora</i> (Myrtaceae) suggest distinct vegetational responses to climate change between the southern and the northern Atlantic Forest. <i>Botanical Journal of the Linnean Society</i> , 2016, 182, 670-688.	0.8	41
10989	Species delimitation and phylogeography of the studfish <i>Fundulus catenatus</i> species group (Ovalentaria: Cyprinodontiformes). <i>Zoological Journal of the Linnean Society</i> , 2016, , .	1.0	1
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10991	Description of <i>Lelenchus brevislitus</i> n. sp. (Nematoda: Tylenchidae), an example of a cryptic species from Iran and its phylogenetic relationships with other species in the family. <i>Nematology</i> , 2016, 18, 987-998.	0.2	18
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10993	<i>Transversotrema</i> Witenberg, 1944 (Trematoda: Transversotrematidae) from inshore fishes of Australia: description of a new species and significant range extensions for three congeners. <i>Systematic Parasitology</i> , 2016, 93, 639-652.	0.5	29
10994	Population dynamics of <i>Anopheles nuneztovari</i> in Colombia. <i>Infection, Genetics and Evolution</i> , 2016, 45, 56-65.	1.0	15
10995	Molecular phylogeny of the Cladophoraceae (Cladophorales, Ulvophyceae), with the resurrection of <i>Acrocladus</i> Nägeli and <i>Willeella</i> BÄrgesen, and the description of <i>Lurbica</i> gen. nov. and <i>Pseudorhizoclonium</i> gen. nov.. <i>Journal of Phycology</i> , 2016, 52, 905-928.	1.0	36
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10997	Characterization of Lamprey BAFF-like Gene: Evolutionary Implications. <i>Journal of Immunology</i> , 2016, 197, 2695-2703.	0.4	33

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11011	Phylogeny and Evolution of Endemic Species on Ulleungdo Island, Korea: The Case of <i>Fagus multinervis</i> (Fagaceae). <i>Systematic Botany</i> , 2016, 41, 617-625.	0.2	10
11012	<i>Caligus rogercresseyi</i> serine proteases: Transcriptomic analysis in response to delousing drugs treatments. <i>Aquaculture</i> , 2016, 465, 65-77.	1.7	15
11013	Morphological and Phylogenetic Description of <i>Trypanosoma noyesi</i> sp. nov.: An Australian Wildlife Trypanosome within the <i>T. cruzi</i> Clade. <i>Protist</i> , 2016, 167, 425-439.	0.6	30
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11021	The Diversification of Plant NBS-LRR Defense Genes Directs the Evolution of MicroRNAs That Target Them. <i>Molecular Biology and Evolution</i> , 2016, 33, 2692-2705.	3.5	200
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11023	Assessment of phylogenetic signal in the germination ability of <i>Phelipanche ramosa</i> on Brassicaceae hosts. <i>Weed Research</i> , 2016, 56, 452-461.	0.8	10
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11025	Regulatory Divergence among Beta-Keratin Genes during Bird Evolution. <i>Molecular Biology and Evolution</i> , 2016, 33, 2769-2780.	3.5	11
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11037	Origin of year-long bean ( <i>Phaseolus dumosus</i> Macfady, Fabaceae) from reticulated hybridization events between multiple <i>Phaseolus</i> species. <i>Annals of Botany</i> , 2016, 118, 957-969.	1.4	23
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11040	Phylogeny, Identification, and Pathogenicity of <i>Lasiodiplodia</i> Associated with Postharvest Stem-End Rot of Coconut in Brazil. <i>Plant Disease</i> , 2016, 100, 561-568.	0.7	36
11041	Exploring glycoside hydrolases and accessory proteins from wood decay fungi to enhance sugarcane bagasse saccharification. <i>Biotechnology for Biofuels</i> , 2016, 9, 110.	6.2	47
11042	<i>Babesia</i> spp. in ticks and wildlife in different habitat types of Slovakia. <i>Parasites and Vectors</i> , 2016, 9, 292.	1.0	48
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11051	Ringhalexin from <i>Hemachatus haemachatus</i> : A novel inhibitor of extrinsic tenase complex. <i>Scientific Reports</i> , 2016, 6, 25935.	1.6	21

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11058	Reciprocal genomic evolution in the ant-fungus agricultural symbiosis. <i>Nature Communications</i> , 2016, 7, 12233.	5.8	106
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11061	One-Step Detection of <i>Monilinia fructicola</i> , <i>M. fructigena</i> , and <i>M. laxa</i> on <i>Prunus</i> and <i>Malus</i> by a Multiplex Real-Time PCR Assay. <i>Plant Disease</i> , 2016, 100, 2465-2474.	0.7	16
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11069	Genomic and phenotypic characterization of the species <i>Acinetobacter venetianus</i> . <i>Scientific Reports</i> , 2016, 6, 21985.	1.6	23

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11074	A natural light-driven inward proton pump. Nature Communications, 2016, 7, 13415.	5.8	124
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11076	The Evolutionary Fates of a Large Segmental Duplication in Mouse. Genetics, 2016, 204, 267-285.	1.2	21
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11092	Functional analysis of iodotyrosine deiodinase from <i>Drosophila melanogaster</i> . <i>Protein Science</i> , 2016, 25, 2187-2195.	3.1	14
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11102	Positive Selection Linked with Generation of Novel Mammalian Dentition Patterns. <i>Genome Biology and Evolution</i> , 2016, 8, 2748-2759.	1.1	9
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11107	A revised generic classification of vittarioid ferns (Pteridaceae) based on molecular, micromorphological, and geographic data. <i>Taxon</i> , 2016, 65, 708-722.	0.4	27
11108	Morphology, Biology, and Phylogenetic Position of the Bivalve <i>Platomysia rugata</i> (Heterodonta). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 66</i> 2016, 33, 441-447.	0.3	3
11109	Numerical encoding of DNA sequences by chaos game representation with application in similarity comparison. <i>Genomics</i> , 2016, 108, 134-142.	1.3	67
11110	Molecular Phylogeny, Revised Higher Classification, and Implications for Conservation of Endangered Hawaiian Leaf-Mining Moths (Lepidoptera: Gracillariidae: Philodoria)1. <i>Pacific Science</i> , 2016, 70, 361.	0.2	5
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11118	Phylogenomic analysis of type 1 NADH:Quinone oxidoreductase. <i>Biochemistry (Moscow)</i> , 2016, 81, 770-784.	0.7	15
11119	Reprint of "Novel mycoviruses discovered from metatranscriptomics survey of soybean phyllosphere phytobiomes". <i>Virus Research</i> , 2016, 219, 11-21.	1.1	13
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11171	The genomic content and context of auxiliary metabolic genes in marine cyanomyoviruses. <i>Virology</i> , 2016, 499, 219-229.	1.1	99
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11222	Exposing the illegal trade in cycad species ( <i>Cycadophyta</i> : <i>Encephalartos</i> ) at two traditional medicine markets in South Africa using DNA barcoding. <i>Genome</i> , 2016, 59, 771-781.	0.9	14
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11235	The Evolution of HD2 Proteins in Green Plants. <i>Trends in Plant Science</i> , 2016, 21, 1008-1016.	4.3	40
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11241	Developmental expression of <i>œgermline</i> and <i>œsex determination</i> -related genes in the ctenophore <i>Mnemiopsis leidyi</i> . <i>EvoDevo</i> , 2016, 7, 17.	1.3	24
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11274	Population Genetics of Overwintering Monarch Butterflies, <i>Danaus plexippus</i> (Linnaeus), from Central Mexico Inferred from Mitochondrial DNA and Microsatellite Markers. <i>Journal of Heredity</i> , 2017, 108, esw071.	1.0	24
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11325	Complete genome sequence of <i>Leuconostoc gelidum</i> subsp. <i>gasicomitatum</i> KG16-1, isolated from vacuum-packaged vegetable sausages. <i>Standards in Genomic Sciences</i> , 2016, 11, 40.	1.5	28
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11378	Evolution of Cadherins and Associated Catenins. , 2016, , 13-37.		6
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11381	Promoter methylation and mRNA expression of HLA-G in relation to HLA-G protein expression in colorectal cancer. <i>Human Immunology</i> , 2016, 77, 764-772.	1.2	9
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11393	Diel regulation of hydrogen peroxide defenses by open ocean microbial communities. <i>Journal of Plankton Research</i> , 2016, 38, 1103-1114.	0.8	35
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11395	Decoding the complete arsenal for cellulose and hemicellulose deconstruction in the highly efficient cellulose decomposer <i>Paenibacillus</i> O199. <i>Biotechnology for Biofuels</i> , 2016, 9, 104.	6.2	56
11396	Genomic Variation in the FT Gene Family of Perennial Ryegrass ( <i>Lolium perenne</i> ). , 2016, , 121-126.		2
11397	Higher Plant and Cyanobacterial Photosystem I: Connected Cytochrome Pathways. <i>Advances in Photosynthesis and Respiration</i> , 2016, , 131-142.	1.0	0
11398	The <i>Rickettsia</i> type IV secretion system: unrealized complexity mired by gene family expansion. <i>Pathogens and Disease</i> , 2016, 74, ftw058.	0.8	45
11399	Biogeographical Patterns of Legume-Nodulating Burkholderia spp.: from African Fynbos to Continental Scales. <i>Applied and Environmental Microbiology</i> , 2016, 82, 5099-5115.	1.4	71
11400	Molecular evidence supports ancient long-distance dispersal for the amphiatlantic disjunction in the giant yellow shrimp plant ( <i>Barleria oenotheroides</i> ). <i>American Journal of Botany</i> , 2016, 103, 1103-1116.	0.8	12
11401	Most Compositae (Asteraceae) are descendants of a paleohexaploid and all share a paleotetraploid ancestor with the Calyceraceae. <i>American Journal of Botany</i> , 2016, 103, 1203-1211.	0.8	98
11402	Evolution of Sulfur Binding by Hemoglobin in Siboglinidae (Annelida) with Special Reference to Bone-Eating Worms, <i>Osedax</i> . <i>Journal of Molecular Evolution</i> , 2016, 82, 219-229.	0.8	5
11403	Symbiont abundance is more important than pre-infection partner choice in a <i>Rhizobium</i> legume mutualism. <i>Systematic and Applied Microbiology</i> , 2016, 39, 345-349.	1.2	11
11404	Evolution of domain peptide interactions to coadapt specificity and affinity to functional diversity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E3862-71.	3.3	36
11405	A molecular palaeobiological exploration of arthropod terrestrialization. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2016, 371, 20150133.	1.8	131
11406	Comparative analysis of prokaryotic diversity in solar salterns in eastern Anatolia (Turkey). <i>Extremophiles</i> , 2016, 20, 589-601.	0.9	51
11407	Distinct Viral Lineages from Fish and Amphibians Reveal the Complex Evolutionary History of Hepadnaviruses. <i>Journal of Virology</i> , 2016, 90, 7920-7933.	1.5	71
11408	Recombinant outer membrane protein C of <i>Aeromonas hydrophila</i> elicits mixed immune response and generates agglutinating antibodies. <i>Immunologic Research</i> , 2016, 64, 1087-1099.	1.3	38
11409	New Insights into the Systematics of the Genus <i>Polyura</i> Billberg, 1820 (Nymphalidae, Charaxinae) with an Emphasis on the <i>P. athamas</i> Group. <i>Journal of the Lepidopterists' Society</i> , 2016, 70, 145-152.	0.0	1
11410	Larval Polychromatism in the Neotropical Hairstreak <i>Strymon bubastus</i> (Stoll) (Lycaenidae, Theclinae.) <i>Tj ETQq1 1 0.784314 rgBT /Overl</i> <i>Lepidopterists' Society</i> , 2016, 70, 153-157.	0.0	5
11411	Population genomics studies identify signatures of global dispersal and drug resistance in <i>Plasmodium vivax</i> . <i>Nature Genetics</i> , 2016, 48, 953-958.	9.4	194
11412	Integrative structural analysis of the UTPB complex, an early assembly factor for eukaryotic small ribosomal subunits. <i>Nucleic Acids Research</i> , 2016, 44, gkw562.	6.5	11



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11413	Water Treaders of Romania and Adjacent Countries and Their Phylogenetic Relationships (Hemiptera: Tj ETQq0 0 0 rgBT /Overlock 10 T	0.4	7
11414	A MLST Clade 2 <i>Clostridium difficile</i> strain with a variant TcdB induces severe inflammatory and oxidative response associated with mucosal disruption. <i>Anaerobe</i> , 2016, 40, 76-84.	1.0	16
11415	Prebiotics and Bioactive Milk Fractions Affect Gut Development, Microbiota, and Neurotransmitter Expression in Piglets. <i>Journal of Pediatric Gastroenterology and Nutrition</i> , 2016, 63, 688-697.	0.9	60
11416	Modulation of the Lytic Activity of the Dedicated Autolysin for Flagellum Formation SlfF by Flagellar Rod Proteins FlgB and FlgF. <i>Journal of Bacteriology</i> , 2016, 198, 1847-1856.	1.0	14
11417	Tree species select diverse soil fungal communities expressing different sets of lignocellulolytic enzyme-encoding genes. <i>Soil Biology and Biochemistry</i> , 2016, 100, 149-159.	4.2	19
11418	Suppressive effects of mycoviral proteins encoded by <i>Magnaporthe oryzae</i> chrysovirus 1 strain A on conidial germination of the rice blast fungus. <i>Virus Research</i> , 2016, 223, 10-19.	1.1	10
11419	Rubisco Catalytic Properties and Temperature Response in Crops. <i>Plant Physiology</i> , 2016, 171, 2549-2561.	2.3	117
11420	Calcium-insensitive splice variants of mammalian E1 subunit of 2-oxoglutarate dehydrogenase complex with tissue-specific patterns of expression. <i>Biochemical Journal</i> , 2016, 473, 1165-1178.	1.7	26
11421	Placing the Fijian Honeyeaters within the meliphagid radiation: implications for origins and conservation. <i>Pacific Conservation Biology</i> , 2016, 22, 262.	0.5	2
11422	Light Remodels Lipid Biosynthesis in <i>Nannochloropsis gaditana</i> by Modulating Carbon Partitioning between Organelles. <i>Plant Physiology</i> , 2016, 171, 2468-2482.	2.3	106
11423	Structure-based virtual screening of hypothetical inhibitors of the enzyme longiborneol synthase—a potential target to reduce <i>Fusarium</i> head blight disease. <i>Journal of Molecular Modeling</i> , 2016, 22, 163.	0.8	3
11424	Single-dose treatment with a humanized neutralizing antibody affords full protection of a human transgenic mouse model from lethal Middle East respiratory syndrome (MERS)-coronavirus infection. <i>Antiviral Research</i> , 2016, 132, 141-148.	1.9	46
11425	<i>Daphnia</i> parasite dynamics across multiple <i>Caullerya</i> epidemics indicate selection against common parasite genotypes. <i>Zoology</i> , 2016, 119, 314-321.	0.6	11
11426	<i>Cryptosporidium</i> and <i>Giardia</i> taxa in faecal samples from animals in catchments supplying the city of Melbourne with drinking water (2011 to 2015). <i>Parasites and Vectors</i> , 2016, 9, 315.	1.0	48
11427	Deep Sequencing of the HIV-1 <i>env</i> Gene Reveals Discrete X4 Lineages and Linkage Disequilibrium between X4 and R5 Viruses in the V1/V2 and V3 Variable Regions. <i>Journal of Virology</i> , 2016, 90, 7142-7158.	1.5	31
11428	The origin of the supernumerary subunits and assembly factors of complex I: A treasure trove of pathway evolution. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2016, 1857, 971-979.	0.5	57
11429	Biological characterization of the hygrobafilomycin antibiotic JBIR-100 and bioinformatic insights into the hygrolide family of natural products. <i>Bioorganic and Medicinal Chemistry</i> , 2016, 24, 6276-6290.	1.4	14
11430	Origin of <i>Chrysanthemum</i> cultivars—Evidence from nuclear low-copy LFY gene sequences. <i>Biochemical Systematics and Ecology</i> , 2016, 65, 129-136.	0.6	19

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11431	Three new species of blood flukes (Digenea: Aporocotylidae) infecting pufferfishes (Teleostei): <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 742</i>	0.6	22
11432	Modulation of NADPH-oxidase gene expression in rolB- transformed calli of <i>Arabidopsis thaliana</i> and <i>Rubia cordifolia</i> . <i>Plant Physiology and Biochemistry</i> , 2016, 105, 282-289.	2.8	10
11433	Morphology and Molecular Phylogeny of Coelomic Gregarines (Apicomplexa) with Different Types of Motility: <i>Urospora ovalis</i> and <i>U. trivisiae</i> from the Polychaete <i>Trivisia forbesii</i> . <i>Protist</i> , 2016, 167, 279-301.	0.6	10
11434	Rapid divergence and gene flow at high latitudes shape the history of Holarctic ground squirrels ( <i>Urocitellus</i> ). <i>Molecular Phylogenetics and Evolution</i> , 2016, 102, 174-188.	1.2	31
11435	Occurrence and molecular characterization of Potato spindle tuber viroid (PSTVd) isolates from potato plants in North China. <i>Journal of Integrative Agriculture</i> , 2016, 15, 349-363.	1.7	14
11436	Engineering control of bacterial cellulose production using a genetic toolkit and a new cellulose-producing strain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E3431-40.	3.3	173
11437	Bacterial communities in termite fungus combs are comprised of consistent gut deposits and contributions from the environment. <i>Microbial Ecology</i> , 2016, 71, 207-220.	1.4	48
11439	Distribution and evolution of the serine/aspartate racemase family in invertebrates. <i>Amino Acids</i> , 2016, 48, 387-402.	1.2	38
11440	Examination of an isolate of Potato leaf roll virus that does not induce visible symptoms in the greenhouse. <i>European Journal of Plant Pathology</i> , 2016, 145, 829-845.	0.8	6
11441	Limited genetic and antigenic diversity within parasite isolates used in a live vaccine against <i>Theileria parva</i> . <i>International Journal for Parasitology</i> , 2016, 46, 495-506.	1.3	41
11442	Characterization of parasite-specific indels and their proposed relevance for selective anthelmintic drug targeting. <i>Infection, Genetics and Evolution</i> , 2016, 39, 201-211.	1.0	7
11443	ANTICALIgN: visualizing, editing and analyzing combined nucleotide and amino acid sequence alignments for combinatorial protein engineering. <i>Protein Engineering, Design and Selection</i> , 2016, 29, 263-270.	1.0	5
11444	Phytochrome Signaling Is Mediated by PHYTOCHROME INTERACTING FACTOR in the Liverwort <i>Marchantia polymorpha</i> . <i>Plant Cell</i> , 2016, 28, 1406-1421.	3.1	94
11445	Evolutionary study of leporid CD4 reveals a hotspot of genetic variability within the D2 domain. <i>Immunogenetics</i> , 2016, 68, 477-482.	1.2	4
11446	<i>Lactarius megalopterus</i> , a new angiocarpous species from a tropical rainforest in Central Africa, shows adaptations to endozoochorous spore dispersal. <i>Mycological Progress</i> , 2016, 15, 1.	0.5	5
11447	Transcription factor SGF1 is critical for the neurodevelopment in the silkworm, <i>Bombyx mori</i> . <i>Gene</i> , 2016, 587, 70-75.	1.0	4
11448	The coiled-coil domain containing protein <i>Ccdc136b</i> antagonizes maternal <i>Wnt/β2-catenin</i> activity during zebrafish dorsoventral axial patterning. <i>Journal of Genetics and Genomics</i> , 2016, 43, 431-438.	1.7	5
11449	Phylogenetic relationships of species of the oesophageal parasitic nematode genera <i>Cyclostrongylus</i> and <i>Spirostrongylus</i> (Strongyloidea: Chabertiidae: Cloacinae) with their wallaby hosts (Marsupialia): <i>Tj ETQq1 1 0 0 0 4314 rgBT /Overlock 10 Tf 50 742</i>	0.6	22

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11451	Genomic and archaeological evidence suggest a dual origin of domestic dogs. Science, 2016, 352, 1228-1231.	6.0	366
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11453	Genetic structure of island and mainland populations of a Neotropical bumble bee species. Journal of Insect Conservation, 2016, 20, 383-394.	0.8	18
11454	Multiple vitellogenins and product yolk proteins in European sea bass ( <i>Dicentrarchus labrax</i> ): Molecular characterization, quantification in plasma, liver and ovary, and maturational proteolysis. Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology, 2016, 194-195, 71-86.	0.7	24
11455	Comparative analysis of expression profiling of the trypsin and chymotrypsin genes from Lepidoptera species with different levels of sensitivity to soybean peptidase inhibitors. Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology, 2016, 196-197, 67-73.	0.7	18
11456	Scale-down studies of membrane bioreactor degrading anionic surfactants wastewater: Isolation of new anionic-surfactant degrading bacteria. International Biodeterioration and Biodegradation, 2016, 114, 14-23.	1.9	41
11457	Redeployment of germ layers related TFs shows regionalized expression during two non-embryonic developments. Developmental Biology, 2016, 416, 235-248.	0.9	17
11458	Combinatorial Gene Regulatory Functions Underlie Ultraconserved Elements in Drosophila. Molecular Biology and Evolution, 2016, 33, 2294-2306.	3.5	18
11459	Characterization and functional analysis of two inhibitor of apoptosis genes in Zhikong scallop <i>Chlamys farreri</i> . Developmental and Comparative Immunology, 2016, 60, 1-11.	1.0	9
11460	Discovery of toll-like receptor 13 exists in the teleost fish: Miiuy croaker (Perciformes, Sciaenidae). Developmental and Comparative Immunology, 2016, 61, 25-33.	1.0	90
11461	Evidence for Dsg3 in regulating Src signaling by competing with it for binding to caveolin-1. Data in Brief, 2016, 6, 124-134.	0.5	9
11462	Data on four apoptosis-related genes in the colonial tunicate <i>Botryllus schlosseri</i> . Data in Brief, 2016, 8, 142-152.	0.5	1
11463	Detection of cryptic species of Rugopharynx (Nematoda: Strongylida) from the stomachs of Australian macropodid marsupials. International Journal for Parasitology: Parasites and Wildlife, 2016, 5, 124-133.	0.6	12
11464	The complete chloroplast genome sequence of <i>Abies nephrolepis</i> (Pinaceae: Abietoideae). Journal of Asia-Pacific Biodiversity, 2016, 9, 245-249.	0.2	16
11465	UbSRD: The Ubiquitin Structural Relational Database. Journal of Molecular Biology, 2016, 428, 679-687.	2.0	18
11466	Structures of the DfsB Protein Family Suggest a Cationic, Helical Sibling Lethal Factor Peptide. Journal of Molecular Biology, 2016, 428, 554-560.	2.0	4
11467	High-intensity cardiac infections of <i>Phthinomita heinigerae</i> n. sp. (Digenea: Aporocotylidae) in the orangeline cardinalfish, <i>Taeniamia fucata</i> (Cantor), off Heron Island on the Great Barrier Reef. Parasitology International, 2016, 65, 371-377.	0.6	10

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11470	Phylogenetically Structured Differences in rRNA Gene Sequence Variation among Species of Arbuscular Mycorrhizal Fungi and Their Implications for Sequence Clustering. <i>Applied and Environmental Microbiology</i> , 2016, 82, 4921-4930.	1.4	31
11471	Evolution of CCL11: genetic characterization in lagomorphs and evidence of positive and purifying selection in mammals. <i>Innate Immunity</i> , 2016, 22, 336-343.	1.1	6
11472	The Rice TCM5 Gene Encoding a Novel Deg Protease Protein is Essential for Chloroplast Development under High Temperatures. <i>Rice</i> , 2016, 9, 13.	1.7	42
11473	Molecular dynamics simulation and bioinformatics study on chloroplast stromal ridge complex from rice ( <i>Oryza sativa</i> L.). <i>BMC Bioinformatics</i> , 2016, 17, 28.	1.2	12
11474	Characterization of multiple sequence alignment errors using complete-likelihood score and position-shift map. <i>BMC Bioinformatics</i> , 2016, 17, 133.	1.2	7
11475	Assessing parallel gene histories in viral genomes. <i>BMC Evolutionary Biology</i> , 2016, 16, 32.	3.2	10
11476	Holding it together: rapid evolution and positive selection in the synaptonemal complex of <i>Drosophila</i> . <i>BMC Evolutionary Biology</i> , 2016, 16, 91.	3.2	24
11477	Identification of the genes involved in odorant reception and detection in the palm weevil <i>Rhynchophorus ferrugineus</i> , an important quarantine pest, by antennal transcriptome analysis. <i>BMC Genomics</i> , 2016, 17, 69.	1.2	102
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11479	Increasing genomic diversity and evidence of constrained lifestyle evolution due to insertion sequences in <i>Aeromonas salmonicida</i> . <i>BMC Genomics</i> , 2016, 17, 44.	1.2	46
11480	Comparative transcriptomics and proteomics of three different aphid species identifies core and diverse effector sets. <i>BMC Genomics</i> , 2016, 17, 172.	1.2	92
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11482	SuperPhy: predictive genomics for the bacterial pathogen <i>Escherichia coli</i> . <i>BMC Microbiology</i> , 2016, 16, 65.	1.3	18
11483	Identification and characterization of abundant repetitive sequences in <i>Eragrostis tef</i> cv. Enatite genome. <i>BMC Plant Biology</i> , 2016, 16, 39.	1.6	16
11484	A metabarcoding framework for facilitated survey of endolithic phototrophs with <i>tufA</i> . <i>BMC Ecology</i> , 2016, 16, 8.	3.0	57
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11488	Genomic characterization and assessment of the virulence and antibiotic resistance of the novel species <i>Paenibacillus</i> sp. strain VT-400, a potentially pathogenic bacterium in the oral cavity of patients with hematological malignancies. <i>Gut Pathogens</i> , 2016, 8, 6.	1.6	20
11489	The contribution of transposable elements to size variations between four teleost genomes. <i>Mobile DNA</i> , 2016, 7, 4.	1.3	71
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11491	Genotyping of enteroviruses isolated in Kenya from pediatric patients using partial VP1 region. <i>SpringerPlus</i> , 2016, 5, 158.	1.2	14
11492	ghost-tree: creating hybrid-gene phylogenetic trees for diversity analyses. <i>Microbiome</i> , 2016, 4, 11.	4.9	51
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11494	Identification and Antifungal Susceptibility of <i>Penicillium</i> -Like Fungi from Clinical Samples in the United States. <i>Journal of Clinical Microbiology</i> , 2016, 54, 2155-2161.	1.8	47
11495	Comprehensive structural analysis of the open and closed conformations of <i>Theileria annulata</i> enolase by molecular modelling and docking. <i>Computational Biology and Chemistry</i> , 2016, 64, 134-144.	1.1	7
11496	Evidence from two independent backcross experiments supports genetic linkage of microsatellite Hcms8a20, but not other candidate loci, to a major ivermectin resistance locus in <i>Haemonchus contortus</i> . <i>International Journal for Parasitology</i> , 2016, 46, 653-661.	1.3	27
11497	Identification of Cyanobacteriochromes Detecting Far-Red Light. <i>Biochemistry</i> , 2016, 55, 3907-3919.	1.2	71
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11500	The Impact of Selection, Gene Conversion, and Biased Sampling on the Assessment of Microbial Demography. <i>Molecular Biology and Evolution</i> , 2016, 33, 1711-1725.	3.5	62
11501	Novel Hydrogenosomes in the Microaerophilic <i>Jakobid</i> <i>Stygiella incarcerata</i> . <i>Molecular Biology and Evolution</i> , 2016, 33, 2318-2336.	3.5	52
11502	Novel modes of RNA editing in mitochondria. <i>Nucleic Acids Research</i> , 2016, 44, 4907-4919.	6.5	49
11503	The non-coding RNA composition of the mitotic chromosome by 5â€²-tag sequencing. <i>Nucleic Acids Research</i> , 2016, 44, 4934-4946.	6.5	16

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11505	Mapping DNA polymerase errors by single-molecule sequencing. <i>Nucleic Acids Research</i> , 2016, 44, e118-e118.	6.5	33
11506	Highly diversified Zika viruses imported to China, 2016. <i>Protein and Cell</i> , 2016, 7, 461-464.	4.8	48
11507	Comparative Genomics of Interreplicore Translocations in Bacteria: A Measure of Chromosome Topology?. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 1597-1606.	0.8	11
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11509	Horizontal gene transfer of acetyltransferases, invertases and chorismate mutases from different bacteria to diverse recipients. <i>BMC Evolutionary Biology</i> , 2016, 16, 74.	3.2	19
11510	The native microbiome of the nematode <i>Caenorhabditis elegans</i> : gateway to a new host-microbiome model. <i>BMC Biology</i> , 2016, 14, 38.	1.7	330
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11513	The Auxin-Deficient Defective Kernel18 ( <i>dek18</i> ) Mutation Alters the Expression of Seed-Specific Biosynthetic Genes in Maize. <i>Journal of Plant Growth Regulation</i> , 2016, 35, 770-777.	2.8	18
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11516	Convergence across a continent: adaptive diversification in a recent radiation of Australian lizards. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016, 283, 20160181.	1.2	41
11517	Characterization of the first cultured representative of <i>Verrucomicrobia</i> subdivision 5 indicates the proposal of a novel phylum. <i>ISME Journal</i> , 2016, 10, 2801-2816.	4.4	173
11518	Comparative Phylogenomics of Pathogenic and Nonpathogenic Species. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 235-244.	0.8	38
11519	<i>Enterobius</i> ( <i>Enterobius</i> ) <i>shriveri</i> n. sp. (Nematoda: Oxyuridae: Enterobiinae) from <i>Macaca fascicularis</i> Raffles, 1821 (Primates: Cercopithecoidea: Cercopithecoidea) and Three Other Cercopithecoidea 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
11520	Brain composition in <i>Heliconius</i> butterflies, posteclosion growth and experience-dependent neuropil plasticity. <i>Journal of Comparative Neurology</i> , 2016, 524, 1747-1769.	0.9	90
11521	Comparative Protein Structure Modeling Using MODELLER. <i>Current Protocols in Bioinformatics</i> , 2016, 54, 5.6.1-5.6.37.	25.8	2,248

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11523	ATP binding by the P-loop NTPase OsYchF1 (an unconventional G protein) contributes to biotic but not abiotic stress responses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 2648-2653.	3.3	31
11524	Longtail tuna <i>Thunnus tonggol</i> (Bleeker, 1851) shows genetic partitioning across, but not within, basins of the Indo-Pacific based on mitochondrial DNA. <i>Journal of Applied Ichthyology</i> , 2016, 32, 318-323.	0.3	7
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11531	Establishing a New Species <i>Encephalitozoon pogonae</i> for the Microsporidian Parasite of Inland Bearded Dragon <i>Pogona vitticeps</i> Ahl 1927 (Reptilia, Squamata, Agamidae). <i>Journal of Eukaryotic Microbiology</i> , 2016, 63, 524-535.	0.8	12
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11659	Evolutionary Dynamics of Influenza A Viruses in US Exhibition Swine. <i>Journal of Infectious Diseases</i> , 2016, 213, 173-182.	1.9	28
11660	Novel <i>Cupriavidus</i> Strains Isolated from Root Nodules of Native Uruguayan <i>Mimosa</i> Species. <i>Applied and Environmental Microbiology</i> , 2016, 82, 3150-3164.	1.4	63
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11667	New features of desiccation tolerance in the lichen photobiont <i>Trebouxia gelatinosa</i> are revealed by a transcriptomic approach. <i>Plant Molecular Biology</i> , 2016, 91, 319-339.	2.0	69
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11669	Transmission dynamics of HIV-1 subtype B in the Basque Country, Spain. <i>Infection, Genetics and Evolution</i> , 2016, 40, 91-97.	1.0	11
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11686	Estimating the number and assignment of clock models in analyses of multigene datasets. <i>Bioinformatics</i> , 2016, 32, 1281-1285.	1.8	13
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11695	JuncDB: an exon–exon junction database. <i>Nucleic Acids Research</i> , 2016, 44, D101-D109.	6.5	7
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11698	Intraspecific Variation in <i>Antherina suraka</i> (Lepidoptera: Saturniidae), an Endemic Resident of Endangered Forests in Madagascar. <i>Annals of the Entomological Society of America</i> , 2016, 109, 384-395.	1.3	1
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11700	Evaluating genomic divergence and parallelism in replicate ecomorphs from young and old cichlid adaptive radiations. <i>Molecular Ecology</i> , 2016, 25, 260-268.	2.0	38
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11710	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
11711	Unusual RNA plant virus integration in the soybean genome leads to the production of small RNAs. <i>Plant Science</i> , 2016, 246, 62-69.	1.7	21
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11713	Evolutionary Relationships among Extinct and Extant Sloths: The Evidence of Mitogenomes and Retroviruses. <i>Genome Biology and Evolution</i> , 2016, 8, 607-621.	1.1	40
11714	<i>Genista anglica</i> (Fabaceae): One very diverse species or one species complex?. <i>Journal of Plant Research</i> , 2016, 129, 411-422.	1.2	2
11715	Ancestral Protein Reconstruction Yields Insights into Adaptive Evolution of Binding Specificity in Solute-Binding Proteins. <i>Cell Chemical Biology</i> , 2016, 23, 236-245.	2.5	84
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11717	Diverse circular replication-associated protein encoding viruses circulating in invertebrates within a lake ecosystem. <i>Infection, Genetics and Evolution</i> , 2016, 39, 304-316.	1.0	66
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11723	Evolutionary history of double-stranded RNA binding proteins in plants: identification of new cofactors involved in easiRNA biogenesis. <i>Plant Molecular Biology</i> , 2016, 91, 131-147.	2.0	16
11724	Host switching of human lice to new world monkeys in South America. <i>Infection, Genetics and Evolution</i> , 2016, 39, 225-231.	1.0	13
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11731	B-type cyclin modulation in response to carbon balance in callus of <i>Populus alba</i> . <i>Plant Cell, Tissue and Organ Culture</i> , 2016, 124, 283-293.	1.2	3
11732	Distinct Processes Drive Diversification in Different Clades of Gesneriaceae. <i>Systematic Biology</i> , 2016, 65, 662-684.	2.7	72
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11734	A putative Type IIS restriction endonuclease <i>GeolCI</i> from <i>Geobacillus</i> sp. - A robust, thermostable alternative to mesophilic prototype <i>BbvI</i> . <i>Journal of Biosciences</i> , 2016, 41, 27-38.	0.5	1
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11736	Mitochondrial comparative genomics and phylogenetic signal assessment of mtDNA among arbuscular mycorrhizal fungi. <i>Molecular Phylogenetics and Evolution</i> , 2016, 98, 74-83.	1.2	50
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11739	Contributions of North American endophytes to the phylogeny, ecology, and taxonomy of Xylariaceae (Sordariomycetes, Ascomycota). <i>Molecular Phylogenetics and Evolution</i> , 2016, 98, 210-232.	1.2	110
11740	The historical biogeography of groupers: Clade diversification patterns and processes. <i>Molecular Phylogenetics and Evolution</i> , 2016, 100, 21-30.	1.2	35
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11742	Dating of the Limnadiidae family suggests an American origin of Eulimnadia. <i>Hydrobiologia</i> , 2016, 773, 149-161.	1.0	9
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11744	Seed-borne viral dsRNA elements in three cultivated <i>Raphanus</i> and <i>Brassicap</i> plants suggest three cryptoviruses. <i>Canadian Journal of Microbiology</i> , 2016, 62, 287-295.	0.8	9
11745	A novel multi-objective genetic algorithm for multiple sequence alignment. <i>International Journal of Data Mining and Bioinformatics</i> , 2016, 14, 139.	0.1	4
11746	Characterization and comparison of putative <i>Stenotrophomonas maltophilia</i> methyl parathion hydrolases. <i>Bioremediation Journal</i> , 2016, 20, 71-79.	1.0	6
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11749	Distribution of rDNA and polyploidy in <i>Deschampsia antarctica</i> E. Desv. in Antarctic and Patagonic populations. <i>Polar Biology</i> , 2016, 39, 1663-1677.	0.5	19
11750	Identification and molecular characterization of a new recombinant begomovirus and associated betasatellite DNA infecting <i>Capsicum annuum</i> in India. <i>Archives of Virology</i> , 2016, 161, 1389-1394.	0.9	13
11751	The arbuscular mycorrhizal fungi colonising roots and root nodules of New Zealand kauri <i>Agathis australis</i> . <i>Fungal Biology</i> , 2016, 120, 807-817.	1.1	23
11752	<i>Rhodophana squamulosa</i> a new species of Entolomataceae from India. <i>Mycoscience</i> , 2016, 57, 90-95.	0.3	8
11753	Structural Insights into <i>Mycobacterium tuberculosis</i> Rv2671 Protein as a Dihydrofolate Reductase Functional Analogue Contributing to <i>para</i> -Aminosalicylic Acid Resistance. <i>Biochemistry</i> , 2016, 55, 1107-1119.	1.2	22
11754	Comprehensive Screening for Naturally Occurring Hepatitis C Virus Resistance to Direct-Acting Antivirals in the NS3, NS5A, and NS5B Genes in Worldwide Isolates of Viral Genotypes 1 to 6. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 2402-2416.	1.4	52
11755	A Fivefold Parallelized Biosynthetic Process Secures Chlorination of <i>Armillaria mellea</i> (Honey) Tj ETQq1 1 0.784314 rgBT /Overlock 10 TF	1.4	31

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11756	Evolution of NADPH-cytochrome P450 oxidoreductases (POR) in Apiales – POR 1 is missing. <i>Molecular Phylogenetics and Evolution</i> , 2016, 98, 21-28.	1.2	9
11757	A computer program for fast and easy typing of a partial endoglucanase gene sequence into genospecies and sequevars 1&2 of the <i>Ralstonia solanacearum</i> species complex. <i>Journal of Microbiological Methods</i> , 2016, 123, 101-107.	0.7	11
11758	Assembly and clustering of natural antibiotics guides target identification. <i>Nature Chemical Biology</i> , 2016, 12, 233-239.	3.9	86
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11760	Characterization of six IL-17 family genes in miiuy croaker and evolution analysis of vertebrate IL-17 family. <i>Fish and Shellfish Immunology</i> , 2016, 49, 243-251.	1.6	20
11761	Identification and characterization of an apoptosis-stimulating protein of p53 (ASPP) gene from <i>Branchiostoma belcheri</i> : Insights into evolution of ASPP gene family. <i>Fish and Shellfish Immunology</i> , 2016, 49, 268-274.	1.6	2
11762	Eastward colonization of the Mediterranean Basin by two geographically structured clades: The case of <i>Odontites Ludw.</i> (Orobanchaceae). <i>Molecular Phylogenetics and Evolution</i> , 2016, 96, 140-149.	1.2	14
11763	Late acquisition of mitochondria by a host with chimaeric prokaryotic ancestry. <i>Nature</i> , 2016, 531, 101-104.	13.7	204
11764	Pleistocene events and present environmental factors have shaped the phylogeography of the intertidal limpet <i>Cellana toreuma</i> (Reeve, 1855) (Gastropoda: Nacellidae) in Southeast Asia and China. <i>Journal of Molluscan Studies</i> , 2016, 82, 378-390.	0.4	13
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11766	Reconsideration of the seven discrete typing units within the species <i>Trypanosoma cruzi</i> , a new proposal of three reliable mitochondrial clades. <i>Infection, Genetics and Evolution</i> , 2016, 39, 176-186.	1.0	30
11767	The noncoding trnH-psbA spacer, as an effective DNA barcode for aquatic freshwater plants, reveals prohibited invasive species in aquarium trade in South Africa. <i>South African Journal of Botany</i> , 2016, 102, 208-216.	1.2	12
11768	Real-time, portable genome sequencing for Ebola surveillance. <i>Nature</i> , 2016, 530, 228-232.	13.7	1,179
11769	Isolation and detection of duck astrovirus CPH: implications for epidemiology and pathogenicity. <i>Avian Pathology</i> , 2016, 45, 221-227.	0.8	17
11770	<i>Ginkgo</i> and <i>Welwitschia</i> Mitogenomes Reveal Extreme Contrasts in Gymnosperm Mitochondrial Evolution. <i>Molecular Biology and Evolution</i> , 2016, 33, 1448-1460.	3.5	151
11771	<i>Arabidopsis</i> CML38, a Calcium Sensor That Localizes to Ribonucleoprotein Complexes under Hypoxia Stress. <i>Plant Physiology</i> , 2016, 170, 1046-1059.	2.3	87
11772	Genomic and proteomic evidence supporting the division of the plant pathogen <i>Ralstonia solanacearum</i> into three species. <i>BMC Genomics</i> , 2016, 17, 90.	1.2	227
11773	– <i>Candidatus Rickettsia mendelii</i> ™, a novel basal group rickettsia detected in <i>Ixodes ricinus</i> ticks in the Czech Republic. <i>Ticks and Tick-borne Diseases</i> , 2016, 7, 482-486.	1.1	29

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11775	First report of the Hawaiian genus <i>Newhousia</i> (Dictyotales, Phaeophyceae) from Madang, Papua New Guinea and description of the new species <i>N. yhaga</i> sp. nov.. <i>Botanica Marina</i> , 2016, 59, 31-37.	0.6	2
11776	Patterns and processes in microbial biogeography: do molecules and morphologies give the same answers?. <i>ISME Journal</i> , 2016, 10, 1779-1790.	4.4	62
11777	Phylogenetic analyses of gazelles reveal repeated transitions of key ecological traits and provide novel insights into the origin of the genus <i>Gazella</i> . <i>Molecular Phylogenetics and Evolution</i> , 2016, 98, 1-10.	1.2	13
11778	The alternate AP-1 adaptor subunit Apm2 interacts with the Mil1 regulatory protein and confers differential cargo sorting. <i>Molecular Biology of the Cell</i> , 2016, 27, 588-598.	0.9	16
11779	A rose by any other name; systematics and diversity in the Chilean giant barnacle <i>Austromegabalanus psittacus</i> (Molina, 1782) (Cirripedia). <i>Journal of Crustacean Biology</i> , 2016, 36, 180-188.	0.3	2
11780	Geographically driven adaptation of chilli veinal mottle virus revealed by genetic diversity analysis of the coat protein gene. <i>Archives of Virology</i> , 2016, 161, 1329-1333.	0.9	26
11781	Enhanced Sphingomyelinase Activity Contributes to the Apoptotic Capacity of Electronegative Low-Density Lipoprotein. <i>Journal of Medicinal Chemistry</i> , 2016, 59, 1032-1040.	2.9	19
11782	Antagonism between <i>Staphylococcus epidermidis</i> and <i>Propionibacterium acnes</i> and its genomic basis. <i>BMC Genomics</i> , 2016, 17, 152.	1.2	131
11783	Maidenhair Ferns, <i>Adiantum</i> , are Indeed Monophyletic and Sister to Shoestring Ferns, Vittarioids (Pteridaceae). <i>Systematic Botany</i> , 2016, 41, 17-23.	0.2	21
11784	A global perspective on Campanulaceae: Biogeographic, genomic, and floral evolution. <i>American Journal of Botany</i> , 2016, 103, 233-245.	0.8	37
11785	Genetic distinctiveness of the damselfly <i>Coenagrion puella</i> in North Africa: an overlooked and endangered taxon. <i>Conservation Genetics</i> , 2016, 17, 985-991.	0.8	12
11786	Mutagenesis and Functional Analysis of the Bacterial Arginine Glycosyltransferase Effector NleB1 from Enteropathogenic <i>Escherichia coli</i> . <i>Infection and Immunity</i> , 2016, 84, 1346-1360.	1.0	20
11787	Large-scale diversification without genetic isolation in nematode symbionts of figs. <i>Science Advances</i> , 2016, 2, e1501031.	4.7	82
11788	Range expansion of the invasive rusty crayfish <i>Orconectes rusticus</i> (Girard, 1852) (Decapoda: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 182	0.3	2
11789	From glacial refugia to wide distribution range: demographic expansion of <i>Loropetalum chinense</i> (Hamamelidaceae) in Chinese subtropical evergreen broadleaved forest. <i>Organisms Diversity and Evolution</i> , 2016, 16, 23-38.	0.7	23
11790	Species composition, activity patterns and blood meal analysis of sand fly populations (Diptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 182 <i>Acta Tropica</i> , 2016, 158, 170-176.	0.9	29
11791	Evidence of horizontal gene transfer between obligate leaf nodule symbionts. <i>ISME Journal</i> , 2016, 10, 2092-2105.	4.4	63

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11804	Colonization of maritime glacier ice by bdelloid Rotifera. <i>Molecular Phylogenetics and Evolution</i> , 2016, 98, 280-287.	1.2	31
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11827	Unarmoured dinoflagellates with a small hyposome: <i>Torodinium</i> and <i>Lebouridinium</i> gen. nov. for <i>Katodinium glaucum</i> (Gymnodinales, Dinophyceae). <i>European Journal of Phycology</i> , 2016, 51, 226-241.	0.9	3

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11888	The genus <i>Retiboletus</i> in China. <i>Mycologia</i> , 2016, 108, 363-380.	0.8	28
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11915	Multiple sequence alignment modeling: methods and applications. <i>Briefings in Bioinformatics</i> , 2016, 17, 1009-1023.	3.2	153
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11917	Norfolk Island Robins are a distinct endangered species: ancient DNA unlocks surprising relationships and phenotypic discordance within the Australo-Pacific Robins. <i>Conservation Genetics</i> , 2016, 17, 321-335.	0.8	13

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11919	Identification of a selenium-dependent glutathione peroxidase in the blood-sucking insect <i>Rhodnius prolixus</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2016, 69, 105-114.	1.2	15
11920	Genomic and metagenomic surveys of hydrogenase distribution indicate H <sub>2</sub> is a widely utilised energy source for microbial growth and survival. <i>ISME Journal</i> , 2016, 10, 761-777.	4.4	503
11921	A Hybrid Multiobjective Memetic Metaheuristic for Multiple Sequence Alignment. <i>IEEE Transactions on Evolutionary Computation</i> , 2016, 20, 499-514.	7.5	37
11922	The systematics of carnivorous sponges. <i>Molecular Phylogenetics and Evolution</i> , 2016, 94, 327-345.	1.2	40
11923	Clarifying phylogenetic relationships and the evolutionary history of the bivalve order Arcida (Mollusca: Bivalvia: Pteriomorpha). <i>Molecular Phylogenetics and Evolution</i> , 2016, 94, 298-312.	1.2	21
11924	Phylogeography of the European sturgeon ( <i>Acipenser sturio</i> ): A critically endangered species. <i>Molecular Phylogenetics and Evolution</i> , 2016, 94, 346-357.	1.2	18
11925	The complete mitochondrial genome of Himalayan Snowcock ( <i>Tetraogallus himalayensis</i> ). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 3751-3752.	0.7	1
11926	Towards a phylogenetic generic classification of Thelypteridaceae: Additional sampling suggests alterations of neotropical taxa and further study of paleotropical genera. <i>Molecular Phylogenetics and Evolution</i> , 2016, 94, 688-700.	1.2	52
11927	A Structure-Based Classification of Class A $\beta$ -Lactamases, a Broadly Diverse Family of Enzymes. <i>Clinical Microbiology Reviews</i> , 2016, 29, 29-57.	5.7	97
11928	<i>Drosophila melanogaster</i> clip-domain serine proteases: Structure, function and regulation. <i>Biochimie</i> , 2016, 122, 255-269.	1.3	109
11929	Differentially methylated obligatory epialleles modulate context-dependent <i>LAM</i> gene expression in the honeybee <i>Apis mellifera</i> . <i>Epigenetics</i> , 2016, 11, 1-10.	1.3	56
11930	New insights about ORF1 coding regions support the proposition of a new genus comprising arthropod viruses in the family Totiviridae. <i>Virus Research</i> , 2016, 211, 159-164.	1.1	14
11931	Diversity of <i>Pseudomonas</i> Genomes, Including <i>Populus</i> -Associated Isolates, as Revealed by Comparative Genome Analysis. <i>Applied and Environmental Microbiology</i> , 2016, 82, 375-383.	1.4	70
11932	Phylogenomic analyses of a Mediterranean earthworm family (Annelida: Hormogastridae). <i>Molecular Phylogenetics and Evolution</i> , 2016, 94, 473-478.	1.2	19
11933	Resolution of Brassicaceae Phylogeny Using Nuclear Genes Uncovers Nested Radiations and Supports Convergent Morphological Evolution. <i>Molecular Biology and Evolution</i> , 2016, 33, 394-412.	3.5	259
11934	Coordinated ultrastructural and phylogenomic analyses shed light on the hidden phycobiont diversity of <i>Trebouxia</i> microalgae in <i>Ramalina fraxinea</i> . <i>Molecular Phylogenetics and Evolution</i> , 2016, 94, 765-777.	1.2	32
11935	DNA deletion as a mechanism for developmentally programmed centromere loss. <i>Nucleic Acids Research</i> , 2016, 44, 1553-1565.	6.5	15

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11937	Switching between monocot and dicot crops in rotation schemes of Argentinean productive fields results in an increment of arbuscular mycorrhizal fungi diversity. <i>Applied Soil Ecology</i> , 2016, 98, 121-131.	2.1	5
11938	Metabarcoding as a tool for investigating arthropod diversity in <i>Nepenthes</i> pitcher plants. <i>Austral Ecology</i> , 2016, 41, 120-132.	0.7	24
11939	Proteomic Tools for the Analysis of Cytoskeleton Proteins. <i>Methods in Molecular Biology</i> , 2016, 1365, 385-413.	0.4	1
11940	Metaproteomics and ultrastructure characterization of <i>Komagataeibacter</i> spp. involved in high-acid spirit vinegar production. <i>Food Microbiology</i> , 2016, 55, 112-122.	2.1	50
11941	Basic leucine zipper (bZIP) transcription factors involved in abiotic stresses: A molecular model of a wheat bZIP factor and implications of its structure in function. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2016, 1860, 46-56.	1.1	122
11942	Molecular Markers Detect Cryptic Predation on Coffee Berry Borer (Coleoptera: Curculionidae) by Silvanid and Laemophloeid Flat Bark Beetles (Coleoptera: Silvanidae, Laemophloeidae) in Coffee Beans. <i>Journal of Economic Entomology</i> , 2016, 109, 100-105.	0.8	12
11943	Identification and Resolution of Microdiversity through Metagenomic Sequencing of Parallel Consortia. <i>Applied and Environmental Microbiology</i> , 2016, 82, 255-267.	1.4	41
11944	Developing an <i>in vivo</i> toxicity assay for RNAi risk assessment in honey bees, <i>Apis mellifera</i> L. <i>Chemosphere</i> , 2016, 144, 1083-1090.	4.2	58
11945	Molecular and morphological analyses of solitary forms of brackish <i>Thalassiosiroid</i> diatoms ( <i>Coscinodiscophyceae</i> ), with emphasis on their phenotypic plasticity. <i>European Journal of Phycology</i> , 2016, 51, 11-30.	0.9	11
11946	Seasonal variation in parasite infection patterns of marine fish species from the Northern Wadden Sea in relation to interannual temperature fluctuations. <i>Journal of Sea Research</i> , 2016, 113, 73-84.	0.6	18
11947	Adaptive selection and coevolution at the proteins of the Polycomb repressive complexes in <i>Drosophila</i> . <i>Heredity</i> , 2016, 116, 213-223.	1.2	4
11948	Five new species of <i>Inocybe</i> (Agaricales) from tropical India. <i>Mycologia</i> , 2016, 108, 110-122.	0.8	14
11949	Magnetotactic bacteria population in a pristine French Atlantic lagoon. <i>Environmental Science and Pollution Research</i> , 2016, 23, 691-697.	2.7	5
11950	Utilizing next-generation sequencing to resolve the backbone of the Core Goodeniaceae and inform future taxonomic and floral form studies. <i>Molecular Phylogenetics and Evolution</i> , 2016, 94, 605-617.	1.2	20
11951	Molecular organization of the 5S rDNA gene type II in elasmobranchs. <i>RNA Biology</i> , 2016, 13, 391-399.	1.5	1
11952	The complete plastome sequence of <i>Gnetum ula</i> (Gnetales: Gnetaceae). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 3721-3722.	0.7	3
11953	The complete mitochondrial genome of Daurian ground squirrel, <i>Spermophilus dauricus</i> . <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 2848-2849.	0.7	5

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11955	The activated sludge ecosystem contains a core community of abundant organisms. <i>ISME Journal</i> , 2016, 10, 11-20.	4.4	416
11956	<i>Pseudamnicola Paulucci</i> , 1878 (Caenogastropoda: Truncatelloidea) from the Aegean Islands: a long or short story?. <i>Organisms Diversity and Evolution</i> , 2016, 16, 121-139.	0.7	40
11957	Phylogeography of the harvestman genus <i>Metasiro</i> (Arthropoda, Arachnida, Opiliones) reveals a potential solution to the Pangean paradox. <i>Organisms Diversity and Evolution</i> , 2016, 16, 167-184.	0.7	16
11958	In Silico Sub-unit Hexavalent Peptide Vaccine Against an <i>Staphylococcus aureus</i> Biofilm-Related Infection. <i>International Journal of Peptide Research and Therapeutics</i> , 2016, 22, 101-117.	0.9	26
11959	How Should Genes and Taxa be Sampled for Phylogenomic Analyses with Missing Data? An Empirical Study in Iguanian Lizards. <i>Systematic Biology</i> , 2016, 65, 128-145.	2.7	155
11960	Structural Insights into KCTD Protein Assembly and Cullin3 Recognition. <i>Journal of Molecular Biology</i> , 2016, 428, 92-107.	2.0	47
11961	The complete mitochondrial genome of <i>Chaenogobius gulosus</i> (Gobiidae, Perciformes) from the South Sea, Korea. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 4207-4208.	0.7	3
11962	Back to monoxeny: <i>Phytomonas nordicus</i> descended from dixenous plant parasites. <i>European Journal of Protistology</i> , 2016, 52, 1-10.	0.5	19
11963	Pathway Tools version 19.0 update: software for pathway/genome informatics and systems biology. <i>Briefings in Bioinformatics</i> , 2016, 17, 877-890.	3.2	250
11964	PqqE from <i>Methylobacterium extorquens</i> AM1: a radical S-adenosyl-L-methionine enzyme with an unusual tolerance to oxygen. <i>Journal of Biochemistry</i> , 2016, 159, 87-99.	0.9	14
11965	The Roles of Compensatory Evolution and Constraint in Aminoacyl tRNA Synthetase Evolution. <i>Molecular Biology and Evolution</i> , 2016, 33, 152-161.	3.5	45
11966	Rapid host switching in generalist <i>Campylobacter</i> strains erodes the signal for tracing human infections. <i>ISME Journal</i> , 2016, 10, 721-729.	4.4	123
11967	Ancestral protein reconstruction: techniques and applications. <i>Biological Chemistry</i> , 2016, 397, 1-21.	1.2	121
11968	Parallelism and Epistasis in Skeletal Evolution Identified through Use of Phylogenomic Mapping Strategies. <i>Molecular Biology and Evolution</i> , 2016, 33, 162-173.	3.5	32
11969	Barn owls ( <i>Tyto alba</i> ) in western North America: phylogeographic structure, connectivity, and genetic diversity. <i>Conservation Genetics</i> , 2016, 17, 357-367.	0.8	9
11970	Phylogenetic characterization and promoter expression analysis of a novel hybrid protein disulfide isomerase/cargo receptor subfamily unique to plants and chromalveolates. <i>Molecular Genetics and Genomics</i> , 2016, 291, 455-469.	1.0	20
11971	Group II late embryogenesis abundant (LEA) proteins: structural and functional aspects in plant abiotic stress. <i>Plant Growth Regulation</i> , 2016, 79, 1-17.	1.8	157

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11973	Extremotolerant rock inhabiting black fungi from Italian monumental sites. <i>Fungal Diversity</i> , 2016, 76, 75-96.	4.7	111
11974	Interglacial refugia preserved high genetic diversity of the Chinese mole shrew in the mountains of southwest China. <i>Heredity</i> , 2016, 116, 23-32.	1.2	37
11975	The Diversity and Co-occurrence Patterns of N <sub>2</sub> -Fixing Communities in a CO <sub>2</sub> -Enriched Grassland Ecosystem. <i>Microbial Ecology</i> , 2016, 71, 604-615.	1.4	52
11976	Comparative mitochondrial genome analysis of <i>Pythium insidiosum</i> and related oomycete species provides new insights into genetic variation and phylogenetic relationships. <i>Gene</i> , 2016, 575, 34-41.	1.0	11
11977	Expression and characterization of a recombinant psychrophilic $\hat{1}^3$ -carbonic anhydrase (NcoCA) identified in the genome of the Antarctic cyanobacteria belonging to the genus <i>Nostoc</i> . <i>Journal of Enzyme Inhibition and Medicinal Chemistry</i> , 2016, 31, 810-817.	2.5	7
11978	The complete mitochondrial genome of dwarf danio, <i>Danio nigrofasciatus</i> . <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 2854-2855.	0.7	2
11979	Four new species of <i>Mesomyzostoma</i> (Myzostomida: Annelida). <i>Journal of Natural History</i> , 2016, 50, 1-23.	0.2	16
11980	An <i>in silico</i> approach towards the identification of novel inhibitors of the TLR-4 signaling pathway. <i>Journal of Biomolecular Structure and Dynamics</i> , 2016, 34, 1345-1362.	2.0	3
11981	Refining the phylum Chlorobi by resolving the phylogeny and metabolic potential of the representative of a deeply branching, uncultivated lineage. <i>ISME Journal</i> , 2016, 10, 833-845.	4.4	62
11982	A Comparison Study for DNA Motif Modeling on Protein Binding Microarray. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2016, 13, 261-271.	1.9	16
11983	ddRAD-seq phylogenetics based on nucleotide, indel, and presence-absence polymorphisms: Analyses of two avian genera with contrasting histories. <i>Molecular Phylogenetics and Evolution</i> , 2016, 94, 122-135.	1.2	61
11984	The complete mitochondrial genome of the killifish <i>Orestias</i> sp. (Cyprinodontiformes, Cyprinodontidae). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 2840-2841.	0.7	3
11985	The complete mitochondrial genome of bearded pig, <i>Sus barbatus</i> , and comparative mitochondrial genomics of Cetartiodactyla. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 2417-2418.	0.7	0
11986	Multiplexed pyrosequencing of nine sea anemone (Cnidaria: Anthozoa: Hexacorallia: Actiniaria) mitochondrial genomes. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 2826-2832.	0.7	21
11987	Late Embryogenesis Abundant (LEA) Gene Family in Maize: Identification, Evolution, and Expression Profiles. <i>Plant Molecular Biology Reporter</i> , 2016, 34, 15-28.	1.0	42
11988	The contribution of endophytic bacteria to <i>Albizia lebbeck</i> -mediated phytoremediation of tannery effluent contaminated soil. <i>International Journal of Phytoremediation</i> , 2016, 18, 77-86.	1.7	4
11989	The complete mitochondrial genome of the endemic and threatened killifish <i>Orestias ascotanensis</i> Parenti, 1984 (Cyprinodontiformes, Cyprinodontidae) from the High Andes. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 2798-2799.	0.7	6



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11990	Genetic diversity of <i>Moestrupia oblonga</i> (Dinophyceae) from coastal areas of Okinawa Island, Japan. <i>Marine Biodiversity</i> , 2016, 46, 197-209.	0.3	2
11991	Phylogeny and physiology of candidate phylum <i>~Atribacteria</i> <sup>™</sup> (OP9/JS1) inferred from cultivation-independent genomics. <i>ISME Journal</i> , 2016, 10, 273-286.	4.4	166
11992	Regulation of <i>Clostridium difficile</i> spore germination by the CspA pseudoprotease domain. <i>Biochimie</i> , 2016, 122, 243-254.	1.3	60
11993	<i>Stenotrophomonas maltophilia</i> as an opportunistic pathogen in cultured African catfish <i>Clarias gariepinus</i> (Burchell, 1822). <i>Aquaculture</i> , 2016, 450, 168-172.	1.7	32
11994	Molecular epidemiology of <i>Mycobacterium abscessus</i> complex isolates in Ireland. <i>Journal of Cystic Fibrosis</i> , 2016, 15, 179-185.	0.3	14
11995	Complete mitochondrial genomes for <i>Icelus spatula</i> , <i>Aspidophoroides olrikii</i> and <i>Leptoclinus maculatus</i> : pan-Arctic marine fishes from Canadian waters. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 2982-2983.	0.7	9
11996	A Novel Approach to Multiple Sequence Alignment Using Multiobjective Evolutionary Algorithm Based on Decomposition. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2016, 20, 717-727.	3.9	35
11997	Complete mitochondrial genome of a sunbird, <i>Aethopyga gouldiae</i> (Aves: Passeriformes), the first representative of Nectariniidae. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 2356-2358.	0.7	1
11998	The complete mitochondrial genome of the rocky reef fish <i>Cheilodactylus variegatus</i> Valenciennes, 1833 (Teleostei: Cheilodactylidae). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 2359-2360.	0.7	1
11999	Variation in ectomycorrhizal fungal communities associated with <i>Oreomunnea mexicana</i> (Juglandaceae) in a Neotropical montane forest. <i>Mycorrhiza</i> , 2016, 26, 1-17.	1.3	72
12000	Elemental sulfur and acetate can support life of a novel strictly anaerobic haloarchaeon. <i>ISME Journal</i> , 2016, 10, 240-252.	4.4	62
12001	Comprehensive DNA barcoding of the herpetofauna of Germany. <i>Molecular Ecology Resources</i> , 2016, 16, 242-253.	2.2	30
12002	<i>Chlorella sorokiniana</i> (formerly <i>C. vulgaris</i> ) UTEX 2714, a non-thermotolerant microalga useful for biotechnological applications and as a reference strain. <i>Journal of Applied Phycology</i> , 2016, 28, 113-121.	1.5	24
12003	The impact of anchored phylogenomics and taxon sampling on phylogenetic inference in narrow-mouthed frogs (Anura, Microhylidae). <i>Cladistics</i> , 2016, 32, 113-140.	1.5	90
12004	Evolutionary diversification of alpine ginger reflects the early uplift of the Himalayan-Tibetan Plateau and rapid extrusion of Indochina. <i>Gondwana Research</i> , 2016, 32, 232-241.	3.0	51
12005	The complete mitochondrial genomes of <i>Opisthopteria orientalis</i> and <i>Blaptica dubia</i> (Blattodea: Tj ETQq1 1 0.784314 rgBT /Qverlock	0.7	4
12006	Multiple maternal origins of Indonesian crowing chickens revealed by mitochondrial DNA analysis. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2017, 28, 254-262.	0.7	9
12007	An anti-DNA antibody prefers damaged dsDNA over native. <i>Journal of Biomolecular Structure and Dynamics</i> , 2017, 35, 219-232.	2.0	7

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12009	Molecular phylogenetic reconstruction and taxonomic investigation of eelpouts (Cottoidei: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 Mapping, Sequencing, and Analysis, 2017, 28, 547-557.	0.7	8
12010	Next-generation sequencing yields the complete mitochondrial genome of the mummichog, <i>Fundulus heteroclitus</i> . Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2017, 28, 121-122.	0.7	0
12011	Strong genetic differentiation among populations of the freshwater shrimp <i>Caridina cantonensis</i> in Hong Kong: implications for conservation of freshwater fauna in urban areas. Marine and Freshwater Research, 2017, 68, 187.	0.7	5
12012	Advances and perspectives in computational prediction of microbial gene essentiality. Briefings in Functional Genomics, 2017, 16, 70-79.	1.3	29
12013	Multiyear Survey of Coccidia, Cryptosporidia, Microsporidia, Histomona, and Hematozoa in Wild Quail in the Rolling Plains Ecoregion of Texas and Oklahoma, USA. Journal of Eukaryotic Microbiology, 2017, 64, 4-17.	0.8	4
12014	Peste Des Petits Ruminants in Benin: Persistence of a Single Virus Genotype in the Country for Over 42 Years. Transboundary and Emerging Diseases, 2017, 64, 1037-1044.	1.3	32
12015	Evolutionary dynamics of satellite DNA repeats from Phaseolus beans. Protoplasma, 2017, 254, 791-801.	1.0	15
12016	On the paraphyly of Cytaeidae and placement of Cytaeis within the suborder Filifera (Hydrozoa: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.3	4
12017	Spatial distribution of aquatic marine fungi across the western Arctic and subarctic. Environmental Microbiology, 2017, 19, 475-484.	1.8	67
12018	<i>Meloidogyne graminicola</i> : a major threat to rice agriculture. Molecular Plant Pathology, 2017, 18, 3-15.	2.0	134
12019	Random Partition Distribution Indexed by Pairwise Information. Journal of the American Statistical Association, 2017, 112, 721-732.	1.8	29
12020	Biodecoloration of Reactive Black 5 by the methylotrophic yeast <i>Candida boidinii</i> MM 4035. Journal of Environmental Sciences, 2017, 53, 78-87.	3.2	29
12021	Diversity and biogeography of larval and juvenile notothenioid fishes in McMurdo Sound, Antarctica. Polar Biology, 2017, 40, 161-176.	0.5	9
12022	Endophytic symbiont yeasts associated with the Antarctic angiosperms <i>Deschampsia antarctica</i> and <i>Colobanthus quitensis</i> . Polar Biology, 2017, 40, 177-183.	0.5	41
12023	Discriminating power of microsatellites in cranberry organelles for taxonomic studies in <i>Vaccinium</i> and <i>Ericaceae</i> . Genetic Resources and Crop Evolution, 2017, 64, 451-466.	0.8	23
12024	Fragmented protein sequence alignment using two-layer particle swarm optimization (FTLPSO). Journal of King Saud University - Science, 2017, 29, 191-205.	1.6	7
12025	Culture-dependent bacteria in commercial fishes: Qualitative assessment and molecular identification using 16S rRNA gene sequencing. Saudi Journal of Biological Sciences, 2017, 24, 1105-1116.	1.8	27

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12026	Müller glia reactivity follows retinal injury despite the absence of the glial fibrillary acidic protein gene in <i>Xenopus</i> . <i>Developmental Biology</i> , 2017, 426, 219-235.	0.9	26
12027	Past lake shore dynamics explain present pattern of unidirectional introgression across a habitat barrier. <i>Hydrobiologia</i> , 2017, 791, 69-82.	1.0	15
12028	Pruning the Pearlsides: Reconciling morphology and molecules in mesopelagic fishes ( <i>Maurolucius</i> ). <i>Trends in Ecology &amp; Evolution</i> , 2017, 32, 1010-1018.	0.6	12
12029	First molecular phylogeny of scorpions of the family Buthidae from India. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2017, 28, 606-611.	0.7	17
12030	Revisiting Coleoptera AT-rich region: structural conservation, phylogenetic and phylogeographic approaches in mitochondrial control region of bioluminescent Elateridae species (Coleoptera). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2017, 28, 671-680.	0.7	6
12031	Genetic diversity and phylogeny of limpets of the genus <i>Nipponacmea</i> (Patellogastropoda: Lottiidae) based on mitochondrial DNA sequences. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2017, 28, 703-710.	0.7	2
12032	All non-indigenous species were introduced recently? The case study of <i>Cassiopea</i> (Cnidaria). <i>Trends in Ecology &amp; Evolution</i> , 2017, 32, 321-328.	0.4	44
12033	Noteworthy habitat and phylogeny updates for eastern US <i>Ulota</i> (Orthotrichaceae, Bryophyta). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2017, 28, 650-654.	0.7	2
12034	Genomic resolution of a cold subsurface aquifer community provides metabolic insights for novel microbes adapted to high CO <sub>2</sub> concentrations. <i>Environmental Microbiology</i> , 2017, 19, 459-474.	1.8	212
12035	A historical biogeography of megadiverse <i>Sericini</i> —another story out of Africa. <i>Cladistics</i> , 2017, 33, 183-197.	1.5	35
12036	Evolution of Pacific Rim diving beetles sheds light on Amphipacific biogeography. <i>Ecography</i> , 2017, 40, 500-510.	2.1	29
12037	The novel fungal-specific gene FUG1 has a role in pathogenicity and fumonisin biosynthesis in <i>Fusarium verticillioides</i> . <i>Molecular Plant Pathology</i> , 2017, 18, 513-528.	2.0	24
12038	Phylogeny and phylogeography of <i>Altolamprologus</i> : ancient introgression and recent divergence in a rock-dwelling Lake Tanganyika cichlid genus. <i>Hydrobiologia</i> , 2017, 791, 35-50.	1.0	24
12039	Fungal phytopathogens encode functional homologues of plant rapid alkalization factor (RALF) peptides. <i>Molecular Plant Pathology</i> , 2017, 18, 811-824.	2.0	95
12040	Molecular phylogeny of the Byrrhoidea–Buprestoidea complex (Coleoptera, Elateriformia). <i>Zoologica Scripta</i> , 2017, 46, 150-164.	0.7	34
12041	Vector soup: high-throughput identification of Neotropical phlebotomine sand flies using metabarcoding. <i>Molecular Ecology Resources</i> , 2017, 17, 172-182.	2.2	31
12042	Phenological shifts in hoverflies (Diptera: Syrphidae): linking measurement and mechanism. <i>Ecography</i> , 2017, 40, 853-863.	2.1	22
12043	Description of <i>Ganymedes yurii</i> sp. n. (Ganymedidae), a New Gregarine Species from the Antarctic Amphipod <i>Gondogeneia</i> sp. (Crustacea). <i>Journal of Eukaryotic Microbiology</i> , 2017, 64, 56-66.	0.8	9

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12044	Ecological dispersal barrier across the equatorial Atlantic in a migratory planktonic copepod. <i>Progress in Oceanography</i> , 2017, 158, 203-212.	1.5	27
12045	Speciation and ecological success in dimly lit waters: horizontal gene transfer in a green sulfur bacteria bloom unveiled by metagenomic assembly. <i>ISME Journal</i> , 2017, 11, 201-211.	4.4	40
12046	Genome Analysis of <i>Pseudoloma neurophilia</i> : A Microsporidian Parasite of Zebrafish ( <i>Danio</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	0.8	27
12047	Identification and characterization of suppressors of plant cell death (SPD) effectors from <i>Magnaporthe oryzae</i> . <i>Molecular Plant Pathology</i> , 2017, 18, 850-863.	2.0	44
12048	The first phylogenetic study of Mesembrinellidae (Diptera: Oestroidea) based on molecular data: clades and congruence with morphological characters. <i>Cladistics</i> , 2017, 33, 134-152.	1.5	26
12049	Molecular phylogeny of the hyperdiverse genus <i>Sarcophaga</i> (Diptera: Sarcophagidae), and comparison between algorithms for identification of rogue taxa. <i>Cladistics</i> , 2017, 33, 109-133.	1.5	28
12050	Morphological and genetic species diversity in ostracods (Crustacea: Oligostraca) from Caribbean reefs. <i>Marine Biodiversity</i> , 2017, 47, 37-53.	0.3	5
12051	Extraction of Chitin from the Shell Wastes of Two Shrimp Species <i>Fenneropenaeus semisulcatus</i> and <i>Fenneropenaeus indicus</i> using Microorganisms. <i>Journal of Aquatic Food Product Technology</i> , 2017, 26, 390-405.	0.6	20
12052	A benchmark testing ground for integrating homology modeling and protein docking. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 10-16.	1.5	29
12053	Endozoicomonas genomes reveal functional adaptation and plasticity in bacterial strains symbiotically associated with diverse marine hosts. <i>Scientific Reports</i> , 2017, 7, 40579.	1.6	207
12054	Comparative genomics reveals convergent evolution between the bamboo-eating giant and red pandas. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 1081-1086.	3.3	196
12055	Species clarification of oyster mushrooms in China and their DNA barcoding. <i>Mycological Progress</i> , 2017, 16, 191-203.	0.5	16
12056	The NBS-LRR architectures of plant R-proteins and metazoan NLRs evolved in independent events. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 1063-1068.	3.3	113
12057	Evolutionary History of the Asian Horned Frogs (Megophryinae): Integrative Approaches to Timetree Dating in the Absence of a Fossil Record. <i>Molecular Biology and Evolution</i> , 2017, 34, msw267.	3.5	46
12058	Human Rhinovirus Diversity and Evolution: How Strange the Change from Major to Minor. <i>Journal of Virology</i> , 2017, 91, .	1.5	20
12059	Taxonomy of <i>Cyrtochilum</i> -alliance (Orchidaceae) in the light of molecular and morphological data. , 2017, 58, 8.		2
12060	<i>Frankia discariae</i> sp. nov.: an infective and effective microsymbiont isolated from the root nodule of <i>Discaria trinervis</i> . <i>Archives of Microbiology</i> , 2017, 199, 641-647.	1.0	33
12061	Molecular Phylogenetic Relations of <i>Achatina fulica</i> Based on Partial Sequence of COI Gene. <i>The National Academy of Sciences, India</i> , 2017, 40, 101-103.	0.8	1

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12062	Four new species of <i>Verrucaria</i> from calcareous rocks in Finland. <i>Lichenologist</i> , 2017, 49, 27-37.	0.5	8
12063	Hydrophobic Residues near the Bilin Chromophore-Binding Pocket Modulate Spectral Tuning of Insert-Cys Subfamily Cyanobacteriochromes. <i>Scientific Reports</i> , 2017, 7, 40576.	1.6	13
12064	Adaptive evolution and demographic history contribute to the divergent population genetic structure of <i>Potato virus Y</i> between China and Japan. <i>Evolutionary Applications</i> , 2017, 10, 379-390.	1.5	40
12065	Historical biogeography and mitogenomics of two endemic Mediterranean gorgonians ( <i>Holaxonia</i> ). <i>Tj ETQq1 1 0.784314 rgBT/Overl</i>	0.7	12
12066	DNA Barcoding of an Assembly of Montane Andean Butterflies ( <i>Satyrinae</i> ): Geographical Scale and Identification Performance. <i>Neotropical Entomology</i> , 2017, 46, 514-523.	0.5	13
12067	Diversity and evolution of TIR-domain-containing proteins in bivalves and Metazoa: New insights from comparative genomics. <i>Developmental and Comparative Immunology</i> , 2017, 70, 145-164.	1.0	43
12068	Evolution of Acid-Sensing Olfactory Circuits in <i>Drosophilids</i> . <i>Neuron</i> , 2017, 93, 661-676.e6.	3.8	182
12069	Molecular investigation into the presence of a <i>Coxiella</i> sp. in <i>Rhipicephalus sanguineus</i> ticks in Australia. <i>Veterinary Microbiology</i> , 2017, 201, 141-145.	0.8	15
12070	VirusSeeker, a computational pipeline for virus discovery and virome composition analysis. <i>Virology</i> , 2017, 503, 21-30.	1.1	115
12071	Whole mitochondrial genome of the <i>Ram</i> 's Horn Squid shines light on the phylogenetic position of the monotypic order <i>Spirulida</i> (Haeckel, 1896). <i>Molecular Phylogenetics and Evolution</i> , 2017, 109, 296-301.	1.2	30
12072	Development and validation of a real-time PCR assay for the glassy-winged sharpshooter <i>Homalodisca vitripennis</i> (Hemiptera: Cicadellidae). <i>Bulletin of Entomological Research</i> , 2017, 107, 332-339.	0.5	0
12073	The first imported case of Rift Valley fever in China reveals a genetic reassortment of different viral lineages. <i>Emerging Microbes and Infections</i> , 2017, 6, 1-7.	3.0	40
12074	MetaSort untangles metagenome assembly by reducing microbial community complexity. <i>Nature Communications</i> , 2017, 8, 14306.	5.8	52
12075	Cross reactivity of immune responses to porcine reproductive and respiratory syndrome virus infection. <i>Vaccine</i> , 2017, 35, 782-788.	1.7	39
12076	Eocene lantern fruits from Gondwanan Patagonia and the early origins of <i>Solanaceae</i> . <i>Science</i> , 2017, 355, 71-75.	6.0	80
12077	Domain Organization and Evolution of the Highly Divergent 5' Coding Region of Genomes of Arteriviruses, Including the Novel Possum Nidovirus. <i>Journal of Virology</i> , 2017, 91, .	1.5	22
12078	Horizontal gene transfer drives the evolution of Rh50 permeases in prokaryotes. <i>BMC Evolutionary Biology</i> , 2017, 17, 2.	3.2	18
12079	Diversity and identification of <i>Neofabraea</i> species causing bull's eye rot in the Czech Republic. <i>European Journal of Plant Pathology</i> , 2017, 147, 683-693.	0.8	22

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12081	Myrteae phylogeny, calibration, biogeography and diversification patterns: Increased understanding in the most species rich tribe of Myrtaceae. <i>Molecular Phylogenetics and Evolution</i> , 2017, 109, 113-137.	1.2	110
12082	Lineage-specific mutational clustering in protein structures predicts evolutionary shifts in function. <i>Bioinformatics</i> , 2017, 33, 1338-1345.	1.8	11
12083	Morphology and molecules reveal the alien <i>Posthodiplostomum centrarchi</i> Hoffman, 1958 as the third species of <i>Posthodiplostomum</i> Dubois, 1936 (Digenea: Diplostomidae) in Europe. <i>Systematic Parasitology</i> , 2017, 94, 1-20.	0.5	34
12084	A meiosis-specific Spt5 homolog involved in non-coding transcription. <i>Nucleic Acids Research</i> , 2017, 45, gkw1318.	6.5	20
12085	Data on taxonomic status and phylogenetic relationship of tits. <i>Data in Brief</i> , 2017, 10, 390-397.	0.5	2
12086	Data on Rad51 amino acid sequences from higher and lower eukaryotic model organisms and parasites. <i>Data in Brief</i> , 2017, 10, 364-368.	0.5	5
12087	The Japanese Red Data book marine mollusk <i>Japonacteon nipponensis</i> and a <i>Japonacteon</i> population from Russia belong to the same species: Molecular evidence and recommendations for conservation. <i>Global Ecology and Conservation</i> , 2017, 9, 82-89.	1.0	1
12088	T-RECs: rapid and large-scale detection of recombination events among different evolutionary lineages of viral genomes. <i>BMC Bioinformatics</i> , 2017, 18, 13.	1.2	9
12090	Multi-spacer typing as an effective method to distinguish the clonal lineage of <i>Clostridium butyricum</i> strains isolated from stool samples during a series of necrotizing enterocolitis cases. <i>Journal of Hospital Infection</i> , 2017, 95, 300-305.	1.4	7
12091	The liver transcriptome of suckermouth armoured catfish ( <i>Pterygoplichthys anisitsi</i> , Loricariidae): Identification of expansions in defensome gene families. <i>Marine Pollution Bulletin</i> , 2017, 115, 352-361.	2.3	14
12092	Induction of resveratrol biosynthesis in <i>Vitis amurensis</i> cells by heterologous expression of the <i>Arabidopsis</i> constitutively active, Ca <sup>2+</sup> -independent form of the AtCPK1 gene. <i>Process Biochemistry</i> , 2017, 54, 144-155.	1.8	13
12093	Variant Ionotropic Receptors in the Malaria Vector Mosquito <i>Anopheles gambiae</i> Tuned to Amines and Carboxylic Acids. <i>Scientific Reports</i> , 2017, 7, 40297.	1.6	81
12094	Testing the contribution of individual genes in mitochondrial genomes for assessing phylogenetic relationships in Vetigastropoda. <i>Journal of Molluscan Studies</i> , 2017, 83, 123-128.	0.4	16
12095	Transcriptomic analysis of human norovirus NS1-2 protein highlights a multifunctional role in murine monocytes. <i>BMC Genomics</i> , 2017, 18, 39.	1.2	32
12096	An incoherent feed-forward loop mediates robustness and tunability in a plant immune network. <i>EMBO Reports</i> , 2017, 18, 464-476.	2.0	51
12097	Comparative analysis of variation and selection in the HCV genome. <i>Infection, Genetics and Evolution</i> , 2017, 49, 104-110.	1.0	17
12098	Cloning, expression, purification and biophysical analysis of two putative halogenases from the glycopeptide A47,934 gene cluster of <i>Streptomyces toyocaensis</i> . <i>Protein Expression and Purification</i> , 2017, 132, 9-18.	0.6	4

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12099	Eggshell palaeogenomics: Palaeognath evolutionary history revealed through ancient nuclear and mitochondrial DNA from Madagascan elephant bird ( <i>Aepyornis</i> sp.) eggshell. <i>Molecular Phylogenetics and Evolution</i> , 2017, 109, 151-163.	1.2	65
12100	Identification of microsporidia host-exposed proteins reveals a repertoire of rapidly evolving proteins. <i>Nature Communications</i> , 2017, 8, 14023.	5.8	88
12101	New species of the giant deep-sea isopod genus <i>Bathynomus</i> (Crustacea, Isopoda, Cirolanidae) from Hainan Island, South China Sea. <i>Integrative Zoology</i> , 2017, 12, 283-291.	1.3	7
12102	Identification of NF- $\kappa$ B related genes in channel catfish and their expression profiles in mucosal tissues after columnaris bacterial infection. <i>Developmental and Comparative Immunology</i> , 2017, 70, 27-38.	1.0	17
12103	Distinct regions of the <i>Phytophthora</i> essential effector Avh238 determine its function in cell death activation and plant immunity suppression. <i>New Phytologist</i> , 2017, 214, 361-375.	3.5	67
12104	Development of <i>oriC</i> -Based Plasmids for <i>Mesoplasma florum</i> . <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	13
12105	Additional data on Iranian trichodorids (Triplonchida: Trichodoridae) and first record of a rare species, <i>Trichodorus variabilis</i> Roca, 1998. <i>Nematology</i> , 2017, 19, 121-129.	0.2	25
12106	What killed Karl Patterson Schmidt? Combined venom gland transcriptomic, venomomic and antivenomic analysis of the South African green tree snake (the boomslang), <i>Dispholidus typus</i> . <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2017, 1861, 814-823.	1.1	56
12107	Characterization and silencing of the fatty acid and retinol binding <i>PpCf1</i> gene in <i>Pratylenchus penetrans</i> . <i>Plant Pathology</i> , 2017, 66, 1214-1224.	1.2	14
12108	Molecular phylogeography and population evolution analysis of <i>Citrus ichangensis</i> (Rutaceae). <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	15
12109	Chalcone isomerase-like genes in <i>Tradescantia</i> BNL4430: identification, molecular characterization, and differential expression profiles under $\gamma$ -radiation stress. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2017, 26, 330-345.	0.9	3
12110	<i>Paracoccidioides</i> spp. catalases and their role in antioxidant defense against host defense responses. <i>Fungal Genetics and Biology</i> , 2017, 100, 22-32.	0.9	16
12111	Characterization of the <i>Xanthomonas translucens</i> Complex Using Draft Genomes, Comparative Genomics, Phylogenetic Analysis, and Diagnostic LAMP Assays. <i>Phytopathology</i> , 2017, 107, 519-527.	1.1	61
12112	The phylogeny of the world's bulbuls (Pycnonotidae) inferred using a supermatrix approach. <i>Ibis</i> , 2017, 159, 498-509.	1.0	38
12113	Studying Vertical Microbiome Transmission from Mothers to Infants by Strain-Level Metagenomic Profiling. <i>MSystems</i> , 2017, 2, .	1.7	329
12114	A phosphorus threshold for mycoheterotrophic plants in tropical forests. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20162093.	1.2	22
12115	Origin and evolutionary implications of introns from analysis of cellulose synthase gene. <i>Journal of Systematics and Evolution</i> , 2017, 55, 142-148.	1.6	6
12116	Evidence for concerted movement of nuclear and mitochondrial clines in a lizard hybrid zone. <i>Molecular Ecology</i> , 2017, 26, 2306-2316.	2.0	23

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12117	Spore Heat Activation Requirements and Germination Responses Correlate with Sequences of Germinant Receptors and with the Presence of a Specific <i>spoVA</i> <sup>2</sup> <i>mob</i> Operon in Foodborne Strains of <i>Bacillus subtilis</i> . <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	27
12118	Phylogenetic relationships and spatial distributions of putative fungal pathogens of seedlings across a rainfall gradient in Panama. <i>Fungal Ecology</i> , 2017, 26, 65-73.	0.7	15
12119	Molecular characterization and morphology of <i>Cochlodinium strangulatum</i> , the type species of <i>Cochlodinium</i> , and <i>Margalefidinium</i> gen. nov. for <i>C. polykrikoides</i> and allied species (Gymnodiniales). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf</i>	1.2	10
12120	A simple model system for identifying arbuscular mycorrhizal fungal taxa that actively colonize rice ( <i>Oryza sativa</i> L.) roots grown in field soil. <i>Soil Science and Plant Nutrition</i> , 2017, 63, 29-36.	0.8	5
12121	Dynamic diversification history with rate upshifts in Holarctic bellflowers ( <i>Campanula</i> ) and <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf</i>	1.5	27
12122	The structurally disordered paramyxovirus nucleocapsid protein tail domain is a regulator of the mRNA transcription gradient. <i>Science Advances</i> , 2017, 3, e1602350.	4.7	29
12123	M Gene Reassortment in H9N2 Influenza Virus Promotes Early Infection and Replication: Contribution to Rising Virus Prevalence in Chickens in China. <i>Journal of Virology</i> , 2017, 91, .	1.5	41
12124	Multiple resistance to pirimiphos-methyl and bifenthrin in <i>Tribolium castaneum</i> involves the activity of lipases, esterases, and laccase2. <i>Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology</i> , 2017, 195, 27-43.	1.3	14
12125	Genomic analysis of a <i>Streptococcus pyogenes</i> strain causing endocarditis in a child. <i>New Microbes and New Infections</i> , 2017, 17, 1-6.	0.8	2
12126	Diversity, distribution, and significance of transposable elements in the genome of the only selfing hermaphroditic vertebrate <i>Kryptolebias marmoratus</i> . <i>Scientific Reports</i> , 2017, 7, 40121.	1.6	28
12127	Different clades and traits yield similar grassland functional responses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 705-710.	3.3	56
12128	Satellite DNA and Transposable Elements in Seabuckthorn ( <i>Hippophae rhamnoides</i> ), a Dioecious Plant with Small Y and Large X Chromosomes. <i>Genome Biology and Evolution</i> , 2017, 9, evw303.	1.1	25
12129	A molecular phylogeny reveals the Cuban enigmatic genus <i>Behaimia</i> as a new piece in the Brongniartieae puzzle of papilionoid legumes. <i>Molecular Phylogenetics and Evolution</i> , 2017, 109, 191-202.	1.2	13
12130	VRprofile: gene-cluster-detection-based profiling of virulence and antibiotic resistance traits encoded within genome sequences of pathogenic bacteria. <i>Briefings in Bioinformatics</i> , 2018, 19, bbw141.	3.2	100
12131	Odorant receptors and antennal lobe morphology offer a new approach to understanding olfaction in the Asian longhorned beetle. <i>Journal of Comparative Physiology A: Neuroethology, Sensory, Neural, and Behavioral Physiology</i> , 2017, 203, 99-109.	0.7	44
12132	Determining the roles of the three alcohol dehydrogenases ( <i>AdhA</i> , <i>AdhB</i> and <i>AdhE</i> ) in <i>Thermoanaerobacter ethanolicus</i> during ethanol formation. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2017, 44, 745-757.	1.4	10
12133	A Novel, Enigmatic Basal Leafhopper Moth Lineage Pollinating a Derived Leafhopper Host Illustrates the Dynamics of Host Shifts, Partner Replacement, and Apparent Coadaptation in Intimate Mutualisms. <i>American Naturalist</i> , 2017, 189, 422-435.	1.0	15
12134	Whole Genome Amplification Provides Suitable Control DNA for Use in DNA Barcoding Applications. <i>Biopreservation and Biobanking</i> , 2017, 15, 277-279.	0.5	2



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12136	The Detection of Spotted Fever Group Rickettsia DNA in Tick Samples From Pastoral Communities in Kenya. <i>Journal of Medical Entomology</i> , 2017, 54, tjw238.	0.9	17
12137	Genome-Wide Convergence during Evolution of Mangroves from Woody Plants. <i>Molecular Biology and Evolution</i> , 2017, 34, msw277.	3.5	43
12138	A Rhizobiales-Specific Unipolar Polysaccharide Adhesin Contributes to <i>Rhodospseudomonas palustris</i> Biofilm Formation across Diverse Photoheterotrophic Conditions. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	42
12139	Characterization of Hepatitis C Virus (HCV) Envelope Diversification from Acute to Chronic Infection within a Sexually Transmitted HCV Cluster by Using Single-Molecule, Real-Time Sequencing. <i>Journal of Virology</i> , 2017, 91, .	1.5	17
12140	Sequence, structure and function relationships in flaviviruses as assessed by evolutive aspects of its conserved non-structural protein domains. <i>Biochemical and Biophysical Research Communications</i> , 2017, 492, 565-571.	1.0	21
12141	Fumarate reductase superfamily: A diverse group of enzymes whose evolution is correlated to the establishment of different metabolic pathways. <i>Mitochondrion</i> , 2017, 34, 56-66.	1.6	25
12142	The Conservation of the Germline Multipotency Program, from Sponges to Vertebrates: A Stepping Stone to Understanding the Somatic and Germline Origins. <i>Genome Biology and Evolution</i> , 2017, 9, evw289.	1.1	39
12143	A comparative genomic analysis of putative pathogenicity genes in the host-specific sibling species <i>Colletotrichum graminicola</i> and <i>Colletotrichum sublineola</i> . <i>BMC Genomics</i> , 2017, 18, 67.	1.2	53
12144	The interplay between natural and sexual selection in the evolution of sexual size dimorphism in <i>Sceloporus</i> lizards (Squamata: Phrynosomatidae). <i>Ecology and Evolution</i> , 2017, 7, 905-917.	0.8	40
12145	Recurrent RNA motifs as scaffolds for genetically encodable small-molecule biosensors. <i>Nature Chemical Biology</i> , 2017, 13, 295-301.	3.9	104
12146	Comparative genomics of canine-isolated <i>Leishmania (Leishmania) amazonensis</i> from an endemic focus of visceral leishmaniasis in Governador Valadares, southeastern Brazil. <i>Scientific Reports</i> , 2017, 7, 40804.	1.6	65
12147	Wilt, Crown, and Root Rot of Common Rose Mallow ( <i>Hibiscus moscheutos</i> ) Caused by a Novel <i>Fusarium</i> sp.. <i>Plant Disease</i> , 2017, 101, 354-358.	0.7	10
12148	HFB7 – A novel orphan hydrophobin of the Harzianum and Virens clades of <i>Trichoderma</i> , is involved in response to biotic and abiotic stresses. <i>Fungal Genetics and Biology</i> , 2017, 102, 63-76.	0.9	30
12149	New roles in hemicellulosic sugar fermentation for the uncultivated Bacteroidetes family BS11. <i>ISME Journal</i> , 2017, 11, 691-703.	4.4	115
12150	Characterization and <i>in vivo</i> regulon determination of an <i>ECF</i> sigma factor and its cognate anti-sigma factor in <i>Nostoc punctiforme</i> . <i>Molecular Microbiology</i> , 2017, 104, 179-194.	1.2	14
12151	Phosphorus acquisition efficiency in arbuscular mycorrhizal maize is correlated with the abundance of root-external hyphae and the accumulation of transcripts encoding PHT1 phosphate transporters. <i>New Phytologist</i> , 2017, 214, 632-643.	3.5	210
12152	The ruminal microbiome associated with methane emissions from ruminant livestock. <i>Journal of Animal Science and Biotechnology</i> , 2017, 8, 7.	2.1	246

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12154	Inflorescence diversity in subtribe Eleusininae (Poaceae: Chloridoideae: Cynodonteae). <i>Flora: Morphology, Distribution, Functional Ecology of Plants</i> , 2017, 228, 50-59.	0.6	7
12155	Identification of a Ligand-Binding Site on the <i>Staphylococcus aureus</i> DnaG Primase C-Terminal Domain. <i>Biochemistry</i> , 2017, 56, 932-943.	1.2	2
12156	<i>Plasmodium malariae</i> and <i>P. ovale</i> genomes provide insights into malaria parasite evolution. <i>Nature</i> , 2017, 542, 101-104.	13.7	150
12157	Insights into the <i>Planktothrix</i> genus: Genomic and metabolic comparison of benthic and planktic strains. <i>Scientific Reports</i> , 2017, 7, 41181.	1.6	53
12158	Chemical and genetic similarity between <i>Dalbergia ecastaphyllum</i> and red propolis from the Northeastern Brazil. <i>Journal of Apicultural Research</i> , 2017, 56, 32-39.	0.7	7
12159	Resolved phylogeny and biogeography of the root pathogen <i>Armillaria</i> and its gasteroid relative, <i>Guyanagaster</i> . <i>BMC Evolutionary Biology</i> , 2017, 17, 33.	3.2	65
12160	Comparative Analysis of Mitochondrial N-Termini from Mouse, Human, and Yeast. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 512-523.	2.5	71
12161	Finless porpoises ( <i>Neophocaena asiaeorientalis</i> ) in the East China Sea: insights into feeding habits using morphological, molecular, and stable isotopic techniques. <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 2017, 74, 1628-1645.	0.7	7
12162	Molecular phylogeny of the family Dicroglossidae (Amphibia: Anura) inferred from complete mitochondrial genomes. <i>Biochemical Systematics and Ecology</i> , 2017, 71, 1-9.	0.6	10
12163	Genetic diversity and evolution of dengue virus serotype 3: A comparative genomics study. <i>Infection, Genetics and Evolution</i> , 2017, 49, 234-240.	1.0	20
12164	Evolution of the Sterol Biosynthetic Pathway of <i>Pythium insidiosum</i> and Related Oomycetes Contributes to Antifungal Drug Resistance. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	53
12165	Employing DNA barcoding as taxonomy and conservation tools for fish species censuses at the southeastern Mediterranean, a hot-spot area for biological invasion. <i>Journal for Nature Conservation</i> , 2017, 36, 1-9.	0.8	19
12166	Exploring the genomic diversity of black yeasts and relatives ( <i>Chaetothyriales</i> , <i>Ascomycota</i> ). <i>Studies in Mycology</i> , 2017, 86, 1-28.	4.5	144
12167	Novel thermostable antibiotic resistance enzymes from the Atlantis II Deep Red Sea brine pool. <i>Microbial Biotechnology</i> , 2017, 10, 189-202.	2.0	20
12168	Low CD21 expression defines a population of recent germinal center graduates primed for plasma cell differentiation. <i>Science Immunology</i> , 2017, 2, .	5.6	203
12169	Both mechanism and age of duplications contribute to biased gene retention patterns in plants. <i>BMC Genomics</i> , 2017, 18, 46.	1.2	30
12170	The mitochondrial genome of <i>Brachycephalus brunneus</i> (Anura: Brachycephalidae), with comments on the phylogenetic position of Brachycephalidae. <i>Biochemical Systematics and Ecology</i> , 2017, 71, 26-31.	0.6	3

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12172	Putative vaccine breakthrough event associated with heterotypic rotavirus infection in newborn calves, Turkey, 2015. <i>Veterinary Microbiology</i> , 2017, 201, 7-13.	0.8	20
12173	Application of high-throughput sequencing to whole rabies viral genome characterisation and its use for phylogenetic re-evaluation of a raccoon strain incursion into the province of Ontario. <i>Virus Research</i> , 2017, 232, 123-133.	1.1	23
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12394	Molecular basis for Cdk1-regulated timing of Mis18 complex assembly and CENP-A deposition. <i>EMBO Reports</i> , 2017, 18, 894-905.	2.0	51
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12446	Cryptosphaeria Canker of <i>Populus nigra</i> Caused by <i>Cryptosphaeria pullmanensis</i> , a New Threat to Poplar Industry in Iran. <i>Journal of Phytopathology</i> , 2017, 165, 387-396.	0.5	4
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12451	Targeted Enrichment for Pathogen Detection and Characterization in Three Felid Species. <i>Journal of Clinical Microbiology</i> , 2017, 55, 1658-1670.	1.8	25
12452	Comparisons between two Antarctic nematodes: cultured <i>Panagrolaimus</i> sp. DAW1 and field-sourced <i>Panagrolaimus davidi</i> . <i>Nematology</i> , 2017, 19, 533-542.	0.2	2
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12454	Decipher the ancestry of the plant-specific LBD gene family. <i>BMC Genomics</i> , 2017, 18, 951.	1.2	27
12455	Returning to the roots: morphology, molecular phylogeny and classification of the Olivoidea (Gastropoda: Neogastropoda). <i>Zoological Journal of the Linnean Society</i> , 2017, 180, 493-541.	1.0	18
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12457	Transcriptomic investigation of wound healing and regeneration in the cnidarian <i>Calliactis polypus</i> . <i>Scientific Reports</i> , 2017, 7, 41458.	1.6	35
12458	AidP, a novel N-Acyl homoserine lactonase gene from Antarctic <i>Planococcus</i> sp.. <i>Scientific Reports</i> , 2017, 7, 42968.	1.6	19
12459	Pipelic Acid Hydroxylases: A Monophyletic Clade among <i>cis</i> -Selective Bacterial Proline Hydroxylases that Discriminates <i>l</i> -Proline. <i>ChemBioChem</i> , 2017, 18, 1523-1528.	1.3	29
12460	Polycladida phylogeny and evolution: integrating evidence from 28S rDNA and morphology. <i>Organisms Diversity and Evolution</i> , 2017, 17, 653-678.	0.7	29
12461	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
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12464	Predicting influenza antigenicity from Hemagglutinin sequence data based on a joint random forest method. <i>Scientific Reports</i> , 2017, 7, 1545.	1.6	40
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12471	A Generative Angular Model of Protein Structure Evolution. <i>Molecular Biology and Evolution</i> , 2017, 34, 2085-2100.	3.5	13
12472	Comparative Genomics of the Ectomycorrhizal Sister Species <i>Rhizopogon vinicolor</i> and <i>Rhizopogon vesiculosus</i> (Basidiomycota: Boletales) Reveals a Divergence of the Mating Type <i>B</i> Locus. <i>Genes, Genomes, Genetics</i> , 2017, 7, 1775-1789.	0.8	17
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12475	Epigeal gammarids survived millions of years of severe climatic fluctuations in high latitude refugia throughout the Western Carpathians. <i>Molecular Phylogenetics and Evolution</i> , 2017, 112, 218-229.	1.2	28
12476	<i>Arabidopsis</i> proteins with a transposon-related domain act in gene silencing. <i>Nature Communications</i> , 2017, 8, 15122.	5.8	32
12477	Influenza C in Lancaster, UK, in the winter of 2014–2015. <i>Scientific Reports</i> , 2017, 7, 46578.	1.6	11
12478	Integrative taxonomy reveals that <i>Charybdis variegata</i> (Fabricius, 1798) (Brachyura: Portunidae) has not been introduced in the South Atlantic Ocean. <i>Journal of Crustacean Biology</i> , 2017, 37, 278-284.	0.3	4
12479	The metabolic potential of the single cell genomes obtained from the Challenger Deep, Mariana Trench within the candidate superphylum <i>P</i> arcubacteria ( <i>OD</i> 1). <i>Environmental Microbiology</i> , 2017, 19, 2769-2784.	1.8	88
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12482	Species-specific regulation of herbivory-induced defoliation tolerance is associated with jasmonate inducibility. <i>Ecology and Evolution</i> , 2017, 7, 3703-3712.	0.8	14
12483	Pan-Genomic Approaches in <i>Lactobacillus reuteri</i> as a Porcine Probiotic: Investigation of Host Adaptation and Antipathogenic Activity. <i>Microbial Ecology</i> , 2017, 74, 709-721.	1.4	15
12484	Evolution of specificity in cartilaginous fish glycoprotein hormones and receptors. <i>General and Comparative Endocrinology</i> , 2017, 246, 309-320.	0.8	13
12485	Phylogeography of the spider <i>Araneus venatrix</i> (Araneidae) suggests past connections between Amazon and Atlantic rainforests. <i>Biological Journal of the Linnean Society</i> , 2017, 121, 771-785.	0.7	21
12486	<i>Staphylococcus aureus</i> Promotes Smed-PGRP-2/Smed-setd8-1 Methyltransferase Signalling in Planarian Neoblasts to Sensitize Anti-bacterial Gene Responses During Re-infection. <i>EBioMedicine</i> , 2017, 20, 150-160.	2.7	24
12487	Simultaneous speciation in the European high mountain flowering plant genus <i>Facchinia</i> ( <i>Minuartia</i> ) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5</i> 2017, 112, 23-35.	1.2	13
12488	Genetic hurdles limit the arms race between <i>Prochlorococcus</i> and the T7-like podoviruses infecting them. <i>ISME Journal</i> , 2017, 11, 1836-1851.	4.4	36
12489	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
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12491	Insights into the Evolution of Hydroxyproline-Rich Glycoproteins from 1000 Plant Transcriptomes. <i>Plant Physiology</i> , 2017, 174, 904-921.	2.3	62
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12498	<i>Anthopleura</i> and the phylogeny of Actinioidea (Cnidaria: Anthozoa: Actiniaria). <i>Organisms Diversity and Evolution</i> , 2017, 17, 545-564.	0.7	26

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12502	Viral gut metagenomics of sympatric wild and domestic canids, and monitoring of viruses: Insights from an endangered wolf population. <i>Ecology and Evolution</i> , 2017, 7, 4135-4146.	0.8	28
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12504	Concerted Divergence after Gene Duplication in Polycomb Repressive Complexes. <i>Plant Physiology</i> , 2017, 174, 1192-1204.	2.3	11
12505	A <i>scn</i> DNA barcode library for Germany's mayflies, stoneflies and caddisflies (Ephemeroptera). <i>Trends in Microbiology</i> , 2017, 25, 67.	2.2	67
12506	Comparative Genomics of Chrysochromulina Ericina Virus and Other Microalga-Infecting Large DNA Viruses Highlights Their Intricate Evolutionary Relationship with the Established Mimiviridae Family. <i>Journal of Virology</i> , 2017, 91, .	1.5	59
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12510	A novel East African monopartite begomovirus-betasatellite complex that infects <i>Vernonia amygdalina</i> . <i>Archives of Virology</i> , 2017, 162, 1079-1082.	0.9	2
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12512	Spatial congruence between taxonomic, phylogenetic and functional hotspots: true pattern or methodological artefact?. <i>Diversity and Distributions</i> , 2017, 23, 209-220.	1.9	23
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12515	Multilocus Sequence Analysis of Phylogroup 1 and 2 Oral <i>Treponema</i> Strains. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	8
12516	Ribosomal RNA Internal Transcribed Regions Identify Possible Misidentification or Mislabeling among <i>Trifolium</i> (Clover) Specimens from Germplasm Collections. <i>Crop Science</i> , 2017, 57, 322-326.	0.8	2

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12518	A cryptic species produced by autoploidy and subsequent introgression involving <i>Medicago prostrata</i> (Fabaceae). Molecular Phylogenetics and Evolution, 2017, 107, 367-381.	1.2	13
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12520	New Arsenate Reductase Gene ( <i>arrA</i> ) PCR Primers for Diversity Assessment and Quantification in Environmental Samples. Applied and Environmental Microbiology, 2017, 83, .	1.4	38
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12530	Minimal barcode distance between two water mite species from Madeira Island: a cautionary tale. Experimental and Applied Acarology, 2017, 72, 133-143.	0.7	10
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12532	Determinants of HIV Phylogenetic Clustering in Chicago Among Young Black Men Who Have Sex With Men From the uConnect Cohort. Journal of Acquired Immune Deficiency Syndromes (1999), 2017, 75, 265-270.	0.9	12
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12534	Coregulation of the cyclic lipopeptides orfamide and sessilin in the biocontrol strain <i>Pseudomonas</i> sp. <sc>CMR</sc>12a. MicrobiologyOpen, 2017, 6, e00499.	1.2	37
12535	Predicting Transcription Factor Binding Sites and Their Cognate Transcription Factors Using Gene Expression Data. Methods in Molecular Biology, 2017, 1629, 271-282.	0.4	3

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12537	New records of <i>Erysiphe</i> sect. <i>Uncinula</i> spp. (Erysiphales) from Thailand and <i>E. liquidambaris</i> var. <i>acalycinae</i> var. nov.. <i>Mycoscience</i> , 2017, 58, 236-241.	0.3	5
12538	Ancient lakes, Pleistocene climates and river avulsions structure the phylogeography of a large but little-known rock scorpion from the Mojave and Sonoran deserts. <i>Biological Journal of the Linnean Society</i> , 2017, 122, 133-146.	0.7	11
12539	A Novel Phylogroup of <i>Pseudomonas cichorii</i> Identified Following an Unusual Disease Outbreak on Tomato. <i>Phytopathology</i> , 2017, 107, 1298-1304.	1.1	13
12540	Comparative analysis of pre- and post-parasitic transcriptomes and mining pioneer effectors of <i>Heterodera avenae</i> . <i>Cell and Bioscience</i> , 2017, 7, 11.	2.1	33
12541	Whole-Genome Sequence and Variant Analysis of W303, a Widely-Used Strain of <i>Saccharomyces cerevisiae</i> . <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2219-2226.	0.8	49
12542	Annotation of the Domestic Pig Genome by Quantitative Proteogenomics. <i>Journal of Proteome Research</i> , 2017, 16, 2887-2898.	1.8	25
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12548	Molecular cloning and structural modelling of gamma-phospholipase A2 inhibitors from <i>Bothrops atrox</i> and <i>Micrurus lemniscatus</i> snakes. <i>International Journal of Biological Macromolecules</i> , 2017, 103, 525-532.	3.6	6
12549	To be or not to be a valid genus: the systematic position of <i>Ophyra</i> R.ÉD. revised (Diptera: Tj ETQq1 1 0.784314 rgBT/Overlo	1.7	15
12550	A Novel A(H7N2) Influenza Virus Isolated from a Veterinarian Caring for Cats in a New York City Animal Shelter Causes Mild Disease and Transmits Poorly in the Ferret Model. <i>Journal of Virology</i> , 2017, 91, .	1.5	35
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12552	Towards Navigating the Minotaur's Labyrinth: Cryptic Diversity and Taxonomic Revision within the Speciose Genus <i>Hipposideros</i> (Hipposideridae). <i>Acta Chiropterologica</i> , 2017, 19, 1-18.	0.2	34
12553	A Taxonomic Revision of the <i>Kerivoula hardwickii</i> Complex (Chiroptera: Vespertilionidae) with the Description of a New Species. <i>Acta Chiropterologica</i> , 2017, 19, 19.	0.2	14

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12555	Contrasting patterns of postglacial range shifts between the northern and southern hemisphere in <i>Herbertus</i> (Herbertaceae, Marchantiophyta). <i>Systematics and Biodiversity</i> , 2017, 15, 541-551.	0.5	5
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12557	Iron-Dependent Enzyme Catalyzes the Initial Step in Biodegradation of <i>N</i> -Nitroglycine by <i>Variovorax</i> sp. Strain JS1663. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	11
12558	Genetic variation of major histocompatibility complex genes in the endangered red-crowned crane. <i>Immunogenetics</i> , 2017, 69, 451-462.	1.2	12
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12561	Morphologic and phylogenetic studies of two hypotrichous ciliates, with notes on morphogenesis in <i>Gastrostyla steinii</i> Engelmann, 1862 (Ciliophora, Hypotrichia). <i>European Journal of Protistology</i> , 2017, 60, 119-133.	0.5	16
12562	Unravelling respiratory syncytial virus outbreaks in Buenos Aires, Argentina: Molecular basis of the spatio-temporal transmission. <i>Virology</i> , 2017, 508, 118-126.	1.1	7
12563	The origin and evolution of human glutaminases and their atypical C-terminal ankyrin repeats. <i>Journal of Biological Chemistry</i> , 2017, 292, 11572-11585.	1.6	19
12564	Complete mitochondrial genome sequence of the freshwater diatom <i>Asterionella formosa</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 97-98.	0.2	13
12565	Genomic Analysis of <i>Calderihabitans maritimus</i> KKC1, a Thermophilic, Hydrogenogenic, Carboxydrotrophic Bacterium Isolated from Marine Sediment. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	26
12566	DNA Barcoding Meets Nanotechnology: Development of a Universal Colorimetric Test for Food Authentication. <i>Angewandte Chemie - International Edition</i> , 2017, 56, 8094-8098.	7.2	50
12567	A null model for microbial diversification. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E5414-E5423.	3.3	9
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12569	Comparative and functional genomics of the <i>Lactococcus lactis</i> taxon; insights into evolution and niche adaptation. <i>BMC Genomics</i> , 2017, 18, 267.	1.2	117
12570	Genomic Epidemiology and Management of <i>Salmonella</i> in Island Ecosystems Used for Takahē Conservation. <i>Microbial Ecology</i> , 2017, 74, 735-744.	1.4	4
12571	Molecular and morphological evidence for nine species in North American <i>Australapatemon</i> (Sudarikov, 1959): a phylogeny expansion with description of the zygoecous <i>Australapatemon mclaughlini</i> n. sp.. <i>Parasitology Research</i> , 2017, 116, 2181-2198.	0.6	23



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12575	The genus <i>Abrawayaomys</i> Cunha and Cruz, 1979 (Rodentia: Cricetidae: Sigmodontinae): geographic variation and species definition. <i>Journal of Mammalogy</i> , 2017, 98, 438-455.	0.6	9
12576	<i>Tobacco rattle virus</i> (TRV)-Mediated Silencing of <i>Nicotiana benthamiana</i> ARGONAUTES ( <i>NbAGO</i> s) Reveals New Antiviral Candidates and Dominant Effects of TRV- <i>NbAGO1</i> . <i>Phytopathology</i> , 2017, 107, 977-987.	1.1	18
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12579	In vitro and in silico characterization of metagenomic soil-derived cellulases capable of hydrolyzing oil palm empty fruit bunch. <i>Biotechnology Reports (Amsterdam, Netherlands)</i> , 2017, 15, 55-62.	2.1	8
12580	The mitogenome phylogeny of Adephaga (Coleoptera). <i>Molecular Phylogenetics and Evolution</i> , 2017, 114, 166-174.	1.2	70
12581	Phylogenetic relationships of a major diversification of <i>Croton</i> (Euphorbiaceae) in the western Indian Ocean region. <i>Botanical Journal of the Linnean Society</i> , 2017, 183, 532-544.	0.8	13
12582	The <i>Candidatus</i> <i>Liberibacter</i> "Host Interface: Insights into Pathogenesis Mechanisms and Disease Control. <i>Annual Review of Phytopathology</i> , 2017, 55, 451-482.	3.5	246
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12584	Surveillance of upper respiratory infections using a new multiplex PCR assay compared to conventional methods during the influenza season in Taiwan. <i>International Journal of Infectious Diseases</i> , 2017, 61, 97-102.	1.5	10
12585	Assessing the potential of RAD-sequencing to resolve phylogenetic relationships within species radiations: The fly genus <i>Chiastocheta</i> (Diptera: Anthomyiidae) as a case study. <i>Molecular Phylogenetics and Evolution</i> , 2017, 114, 189-198.	1.2	18
12586	<i>Coronavirus HKU15</i> in respiratory tract of pigs and first discovery of coronavirus quasispecies in 5' untranslated region. <i>Emerging Microbes and Infections</i> , 2017, 6, 1-7.	3.0	29
12587	Unexpected genomic features in widespread intracellular bacteria: evidence for motility of marine chlamydiae. <i>ISME Journal</i> , 2017, 11, 2334-2344.	4.4	34
12588	Identification of introns harboring functional sequence elements through positional conservation. <i>Scientific Reports</i> , 2017, 7, 4201.	1.6	17
12589	Phylogenetic and biogeographical history of the Afro-Madagascan genera <i>Delonix</i> , <i>Colvillea</i> and <i>Lemuropisum</i> (Fabaceae: Caesalpinioideae). <i>Botanical Journal of the Linnean Society</i> , 2017, 184, 59-78.	0.8	10

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12592	A Phylogenomic Solution to the Origin of Insects by Resolving Crustacean-Hexapod Relationships. Current Biology, 2017, 27, 1818-1824.e5.	1.8	156
12593	Gene-enriched draft genome of the cattle tick Rhipicephalus microplus: assembly by the hybrid Pacific Biosciences/Illumina approach enabled analysis of the highly repetitive genome. International Journal for Parasitology, 2017, 47, 569-583.	1.3	48
12594	Structural and Dynamics Characterization of the MerR Family Metalloregulator CueR in its Repression and Activation States. Structure, 2017, 25, 988-996.e3.	1.6	38
12595	Lineage-specific expansion and loss of tyrosinase genes across platyhelminths and their induction profiles in the carcinogenic oriental liver fluke, <i>Clonorchis sinensis</i> . Parasitology, 2017, 144, 1316-1327.	0.7	4
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12599	Phytochromes from <i>Agrobacterium fabrum</i> . Photochemistry and Photobiology, 2017, 93, 642-655.	1.3	23
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12601	Reducing the information gap on Loricarioidei (Siluriformes) mitochondrial genomics. BMC Genomics, 2017, 18, 345.	1.2	12
12602	Adaptive Roles of <i>SSY1</i> and <i>SIR3</i> During Cycles of Growth and Starvation in <i>Saccharomyces cerevisiae</i> Populations Enriched for Quiescent or Nonquiescent Cells. G3: Genes, Genomes, Genetics, 2017, 7, 1899-1911.	0.8	13
12603	Phylogenetic Systematics of Cochlospermaceae (Malvales) Based on Molecular and Morphological Evidence. Systematic Botany, 2017, 42, 271-282.	0.2	14
12604	A New Species of Hylodes (Anura, Hylodidae) from Serra do Mar, Southeastern Brazil: The Fourth with Nuptial Thumb Tubercles. Herpetologica, 2017, 73, 136.	0.2	10
12605	Low Genetic Variation of Red-Crowned Cranes on Hokkaido Island, Japan, Over the Hundred Years. Zoological Science, 2017, 34, 211-216.	0.3	7
12606	Phylogenomic Reconstruction of the Oomycete Phylogeny Derived from 37 Genomes. MSphere, 2017, 2, .	1.3	84
12607	First Record of the <i>Pseudogekko brevipes</i> Complex from the Northern Philippines, with Description of a New Species. Herpetologica, 2017, 73, 162-175.	0.2	5

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12609	Phylogenies of symbiotic genes of <i>Bradyrhizobium</i> symbionts of legumes of economic and environmental importance in Brazil support the definition of the new symbiovars pachyrhizi and sojae. <i>Systematic and Applied Microbiology</i> , 2017, 40, 254-265.	1.2	45
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12611	Fungal communities associated with bark and ambrosia beetles trapped at international harbours. <i>Fungal Ecology</i> , 2017, 28, 44-52.	0.7	44
12612	Molecular phylogeny and taxonomy of <i>Parauncinula</i> (Erysiphales) and two new species <i>P.Âpolyspora</i> and <i>P. uncinata</i> . <i>Mycoscience</i> , 2017, 58, 361-368.	0.3	16
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12614	Venom of the Peruvian snake <i>Bothriopsis oligolepis</i> : Detection of antibacterial activity and involvement of proteolytic enzymes and C-type lectins in growth inhibition of <i>Staphylococcus aureus</i> . <i>Toxicon</i> , 2017, 134, 30-40.	0.8	7
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12616	Integrative modeling of gene and genome evolution roots the archaeal tree of life. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E4602-E4611.	3.3	232
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12618	Integrative taxonomy of the Central African forest chameleon, <i>Kinyongia adolfifrideric</i> (Sauria: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 34 the Linnean Society, 0, , .	1.0	6
12619	Gene rearrangement and sequence analysis of mitogenomes suggest polyphyly of Archaeobalanid and Balanid barnacles (Cirripedia: Balanomorpha). <i>Zoologica Scripta</i> , 2017, 46, 729-739.	0.7	15
12620	PvGAMA reticulocyte binding activity: predicting conserved functional regions by natural selection analysis. <i>Parasites and Vectors</i> , 2017, 10, 251.	1.0	36
12621	Examination of species delimitation of ambiguous DNA-based <i>Ulva</i> ( <i>Ulvophyceae</i> , Chlorophyta) clades by culturing and hybridisation. <i>Phycologia</i> , 2017, 56, 517-532.	0.6	22
12622	An 18S rRNA Workflow for Characterizing Protists in Sewage, with a Focus on Zoonotic Trichomonads. <i>Microbial Ecology</i> , 2017, 74, 923-936.	1.4	36
12623	Characterization of <i>Phormidium lacuna</i> strains from the North Sea and the Mediterranean Sea for biotechnological applications. <i>Process Biochemistry</i> , 2017, 59, 194-206.	1.8	14
12624	Fin-fold development in paddlefish and catshark and implications for the evolution of the autopod. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20162780.	1.2	27
12625	Tropical specialist vs. climate generalist: Diversification and demographic history of sister species of <i>Carlia</i> skinks from northwestern Australia. <i>Molecular Ecology</i> , 2017, 26, 4045-4058.	2.0	25

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12627	An Unusual New Species of <i>Bidens</i> (Asteraceae, Coreopsidae) with its Phylogenetic Position and Taxonomic Notes. <i>Systematic Botany</i> , 2017, 42, 301-312.	0.2	4
12628	Draft genome of spinach and transcriptome diversity of 120 <i>Spinacia</i> accessions. <i>Nature Communications</i> , 2017, 8, 15275.	5.8	156
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12630	A Novel Strain of the Mastrevirus <i>Chickpea chlorotic dwarf virus</i> Infecting Papaya in Nigeria. <i>Plant Disease</i> , 2017, 101, 1684-1684.	0.7	7
12631	Evolutionary History and Taxonomy of the <i>Euphorbia polycarpa</i> Complex ( <i>Euphorbia</i> subg. <i>Chamaesyce</i> ) Tj ETQq1 1.0,784314 rgBT /Ove 0.2	0.2	0
12632	Genome Size in North American Fireflies: Substantial Variation Likely Driven by Neutral Processes. <i>Genome Biology and Evolution</i> , 2017, 9, 1499-1512.	1.1	41
12633	DNA Barcoding Meets Nanotechnology: Development of a Universal Colorimetric Test for Food Authentication. <i>Angewandte Chemie</i> , 2017, 129, 8206-8210.	1.6	7
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12636	The Evolutionary Basis of Translational Accuracy in Plants. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2363-2373.	0.8	5
12637	Exploring Components of the CO <sub>2</sub> -Concentrating Mechanism in Alkaliphilic Cyanobacteria Through Genome-Based Analysis. <i>Computational and Structural Biotechnology Journal</i> , 2017, 15, 340-350.	1.9	37
12638	Identification and expression profiling of novel plant cell wall degrading enzymes from a destructive pest of palm trees, <i>Rhynchophorus ferrugineus</i> . <i>Insect Molecular Biology</i> , 2017, 26, 469-484.	1.0	21
12639	Taxonomic revision of <i>Dactyloctenium</i> ( <i>Dactyloctenium</i> ) based on morphological, ultrastructural, biochemical and molecular data. <i>Phycological Research</i> , 2017, 65, 235-247.	0.8	12
12640	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
12641	Discovery of extremely halophilic, methyl-reducing euryarchaea provides insights into the evolutionary origin of methanogenesis. <i>Nature Microbiology</i> , 2017, 2, 17081.	5.9	213
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12643	Pseudoheterocaryum, a new genus segregated from <i>Heterocaryum</i> (Boraginaceae) on the basis of molecular data. <i>Australian Systematic Botany</i> , 2017, 30, 105.	0.3	5

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12645	A six-gene phylogenetic overview of Basidiomycota and allied phyla with estimated divergence times of higher taxa and a phyloproteomics perspective. <i>Fungal Diversity</i> , 2017, 84, 43-74.	4.7	124
12646	The diversity and co-occurrence patterns of diazotrophs in the steppes of Inner Mongolia. <i>Catena</i> , 2017, 157, 130-138.	2.2	27
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12649	Evolutionary relationships and expression analysis of EUL domain proteins in rice ( <i>Oryza sativa</i> ). <i>Rice</i> , 2017, 10, 26.	1.7	31
12650	Four new species of <i>Paradiscogaster</i> Yamaguti, 1934 (Digenea: Faustulidae) from batfishes (Perciformes: Ephippidae) on the Great Barrier Reef, Australia. <i>Systematic Parasitology</i> , 2017, 94, 339-349.	0.5	2
12651	Biogeography of bloom-forming microcystin producing and non-toxigenic populations of <i>Dolichospermum lemmermannii</i> (Cyanobacteria). <i>Harmful Algae</i> , 2017, 67, 1-12.	2.2	40
12652	Detection and phylogenetic characterisation of novel <i>Anaplasma</i> and <i>Ehrlichia</i> species in <i>Amblyomma triguttatum</i> subsp. from four allopatric populations in Australia. <i>Ticks and Tick-borne Diseases</i> , 2017, 8, 749-756.	1.1	32
12653	Adaptive Patterns of Mitogenome Evolution Are Associated with the Loss of Shell Scutes in Turtles. <i>Molecular Biology and Evolution</i> , 2017, 34, 2522-2536.	3.5	21
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12655	Protein and pathway engineering for the biosynthesis of 5-hydroxytryptophan in <i>Escherichia coli</i> . <i>Engineering in Life Sciences</i> , 2017, 17, 892-899.	2.0	13
12656	On the relationship between residue structural environment and sequence conservation in proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 1713-1723.	1.5	4
12657	Taking a detour: invasion of an octocoral into the Tropical Eastern Pacific. <i>Biological Invasions</i> , 2017, 19, 2583-2597.	1.2	7
12658	Sulfonamide inhibition profiles of the $\Gamma^2$ -carbonic anhydrase from the pathogenic bacterium <i>Francisella tularensis</i> responsible of the febrile illness tularemia. <i>Bioorganic and Medicinal Chemistry</i> , 2017, 25, 3555-3561.	1.4	20
12659	Plant pectin acetyltransferase structure and function: new insights from bioinformatic analysis. <i>BMC Genomics</i> , 2017, 18, 456.	1.2	60
12660	High quality permanent draft genome sequence of <i>Chryseobacterium bovis</i> DSM 19482T, isolated from raw cow milk. <i>Standards in Genomic Sciences</i> , 2017, 12, 31.	1.5	2
12661	<i>Bradyrhizobium sacchari</i> sp. nov., a legume nodulating bacterium isolated from sugarcane roots. <i>Archives of Microbiology</i> , 2017, 199, 1251-1258.	1.0	29

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12663	A novel alignment-free vector method to cluster protein sequences. <i>Journal of Theoretical Biology</i> , 2017, 427, 41-52.	0.8	6
12664	Variation analysis of norovirus among children with diarrhea in rural Hebei Province, north of China. <i>Infection, Genetics and Evolution</i> , 2017, 53, 199-205.	1.0	7
12665	Characterization of recombinant <i>Trypanosoma brucei gambiense</i> Translationally Controlled Tumor Protein ( <i>TbTCTP</i> ) and its interaction with <i>Glossina</i> midgut bacteria. <i>Gut Microbes</i> , 2017, 8, 413-427.	4.3	8
12666	External diversity is restrained by internal conservatism: New nudibranch mollusc contributes to the cryptic species problem. <i>Zoologica Scripta</i> , 2017, 46, 683-692.	0.7	41
12667	Restoring the species status of <i>Catharus maculatus</i> (Aves: Turdidae), a secretive Andean thrush, with a critique of the yardstick approach to species delimitation. <i>Zootaxa</i> , 2017, 4276, .	0.2	11
12668	Complete genome sequences of two novel autographiviruses infecting a bacterium from the <i>Pseudomonas fluorescens</i> group. <i>Archives of Virology</i> , 2017, 162, 2907-2911.	0.9	7
12669	Species boundaries in the <i>Astragalus cusickii</i> complex delimited using molecular phylogenetic techniques. <i>Molecular Phylogenetics and Evolution</i> , 2017, 114, 93-110.	1.2	5
12670	Supporting precision medicine by data mining across multi-disciplines: an integrative approach for generating comprehensive linkages between single nucleotide variants (SNVs) and drug-binding sites. <i>Bioinformatics</i> , 2017, 33, 1621-1629.	1.8	11
12671	Genetic diversity of symbiotic <i>Paraburkholderia</i> species isolated from nodules of <i>Mimosa pudica</i> (L.) and <i>Phaseolus vulgaris</i> (L.) grown in soils of the Brazilian Atlantic Forest (Mata Atlântica). <i>FEMS Microbiology Ecology</i> , 2017, 93, .	1.3	25
12672	Comparative genomics of free-living Gammaproteobacteria: pathogenesis-related genes or interaction-related genes?. <i>Pathogens and Disease</i> , 2017, 75, .	0.8	23
12673	Evolutionary and Functional Mitogenomics Associated With the Genetic Restoration of the Florida Panther. <i>Journal of Heredity</i> , 2017, 108, 449-455.	1.0	9
12674	The Genome Sizes of Ostracod Crustaceans Correlate with Body Size and Evolutionary History, but not Environment. <i>Journal of Heredity</i> , 2017, 108, 701-706.	1.0	17
12675	Signatures of adaptive molecular evolution in American pikas ( <i>Ochotona princeps</i> ). <i>Journal of Mammalogy</i> , 2017, 98, 1156-1167.	0.6	7
12676	Purifying and Positive Selection Influence Patterns of Gene Loss and Gene Expression in the Evolution of a Plant Sex Chromosome System. <i>Molecular Biology and Evolution</i> , 2017, 34, 1140-1154.	3.5	50
12677	Identification and Evolutionary Characterization of ARGONAUTE-Binding Platforms. <i>Methods in Molecular Biology</i> , 2017, 1640, 257-266.	0.4	1
12678	Phylodynamics of foot-and-mouth disease virus O/PanAsia in Vietnam 2010–2014. <i>Veterinary Research</i> , 2017, 48, 24.	1.1	24
12679	Phylogenetic and Evolutionary Analysis of Plant ARGONAUTES. <i>Methods in Molecular Biology</i> , 2017, 1640, 267-294.	0.4	9

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12681	The Tale of a Neglected Energy Source: Elevated Hydrogen Exposure Affects both Microbial Diversity and Function in Soil. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	26
12682	Sex combs reduced (Scr) regulatory region of <i>Drosophila</i> revisited. <i>Molecular Genetics and Genomics</i> , 2017, 292, 773-787.	1.0	3
12683	Agricultural management practices influence AMF diversity and community composition with cascading effects on plant productivity. <i>Applied Soil Ecology</i> , 2017, 115, 53-59.	2.1	70
12684	Metagenomic analysis in Lake Onego (Russia) <i>Synechococcus</i> cyanobacteria. <i>Journal of Great Lakes Research</i> , 2017, 43, 43-54.	0.8	2
12685	Structural analysis and insight into Zika virus NS5 mediated interferon inhibition. <i>Infection, Genetics and Evolution</i> , 2017, 51, 143-152.	1.0	12
12686	Coral hybridization or phenotypic variation? Genomic data reveal gene flow between <i>Porites lobata</i> and <i>P. Compressa</i> . <i>Molecular Phylogenetics and Evolution</i> , 2017, 111, 132-148.	1.2	59
12687	Lipidome determinants of maximal lifespan in mammals. <i>Scientific Reports</i> , 2017, 7, 5.	1.6	60
12688	New Insights into the Systematics of the <i>Schoenoxiphium</i> Clade ( <i>Carex</i> , Cyperaceae). <i>International Journal of Plant Sciences</i> , 2017, 178, 320-329.	0.6	7
12689	Diversity, Phylogeny, anticancer and antimicrobial potential of fungal endophytes associated with <i>Monarda citriodora</i> L. <i>BMC Microbiology</i> , 2017, 17, 44.	1.3	40
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12691	Genetic entanglement between <i>Cercospora</i> species associating soybean purple seed stain. <i>Mycological Progress</i> , 2017, 16, 593-603.	0.5	10
12692	Adaptive evolution of insect selective excitatory $\hat{I}^2$ -type sodium channel neurotoxins from scorpion venom. <i>Peptides</i> , 2017, 92, 31-37.	1.2	2
12693	Global analysis of biosynthetic gene clusters reveals vast potential of secondary metabolite production in <i>Penicillium</i> species. <i>Nature Microbiology</i> , 2017, 2, 17044.	5.9	198
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12695	Large-scale 16S gene assembly using metagenomics shotgun sequences. <i>Bioinformatics</i> , 2017, 33, 1447-1456.	1.8	13
12696	WGS to predict antibiotic MICs for <i>Neisseria gonorrhoeae</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, 1937-1947.	1.3	169
12697	Why Do Phylogenomic Data Sets Yield Conflicting Trees? Data Type Influences the Avian Tree of Life more than Taxon Sampling. <i>Systematic Biology</i> , 2017, 66, 857-879.	2.7	242

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12698	Protective effects of mannan oligosaccharides on turbot <i>Scophthalmus maximus</i> suffering from soy enteropathy. <i>Aquaculture</i> , 2017, 476, 141-151.	1.7	40
12699	First found of <i>Erysiphe elevata</i> on <i>Eucalyptus camaldulensis</i> and <i>Phyllactinia lagerstroemiae</i> sp. nov. on <i>Lagerstroemia</i> from Thailand. <i>Mycoscience</i> , 2017, 58, 253-260.	0.3	10
12700	Scallop genome provides insights into evolution of bilaterian karyotype and development. <i>Nature Ecology and Evolution</i> , 2017, 1, 120.	3.4	353
12701	Genome-wide sequencing of longan ( <i>Dimocarpus longan</i> Lour.) provides insights into molecular basis of its polyphenol-rich characteristics. <i>GigaScience</i> , 2017, 6, 1-14.	3.3	103
12702	Mapping Transposon Insertions in Bacterial Genomes by Arbitrarily Primed PCR. <i>Current Protocols in Molecular Biology</i> , 2017, 118, 15.15.1-15.15.15.	2.9	19
12703	Bioinformatics Applications in Clinical Microbiology. <i>Translational Medicine Research</i> , 2017, , 353-367.	0.0	0
12704	Testing for the Occurrence of Selective Episodes During the Divergence of Otophysan Fishes: Insights from Mitogenomics. <i>Journal of Molecular Evolution</i> , 2017, 84, 162-173.	0.8	5
12705	Phylogenetic analysis reveals cryptic species diversity within minute intestinal fluke, <i>Stellantchasmus falcatus</i> Onji and Nishio, 1916 (Trematoda, Heterophyidae). <i>Asian Pacific Journal of Tropical Medicine</i> , 2017, 10, 165-170.	0.4	10
12706	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
12707	Diversity, Distribution, and Evolution of Tomato Viruses in China Uncovered by Small RNA Sequencing. <i>Journal of Virology</i> , 2017, 91, .	1.5	63
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12709	Do dams also stop frogs? Assessing population connectivity of coastal tailed frogs ( <i>Ascaphus truei</i> ) in the North Cascades National Park Service Complex. <i>Conservation Genetics</i> , 2017, 18, 439-451.	0.8	7
12710	Translation of CircRNAs. <i>Molecular Cell</i> , 2017, 66, 9-21.e7.	4.5	1,431
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12712	Identification of new BMP6 pro-peptide mutations in patients with iron overload. <i>American Journal of Hematology</i> , 2017, 92, 562-568.	2.0	35
12713	Translating the microRNA signature of microvesicles derived from human coronary artery smooth muscle cells in patients with familial hypercholesterolemia and coronary artery disease. <i>Journal of Molecular and Cellular Cardiology</i> , 2017, 106, 55-67.	0.9	45
12714	Selective modes determine evolutionary rates, gene compactness and expression patterns in <i>Brassica</i> . <i>Plant Journal</i> , 2017, 91, 34-44.	2.8	57
12715	Genetic basis of benzimidazole resistance in <i>Teladorsagia circumcincta</i> in Ireland. <i>Irish Veterinary Journal</i> , 2017, 70, 8.	0.8	20



#	ARTICLE	IF	CITATIONS
12716	Identification and characterization of lactic acid bacteria and yeasts of PDO Tuscan bread sourdough by culture dependent and independent methods. <i>International Journal of Food Microbiology</i> , 2017, 250, 19-26.	2.1	54
12717	Evolutionary insights into T-type Ca <sup>2+</sup> channel structure, function, and ion selectivity from the <i>Trichoplax adhaerens</i> homologue. <i>Journal of General Physiology</i> , 2017, 149, 483-510.	0.9	30
12718	<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
12719	Description of <i>Flamella daurica</i> n. sp., with notes on the phylogeny of the genus <i>Flamella</i> and related taxa. <i>European Journal of Protistology</i> , 2017, 58, 164-174.	0.5	1
12720	Human MFAP1 is a cryptic ortholog of the <i>Saccharomyces cerevisiae</i> Spp381 splicing factor. <i>BMC Evolutionary Biology</i> , 2017, 17, 91.	3.2	13
12721	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
12722	Peritoneal bacterial infection repressed the expression of IL17D in Siberia sturgeon a chondrosteian fish in the early immune response. <i>Fish and Shellfish Immunology</i> , 2017, 64, 39-48.	1.6	12
12723	Phylogenetically diverse group of native bacterial symbionts isolated from root nodules of groundnut ( <i>Arachis hypogaea</i> L.) in South Africa. <i>Systematic and Applied Microbiology</i> , 2017, 40, 215-226.	1.2	31
12724	Genomic innovations linked to infection strategies across emerging pathogenic chytrid fungi. <i>Nature Communications</i> , 2017, 8, 14742.	5.8	96
12725	Protein interaction evolution from promiscuity to specificity with reduced flexibility in an increasingly complex network. <i>Scientific Reports</i> , 2017, 7, 44948.	1.6	40
12726	Non-biting midges (Diptera: Chironomidae) research in South America: subsidizing biogeographic hypotheses. <i>Annales De Limnologie</i> , 2017, 53, 111-128.	0.6	9
12727	Endophytic <i>Colletotrichum</i> spp. from <i>Cinchona calisaya</i> wedd. and its potential quinine production as antibacterial and antimalaria. , 2017, , .		2
12728	Generation and characterization of a collection of knock-down lines for the chloroplast Clp protease complex in tobacco. <i>Journal of Experimental Botany</i> , 2017, 68, 2199-2218.	2.4	31
12729	Crystal structure and RNA-binding properties of an Hfq homolog from the deep-branching Aquificae: conservation of the lateral RNA-binding mode. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 294-315.	1.1	17
12730	Unlocking the story in the swab: A new genotyping assay for the amphibian chytrid fungus <i>Batrachochytrium dendrobatidis</i> . <i>Molecular Ecology Resources</i> , 2017, 17, 1283-1292.	2.2	33
12731	Giant viruses with an expanded complement of translation system components. <i>Science</i> , 2017, 356, 82-85.	6.0	234
12732	Genetic diversity of Atlantic Bluefin tuna in the Mediterranean Sea: insights from genome-wide SNPs and microsatellites. <i>Journal of Biological Research</i> , 2017, 24, 3.	2.2	9
12733	Identification and characterization of a 20 <sup>12</sup> -HSDH from the anaerobic gut bacterium <i>Butyricoccus desmolans</i> ATCC 43058. <i>Journal of Lipid Research</i> , 2017, 58, 916-925.	2.0	29

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12734	Unveiling Members of <i>Colletotrichum acutatum</i> Species Complex Causing <i>Colletotrichum</i> Leaf Disease of <i>Hevea brasiliensis</i> in Sri Lanka. <i>Current Microbiology</i> , 2017, 74, 747-756.	1.0	11
12735	Identification of residues critical for proton-coupled glutathione translocation in the yeast glutathione transporter, Hgt1p. <i>Biochemical Journal</i> , 2017, 474, 1807-1821.	1.7	0
12736	High-quality genome assembly of <i>Capsella bursa-pastoris</i> reveals asymmetry of regulatory elements at early stages of polyploid genome evolution. <i>Plant Journal</i> , 2017, 91, 278-291.	2.8	40
12737	A Genome-Scale Model of <i>Shewanella piezotolerans</i> Simulates Mechanisms of Metabolic Diversity and Energy Conservation. <i>MSystems</i> , 2017, 2, .	1.7	14
12738	Reconstruction of the evolution of microbial defense systems. <i>BMC Evolutionary Biology</i> , 2017, 17, 94.	3.2	46
12739	The revision of <i>Prangos</i> subsections <i>Koelzella</i> and <i>Fedtschenkoana</i> (Apiaceae) with some notes to phylogeny and biogeography of the genus: molecular and morphological evidences. <i>Plant Systematics and Evolution</i> , 2017, 303, 815-826.	0.3	12
12740	Diverse origins of enzymes involved in the biosynthesis of chloroplast peptidoglycan. <i>Journal of Plant Research</i> , 2017, 130, 635-645.	1.2	28
12741	Carbonate biomineralization and heavy metal remediation by calcifying fungi isolated from karstic caves. <i>Ecological Engineering</i> , 2017, 103, 106-117.	1.6	68
12742	A contribution to the phylogeny of agglutinating <i>Arcellinida</i> (Amoebozoa) based on SSU rRNA gene sequences. <i>European Journal of Protistology</i> , 2017, 59, 99-107.	0.5	16
12743	Phylogenomic evolutionary surveys of subtilase superfamily genes in fungi. <i>Scientific Reports</i> , 2017, 7, 45456.	1.6	48
12744	Molecular characterisation of <i>Chlamydia pneumoniae</i> associated to atherosclerosis. <i>Pathogens and Disease</i> , 2017, 75, .	0.8	10
12745	Draft genome of the Northern snakehead, <i>Channa argus</i> . <i>GigaScience</i> , 2017, 6, 1-5.	3.3	45
12746	Evolution of the endomembrane systems of trypanosomatids: conservation and specialisation. <i>Journal of Cell Science</i> , 2017, 130, 1421-1434.	1.2	23
12747	Bioresolution of racemic phenyl glycidyl ether by a putative recombinant epoxide hydrolase from <i>Streptomyces griseus</i> NBRC 13350. <i>World Journal of Microbiology and Biotechnology</i> , 2017, 33, 82.	1.7	5
12748	BuddySuite: Command-Line Toolkits for Manipulating Sequences, Alignments, and Phylogenetic Trees. <i>Molecular Biology and Evolution</i> , 2017, 34, 1543-1546.	3.5	8
12749	Complete genome sequence and comparative genomics of the probiotic yeast <i>Saccharomyces boulardii</i> . <i>Scientific Reports</i> , 2017, 7, 371.	1.6	85
12750	Genomic characterization of Nontuberculous Mycobacteria. <i>Scientific Reports</i> , 2017, 7, 45258.	1.6	176
12751	Survival, recovery, and reproduction of apple snails ( <i>Pomacea</i> spp.) following exposure to drought conditions. <i>Freshwater Science</i> , 2017, 36, 316-324.	0.9	19

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12752	Triggering dieback in an invasive plant: endophyte diversity and pathogenicity. <i>Australasian Plant Pathology</i> , 2017, 46, 157-170.	0.5	14
12753	Isolation and characterization of a novel putative human polyomavirus. <i>Virology</i> , 2017, 506, 45-54.	1.1	77
12754	Comammox in drinking water systems. <i>Water Research</i> , 2017, 116, 332-341.	5.3	163
12755	Panfungal Polymerase Chain Reaction for Identification of Fungal Pathogens in Formalin-Fixed Animal Tissues. <i>Veterinary Pathology</i> , 2017, 54, 640-648.	0.8	47
12756	Comparative transcriptome analyses of flower development in four species of <i>Achimenes</i> (Gesneriaceae). <i>BMC Genomics</i> , 2017, 18, 240.	1.2	41
12757	WRN conditioned media is sufficient for <i>in vitro</i> propagation of intestinal organoids from large farm and small companion animals. <i>Biology Open</i> , 2017, 6, 698-705.	0.6	88
12758	Substrates of <i>Peltigera</i> Lichens as a Potential Source of Cyanobionts. <i>Microbial Ecology</i> , 2017, 74, 561-569.	1.4	25
12759	The influence of O <sub>2</sub> availability and Fe(III) mineralogy on Fe metabolism by an acidophilic bacterial culture. <i>Chemical Geology</i> , 2017, 457, 107-117.	1.4	5
12760	Persistence of historical population structure in an endangered species despite near-complete biome conversion in California's San Joaquin Desert. <i>Molecular Ecology</i> , 2017, 26, 3618-3635.	2.0	23
12761	The Regulation of Uterine Proinflammatory Gene Expression during Pregnancy in the Live-Bearing Lizard, <i>Pseudemoia entrecasteauxii</i> . <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2017, 328, 334-346.	0.6	8
12762	Identification and evolution of a plant cell wall specific glycoprotein glycosyl transferase, ExAD. <i>Scientific Reports</i> , 2017, 7, 45341.	1.6	29
12763	Endemic palm species shed light on habitat shifts and the assembly of the Cerrado and Restinga floras. <i>Molecular Phylogenetics and Evolution</i> , 2017, 110, 127-133.	1.2	24
12764	Reduction of antinutritional glucosinolates in Brassica oilseeds by mutation of genes encoding transporters. <i>Nature Biotechnology</i> , 2017, 35, 377-382.	9.4	84
12765	Systematics of <i>Cladophora</i> spp. (Chlorophyta) from North Carolina, USA, based upon morphology and DNA sequence data with a description of <i>Cladophora subtilissima</i> sp. nov.. <i>Journal of Phycology</i> , 2017, 53, 541-556.	1.0	15
12766	<i>Jacksonvillea apiculata</i> (Oscillatoriales, Cyanobacteria) gen. & sp. nov.: a new genus of filamentous, epipsamic cyanobacteria from North Florida. <i>Phycologia</i> , 2017, 56, 284-295.	0.6	19
12767	Additions to <i>Lindgomyces</i> (Lindgomycetaceae, Pleosporales, Dothideomycetes), including two new species occurring on submerged wood from North Carolina, USA, with notes on secondary metabolite profiles. <i>Mycological Progress</i> , 2017, 16, 535-552.	0.5	14
12768	Draft genome of the fungus-growing termite pathogenic fungus <i>Ophiocordyceps bispora</i> (Ophiocordycipitaceae, Hypocreales, Ascomycota). <i>Data in Brief</i> , 2017, 11, 537-542.	0.5	9
12769	Molecular analyses reveal high species diversity of trematodes in a sub-Arctic lake. <i>International Journal for Parasitology</i> , 2017, 47, 327-345.	1.3	72

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12771	A New Crown-Group Frog (Amphibia: Anura) from the Early Cretaceous of Northeastern Inner Mongolia, China. <i>American Museum Novitates</i> , 2017, 3876, 1-39.	0.2	19
12772	Evidence of respiratory syncytial virus and parainfluenza-3 virus in Mexican sheep. <i>VirusDisease</i> , 2017, 28, 102-110.	1.0	8
12773	DExD/H-box RNA helicase genes are differentially expressed between males and females during the critical period of male sex differentiation in channel catfish. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2017, 22, 109-119.	0.4	8
12774	Finding hot singles: matching males to females in dimorphic spiders (Araneidae: Micrathena) using phylogenetic placement and DNA barcoding. <i>Invertebrate Systematics</i> , 2017, 31, 8.	0.5	11
12775	Nucleotide diversity and phylogenetic relationships among <i>Gladiolus</i> cultivars and related taxa of family Iridaceae. <i>Journal of Genetics</i> , 2017, 96, 135-145.	0.4	6
12776	The Unique Domain Forms a Fuzzy Intramolecular Complex in Src Family Kinases. <i>Structure</i> , 2017, 25, 630-640.e4.	1.6	72
12777	Altered expression of maize PLASTOCHRON1 enhances biomass and seed yield by extending cell division duration. <i>Nature Communications</i> , 2017, 8, 14752.	5.8	89
12778	Highly pathogenic H5N6 influenza A viruses recovered from wild birds in Guangdong, southern China, 2014–2015. <i>Scientific Reports</i> , 2017, 7, 44410.	1.6	18
12779	A phylogenetically distinctive and extremely heat stable light-driven proton pump from the eubacterium <i>Rubrobacter xylanophilus</i> DSM 9941T. <i>Scientific Reports</i> , 2017, 7, 44427.	1.6	26
12780	Phylogenetic systematics of <i>Syncephalis</i> (Zoopagales, Zoopagomycotina), a genus of ubiquitous mycoparasites. <i>Mycologia</i> , 2017, 109, 333-349.	0.8	20
12781	Elevated mitochondrial genome variation after 50 generations of radiation exposure in a wild rodent. <i>Evolutionary Applications</i> , 2017, 10, 784-791.	1.5	40
12782	GS-5734 and its parent nucleoside analog inhibit Filo-, Pneumo-, and Paramyxoviruses. <i>Scientific Reports</i> , 2017, 7, 43395.	1.6	373
12783	Bushmeat Hunting and Zoonotic Transmission of Simian T-Lymphotropic Virus 1 in Tropical West and Central Africa. <i>Journal of Virology</i> , 2017, 91, .	1.5	30
12784	On Wet Rocks with Snorkels: Immature Stages of Tritonus Cascade Beetles with Unusual Modification of Spiracles (Coleoptera: Hydrophilidae: Laccobiini). <i>Annales Zoologici</i> , 2017, 67, 91-107.	0.1	8
12785	Characterization of <i>Theileria equi</i> genotypes in horses in Israel, the Palestinian Authority and Jordan. <i>Ticks and Tick-borne Diseases</i> , 2017, 8, 499-505.	1.1	18
12786	A Mixed Infection of <i>Lettuce chlorosis virus</i> , <i>Papaya ringspot virus</i> , and <i>Tomato yellow leaf curl virus-IL</i> Detected in a Texas Papaya Orchard Affected by a Virus-Like Disease Outbreak. <i>Plant Disease</i> , 2017, 101, 1094-1102.	0.7	11
12787	The floating <i>Sargassum</i> (Phaeophyceae) of the South Atlantic Ocean – likely scenarios. <i>Phycologia</i> , 2017, 56, 321-328.	0.6	85

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12788	Lichen acclimation to changing environments: Photobiont switching vs. climate-specific uniqueness in <i>Psora decipiens</i> . Ecology and Evolution, 2017, 7, 2560-2574.	0.8	46
12789	Revisiting the taxonomy of the family Circoviridae: establishment of the genus Cyclovirus and removal of the genus Gyrovirus. Archives of Virology, 2017, 162, 1447-1463.	0.9	285
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12791	Evolution of the ability to modulate host chemokine networks via gene duplication in human cytomegalovirus (HCMV). Infection, Genetics and Evolution, 2017, 51, 46-53.	1.0	19
12792	Self-identity reprogrammed by a single residue switch in a cell surface receptor of a social bacterium. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 3732-3737.	3.3	30
12793	Molecular phylogeny and taxonomic revision of the genus <i>Wittrockiella</i> (Pithophoraceae), nov.. Journal of Phycology, 2017, 53, 522-540.	1.0	4
12794	Evolutionary ecology of beta-lactam gene clusters in animals. Molecular Ecology, 2017, 26, 3217-3229.	2.0	24
12795	Molecular and morphological data support the transfer of the monotypic Iranian genus <i>Alococarpum</i> to <i>Prangos</i> (Apiaceae). Phytotaxa, 2017, 299, 223.	0.1	8
12796	Computational Biosensors: Molecules, Algorithms, and Detection Platforms. Modeling and Optimization in Science and Technologies, 2017, , 541-577.	0.7	2
12797	Eucalypt powdery mildew caused by <i>Podosphaera pannosa</i> in Brazil. Tropical Plant Pathology, 2017, 42, 261-272.	0.8	5
12798	Estimation of main diversification time-points of hantaviruses using phylogenetic analyses of complete genomes. Virus Research, 2017, 233, 60-69.	1.1	8
12799	Recurrent rewiring and emergence of RNA regulatory networks. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E2816-E2825.	3.3	32
12800	Phylogenetic study of the tribe Potentilleae (Rosaceae), with further insight into the disintegration of <i>Sibbaldia</i> . Journal of Systematics and Evolution, 2017, 55, 177-191.	1.6	25
12801	Novel RNA viruses producing simultaneous covert infections in <i>Ceratitis capitata</i> . Correlations between viral titers and host fitness, and implications for SIT programs. Journal of Invertebrate Pathology, 2017, 143, 50-60.	1.5	17
12802	Diverse Mesorhizobium bacteria nodulate native Astragalus and Oxytropis in arctic and subarctic areas in Eurasia. Systematic and Applied Microbiology, 2017, 40, 51-58.	1.2	9
12803	The apicoplast genomes of two taxonomic units of Babesia from sheep. Veterinary Parasitology, 2017, 233, 123-128.	0.7	10
12804	Genetic Evidence for Cytochrome <i>b</i> Q Site Inhibition by 4(1-H) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 107 Td Chemotherapy, 2017, 61, .	1.4	46
12805	Challenges in assignment of allosteric effects in cytochrome P450-catalyzed substrate oxidations to structural dynamics in the hemoprotein architecture. Journal of Inorganic Biochemistry, 2017, 167, 100-115.	1.5	19

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12806	A Novel Transcriptional Regulator Related to Thiamine Phosphate Synthase Controls Thiamine Metabolism Genes in Archaea. <i>Journal of Bacteriology</i> , 2017, 199, .	1.0	38
12807	Transcriptome-wide identification and expression analyses of ABC transporters in dwarf polish wheat under metal stresses. <i>Biologia Plantarum</i> , 2017, 61, 293-304.	1.9	30
12808	Phylogenetic relationships of weaverbirds (Aves: Ploceidae): A first robust phylogeny based on mitochondrial and nuclear markers. <i>Molecular Phylogenetics and Evolution</i> , 2017, 109, 21-32.	1.2	19
12809	Feline Immunodeficiency Virus Cross-Species Transmission: Implications for Emergence of New Lentiviral Infections. <i>Journal of Virology</i> , 2017, 91, .	1.5	39
12810	Supermatrix phylogeny and biogeography of the Australasian Meliphagides radiation (Aves:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 582 T	1.2	77
12811	Ex-situ biogas upgrading and enhancement in different reactor systems. <i>Bioresource Technology</i> , 2017, 225, 429-437.	4.8	249
12812	Elucidation of the first definitively identified life cycle for a marine turtle blood fluke (Trematoda:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 582 T	1.3	38
12813	Co-phylogeographic study of the flatworm <i>Gyrodactylus gondae</i> and its goby host <i>Pomatoschistus minutus</i> . <i>Parasitology International</i> , 2017, 66, 119-125.	0.6	15
12814	Diversification shifts in leafroller moths linked to continental colonization and the rise of angiosperms. <i>Cladistics</i> , 2017, 33, 449-466.	1.5	24
12815	Genome sequence and genetic diversity of European ash trees. <i>Nature</i> , 2017, 541, 212-216.	13.7	166
12816	Molecular Identification of d-Ribulokinase in Budding Yeast and Mammals. <i>Journal of Biological Chemistry</i> , 2017, 292, 1005-1028.	1.6	17
12817	Contrasting patterns of adaptive sequence convergence among echolocating mammals. <i>Gene</i> , 2017, 605, 1-4.	1.0	8
12818	Exploring the past and the future of protein evolution with ancestral sequence reconstruction: the "retro" approach to protein engineering. <i>Biochemical Journal</i> , 2017, 474, 1-19.	1.7	100
12819	1,2-Diacylglycerol choline phosphotransferase catalyzes the final step in the unique <i>Treponema denticola</i> phosphatidylcholine biosynthesis pathway. <i>Molecular Microbiology</i> , 2017, 103, 896-912.	1.2	8
12820	Analysis of morphological, ecological and molecular characters of <i>Russula pectinatoides</i> Peck and <i>Russula praetervisa</i> Sarnari, with a description of the new taxon <i>Russula recondita</i> Melera & Ostellari. <i>Mycological Progress</i> , 2017, 16, 117-134.	0.5	15
12821	microRNA-145 regulates the RLR signaling pathway in miiuy croaker after poly(I:C) stimulation via targeting MDA5. <i>Developmental and Comparative Immunology</i> , 2017, 68, 79-86.	1.0	32
12822	Methane fates in the benthos and water column at cold seep sites along the continental margin of Central and North America. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2017, 120, 122-131.	0.6	7
12823	Characterization of founder viruses in very early SIV rectal transmission. <i>Virology</i> , 2017, 502, 97-105.	1.1	18

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12824	Synthesis of arborane triterpenols by a bacterial oxidosqualene cyclase. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 245-250.	3.3	45
12825	Genomewide <i>scn</i> SNP data reveal cryptic phylogeographic structure and microallopatric divergence in a rapidly adapted clade of cichlids from the Congo River. Molecular Ecology, 2017, 26, 1401-1419.	2.0	38
12826	Shifting Clade Distribution, Reassortment, and Emergence of New Subtypes of Highly Pathogenic Avian Influenza A(H5) Viruses Collected from Vietnamese Poultry from 2012 to 2015. Journal of Virology, 2017, 91, .	1.5	41
12827	Inhibition of CRISPR-Cas9 with Bacteriophage Proteins. Cell, 2017, 168, 150-158.e10.	13.5	409
12828	Identification of Triplophysa species from the Qinghai-Tibetan Plateau (QTP) and its adjacent regions through DNA barcodes. Gene, 2017, 605, 12-19.	1.0	12
12829	<i>Xenopus</i> Piwi proteins interact with a broad proportion of the oocyte transcriptome. Rna, 2017, 23, 504-520.	1.6	14
12830	Phylogenetic analysis of Micracidini bark beetles (Coleoptera: Curculionidae) demonstrates a single trans-Atlantic disjunction and inclusion of Cactopinus in the New World clade. Canadian Entomologist, 2017, 149, 8-25.	0.4	6
12831	Molecular pathological study on LRR10 in sudden unexplained nocturnal death syndrome in the Chinese Han population. International Journal of Legal Medicine, 2017, 131, 621-628.	1.2	9
12832	Two for one: inadvertent introduction of Euglandina species during failed bio-control efforts in Hawaii. Biological Invasions, 2017, 19, 1399-1405.	1.2	20
12833	Phylogeography of Toxoplasma gondii points to a South American origin. Infection, Genetics and Evolution, 2017, 48, 150-155.	1.0	56
12834	Enhanced virulence of clade 2.3.2.1 highly pathogenic avian influenza A H5N1 viruses in ferrets. Virology, 2017, 502, 114-122.	1.1	19
12835	<i>DRO1</i> influences root system architecture in Arabidopsis and Prunus species. Plant Journal, 2017, 89, 1093-1105.	2.8	125
12836	Relationships Among Powered Flight, Metabolic Rate, Body Mass, Genome Size, and the Retrotransposon Complement of Volant Birds. Evolutionary Biology, 2017, 44, 261-272.	0.5	10
12837	Structure and expression of dna methyltransferase genes from apomictic and sexual Boechera species. Computational Biology and Chemistry, 2017, 67, 15-21.	1.1	6
12838	Arbuscular mycorrhizal fungal community composition is altered by long-term litter removal but not litter addition in a lowland tropical forest. New Phytologist, 2017, 214, 455-467.	3.5	45
12839	Draft genome and description of Orrella dioscoreae gen. nov. sp. nov., a new species of Alcaligenaceae isolated from leaf acumens of Dioscorea sansibarensis. Systematic and Applied Microbiology, 2017, 40, 11-21.	1.2	42
12840	<i>AvrPm2</i> encodes an <i>RNase</i> -like avirulence effector which is conserved in the two different specialized forms of wheat and rye powdery mildew fungus. New Phytologist, 2017, 213, 1301-1314.	3.5	112
12841	Expression of the Antisense-to-Latency Transcript Long Noncoding RNA in Kaposi's Sarcoma-Associated Herpesvirus. Journal of Virology, 2017, 91, .	1.5	31

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12842	BindML/BindML+: Detecting Protein-Protein Interaction Interface Propensity from Amino Acid Substitution Patterns. <i>Methods in Molecular Biology</i> , 2017, 1529, 279-289.	0.4	4
12843	Molecular characterization of a new soybean-infecting member of the genus <i>Nepovirus</i> identified by high-throughput sequencing. <i>Archives of Virology</i> , 2017, 162, 1089-1092.	0.9	8
12844	<i>Ascaris</i> phylogeny based on multiple whole mtDNA genomes. <i>Infection, Genetics and Evolution</i> , 2017, 48, 4-9.	1.0	19
12845	In the shadows: Phylogenomics and coalescent species delimitation unveil cryptic diversity in a Cerrado endemic lizard ( <i>Squamata: Tropicurus</i> ). <i>Molecular Phylogenetics and Evolution</i> , 2017, 107, 455-465.	1.2	37
12846	The complex evolutionary history of aminoacyl-tRNA synthetases. <i>Nucleic Acids Research</i> , 2017, 45, 1059-1068.	6.5	75
12847	Zinc Cluster Transcription Factors Alter Virulence in <i>Candida albicans</i> . <i>Genetics</i> , 2017, 205, 559-576.	1.2	31
12848	High levels of benzimidazole resistance and $\beta$ -tubulin isotype 1 SNP F167Y in <i>Haemonchus contortus</i> populations from Cear� State, Brazil. <i>Small Ruminant Research</i> , 2017, 146, 48-52.	0.6	12
12849	The complete maternal and paternal mitochondrial genomes of <i>Unio crassus</i> : Mitochondrial molecular clock and the overconfidence of molecular dating. <i>Molecular Phylogenetics and Evolution</i> , 2017, 107, 605-608.	1.2	12
12850	<i>Hepatozoon silvestris</i> sp. nov.: morphological and molecular characterization of a new species of <i>Hepatozoon</i> (Adeleorina: Hepatozoidae) from the European wild cat ( <i>Felis silvestris</i> ) Tj ETQq0 0 0 rgBT0/0 Overlock 40 Tf 50 4		
12851	The spider tree of life: phylogeny of Araneae based on target� gene analyses from an extensive taxon sampling. <i>Cladistics</i> , 2017, 33, 574-616.	1.5	341
12852	Eosinophilic airway inflammation in asthmatic patients is associated with an altered airway microbiome. <i>Journal of Allergy and Clinical Immunology</i> , 2017, 140, 407-417.e11.	1.5	89
12853	Insights into the lifestyle of uncultured bacterial natural product factories associated with marine sponges. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E347-E356.	3.3	114
12854	An Effective Counterselection System for <i>Listeria monocytogenes</i> and Its Use To Characterize the Monocin Genomic Region of Strain 10403S. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	31
12855	Evolutionary conservation and in vitro reconstitution of microsporidian iron� sulfur cluster biosynthesis. <i>Nature Communications</i> , 2017, 8, 13932.	5.8	67
12856	Diverse evolutionary patterns of pneumococcal antigens identified by pangenome-wide immunological screening. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E357-E366.	3.3	68
12857	Museomics resolve the systematics of an endangered grass lineage endemic to north-western Madagascar. <i>Annals of Botany</i> , 2017, 119, 339-351.	1.4	34
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12859	Involvement of an RNA binding protein containing Alba domain in the stage-specific regulation of beta-amastin expression in <i>Trypanosoma cruzi</i> . <i>Molecular and Biochemical Parasitology</i> , 2017, 211, 1-8.	0.5	11



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12861	The regulation of antimicrobial peptide resistance in the transition to insect symbiosis. <i>Molecular Microbiology</i> , 2017, 103, 958-972.	1.2	27
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12863	<i>Pandora formicae</i> , a specialist ant pathogenic fungus: New insights into biology and taxonomy. <i>Journal of Invertebrate Pathology</i> , 2017, 143, 108-114.	1.5	32
12864	Phylogenetic relationships of <i>Burmeistera</i> (Campanulaceae: Lobelioideae): Combining whole plastome with targeted loci data in a recent radiation. <i>Molecular Phylogenetics and Evolution</i> , 2017, 107, 551-563.	1.2	31
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12866	New case of lateral asymmetry in fishes: A new subfamily, genus and species of deep water clingfishes from Papua New Guinea, western Pacific Ocean. <i>Comptes Rendus - Biologies</i> , 2017, 340, 47-62.	0.1	9
12867	Characterization of S-nitrosoglutathione reductase from <i>Brassica</i> and <i>Lactuca</i> spp. and its modulation during plant development. <i>Nitric Oxide - Biology and Chemistry</i> , 2017, 68, 68-76.	1.2	27
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12870	Evolution and systematics of Green Bush-crickets (Orthoptera: Tettigoniidae: Tettigonia) in the Western Palaearctic: testing concordance between molecular, acoustic, and morphological data. <i>Organisms Diversity and Evolution</i> , 2017, 17, 213-228.	0.7	6
12871	<i>Prototheca tumulicola</i> sp. nov., a novel achlorophyllous, yeast-like microalga isolated from the stone chamber interior of the Takamatsuzuka Tumulus. <i>Mycoscience</i> , 2017, 58, 53-59.	0.3	13
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12873	Dynein light chain family genes in 15 plant species: Identification, evolution and expression profiles. <i>Plant Science</i> , 2017, 254, 70-81.	1.7	14
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12876	Effects of initial moisture content of Korean traditional wheat-based fermentation starter nuruk on microbial abundance and diversity. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 2093-2106.	1.7	19
12877	A reappraisal of <i>Stegastes</i> species occurring in the South Atlantic using morphological and molecular data. <i>Helgoland Marine Research</i> , 2017, 70, .	1.3	5

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12879	The genome draft of coconut ( <i>Cocos nucifera</i> ). <i>GigaScience</i> , 2017, 6, 1-11.	3.3	96
12880	Evolution-informed forecasting of seasonal influenza A (H3N2). <i>Science Translational Medicine</i> , 2017, 9, .	5.8	51
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12885	Obstruction of pilus retraction stimulates bacterial surface sensing. <i>Science</i> , 2017, 358, 535-538.	6.0	231
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12887	Ability of phages to infect <i>Acinetobacter calcoaceticus</i> – <i>Acinetobacter baumannii</i> complex species through acquisition of different pectate lyase depolymerase domains. <i>Environmental Microbiology</i> , 2017, 19, 5060-5077.	1.8	81
12888	Keeping it complicated: Mitochondrial genome plasticity across diplomonads. <i>Scientific Reports</i> , 2017, 7, 14166.	1.6	18
12889	Structure of PINK1 in complex with its substrate ubiquitin. <i>Nature</i> , 2017, 552, 51-56.	13.7	114
12890	Contaminants of emerging concern affect <i>Trichoplusia ni</i> growth and development on artificial diets and a key host plant. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E9923-E9931.	3.3	23
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12892	Tracing the Evolutionary History of the CAP Superfamily of Proteins Using Amino Acid Sequence Homology and Conservation of Splice Sites. <i>Journal of Molecular Evolution</i> , 2017, 85, 137-157.	0.8	21
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12895	Convergence of plasmid architectures drives emergence of multi-drug resistance in a clonally diverse <i>Escherichia coli</i> population from a veterinary clinical care setting. <i>Veterinary Microbiology</i> , 2017, 211, 6-14.	0.8	15

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12897	The TLR13-MyD88-NF- $\kappa$ B signalling pathway of <i>Cyclina sinensis</i> plays vital roles in innate immune responses. <i>Fish and Shellfish Immunology</i> , 2017, 70, 720-730.	1.6	36
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12908	TM-Aligner: Multiple sequence alignment tool for transmembrane proteins with reduced time and improved accuracy. <i>Scientific Reports</i> , 2017, 7, 12543.	1.6	23
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12910	Notes on <i>Amanita</i> section <i>Caesareae</i> from Malaysia. <i>Mycologia</i> , 2017, 109, 1-11.	0.8	6
12911	Geographically widespread honeybee gut symbiont subgroups show locally distinct antibiotic-resistant patterns. <i>Molecular Ecology</i> , 2017, 26, 6590-6607.	2.0	26
12912	Human microbiome signatures of differential colorectal cancer drug metabolism. <i>Npj Biofilms and Microbiomes</i> , 2017, 3, 27.	2.9	103
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12914	Evolution of Single-Domain Globins in Hydrothermal Vent Scale-Worms. <i>Journal of Molecular Evolution</i> , 2017, 85, 172-187.	0.8	25

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12931	Genomic adaptation to polyphagy and insecticides in a major East Asian noctuid pest. <i>Nature Ecology and Evolution</i> , 2017, 1, 1747-1756.	3.4	269
12932	The roles of barriers, refugia, and chromosomal clines underlying diversification in Atlantic Forest social wasps. <i>Scientific Reports</i> , 2017, 7, 7689.	1.6	33

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12934	<i>Lactobacillus plantarum</i> LP-Onlly alters the gut flora and attenuates colitis by inducing microbiome alteration in interleukin-10 knockout mice. <i>Molecular Medicine Reports</i> , 2017, 16, 5979-5985.	1.1	24
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12949	In silico design of knowledge-based <i>Plasmodium falciparum</i> epitope ensemble vaccines. <i>Journal of Molecular Graphics and Modelling</i> , 2017, 78, 195-205.	1.3	20
12950	Barley SIX-ROWED SPIKE3 encodes a putative Jumonji C-type H3K9me2/me3 demethylase that represses lateral spikelet fertility. <i>Nature Communications</i> , 2017, 8, 936.	5.8	78

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12965	Mirnova: genome-free prediction of microRNAs from small RNA sequencing data and single-cells using decision forests. <i>Nucleic Acids Research</i> , 2017, 45, e177-e177.	6.5	54
12966	Structure of human lysosomal acid $\beta$ -glucosidase—a guide for the treatment of Pompe disease. <i>Nature Communications</i> , 2017, 8, 1111.	5.8	169
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13018	High-yield production of indole-3-acetic acid by <i>Enterobacter</i> sp. DMKU-RP206, a rice phyllosphere bacterium that possesses plant growth-promoting traits. <i>3 Biotech</i> , 2017, 7, 305.	1.1	42
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13042	The <i>Apostasia</i> genome and the evolution of orchids. <i>Nature</i> , 2017, 549, 379-383.	13.7	305
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13050	mtDNA screening: Disease vectors as vertebrate samplers. <i>Molecular Ecology</i> , 2017, 26, 6478-6486.	2.0	57
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13073	Population entropies estimates of proteins. <i>AIP Conference Proceedings</i> , 2017, , .	0.3	1
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13091	Oral insecticidal activity of new bacterial isolates against insects in two orders. <i>Biocontrol Science and Technology</i> , 2017, 27, 886-902.	0.5	14
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13128	The <i>ALDH21</i> gene found in lower plants and some vascular plants codes for a NADP <sup>+</sup> -dependent succinic semialdehyde dehydrogenase. <i>Plant Journal</i> , 2017, 92, 229-243.	2.8	10
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13130	Powdery mildew of <i>Chrysanthemum morifolium</i> : phylogeny and taxonomy in the context of <i>Golovinomyces</i> species on <i>Asteraceae</i> hosts. <i>Mycologia</i> , 2017, 109, 508-519.	0.8	12

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13132	PCR cycles above routine numbers do not compromise high-throughput DNA barcoding results. <i>Genome</i> , 2017, 60, 868-873.	0.9	26
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13138	Multiple viral infections in <i>Agaricus bisporus</i> - Characterisation of 18 unique RNA viruses and 8 ORFans identified by deep sequencing. <i>Scientific Reports</i> , 2017, 7, 2469.	1.6	59
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13164	Phylogenetic community structure of fungal endophytes in seagrass species. <i>Botanica Marina</i> , 2017, 60, .	0.6	27
13165	Development of reliable detection assays for blueberry mosaic- and blackberry vein banding-associated viruses based on their population structures. <i>Journal of Virological Methods</i> , 2017, 248, 191-194.	1.0	7
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13174	Early events in speciation: Cryptic species of <i>Drosophila aldrichi</i> . <i>Ecology and Evolution</i> , 2017, 7, 4220-4228.	0.8	6
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13177	A re-evaluation of diversity of the Aporocotylidae Oehner, 1912 in <i>Siganus fuscescens</i> (Houttuyn) (Perciformes: Siganidae) and associated species. <i>Systematic Parasitology</i> , 2017, 94, 717-737.	0.5	14
13178	Evolution of mitochondrial energy metabolism genes associated with hydrothermal vent adaption of Alvinocaridid shrimps. <i>Genes and Genomics</i> , 2017, 39, 1367-1376.	0.5	21
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13180	Redescription of the halophile ciliate, <i>Blepharisma halophilum</i> Ruinen, 1938 (Ciliophora,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 502 <i>Journal of Protistology</i> , 2017, 61, 20-28.	0.5	16
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13195	MtDNA genomes reveal a relaxation of selective constraints in low-BMI individuals in a Uyghur population. <i>Human Genetics</i> , 2017, 136, 1353-1362.	1.8	8
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13201	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
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13204	Recruitment of CRISPR-Cas systems by Tn7-like transposons. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E7358-E7366.	3.3	210
13205	Navigating the conformational landscape of G protein-coupled receptor kinases during allosteric activation. <i>Journal of Biological Chemistry</i> , 2017, 292, 16032-16043.	1.6	16
13206	ALIGNSEC: viewing protein secondary structure predictions within large multiple sequence alignments. <i>Bioinformatics</i> , 2017, 33, 3991-3992.	1.8	47
13207	Release from prey preservation behavior via prey switch allowed diversification of cuticular hydrocarbon profiles in digger wasps. <i>Evolution; International Journal of Organic Evolution</i> , 2017, 71, 2562-2571.	1.1	5
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13210	New insights into the origin and the genetic status of the Balkan donkey from Serbia. <i>Animal Genetics</i> , 2017, 48, 580-590.	0.6	10
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13219	Evidence that blood flukes (Trematoda: Aporocotylidae) of chondrichthyans infect bivalves as intermediate hosts: indications of an ancient diversification of the Schistosomatoidea. <i>International Journal for Parasitology</i> , 2017, 47, 885-891.	1.3	33
13220	<i>Loimia ramzega</i> sp. nov., a new giant species of Terebellidae (Polychaeta) from French waters (Brittany, English Channel). <i>Journal of the Marine Biological Association of the United Kingdom</i> , 2017, 97, 935-942.	0.4	7

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13224	Evolutionarily diverse <i>SYP1</i> and <i>SNARE</i> s jointly sustain pollen tube growth in <i>Arabidopsis</i> . <i>Plant Journal</i> , 2017, 92, 375-385.	2.8	43
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13227	The first entomophthorean killing millipedes, <i>Arthropaga myriapodina</i> n. gen. n. sp., causes climbing before host death. <i>Journal of Invertebrate Pathology</i> , 2017, 149, 135-140.	1.5	15
13228	Novel thiosemicarbazide derivatives with 4-nitrophenyl group as multi-target drugs: $\alpha$ -glucosidase inhibitors with antibacterial and antiproliferative activity. <i>Biomedicine and Pharmacotherapy</i> , 2017, 93, 1269-1276.	2.5	25
13229	Comparative mitogenomics, phylogeny and evolutionary history of <i>Leptogorgia</i> (Gorgoniidae). <i>Molecular Phylogenetics and Evolution</i> , 2017, 115, 181-189.	1.2	25
13230	Cradles and museums of Antarctic teleost biodiversity. <i>Nature Ecology and Evolution</i> , 2017, 1, 1379-1384.	3.4	44
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13232	Characterization of the complete plastid genome of <i>Porphyridium purpureum</i> strain CCMP1328. <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 489-490.	0.2	1
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13235	The role of <i>ZIP</i> transporters and group F <i>bZIP</i> transcription factors in the Zn-deficiency response of wheat ( <i>Triticum aestivum</i> ). <i>Plant Journal</i> , 2017, 92, 291-304.	2.8	132
13236	Discovery of new orbiviruses and totivirus from <i>Anopheles</i> mosquitoes in Eastern Australia. <i>Archives of Virology</i> , 2017, 162, 3529-3534.	0.9	21
13237	<i>Bifiguratus adelaidae</i> , gen. et sp. nov., a new member of Mucoromycotina in endophytic and soil-dwelling habitats. <i>Mycologia</i> , 2017, 109, 363-378.	0.8	27
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13240	Exploring DNA Barcodes of Neotropical and Afrotropical Species of <i>EccopsisZeller</i> (Lepidoptera: Tj ETQq1 1 0.7843 14 rgBT /Qoverlock 10	0.0	2
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13243	The Taxonomy of Neotenic Net-Winged Beetles from China Based on Morphology and Molecular Data (Coleoptera: Lycidae). <i>Annales Zoologici</i> , 2017, 67, 679-687.	0.1	7
13244	Stable transgenerational epigenetic inheritance requires a DNA methylation-sensing circuit. <i>Nature Communications</i> , 2017, 8, 2124.	5.8	69
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13252	Evolutionary analysis of mumps viruses of genotype F collected in mainland China in 2001-2015. <i>Scientific Reports</i> , 2017, 7, 17144.	1.6	12
13253	<i>Alectryon vitiensis</i> : A New Species of Sapindaceae Endemic to Fiji. <i>Novon</i> , 2017, 25, 421-429.	0.3	2
13254	Major role of nitrite-oxidizing bacteria in dark ocean carbon fixation. <i>Science</i> , 2017, 358, 1046-1051.	6.0	229
13255	Molecular detection of influenza A(H1N1)pdm09 viruses with M genes from human pandemic strains among Nigerian pigs, 2013-2015: implications and associated risk factors. <i>Epidemiology and Infection</i> , 2017, 145, 3345-3360.	1.0	11
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13258	Focused conformational sampling in proteins. <i>Journal of Chemical Physics</i> , 2017, 147, 195102.	1.2	8
13259	Receptor-binding loops in alphacoronavirus adaptation and evolution. <i>Nature Communications</i> , 2017, 8, 1735.	5.8	82
13260	SID-1 Domains Important for dsRNA Import in <i>Caenorhabditis elegans</i> . <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3887-3899.	0.8	30
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13347	Molecular phylogeny of the Haplospianchnata Olson, Cribb, Tkach, Bray and Littlewood, 2003, with a description of <i>Schikhobalotrema huffmanii</i> n. sp.. <i>Acta Parasitologica</i> , 2017, 62, 502-512.	0.4	7

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13369	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
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13405	Whole genome sequencing of an ExPEC that caused fatal pneumonia at a pig farm in Changchun, China. <i>BMC Veterinary Research</i> , 2017, 13, 169.	0.7	10
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13410	A comparative molecular and 3-dimensional structural investigation into cross-continental and novel avian <i>Trypanosoma</i> spp. in Australia. <i>Parasites and Vectors</i> , 2017, 10, 234.	1.0	9
13411	The use of kDNA minicircle subclass relative abundance to differentiate between <i>Leishmania</i> (L.) infantum and <i>Leishmania</i> (L.) amazonensis. <i>Parasites and Vectors</i> , 2017, 10, 239.	1.0	34
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13450	Genome of <i>Ca. Desulfovibrio trichonymphae</i> <sup>TM</sup> , an H <sub>2</sub> -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
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13457	Evolution of the RH gene family in vertebrates revealed by brown hagfish ( <i>Eptatretus atami</i> ) genome sequences. <i>Molecular Phylogenetics and Evolution</i> , 2017, 107, 1-9.	1.2	7
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13459	Genetic diversity and structure in apple-infesting pests of <i>Carposina sasakii</i> , <i>Grapholita dimorpha</i> and <i>Grapholita molesta</i> in Korea. <i>Journal of Asia-Pacific Entomology</i> , 2017, 20, 13-16.	0.4	4
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13466	Two Isoforms of Clp Peptidase in <i>Pseudomonas aeruginosa</i> Control Distinct Aspects of Cellular Physiology. <i>Journal of Bacteriology</i> , 2017, 199, .	1.0	37
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13472	Horizontal transfer of a novel Helentron in insects. <i>Molecular Genetics and Genomics</i> , 2017, 292, 243-250.	1.0	7
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13481	Structural-functional adaptations of porcine CYP1A1 to metabolize polychlorinated dibenzo-p-dioxins. <i>Chemosphere</i> , 2017, 168, 205-216.	4.2	9
13482	Identification, annotation and expression analysis of 29 Rho GTPase genes from channel catfish ( <i>Ictalurus punctatus</i> ) after bacterial infections. <i>Developmental and Comparative Immunology</i> , 2017, 67, 445-451.	1.0	9
13483	Short Communication: Phylogenetic Evidence of HIV-1 Transmission Between Adult and Adolescent Men Who Have Sex with Men. <i>AIDS Research and Human Retroviruses</i> , 2017, 33, 318-322.	0.5	23
13484	Genomic Basis of Adaptive Evolution: The Survival of Amur Ide ( <i>Leuciscus waleckii</i> ) in an Extremely Alkaline Environment. <i>Molecular Biology and Evolution</i> , 2017, 34, 145-159.	3.5	66
13485	Investigation of epizootic papillomatosis in bluegill <i>Lepomis macrochirus</i> (Rafinesque 1810) using next-generation sequencing. <i>Journal of Fish Diseases</i> , 2017, 40, 947-952.	0.9	2
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13488	Phylogeny and Systematics of Leptomyxid Amoebae (Amoebozoa, Tubulinea, Leptomyxida). <i>Protist</i> , 2017, 168, 220-252.	0.6	11
13489	Molecular phylogeny of the aquatic beetle family Noteridae (Coleoptera: Adephaga) with an emphasis on data partitioning strategies. <i>Molecular Phylogenetics and Evolution</i> , 2017, 107, 282-292.	1.2	49
13490	Chemosynthetic symbionts of marine invertebrate animals are capable of nitrogen fixation. <i>Nature Microbiology</i> , 2017, 2, 16195.	5.9	151
13491	Is the Antarctic <i>Ophryotrocha orensanzi</i> (Annelida: Dorvilleidae) a circumpolar non-specialized opportunist?. <i>Systematics and Biodiversity</i> , 2017, 15, 105-114.	0.5	6

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13494	Genetic typing of bovine viral diarrhoea virus in cattle on Irish farms. <i>Research in Veterinary Science</i> , 2017, 111, 14-20.	0.9	4
13495	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
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13501	Evolution in African tropical trees displaying ploidy-habitat association: The genus <i>Afzelia</i> (Leguminosae). <i>Molecular Phylogenetics and Evolution</i> , 2017, 107, 270-281.	1.2	32
13502	Sweet Tetra-Trophic Interactions: Multiple Evolution of Nectar Secretion, a Defensive Extended Phenotype in Cynipid Gall Wasps. <i>American Naturalist</i> , 2017, 189, 67-77.	1.0	38
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13506	Microbial and viral-like rhodopsins present in coastal marine sediments from four polar and subpolar regions. <i>FEMS Microbiology Ecology</i> , 2017, 93, fiw216.	1.3	9
13507	A complete molecular phylogeny of <i>Claravis</i> confirms its paraphyly within small New World ground-doves (Aves: Peristerinae) and implies multiple plumage state transitions. <i>Journal of Avian Biology</i> , 2017, 48, 459-464.	0.6	7
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13512	Morphologically tortured: taxonomic placement of an Antarctic springtail (Collembola: Isotomidae) misguided by morphology and ecology. <i>Zoologica Scripta</i> , 2017, 46, 180-187.	0.7	14
13513	Comparative performance of double-digest RAD sequencing across divergent arachnid lineages. <i>Molecular Ecology Resources</i> , 2017, 17, 418-430.	2.2	24
13514	Assessing the phylogenetic placement and redundancy of Aspidotheliaceae (Ascomycota), an orphaned family of lichen-forming fungi. <i>Systematics and Biodiversity</i> , 2017, 15, 63-73.	0.5	5
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13516	<i>Cryptococcus neoformans</i> UGT1 encodes a UDP-Galactose/UDP-GalNAc transporter. <i>Glycobiology</i> , 2017, 27, 87-98.	1.3	20
13517	Morphological and taxonomic demarcation of <i>Brachionus asplanchnoidis</i> Charin within the <i>Brachionus plicatilis</i> cryptic species complex (Rotifera, Monogononta). <i>Hydrobiologia</i> , 2017, 796, 19-37.	1.0	28
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13521	Rare or cryptic? The first report of an Omura's whale ( <i>Balaenoptera omurai</i> ) in the South Atlantic Ocean. <i>Marine Mammal Science</i> , 2017, 33, 80-95.	0.9	14
13522	Functional Diversification of the Four MARCKS Family Members in Zebrafish Neural Development. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2017, 328, 119-138.	0.6	14
13523	Molecular characterization of a recently identified circovirus in zebra finches ( <i>Taeniopygia</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T. <i>Journal of Virology</i> , 2017, 91, 106-116.	0.8	11
13524	<i>Drosophila yakuba mayottensis</i> , a new model for the study of incipient ecological speciation. <i>Fly</i> , 2017, 11, 37-45.	0.9	7
13525	Morphology, morphogenesis, and molecular phylogeny of <i>Uroleptus</i> ( <i>Caudiholosticha</i> ) <i>stueberi</i> (Foissner, 1987) comb. nov. (Ciliophora, Hypotricha), and reclassification of the remaining <i>Caudiholosticha</i> species. <i>European Journal of Protistology</i> , 2017, 59, 82-98.	0.5	20
13526	Phylogenetic regionalization of marine plants reveals close evolutionary affinities among disjunct temperate assemblages. <i>Biological Conservation</i> , 2017, 213, 351-356.	1.9	17
13527	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

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13530	High-Sequence Diversity and Rapid Virus Turnover Contribute to Higher Rates of Coreceptor Switching in Treatment-Experienced Subjects with HIV-1 Viremia. <i>AIDS Research and Human Retroviruses</i> , 2017, 33, 234-245.	0.5	3
13531	Serpins in arthropod biology. <i>Seminars in Cell and Developmental Biology</i> , 2017, 62, 105-119.	2.3	121
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13536	HIV-1 antiretroviral drug resistance patterns in patients failing NNRTI-based treatment: results from a national survey in South Africa. <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, 210-219.	1.3	37
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13539	Molecular phylogenies challenge the classification of Polymastiidae (Porifera, Demospongiae) based on morphology. <i>Organisms Diversity and Evolution</i> , 2017, 17, 45-66.	0.7	13
13540	Evolutionary divergence in <i>Chenopodium</i> and validation of SNPs in chloroplast <i>rbcl</i> and <i>matk</i> genes by allele-specific PCR for development of <i>Chenopodium</i> quinoa-specific markers. <i>Crop Journal</i> , 2017, 5, 32-42.	2.3	8
13541	Importance of incomplete lineage sorting and introgression in the origin of shared genetic variation between two closely related pines with overlapping distributions. <i>Heredity</i> , 2017, 118, 211-220.	1.2	73
13542	Relief of Xylose Binding to Cellobiose Phosphorylase by a Single Distal Mutation. <i>ACS Synthetic Biology</i> , 2017, 6, 206-210.	1.9	5
13543	DNA barcodes of the native ray-finned fishes in Taiwan. <i>Molecular Ecology Resources</i> , 2017, 17, 796-805.	2.2	62
13544	Analysis of apolipoprotein genes and their involvement in disease response of channel catfish after bacterial infection. <i>Developmental and Comparative Immunology</i> , 2017, 67, 464-470.	1.0	31
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13549	Full-length and mini-length DNA barcoding for the identification of seafood commercially traded in Germany. <i>Food Control</i> , 2017, 73, 922-929.	2.8	43
13550	A Metabarcoding Survey on the Fungal Microbiota Associated to the Olive Fruit Fly. <i>Microbial Ecology</i> , 2017, 73, 677-684.	1.4	38
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13552	Phylogenomics and species delimitation in the knob-scaled lizards of the genus <i>Xenosaurus</i> (Squamata: Xenosauridae) using ddRADseq data reveal a substantial underestimation of diversity. <i>Molecular Phylogenetics and Evolution</i> , 2017, 106, 241-253.	1.2	63
13553	Transmission between Archaic and Modern Human Ancestors during the Evolution of the Oncogenic Human Papillomavirus 16. <i>Molecular Biology and Evolution</i> , 2017, 34, 4-19.	3.5	103
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13555	Independent Evolution of Acetolactate Synthase-inhibiting Herbicide Resistance in Weedy Sorghum Populations across Common Geographic Regions. <i>Weed Science</i> , 2017, 65, 164-176.	0.8	13
13556	Chloroplast genome structures in <i>Gentiana</i> (Gentianaceae), based on three medicinal alpine plants used in Tibetan herbal medicine. <i>Current Genetics</i> , 2017, 63, 241-252.	0.8	34
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13558	Multiple origins of Hawaiian drosophilids: Phylogeography of <i>Scaptomyza</i> Hardy (Diptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.3	23
13559	Statistically Consistent <i>k</i> -mer Methods for Phylogenetic Tree Reconstruction. <i>Journal of Computational Biology</i> , 2017, 24, 153-171.	0.8	19
13560	Species diversity can be overestimated by a fixed empirical threshold: insights from DNA barcoding of the genus <i>Cletus</i> (Hemiptera: Coreidae) and the meta-analysis of COI data from previous phylogeographical studies. <i>Molecular Ecology Resources</i> , 2017, 17, 314-323.	2.2	13
13561	DNA barcoding for identification of consumer-relevant mushrooms: A partial solution for product certification?. <i>Food Chemistry</i> , 2017, 214, 383-392.	4.2	68
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13565	Characterization of Class III Peroxidases from Switchgrass. <i>Plant Physiology</i> , 2017, 173, 417-433.	2.3	43
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13567	Climate-induced glacier and snow loss imperils alpine stream insects. <i>Global Change Biology</i> , 2017, 23, 2577-2589.	4.2	75
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13571	Characterization of <i>Gambierdiscus lapillus</i> sp. nov. (Gonyaulacales, Dinophyceae): a new toxic dinoflagellate from the Great Barrier Reef (Australia). <i>Journal of Phycology</i> , 2017, 53, 283-297.	1.0	56
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13578	Diversity of free-Living nitrogen fixing <i>Streptomyces</i> in soils of the badlands of South Dakota. <i>Microbiological Research</i> , 2017, 195, 31-39.	2.5	98
13579	Development of rubber-enriched dandelion varieties by metabolic engineering of the inulin pathway. <i>Plant Biotechnology Journal</i> , 2017, 15, 740-753.	4.1	58
13580	In-silico prediction of dual function of DksA like hypothetical protein in <i>V. cholerae</i> O395 genome. <i>Microbiological Research</i> , 2017, 195, 60-70.	2.5	1
13581	Multiple transporters are involved in natamycin efflux in <i>Streptomyces chattanoogensis</i> L10. <i>Molecular Microbiology</i> , 2017, 103, 713-728.	1.2	21



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13583	Estimation of long terminal repeat element content in the <i>Helicoverpa zea</i> genome from high-throughput sequencing of bacterial artificial chromosome pools. <i>Genome</i> , 2017, 60, 310-324.	0.9	7
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13585	Molecular characterisation of <i>Theileria orientalis</i> in imported and native bovines from Pakistan. <i>Infection, Genetics and Evolution</i> , 2017, 47, 19-25.	1.0	22
13586	Phylogeography of a freshwater crustacean species complex reflects a longgone archipelago. <i>Journal of Biogeography</i> , 2017, 44, 421-432.	1.4	43
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13588	Phenotypic and genomic characterization of the antimicrobial producer <i>Rheinheimera</i> sp. EpRS3 isolated from the medicinal plant <i>Echinacea purpurea</i> : insights into its biotechnological relevance. <i>Research in Microbiology</i> , 2017, 168, 293-305.	1.0	39
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13590	How petals change their spots: cis-regulatory rewiring in <i>Clarkia</i> (Onagraceae). <i>New Phytologist</i> , 2017, 216, 510-518.	3.5	50
13591	Transcriptome and secretome of two <i>Pythium</i> species during infection and saprophytic growth. <i>Physiological and Molecular Plant Pathology</i> , 2017, 99, 41-54.	1.3	3
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13596	Lineage diversification of fringe-toed lizards (Phrynosomatidae: <i>Uma notata</i> complex) in the Colorado Desert: Delimiting species in the presence of gene flow. <i>Molecular Phylogenetics and Evolution</i> , 2017, 106, 103-117.	1.2	28
13597	MetaMLST: multi-locus strain-level bacterial typing from metagenomic samples. <i>Nucleic Acids Research</i> , 2017, 45, e7-e7.	6.5	88
13598	Phylogeographic structure across one of the largest intact tropical savannahs: Molecular and morphological analysis of Australia's iconic frilled lizard <i>Chlamydosaurus kingii</i> . <i>Molecular Phylogenetics and Evolution</i> , 2017, 106, 217-227.	1.2	11
13599	Long-term agricultural fertilization alters arbuscular mycorrhizal fungal community composition and barley ( <i>Hordeum vulgare</i> ) mycorrhizal carbon and phosphorus exchange. <i>New Phytologist</i> , 2017, 213, 874-885.	3.5	121

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13601	The major outer sheath protein forms distinct conformers and multimeric complexes in the outer membrane and periplasm of <i>Treponema denticola</i> . <i>Scientific Reports</i> , 2017, 7, 13260.	1.6	10
13602	Molecular phylogenetic analysis of new <i>Entoloma rhodopolium</i> -related species in Japan and its identification method using PCR-RFLP. <i>Scientific Reports</i> , 2017, 7, 14942.	1.6	13
13603	Rebound of Cotton leaf curl Multan virus and its exclusive detection in cotton leaf curl disease outbreak, Punjab (India), 2015. <i>Scientific Reports</i> , 2017, 7, 17361.	1.6	25
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13606	The use of Oxford Nanopore native barcoding for complete genome assembly. <i>GigaScience</i> , 2017, 6, 1-6.	3.3	19
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13608	mutLBSgeneDB: mutated ligand binding site gene DataBase. <i>Nucleic Acids Research</i> , 2017, 45, D256-D263.	6.5	21
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13616	Copy Number Variation and Expression Analysis Reveals a Nonorthologous Pinta Gene Family Member Involved in Butterfly Vision. <i>Genome Biology and Evolution</i> , 2017, 9, 3398-3412.	1.1	3
13617	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
13618	Evidence of Diversity, Site, and Host Specificity of Sea Turtle Blood Flukes (Digenea: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 67 103, 756-767.	0.3	17

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13620	<i>Phytophthora megakarya</i> and <i>Phytophthora palmivora</i> , Closely Related Causal Agents of Cacao Black Pod Rot, Underwent Increases in Genome Sizes and Gene Numbers by Different Mechanisms. <i>Genome Biology and Evolution</i> , 2017, 9, 536-557.	1.1	71
13621	Whole genome sequencing of Chinese clearhead icefish, <i>Protosalanx hyalocranius</i> . <i>GigaScience</i> , 2017, 6, 1-6.	3.3	15
13622	The occurrence of three species of the genus <i>Oscheius</i> Andr�ssy, 1976 (Nematoda: Rhabditida) in Iran. <i>Journal of Plant Protection Research</i> , 2017, 57, 248-255.	1.0	8
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13624	<i>Sporolithon indopacificum</i> sp. nov. (Sporolithales, Rhodophyta) from tropical western Indian and western Pacific oceans: First report, confirmed by DNA sequence data, of a widely distributed species of <i>Sporolithon</i> . <i>Phytotaxa</i> , 2017, 326, 115.	0.1	18
13625	Cloud-POA: A cloud-based map only implementation of PO-MSA on Amazon multi-node EC2 Hadoop Cluster. , 2017, , .		2
13626	Identification of an enterovirus recombinant with a torovirus-like gene insertion during a diarrhea outbreak in fattening pigs. <i>Virus Evolution</i> , 2017, 3, vex024.	2.2	30
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13630	Identification of Oxa1 Homologs Operating in the Eukaryotic Endoplasmic Reticulum. <i>Cell Reports</i> , 2017, 21, 3708-3716.	2.9	107
13631	<i>Hedera caerulescens</i> (Alcyonacea : Alcyoniidae), a new genus and species of soft coral from the temperate North Atlantic: invasive in its known range?. <i>Invertebrate Systematics</i> , 2017, 31, 723.	0.5	4
13632	The Tc1/mariner DNA transposons in the genome of mollusk <i>Littorina saxatilis</i> . <i>Russian Journal of Genetics</i> , 2017, 53, 1358-1365.	0.2	2
13633	Comparative analysis of the genomes of <i>Stylophora pistillata</i> and <i>Acropora digitifera</i> provides evidence for extensive differences between species of corals. <i>Scientific Reports</i> , 2017, 7, 17583.	1.6	121
13634	Diversification of Type VI Secretion System Toxins Reveals Ancient Antagonism among Bee Gut Microbes. <i>MBio</i> , 2017, 8, .	1.8	94
13635	Evolution of sequence-specific anti-silencing systems in <i>Arabidopsis</i> . <i>Nature Communications</i> , 2017, 8, 2161.	5.8	26
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13637	Complete mitochondrial genome of Siberian musk deer <i>Moschus moschiferus</i> (Artiodactyla): Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 Part B: Resources, 2017, 2, 860-861.	0.2	3
13638	<i>Ipomoea gilana</i> : A New and Endemic Morning Glory (Ipomoeaceae, Convolvulaceae) in the Gila National Forest, New Mexico. Systematic Botany, 2017, 42, 974-978.	0.2	0
13639	A Comprehensive Analysis of Transcript-Supported De Novo Genes in <i>Saccharomyces sensu stricto</i> Yeasts. Molecular Biology and Evolution, 2017, 34, 2823-2838.	3.5	28
13640	Lichenicolous species of <i>Hainesia</i> belong to Phacidiales (Leotiomyces) and are included in an extended concept of <i>Epithamnolia</i> . Mycologia, 2017, 109, 882-899.	0.8	13
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13642	Origins of the fern genus <i>Hymenophyllum</i> (Hymenophyllaceae) in New Caledonia: Multiple independent colonizations from surrounding territories and limited in situ diversification. Taxon, 2017, 66, 1041-1064.	0.4	17
13643	Draft genome of the lined seahorse, <i>Hippocampus erectus</i> . GigaScience, 2017, 6, 1-6.	3.3	38
13644	Molecular data, based on an exhaustive species sampling of the fern genus <i>Rumohra</i> (Dryopteridaceae), reveal a biogeographical history mostly shaped by dispersal and several cryptic species in the widely distributed <i>Rumohra adiantiformis</i> . Botanical Journal of the Linnean Society, 2017, 185, 463-481.	0.8	21
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13647	A Poissonian Model of Indel Rate Variation for Phylogenetic Tree Inference. Systematic Biology, 2017, 66, 698-714.	2.7	4
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13650	Genomic characterization of environmental <i>Pseudomonas aeruginosa</i> isolated from dental unit waterlines revealed the insertion sequence ISPa11 as a chaotropic element. FEMS Microbiology Ecology, 2017, 93, .	1.3	21
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13652	Evolutionary Origins of Pax6 Control of Crystallin Genes. Genome Biology and Evolution, 2017, 9, 2075-2092.	1.1	20
13653	Complete Mitochondrial Genomes of the Cherskiiâ€™s Sculpin <i>Cottus czerskii</i> and Siberian Taimen <i>Hucho taimen</i> Reveal GenBank Entry Errors: Incorrect Species Identification and Recombinant Mitochondrial Genome. Evolutionary Bioinformatics, 2017, 13, 117693431772678.	0.6	12
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13795	Impact of Clinical Parameters in the Intra-host Evolution of HIV-1 Subtype B in Pediatric Patients: A Machine Learning Approach. <i>Genome Biology and Evolution</i> , 2017, 9, 2715-2726.	1.1	5
13796	Origin and Spread of Spliceosomal Introns: Insights from the Fungal Clade <i>Zygomycota</i> . <i>Genome Biology and Evolution</i> , 2017, 9, 2658-2667.	1.1	16
13797	Defining the Roles of the Cation Diffusion Facilitators in Fe <sup>2+</sup> /Zn <sup>2+</sup> Homeostasis and Establishment of Their Participation in Virulence in <i>Pseudomonas aeruginosa</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 84.	1.8	36
13798	Sequencing of <i>bla</i> MP-Carrying <i>IncN2</i> Plasmids, and Comparative Genomics of <i>IncN2</i> Plasmids Harboring Class 1 Integrons. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 102.	1.8	22

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13800	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
13801	Activity of Bacteriophages in Removing Biofilms of <i>Pseudomonas aeruginosa</i> Isolates from Chronic Rhinosinusitis Patients. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 418.	1.8	132
13802	Analysis of the Salivary Gland Transcriptome of Unfed and Partially Fed <i>Amblyomma sculptum</i> Ticks and Descriptive Proteome of the Saliva. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 476.	1.8	79
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13804	Recent Positive Selection in Genes of the Mammalian Epidermal Differentiation Complex Locus. <i>Frontiers in Genetics</i> , 2016, 7, 227.	1.1	20
13805	Transcription Factors in Fungi: TFome Dynamics, Three Major Families, and Dual-Specificity TFs. <i>Frontiers in Genetics</i> , 2017, 8, 53.	1.1	105
13806	A Glimpse into the Satellite DNA Library in Characidae Fish (Teleostei, Characiformes). <i>Frontiers in Genetics</i> , 2017, 8, 103.	1.1	27
13807	Comparative Genomic Analysis of the Human Gut Microbiome Reveals a Broad Distribution of Metabolic Pathways for the Degradation of Host-Synthesized Mucin Glycans and Utilization of Mucin-Derived Monosaccharides. <i>Frontiers in Genetics</i> , 2017, 8, 111.	1.1	79
13808	New Tools in Orthology Analysis: A Brief Review of Promising Perspectives. <i>Frontiers in Genetics</i> , 2017, 8, 165.	1.1	49
13809	Draft Sequencing of the Heterozygous Diploid Genome of Satsuma ( <i>Citrus unshiu</i> Marc.) Using a Hybrid Assembly Approach. <i>Frontiers in Genetics</i> , 2017, 8, 180.	1.1	49
13810	Headwater Capture Evidenced by Paleo-Rivers Reconstruction and Population Genetic Structure of the Armored Catfish ( <i>Pareiorhaphis garbei</i> ) in the Serra do Mar Mountains of Southeastern Brazil. <i>Frontiers in Genetics</i> , 2017, 8, 199.	1.1	28
13811	Specificity, Privacy, and Degeneracy in the CD4 T Cell Receptor Repertoire Following Immunization. <i>Frontiers in Immunology</i> , 2017, 8, 430.	2.2	52
13812	Discovery of Novel Leptospirosis Vaccine Candidates Using Reverse and Structural Vaccinology. <i>Frontiers in Immunology</i> , 2017, 8, 463.	2.2	44
13813	Hidden Lineage Complexity of Glycan-Dependent HIV-1 Broadly Neutralizing Antibodies Uncovered by Digital Panning and Native-Like gp140 Trimer. <i>Frontiers in Immunology</i> , 2017, 8, 1025.	2.2	21
13814	Detection of Increased Plasma Interleukin-6 Levels and Prevalence of <i>Prevotella copri</i> and <i>Bacteroides vulgatus</i> in the Feces of Type 2 Diabetes Patients. <i>Frontiers in Immunology</i> , 2017, 8, 1107.	2.2	113
13815	Local Chromatin Features Including PU.1 and IKAROS Binding and H3K4 Methylation Shape the Repertoire of Immunoglobulin Kappa Genes Chosen for V(D)J Recombination. <i>Frontiers in Immunology</i> , 2017, 8, 1550.	2.2	40
13816	Cu,Zn Superoxide Dismutase Genes in <i>Tribolium castaneum</i> : Evolution, Molecular Characterisation, and Gene Expression during Immune Priming. <i>Frontiers in Immunology</i> , 2017, 8, 1811.	2.2	28

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13818	Colonial Tube-Dwelling Ciliates Influence Methane Cycling and Microbial Diversity within Methane Seep Ecosystems. <i>Frontiers in Marine Science</i> , 2017, 3, .	1.2	17
13819	Metagenomic Binning Recovers a Transcriptionally Active Gammaproteobacterium Linking Methanotrophy to Partial Denitrification in an Anoxic Oxygen Minimum Zone. <i>Frontiers in Marine Science</i> , 2017, 4, .	1.2	44
13820	Diversity and Transcriptional Levels of RuBisCO Form II of Sulfur-Oxidizing $\hat{\text{I}}^3$ -Proteobacteria in Coastal-Upwelling Waters with Seasonal Anoxia. <i>Frontiers in Marine Science</i> , 2017, 4, .	1.2	4
13821	Diatom Transcriptional and Physiological Responses to Changes in Iron Bioavailability across Ocean Provinces. <i>Frontiers in Marine Science</i> , 2017, 4, .	1.2	55
13822	Transcriptomic Resilience of the <i>Montipora digitata</i> Holobiont to Low pH. <i>Frontiers in Marine Science</i> , 2017, 4, .	1.2	16
13823	Genome Analysis of <i>Clostridium difficile</i> PCR Ribotype 014 Lineage in Australian Pigs and Humans Reveals a Diverse Genetic Repertoire and Signatures of Long-Range Interspecies Transmission. <i>Frontiers in Microbiology</i> , 2016, 7, 2138.	1.5	117
13824	The <i>sil</i> Locus in <i>Streptococcus Anginosus</i> Group: Interspecies Competition and a Hotspot of Genetic Diversity. <i>Frontiers in Microbiology</i> , 2017, 7, 2156.	1.5	14
13825	Phenotypic Microdiversity and Phylogenetic Signal Analysis of Traits Related to Social Interaction in <i>Bacillus</i> spp. from Sediment Communities. <i>Frontiers in Microbiology</i> , 2017, 8, 29.	1.5	21
13826	Metatranscriptomic Analysis Reveals Unexpectedly Diverse Microbial Metabolism in a Biogeochemical Hot Spot in an Alluvial Aquifer. <i>Frontiers in Microbiology</i> , 2017, 8, 40.	1.5	14
13827	Production of Potent Antimicrobial Compounds from <i>Streptomyces cyaneofuscatus</i> Associated with Fresh Water Sediment. <i>Frontiers in Microbiology</i> , 2017, 8, 68.	1.5	46
13828	Characterization of the Genomic Diversity of Norovirus in Linked Patients Using a Metagenomic Deep Sequencing Approach. <i>Frontiers in Microbiology</i> , 2017, 8, 73.	1.5	34
13829	Freshwater Recirculating Aquaculture System Operations Drive Biofilter Bacterial Community Shifts around a Stable Nitrifying Consortium of Ammonia-Oxidizing Archaea and Comammox Nitrospira. <i>Frontiers in Microbiology</i> , 2017, 8, 101.	1.5	178
13830	Genome Wide In silico Analysis of the Mismatch Repair Components of <i>Plasmodium falciparum</i> and Their Comparison with Human Host. <i>Frontiers in Microbiology</i> , 2017, 08, 130.	1.5	16
13831	<i>Listeria monocytogenes</i> 10403S Arginine Repressor ArgR Finely Tunes Arginine Metabolism Regulation under Acidic Conditions. <i>Frontiers in Microbiology</i> , 2017, 8, 145.	1.5	44
13832	Diverse Plant-Associated Pleosporalean Fungi from Saline Areas: Ecological Tolerance and Nitrogen-Status Dependent Effects on Plant Growth. <i>Frontiers in Microbiology</i> , 2017, 8, 158.	1.5	48
13833	Plant Growth Promoting Bacteria Associated with <i>Langsdorffia hypogaea</i> -Rhizosphere-Host Biological Interface: A Neglected Model of Bacterial Prospection. <i>Frontiers in Microbiology</i> , 2017, 08, 172.	1.5	32
13834	The Histidine Decarboxylase Gene Cluster of <i>Lactobacillus parabuchneri</i> Was Gained by Horizontal Gene Transfer and Is Mobile within the Species. <i>Frontiers in Microbiology</i> , 2017, 8, 218.	1.5	40

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13835	Diversity and Activity of Alternative Nitrogenases in Sequenced Genomes and Coastal Environments. <i>Frontiers in Microbiology</i> , 2017, 8, 267.	1.5	56
13836	Genomic Characterization of Recent Chicken Anemia Virus Isolates in China. <i>Frontiers in Microbiology</i> , 2017, 8, 401.	1.5	34
13837	Identification and Characterization of a Novel Salt-Tolerant Esterase from the Deep-Sea Sediment of the South China Sea. <i>Frontiers in Microbiology</i> , 2017, 08, 441.	1.5	40
13838	Untangling Genomes of Novel Planctomycetal and Verrucomicrobial Species from Monterey Bay Kelp Forest Metagenomes by Refined Binning. <i>Frontiers in Microbiology</i> , 2017, 8, 472.	1.5	70
13839	Mosquito Microbiome Dynamics, a Background for Prevalence and Seasonality of West Nile Virus. <i>Frontiers in Microbiology</i> , 2017, 8, 526.	1.5	114
13840	Intriguing Interaction of Bacteriophage-Host Association: An Understanding in the Era of Omics. <i>Frontiers in Microbiology</i> , 2017, 8, 559.	1.5	37
13841	Computational Exploration of Putative LuxR Solos in Archaea and Their Functional Implications in Quorum Sensing. <i>Frontiers in Microbiology</i> , 2017, 8, 798.	1.5	22
13842	The Bacteriophage EF-P29 Efficiently Protects against Lethal Vancomycin-Resistant <i>Enterococcus faecalis</i> and Alleviates Gut Microbiota Imbalance in a Murine Bacteremia Model. <i>Frontiers in Microbiology</i> , 2017, 8, 837.	1.5	78
13843	In silico Prediction, in vitro Antibacterial Spectrum, and Physicochemical Properties of a Putative Bacteriocin Produced by <i>Lactobacillus rhamnosus</i> Strain L156.4. <i>Frontiers in Microbiology</i> , 2017, 8, 876.	1.5	29
13844	Positively Selected Sites at HCMV gB Furin Processing Region and Their Effects in Cleavage Efficiency. <i>Frontiers in Microbiology</i> , 2017, 8, 934.	1.5	17
13845	Novel <i>Synechococcus</i> Genomes Reconstructed from Freshwater Reservoirs. <i>Frontiers in Microbiology</i> , 2017, 8, 1151.	1.5	69
13846	Genome Data Provides High Support for Generic Boundaries in <i>Burkholderia</i> Sensu Lato. <i>Frontiers in Microbiology</i> , 2017, 8, 1154.	1.5	122
13847	Dynamic Co-evolution and Interaction of Avian Leukosis Virus Genetic Variants and Host Immune Responses. <i>Frontiers in Microbiology</i> , 2017, 8, 1168.	1.5	11
13848	Comparative Genomics Identifies a Novel Conserved Protein, HpaT, in Proteobacterial Type III Secretion Systems that Do Not Possess the Putative Translocon Protein HrpF. <i>Frontiers in Microbiology</i> , 2017, 8, 1177.	1.5	26
13849	Detecting the Diversity of <i>Mycoplasma</i> and <i>Ureaplasma</i> Endosymbionts Hosted by <i>Trichomonas vaginalis</i> Isolates. <i>Frontiers in Microbiology</i> , 2017, 8, 1188.	1.5	14
13850	Distribution of 2,4-Diacetylphloroglucinol Biosynthetic Genes among the <i>Pseudomonas</i> spp. Reveals Unexpected Polyphyletism. <i>Frontiers in Microbiology</i> , 2017, 8, 1218.	1.5	55
13851	Generic Amplicon Deep Sequencing to Determine Ilarvirus Species Diversity in Australian Prunus. <i>Frontiers in Microbiology</i> , 2017, 8, 1219.	1.5	25
13852	In-silico Taxonomic Classification of 373 Genomes Reveals Species Misidentification and New Genospecies within the Genus <i>Pseudomonas</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 1296.	1.5	43

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13853	Molecular Identification and Genetic Characterization of <i>Macrophomina phaseolina</i> Strains Causing Pathogenicity on Sunflower and Chickpea. <i>Frontiers in Microbiology</i> , 2017, 8, 1309.	1.5	50
13854	A Multilocus Sequence Analysis Scheme for Phylogeny of <i>Thioclava</i> Bacteria and Proposal of Two Novel Species. <i>Frontiers in Microbiology</i> , 2017, 8, 1321.	1.5	24
13855	Nitrate Sensing and Metabolism Inhibit Biofilm Formation in the Opportunistic Pathogen <i>Burkholderia pseudomallei</i> by Reducing the Intracellular Concentration of c-di-GMP. <i>Frontiers in Microbiology</i> , 2017, 8, 1353.	1.5	48
13856	Comparative Analysis of the <i>Flavobacterium columnare</i> Genomovar I and II Genomes. <i>Frontiers in Microbiology</i> , 2017, 8, 1375.	1.5	37
13857	Complete Genome Analysis of <i>Thermus parvatiensis</i> and Comparative Genomics of <i>Thermus</i> spp. Provide Insights into Genetic Variability and Evolution of Natural Competence as Strategic Survival Attributes. <i>Frontiers in Microbiology</i> , 2017, 8, 1410.	1.5	16
13858	Microbial Community Structure and the Persistence of Cyanobacterial Populations in Salt Crusts of the Hyperarid Atacama Desert from Genome-Resolved Metagenomics. <i>Frontiers in Microbiology</i> , 2017, 8, 1435.	1.5	73
13859	Genomic, Physiologic, and Symbiotic Characterization of <i>Serratia marcescens</i> Strains Isolated from the Mosquito <i>Anopheles stephensi</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 1483.	1.5	52
13860	Genome Sequencing Reveals the Potential of <i>Achromobacter</i> sp. HZ01 for Bioremediation. <i>Frontiers in Microbiology</i> , 2017, 8, 1507.	1.5	43
13861	<i>AmoA</i> -Targeted Polymerase Chain Reaction Primers for the Specific Detection and Quantification of <i>Comammox Nitrospira</i> in the Environment. <i>Frontiers in Microbiology</i> , 2017, 8, 1508.	1.5	313
13862	Zika Virus: What Have We Learnt Since the Start of the Recent Epidemic?. <i>Frontiers in Microbiology</i> , 2017, 8, 1554.	1.5	44
13863	Microbial Diversity in Sulfate-Reducing Marine Sediment Enrichment Cultures Associated with Anaerobic Biotransformation of Coastal Stockpiled Phosphogypsum (Sfax, Tunisia). <i>Frontiers in Microbiology</i> , 2017, 8, 1583.	1.5	31
13864	Identification of Fungal Communities Associated with the Biodeterioration of Waterlogged Archeological Wood in a Han Dynasty Tomb in China. <i>Frontiers in Microbiology</i> , 2017, 8, 1633.	1.5	27
13865	Comparative Genomics of <i>Burkholderia singularis</i> sp. nov., a Low G+C Content, Free-Living Bacterium That Defies Taxonomic Dissection of the Genus <i>Burkholderia</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 1679.	1.5	36
13866	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
13867	Reclassification of <i>Paenibacillus riograndensis</i> as a Genomovar of <i>Paenibacillus sonchi</i> : Genome-Based Metrics Improve Bacterial Taxonomic Classification. <i>Frontiers in Microbiology</i> , 2017, 8, 1849.	1.5	27
13868	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
13869	Characterization of Four Multidrug Resistance Plasmids Captured from the Sediments of an Urban Coastal Wetland. <i>Frontiers in Microbiology</i> , 2017, 8, 1922.	1.5	33
13870	An Investigation into Rumen Fungal and Protozoal Diversity in Three Rumen Fractions, during High-Fiber or Grain-Induced Sub-Acute Ruminal Acidosis Conditions, with or without Active Dry Yeast Supplementation. <i>Frontiers in Microbiology</i> , 2017, 8, 1943.	1.5	40



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13871	Cadaver Thanatomicrobiome Signatures: The Ubiquitous Nature of Clostridium Species in Human Decomposition. <i>Frontiers in Microbiology</i> , 2017, 8, 2096.	1.5	61
13872	Reconstruction of Diverse Verrucomicrobial Genomes from Metagenome Datasets of Freshwater Reservoirs. <i>Frontiers in Microbiology</i> , 2017, 8, 2131.	1.5	68
13873	Ecogenomics and Taxonomy of Cyanobacteria Phylum. <i>Frontiers in Microbiology</i> , 2017, 8, 2132.	1.5	99
13874	A Novel IncA/C1 Group Conjugative Plasmid, Encoding VIM-1 Metallo-Beta-Lactamase, Mediates the Acquisition of Carbapenem Resistance in ST104 <i>Klebsiella pneumoniae</i> Isolates from Neonates in the Intensive Care Unit of V. Monaldi Hospital in Naples. <i>Frontiers in Microbiology</i> , 2017, 8, 2135.	1.5	25
13875	Phylogenetic Network Analysis Revealed the Occurrence of Horizontal Gene Transfer of 16S rRNA in the Genus <i>Enterobacter</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 2225.	1.5	19
13876	To Be or Not To Be T4: Evidence of a Complex Evolutionary Pathway of Head Structure and Assembly in Giant Salmonella Virus SPN3US. <i>Frontiers in Microbiology</i> , 2017, 8, 2251.	1.5	23
13877	PifC and Osa, Plasmid Weapons against Rival Conjugative Coupling Proteins. <i>Frontiers in Microbiology</i> , 2017, 8, 2260.	1.5	17
13878	An Assessment of Different Genomic Approaches for Inferring Phylogeny of <i>Listeria monocytogenes</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 2351.	1.5	66
13879	Niche Partitioning of the N Cycling Microbial Community of an Offshore Oxygen Deficient Zone. <i>Frontiers in Microbiology</i> , 2017, 8, 2384.	1.5	60
13880	Complete Genome Sequencing of <i>Mycobacterium bovis</i> SP38 and Comparative Genomics of <i>Mycobacterium bovis</i> and <i>M. tuberculosis</i> Strains. <i>Frontiers in Microbiology</i> , 2017, 8, 2389.	1.5	40
13881	Strong Genomic and Phenotypic Heterogeneity in the <i>Aeromonas sobria</i> Species Complex. <i>Frontiers in Microbiology</i> , 2017, 8, 2434.	1.5	20
13882	Probing Genomic Aspects of the Multi-Host Pathogen <i>Clostridium perfringens</i> Reveals Significant Pangenome Diversity, and a Diverse Array of Virulence Factors. <i>Frontiers in Microbiology</i> , 2017, 8, 2485.	1.5	70
13883	Aerobic and Anaerobic Methanotrophic Communities Associated with Methane Hydrates Exposed on the Seafloor: A High-Pressure Sampling and Stable Isotope-Incubation Experiment. <i>Frontiers in Microbiology</i> , 2017, 8, 2569.	1.5	18
13884	Expression of <i>sept3</i> , <i>sept5a</i> and <i>sept5b</i> in the Developing and Adult Nervous System of the Zebrafish ( <i>Danio rerio</i> ). <i>Frontiers in Neuroanatomy</i> , 2017, 11, 6.	0.9	3
13885	Post-translational thioamidation of methyl-coenzyme M reductase, a key enzyme in methanogenic and methanotrophic Archaea. <i>ELife</i> , 2017, 6, .	2.8	82
13886	Molecular Phylogeny and Morphological Distinctions of Two Popular Bivalves, <i>Ctenoides scaber</i> and <i>Ctenoides mitis</i> . <i>Journal of Marine Biology</i> , 2017, 2017, 1-9.	1.0	2
13887	Diversity of Aerobic Bacteria Isolated from Oral and Cloacal Cavities from Free-Living Snakes Species in Costa Rica Rainforest. <i>International Scholarly Research Notices</i> , 2017, 2017, 1-9.	0.9	12
13888	Computer-Aided Design of an Epitope-Based Vaccine against Epstein-Barr Virus. <i>Journal of Immunology Research</i> , 2017, 2017, 1-15.	0.9	34

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13889	Imported Asymptomatic Bancroftian Filariasis Discovered from a <i>Plasmodium vivax</i> Infected Patient: A Case Report from Singapore. <i>Case Reports in Infectious Diseases</i> , 2017, 2017, 1-8.	0.2	5
13890	Phylogeny of Ten Kenyan <i>Plectranthus</i> Species in the <i>Coleus</i> Clade Inferred from Leaf Micromorphology, <i>RbcL</i> and <i>MatK</i> Genes. <i>Journal of Botany</i> , 2017, 2017, 1-16.	1.2	2
13891	A Novel Genetic Group of Bovine <i>Hepacivirus</i> in Archival Serum Samples from Brazilian Cattle. <i>BioMed Research International</i> , 2017, 2017, 1-4.	0.9	19
13892	L-Glutamine Supplementation Alleviates Constipation during Late Gestation of Mini Sows by Modifying the Microbiota Composition in Feces. <i>BioMed Research International</i> , 2017, 2017, 1-9.	0.9	28
13893	Complete Chloroplast Genome Sequence of <i>Coptis chinensis</i> Franch. and Its Evolutionary History. <i>BioMed Research International</i> , 2017, 2017, 1-7.	0.9	6
13894	Describing Genomic and Epigenomic Traits Underpinning Emerging Fungal Pathogens. <i>Advances in Genetics</i> , 2017, 100, 73-140.	0.8	17
13895	Where Fossils Dare and Males Matter: combined morphological and molecular analysis untangles the evolutionary history of the spider ant genus <i>Leptomymex</i> Mayr (Hymenoptera : Dolichoderinae). <i>Invertebrate Systematics</i> , 2017, 31, 765.	0.5	14
13896	Subterranean mammals show convergent regression in ocular genes and enhancers, along with adaptation to tunneling. <i>ELife</i> , 2017, 6, .	2.8	138
13897	Comparative analysis estimates the relative frequencies of co-divergence and cross-species transmission within viral families. <i>PLoS Pathogens</i> , 2017, 13, e1006215.	2.1	224
13898	HLA genotyping by next-generation sequencing of complementary DNA. <i>BMC Genomics</i> , 2017, 18, 914.	1.2	19
13899	Advances in cytogenetics of Brazilian rodents: cytotaxonomy, chromosome evolution and new karyotypic data. <i>Comparative Cytogenetics</i> , 2017, 11, 833-892.	0.3	22
13900	Improved annotation of the insect vector of citrus greening disease: biocuration by a diverse genomics community. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	1.4	62
13901	Characteristics and Lethality of a Novel Recombinant Dermonecrotic Venom Phospholipase from <i>Hemiscorpius lepturus</i> . <i>Toxins</i> , 2017, 9, 102.	1.5	14
13902	Genomic divergence and cohesion in a species of pelagic freshwater bacteria. <i>BMC Genomics</i> , 2017, 18, 794.	1.2	14
13903	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
13904	Molecular phylogenetics of cool-season grasses in the subtribes Agrostidinae, Anthoxanthinae, Aveninae, Brizinae, Calothecinae, Koeleriinae and Phalaridinae (Poaceae, Pooideae, Poaeae, Poaeae) <a href="#">Tj ETQq1 1 0.784614 rgBT 43</a> <a href="#">overlock 1</a>	1.4	14
13905	<i>Bradyrhizobium elkanii</i> nod regulon: insights through genomic analysis. <i>Genetics and Molecular Biology</i> , 2017, 40, 703-716.	0.6	5
13906	The importance of validated alpha taxonomy for phylogenetic and DNA barcoding studies: a comment on species identification of pygmy grasshoppers (Orthoptera, Tetrigidae). <i>ZooKeys</i> , 2017, 679, 139-144.	0.5	17

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13907	Identification and characterization of a subtelomeric satellite DNA in Callitrichini monkeys. <i>DNA Research</i> , 2017, 24, 377-385.	1.5	8
13908	Evolutionary history and functional divergence of the cytochrome P450 gene superfamily between <i>Arabidopsis thaliana</i> and Brassica species uncover effects of whole genome and tandem duplications. <i>BMC Genomics</i> , 2017, 18, 733.	1.2	37
13909	Bioprospection and characterization of the amyolytic activity by filamentous fungi from Brazilian Atlantic Forest. <i>Biota Neotropica</i> , 2017, 17, .	1.0	14
13910	IPD-MHC 2.0: an improved inter-species database for the study of the major histocompatibility complex. <i>Nucleic Acids Research</i> , 2017, 45, D860-D864.	6.5	168
13911	Mitochondrial genomes reveal recombination in the presumed asexual <i>Fusarium oxysporum</i> species complex. <i>BMC Genomics</i> , 2017, 18, 735.	1.2	65
13912	Alu Insertion Polymorphisms as Evidence for Population Structure in Baboons. <i>Genome Biology and Evolution</i> , 2017, 9, 2418-2427.	1.1	13
13913	Arginine and Lysine Transporters Are Essential for <i>Trypanosoma brucei</i> . <i>PLoS ONE</i> , 2017, 12, e0168775.	1.1	24
13914	Improving protein-protein interaction prediction using evolutionary information from low-quality MSAs. <i>PLoS ONE</i> , 2017, 12, e0169356.	1.1	7
13915	Clarifying the Cryptic Host Specificity of <i>Blastocystis</i> spp. Isolates from <i>Alouatta palliata</i> and <i>A. pigra</i> Howler Monkeys. <i>PLoS ONE</i> , 2017, 12, e0169637.	1.1	24
13916	Molecular Detection of <i>Plasmodium malariae</i> / <i>Plasmodium brasilianum</i> in Non-Human Primates in Captivity in Costa Rica. <i>PLoS ONE</i> , 2017, 12, e0170704.	1.1	13
13917	Cell reproductive patterns in the green alga <i>Pseudokirchneriella subcapitata</i> (=Selenastrum) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 347 T and 3,5-DCP. <i>PLoS ONE</i> , 2017, 12, e0171259.	1.1	32
13918	Whole-genome duplication and molecular evolution in <i>Cornus</i> L. (Cornaceae) Insights from transcriptome sequences. <i>PLoS ONE</i> , 2017, 12, e0171361.	1.1	17
13919	Molecular identification of two <i>Culex</i> ( <i>Culex</i> ) species of the neotropical region (Diptera: Culicidae). <i>PLoS ONE</i> , 2017, 12, e0173052.	1.1	9
13920	Genomic diversity within the haloalkaliphilic genus <i>Thioalkalivibrio</i> . <i>PLoS ONE</i> , 2017, 12, e0173517.	1.1	42
13921	IsoSel: Protein Isoform Selector for phylogenetic reconstructions. <i>PLoS ONE</i> , 2017, 12, e0174250.	1.1	7
13922	Differential transcriptome analysis supports <i>Rhodnius montenegrensis</i> and <i>Rhodnius robustus</i> (Hemiptera, Reduviidae, Triatominae) as distinct species. <i>PLoS ONE</i> , 2017, 12, e0174997.	1.1	15
13923	Analyses of the probiotic property and stress resistance-related genes of <i>Lactococcus lactis</i> subsp. <i>lactis</i> NCDO 2118 through comparative genomics and in vitro assays. <i>PLoS ONE</i> , 2017, 12, e0175116.	1.1	51
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13936	Northward dispersal of sea kraits ( <i>Laticauda semifasciata</i> ) beyond their typical range. PLoS ONE, 2017, 12, e0179871.	1.1	14
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13940	Analysis of aquaporins from the euryhaline barnacle <i>Balanus improvisus</i> reveals differential expression in response to changes in salinity. PLoS ONE, 2017, 12, e0181192.	1.1	27
13941	Sexual reproduction in plagiogrammecean diatoms: First insights into the early pennates. PLoS ONE, 2017, 12, e0181413.	1.1	9
13942	Solution NMR structure of the TRIM21 B-box2 and identification of residues involved in its interaction with the RING domain. PLoS ONE, 2017, 12, e0181551.	1.1	9

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13944	Molecular cloning and characterization of pirarucu ( <i>Arapaima gigas</i> ) follicle-stimulating hormone and luteinizing hormone $\beta$ -subunit cDNAs. <i>PLoS ONE</i> , 2017, 12, e0183545.	1.1	9
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13948	Genetic structure in the southernmost populations of black-and-gold howler monkeys ( <i>Alouatta</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 21	1.1	21
13949	Fungal communities in ancient peatlands developed from different periods in the Sanjiang Plain, China. <i>PLoS ONE</i> , 2017, 12, e0187575.	1.1	18
13950	Insights into the molecular evolution of peptidase inhibitors in arthropods. <i>PLoS ONE</i> , 2017, 12, e0187643.	1.1	1
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13952	Deep sequencing of near full-length HIV-1 genomes from plasma identifies circulating subtype C and infrequent occurrence of AC recombinant form in Southern India. <i>PLoS ONE</i> , 2017, 12, e0188603.	1.1	6
13953	Genetic signatures for <i>Helicobacter pylori</i> strains of West African origin. <i>PLoS ONE</i> , 2017, 12, e0188804.	1.1	2
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13955	Molecular characterization of hepatitis B virus in Bangladesh reveals a highly recombinant population. <i>PLoS ONE</i> , 2017, 12, e0188944.	1.1	25
13956	Characterization of <i>Mycosphaerellaceae</i> species associated with citrus greasy spot in Panama and Spain. <i>PLoS ONE</i> , 2017, 12, e0189585.	1.1	25
13957	Extra-epitopic hepatitis C virus polymorphisms confer resistance to broadly neutralizing antibodies by modulating binding to scavenger receptor B1. <i>PLoS Pathogens</i> , 2017, 13, e1006235.	2.1	47
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13960	The first initiative of DNA barcoding of ornamental plants from Egypt and potential applications in horticulture industry. <i>PLoS ONE</i> , 2017, 12, e0172170.	1.1	17

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13964	African origin of <i>Bradyrhizobium</i> populations nodulating Bambara groundnut ( <i>Vigna subterranea</i> L.) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T	1.1	30
13965	<i>Cortinarius</i> section <i>Bicolores</i> and section <i>Saturnini</i> (<i>Basidiomycota</i>, <i></i>) Tj ETQq0 0 0 rgBT /Overlock 10 T Molecular Phylogeny and Evolution of Fungi, 2017, 39, 175-200.	1.6	13
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13970	Antigenicity of the 2015â€“2016 seasonal H1N1 human influenza virus HA and NA proteins. PLoS ONE, 2017, 12, e0188267.	1.1	46
13971	Natural variation of a sensor kinase controlling a conserved stress response pathway in <i>Escherichia coli</i> . PLoS Genetics, 2017, 13, e1007101.	1.5	23
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13985	Co-occurring protein phosphorylation are functionally associated. PLoS Computational Biology, 2017, 13, e1005502.	1.5	26
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13992	Phylogeographic structure, cryptic speciation and demographic history of the sharpbelly (Hemiculter) Tj ETQq1 1 0.784314 rgBT /Ove	3.2	45
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13995	Genome-wide identification, characterization, and evolutionary analysis of flowering genes in radish (Raphanus sativus L.). BMC Genomics, 2017, 18, 981.	1.2	17
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14024	Genetic diversity of <i>Haemonchus contortus</i> isolated from sympatric wild blue sheep ( <i>Pseudois</i> ) and <i>Vectors</i> , 2017, 10, 340.	1.0	10
14025	Incidence of dengue and chikungunya viruses in mosquitoes and human patients in border provinces of Vietnam. <i>Parasites and Vectors</i> , 2017, 10, 556.	1.0	25
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14027	TGTT and AACA: two transcriptionally active LTR retrotransposon subfamilies with a specific LTR structure and horizontal transfer in four Rosaceae species. <i>Mobile DNA</i> , 2017, 8, 14.	1.3	2
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14037	Genome overview of eight <i>Candida boidinii</i> strains isolated from human activities and wild environments. <i>Standards in Genomic Sciences</i> , 2017, 12, 70.	1.5	13
14038	Draft genome of <i>Paraburkholderia caballeronis</i> TNe-841T, a free-living, nitrogen-fixing, tomato plant-associated bacterium. <i>Standards in Genomic Sciences</i> , 2017, 12, 80.	1.5	7
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14048	Rising prevalence of non-B HIV-1 subtypes in North Carolina and evidence for local onward transmission. <i>Virus Evolution</i> , 2017, 3, vex013.	2.2	22
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14058	A Shared Memory Method For Enhancing The HTNGH AlgorithmPerformance. , 2017, , .		3
14059	Molecular surveillance of spotted fever group rickettsioses in wildlife and detection of <i>Rickettsia sibirica</i> in a Topi ( <i>Damaliscus lunatus</i> ssp. <i>jimela</i> ) in Kenya. <i>Onderstepoort Journal of Veterinary Research</i> , 2017, 84, e1-e7.	0.6	1
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14066	AllerBase: a comprehensive allergen knowledgebase. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	1.4	27
14067	Influence of the Culture Media and the Organic Matter in the Growth of <i>Paxillus ammoniavirescens</i> (Contu & Dessi). <i>Mycobiology</i> , 2017, 45, 172-177.	0.6	6
14068	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 rgBT/Overlook 10 Tf 00		10
14069	Ubiquitin related enzymes and plant-specific ubiquitin ligase ATL family in tomato plants. <i>Plant Biotechnology</i> , 2017, 34, 71-78.	0.5	6

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14189	Large-scale phylogenetic analyses provide insights into unrecognized diversity and historical biogeography of Asian leaf-litter frogs, genus <i>Leptolalax</i> (Anura: Megophryidae). <i>Molecular Phylogenetics and Evolution</i> , 2018, 124, 162-171.	1.2	68
14190	Genetic variability of <i>Ganoderma zonatum</i> infecting palms in Florida. <i>Mycologia</i> , 2018, 110, 339-346.	0.8	10
14191	The complete mitochondrial genomes of five lichenized fungi in the genus <i>Usnea</i> (Ascomycota: Tj ETQq1 1 0,784314 rgBT /Over	0.2	16
14192	A New Gall Midge Species of <i>Asphondylia</i> (Diptera: Cecidomyiidae) Inducing Flower Galls on <i>Clinopodium nepeta</i> (Lamiaceae) From Europe, Its Phenology, and Associated Fungi. <i>Environmental Entomology</i> , 2018, 47, 609-622.	0.7	9
14193	Genomes of ubiquitous marine and hypersaline <i>Hydrogenovibrio</i> , <i>Thiomicrobacter</i> and <i>Thiomicrospira</i> spp. encode a diversity of mechanisms to sustain chemolithoautotrophy in heterogeneous environments. <i>Environmental Microbiology</i> , 2018, 20, 2686-2708.	1.8	32
14194	Studying AMPK in an Evolutionary Context. <i>Methods in Molecular Biology</i> , 2018, 1732, 111-142.	0.4	3
14195	Crystal structure of IspF from <i>Bacillus subtilis</i> and absence of protein complex assembly amongst IspD/IspE/IspF enzymes in the MEP pathway. <i>Bioscience Reports</i> , 2018, 38, .	1.1	4

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14197	High genetic diversity and demographic stability in <i>Aechmea kertesziae</i> (Bromeliaceae), a species of sandy coastal plains (restinga habitat) in southern Brazil. <i>Botanical Journal of the Linnean Society</i> , 2018, 186, 374-388.	0.8	13
14198	Genome-reconstruction for eukaryotes from complex natural microbial communities. <i>Genome Research</i> , 2018, 28, 569-580.	2.4	163
14199	Identification of multiple isomeric core chitobiose- $\alpha$ -modified high-mannose and paucimannose N-glycans in the planarian <i>Schmidtea mediterranea</i> . <i>Journal of Biological Chemistry</i> , 2018, 293, 6707-6720.	1.6	9
14200	Satellite DNAs are conserved and differentially transcribed among <i>Gryllus</i> cricket species. <i>DNA Research</i> , 2018, 25, 137-147.	1.5	18
14201	Comparative phylogeography of capitulate <i>Campanula</i> species from the Balkans, with description of a new species, <i>C. daucoides</i> . <i>Plant Systematics and Evolution</i> , 2018, 304, 549-575.	0.3	11
14202	Leapfrogging the Mexican highlands: influence of biogeographical and ecological factors on the diversification of highland species. <i>Biological Journal of the Linnean Society</i> , 2018, 123, 767-781.	0.7	12
14203	Patterns of <i>Midichloria</i> infection in avian-borne African ticks and their trans-Saharan migratory hosts. <i>Parasites and Vectors</i> , 2018, 11, 106.	1.0	18
14204	Identification and expression of the CEP gene family in apple ( <i>Malus domestica</i> ). <i>Journal of Integrative Agriculture</i> , 2018, 17, 348-358.	1.7	9
14205	Food availability on the shore: Linking epilithic and planktonic microalgae to the food ingested by two intertidal gastropods. <i>Marine Environmental Research</i> , 2018, 136, 71-77.	1.1	13
14206	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
14207	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
14208	Discovery and Biosynthesis of the Antibiotic Bicyclomycin in Distantly Related Bacterial Classes. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	36
14209	Can we build it? Yes we can, but should we use it? Assessing the quality and value of a very large phylogeny of <i>Campanulid</i> angiosperms. <i>American Journal of Botany</i> , 2018, 105, 417-432.	0.8	45
14210	One More Decade of <i>Agrobacterium</i> Taxonomy. <i>Current Topics in Microbiology and Immunology</i> , 2018, 418, 1-14.	0.7	21
14211	Complete genome sequence of uropathogenic <i>Escherichia coli</i> isolate UPEC 26-1. <i>Genes and Genomics</i> , 2018, 40, 643-655.	0.5	3
14212	Remodeling the Specificity of an Endosomal CORVET Tether Underlies Formation of Regulated Secretory Vesicles in the Ciliate <i>Tetrahymena thermophila</i> . <i>Current Biology</i> , 2018, 28, 697-710.e13.	1.8	25
14213	Assessing the functionality and genetic diversity of lactococcal prophages. <i>International Journal of Food Microbiology</i> , 2018, 272, 29-40.	2.1	26

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14215	<i>Peptoniphilus lacydonensis</i> sp. nov., a new human-associated species isolated from a patient with chronic refractory sinusitis. <i>New Microbes and New Infections</i> , 2018, 23, 61-69.	0.8	14
14216	Novel and interesting <i>Ophiocordyceps</i> spp. ( <i>Ophiocordycipitaceae</i> , <i>Hypocreales</i> ) with superficial perithecia from Thailand. <i>Studies in Mycology</i> , 2018, 89, 125-142.	4.5	42
14217	Phylogenetic and molecular epidemiological studies reveal evidence of recombination among Marek's disease viruses. <i>Virology</i> , 2018, 516, 202-209.	1.1	12
14218	Anti-CRISPR proteins encoded by archaeal lytic viruses inhibit subtype I-D immunity. <i>Nature Microbiology</i> , 2018, 3, 461-469.	5.9	118
14219	Identification, expression, and endocrine-disruption of three ecdysone-responsive genes in the sentinel species <i>Gammarus fossarum</i> . <i>Scientific Reports</i> , 2018, 8, 3793.	1.6	17
14220	The Apicomplexa-specific glucosamine-6-phosphate N-acetyltransferase gene family encodes a key enzyme for glycoconjugate synthesis with potential as therapeutic target. <i>Scientific Reports</i> , 2018, 8, 4005.	1.6	14
14221	The mycoparasitic fungus <i>Clonostachys rosea</i> responds with both common and specific gene expression during interspecific interactions with fungal prey. <i>Evolutionary Applications</i> , 2018, 11, 931-949.	1.5	96
14222	Dense infraspecific sampling reveals rapid and independent trajectories of plastome degradation in a heterotrophic orchid complex. <i>New Phytologist</i> , 2018, 218, 1192-1204.	3.5	56
14223	Extensive T cell cross-reactivity between diverse seasonal influenza strains in the ferret model. <i>Scientific Reports</i> , 2018, 8, 6112.	1.6	23
14224	Novel plasmid-mediated colistin resistance gene <i>mcr-7.1</i> in <i>Klebsiella pneumoniae</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2018, 73, 1791-1795.	1.3	305
14225	A Whole Genome Assembly of the Horn Fly, <i>Haematobia irritans</i> , and Prediction of Genes with Roles in Metabolism and Sex Determination. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 1675-1686.	0.8	12
14226	Endophytic yeast diversity in leaf tissue of rice, corn and sugarcane cultivated in Thailand assessed by a culture-dependent approach. <i>Fungal Biology</i> , 2018, 122, 785-799.	1.1	36
14227	<i>Acetobacter oryzafermentans</i> sp. nov., isolated from Korean traditional vinegar and reclassification of the type strains of <i>Acetobacter pasteurianus</i> subsp. <i>ascendens</i> (Henneberg 1898) and <i>Acetobacter pasteurianus</i> subsp. <i>paradoxus</i> (Frateur 1950) as <i>Acetobacter ascendens</i> sp. nov., comb. nov.. <i>Systematic and Applied Microbiology</i> , 2018, 41, 324-332.	1.2	25
14228	Morphological and molecular evidence for two new species in <i>Lepiota</i> from China. <i>Mycologia</i> , 2018, 110, 494-501.	0.8	11
14229	A Parallel Multiobjective Metaheuristic for Multiple Sequence Alignment. <i>Journal of Computational Biology</i> , 2018, 25, 1009-1022.	0.8	3
14230	The IMD pathway regulates lysozyme-like proteins (LLPs) in the silkworm <i>Antheraea mylitta</i> . <i>Journal of Invertebrate Pathology</i> , 2018, 154, 102-108.	1.5	13
14231	Phylogenetic relationship and genetic diversity of citrus psyllid populations from China and Pakistan and their associated <i>Candidatus</i> bacterium. <i>Molecular Phylogenetics and Evolution</i> , 2018, 126, 173-180.	1.2	16

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14233	Recognition of a new generic level swallow taxon from central Africa. <i>Journal of Avian Biology</i> , 2018, 49, e01698.	0.6	2
14234	Assembly and annotation of a draft genome sequence for <i>Glycine latifolia</i> , a perennial wild relative of soybean. <i>Plant Journal</i> , 2018, 95, 71-85.	2.8	33
14235	Genomic Inference of Recombination-Mediated Evolution in <i>Xanthomonas euvesicatoria</i> and <i>X. perforans</i> . <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	35
14236	Sequencing of pT5282-CTXM, p13190-KPC and p30860-NR, and comparative genomics analysis of IncX8 plasmids. <i>International Journal of Antimicrobial Agents</i> , 2018, 52, 210-217.	1.1	13
14237	Structural and thermodynamic insights into $\beta$ -1,2-glucooligosaccharide capture by a solute-binding protein in <i>Listeria innocua</i> . <i>Journal of Biological Chemistry</i> , 2018, 293, 8812-8828.	1.6	19
14238	<i>Vibrio</i> Ecology in the Neuse River Estuary, North Carolina, Characterized by Next-Generation Amplicon Sequencing of the Gene Encoding Heat Shock Protein 60 ( <i>hsp60</i> ). <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	48
14239	Discrepancies Between Molecular and Morphological Databases of Soil Ciliates Studied for Temperate Grasslands of Central Europe. <i>Protist</i> , 2018, 169, 521-538.	0.6	10
14240	Phylogeny and evolutionary radiation of the marine mussels (Bivalvia: Mytilidae) based on mitochondrial and nuclear genes. <i>Molecular Phylogenetics and Evolution</i> , 2018, 126, 233-240.	1.2	39
14241	Evolution of cyclohexadienyl dehydratase from an ancestral solute-binding protein. <i>Nature Chemical Biology</i> , 2018, 14, 542-547.	3.9	79
14242	Information Dropout Patterns in Restriction Site Associated DNA Phylogenomics and a Comparison with Multilocus Sanger Data in a Species-Rich Moth Genus. <i>Systematic Biology</i> , 2018, 67, 925-939.	2.7	46
14243	Phylogenetic analysis of <i>Dunaliella</i> (Chlorophyta) emphasizing new benthic and supralittoral isolates from Great Salt Lake. <i>Journal of Phycology</i> , 2018, 54, 483-493.	1.0	7
14244	Phylogenetic and Phylogenomic Definition of <i>Rhizopus</i> Species. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2007-2018.	0.8	47
14245	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
14246	Diversification of African tree frogs (genus <i>Leptopelis</i> ) in the highlands of Ethiopia. <i>Molecular Ecology</i> , 2018, 27, 2256-2270.	2.0	14
14247	Mitogenomics reveals phylogenetic relationships of caudofoveate aplacophoran molluscs. <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 429-436.	1.2	17
14248	The <i>Gastrodia elata</i> genome provides insights into plant adaptation to heterotrophy. <i>Nature Communications</i> , 2018, 9, 1615.	5.8	170
14249	Evolutionary diversification of the African achyranthoid clade (Amaranthaceae) in the context of sterile flower evolution and epizoochory. <i>Annals of Botany</i> , 2018, 122, 69-85.	1.4	12

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14251	The Codon Usage of Lowly Expressed Genes Is Subject to Natural Selection. <i>Genome Biology and Evolution</i> , 2018, 10, 1237-1246.	1.1	45
14252	Does biological intimacy shape ecological network structure? A test using a brood pollination mutualism on continental and oceanic islands. <i>Journal of Animal Ecology</i> , 2018, 87, 1160-1171.	1.3	20
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14254	Targeting of RNA Polymerase II by a nuclear <i>Legionella pneumophila</i> Dot/Icm effector SnpL. <i>Cellular Microbiology</i> , 2018, 20, e12852.	1.1	21
14255	Pathogenic and molecular comparison of <i>Puccinia kuehnii</i> isolates and reactions of sugarcane varieties to orange rust. <i>Plant Pathology</i> , 2018, 67, 1687-1696.	1.2	9
14256	Successive duplication-divergence mechanisms at the <i>RCO</i> locus contributed to leaf shape diversity in the Brassicaceae. <i>Development (Cambridge)</i> , 2018, 145, .	1.2	11
14257	Population genomics and geographical parthenogenesis in Japanese harvestmen (Opiliones). <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 ff</i>	0.8	11
14258	What factors potentially influence the ability of phylogenetic distance to predict trait dispersion in a temperate forest?. <i>Ecology and Evolution</i> , 2018, 8, 1107-1116.	0.8	3
14259	The Egyptian Roussette Genome Reveals Unexpected Features of Bat Antiviral Immunity. <i>Cell</i> , 2018, 173, 1098-1110.e18.	13.5	220
14260	Comparative transcriptome analysis of genes involved in anthocyanin synthesis in blueberry. <i>Plant Physiology and Biochemistry</i> , 2018, 127, 561-572.	2.8	76
14261	Genomic analyses identify multiple Asian origins and deeply diverged mitochondrial clades in inbred brown rats ( <i>Rattus norvegicus</i> ). <i>Evolutionary Applications</i> , 2018, 11, 718-726.	1.5	12
14262	Genomic analysis of oral <i>Campylobacter concisus</i> strains identified a potential bacterial molecular marker associated with active Crohn's disease. <i>Emerging Microbes and Infections</i> , 2018, 7, 1-14.	3.0	25
14263	DNA barcodes successfully delimit morphospecies in a superdiverse insect genus. <i>Zoologica Scripta</i> , 2018, 47, 311-324.	0.7	51
14264	Lignolytic mushroom <i>Lenzites elegans</i> WDP2: Laccase production, characterization, and bioremediation of synthetic dyes. <i>Ecotoxicology and Environmental Safety</i> , 2018, 158, 50-58.	2.9	55
14265	Evolution of a xenobiotic degradation pathway: formation and capture of the labile phthaloyl-CoA intermediate during anaerobic phthalate degradation. <i>Molecular Microbiology</i> , 2018, 108, 614-626.	1.2	15
14266	Redefinition and Unification of the SXT/R391 Family of Integrative and Conjugative Elements. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	35
14267	Tracking the Rules of Transmission and Introgression with Networks. <i>Microbiology Spectrum</i> , 2018, 6, .	1.2	3

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14268	A novel gene family involved in spermatophore generation in the economically important salmon louse <i>Lepeophtheirus salmonis</i> . <i>Molecular Reproduction and Development</i> , 2018, 85, 478-489.	1.0	7
14269	Comparative genome and transcriptome analysis reveal the medicinal basis and environmental adaptation of artificially cultivated <i>Taiwanofungus camphoratus</i> . <i>Mycological Progress</i> , 2018, 17, 871-883.	0.5	9
14270	Molecular phylogeny of the paper wasp subgenus <i>Polistes</i> ( <i>Polistella</i> ) Ashmead, 1904 (Hymenoptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf	0.4	4
14271	A tripartite survey of hyperparasitic fungi associated with ectoparasitic flies on bats (Mammalia: Tj ETQq1 1 0.784314 rgBT /Overlock 11	0.8	21
14272	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
14273	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
14274	Low prevalence of transmitted HIV-1 drug resistance detected by a dried blood spot (DBS)-based next-generation sequencing (NGS) method in newly diagnosed individuals in Cameroon in the years 2015-16. <i>Journal of Antimicrobial Chemotherapy</i> , 2018, 73, 1917-1929.	1.3	16
14275	What explains high plant richness in East Asia? Time and diversification in the tribe <i>Lysimachieae</i> ( <i>Primulaceae</i> ). <i>New Phytologist</i> , 2018, 219, 436-448.	3.5	34
14276	Glutathione transferases catalyze recycling of auto-toxic cyanogenic glucosides in sorghum. <i>Plant Journal</i> , 2018, 94, 1109-1125.	2.8	60
14277	Survival in northern microrefugia in an endemic Carpathian gammarid (Crustacea: Amphipoda). <i>Zoologica Scripta</i> , 2018, 47, 357-372.	0.7	18
14278	MEMSA: A Robust Parisian EA for Multidimensional Multiple Sequence Alignment. <i>Lecture Notes in Computer Science</i> , 2018, , 88-99.	1.0	0
14279	Molecular characterization and lesions associated with <i>Diomedonema diomedae</i> (Aproctoidea: Tj ETQq1 1 0.784314 rgBT /Overlock 11	0.6	5
14280	High-throughput sequencing for algal systematics. <i>European Journal of Phycology</i> , 2018, 53, 256-272.	0.9	33
14281	Donor-Derived <i>Candida dubliniensis</i> Resulting in Perigraft Abscesses in a Liver Transplant Recipient Proven by Whole Genome Sequencing: A Case Report. <i>Transplantation Proceedings</i> , 2018, 50, 915-919.	0.3	1
14282	Phylogeny, evolution and mitochondrial gene order rearrangement in scale worms (Aphroditiformia, Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.2	67
14283	A Review on the Phylogeography of Potentially Chemoautotrophic Bacteria from Major Vent and Seep Fauna and Their Contribution to Primary Production. <i>Geomicrobiology Journal</i> , 2018, 35, 612-634.	1.0	10
14284	Phylotranscriptomic analysis and genome evolution of the <i>Cypripedioideae</i> ( <i>Orchidaceae</i> ). <i>American Journal of Botany</i> , 2018, 105, 631-640.	0.8	25
14285	Diversity of dengue virus-3 genotype III in Jeddah, Saudi Arabia. <i>Acta Tropica</i> , 2018, 183, 114-118.	0.9	6

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14286	Identification of novel enzymes to enhance the ruminal digestion of barley straw. <i>Bioresource Technology</i> , 2018, 260, 76-84.	4.8	13
14287	Quantifying known and emerging uterine pathogens, and evaluating their association with metritis and fever in dairy cows. <i>Theriogenology</i> , 2018, 114, 25-33.	0.9	47
14288	Testing Wallace's intuition: water type, reproductive isolation and divergence in an Amazonian fish. <i>Journal of Evolutionary Biology</i> , 2018, 31, 882-892.	0.8	16
14289	Regulation of early endosomes across eukaryotes: Evolution and functional homology of Vps9 proteins. <i>Traffic</i> , 2018, 19, 546-563.	1.3	12
14290	Brassicales phylogeny inferred from 72 plastid genes: A reanalysis of the phylogenetic localization of two paleopolyploid events and origin of novel chemical defenses. <i>American Journal of Botany</i> , 2018, 105, 463-469.	0.8	76
14291	Phylogenomic and comparative analysis of the distribution and regulatory patterns of TPP riboswitches in fungi. <i>Scientific Reports</i> , 2018, 8, 5563.	1.6	20
14292	Complete mitochondrial genome of the green-lipped mussel, <i>Perna canaliculus</i> (Mollusca: Mytiloidea), from long nanopore sequencing reads. <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 175-176.	0.2	12
14293	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
14294	Structure of the mouse acidic amino acid decarboxylase GADL1. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018, 74, 65-73.	0.4	8
14295	Evidence for selective bacterial community structuring on microplastics. <i>Environmental Microbiology</i> , 2018, 20, 2796-2808.	1.8	261
14296	Defining and Evaluating a Core Genome Multilocus Sequence Typing Scheme for Genome-Wide Typing of <i>Clostridium difficile</i> . <i>Journal of Clinical Microbiology</i> , 2018, 56, .	1.8	64
14297	Nucleoprotein from the unique human infecting Orthobunyavirus of Simbu serogroup (Oropouche) Tj ETQq1 1 0.784314 rgBT /Overlaid 711-721.	1.2	4
14298	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. <i>Cell Reports</i> , 2018, 23, 213-226.e3.	2.9	83
14299	Retained duplications and deletions of CYP2C genes among primates. <i>Molecular Phylogenetics and Evolution</i> , 2018, 125, 204-212.	1.2	3
14300	Dopamine-mediated calcium channel regulation in synaptic suppression in <i>L. stagnalis</i> interneurons. <i>Channels</i> , 2018, 12, 153-173.	1.5	6
14301	Alignment Modulates Ancestral Sequence Reconstruction Accuracy. <i>Molecular Biology and Evolution</i> , 2018, 35, 1783-1797.	3.5	70
14302	Postgenomics Characterization of an Essential Genetic Determinant of Mammary Pathogenic <i>Escherichia coli</i> . <i>MBio</i> , 2018, 9, .	1.8	46
14303	Effect of vaccination on cattle subclinically infected with foot-and-mouth disease virus in Cameroon. <i>Preventive Veterinary Medicine</i> , 2018, 155, 1-10.	0.7	19



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14304	Genome Sequences of <i>Apibacter</i> spp., Gut Symbionts of Asian Honey Bees. <i>Genome Biology and Evolution</i> , 2018, 10, 1174-1179.	1.1	27
14305	Draft genome of the Peruvian scallop <i>Argopecten purpuratus</i> . <i>GigaScience</i> , 2018, 7, .	3.3	60
14306	Accelerated evolution of toxin genes: Exonization and intronization in snake venom disintegrin/metalloprotease genes. <i>Toxicon</i> , 2018, 148, 16-25.	0.8	17
14307	Cultivation and genomics of the first freshwater SAR11 (LD12) isolate. <i>ISME Journal</i> , 2018, 12, 1846-1860.	4.4	123
14308	Bacterial diversity and community structure in the rhizosphere of four <i>Ferula</i> species. <i>Scientific Reports</i> , 2018, 8, 5345.	1.6	33
14309	Sequence Analysis of IncA/C and IncI1 Plasmids Isolated from Multidrug-Resistant <i>Salmonella</i> Newport Using Single-Molecule Real-Time Sequencing. <i>Foodborne Pathogens and Disease</i> , 2018, 15, 361-371.	0.8	16
14310	Molecular phylogeny and temporal diversification of <i>Tanytarsus</i> van der Wulp (Diptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 100 Entomology, 2018, 43, 659-677.	1.7	23
14311	Sesquiterpene Synthase-3-Hydroxy-3-Methylglutaryl Coenzyme A Synthase Fusion Protein Responsible for Hirsutene Biosynthesis in <i>Stereum hirsutum</i> . <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	25
14312	Role of a membrane-bound aldehyde dehydrogenase complex AldFGH in acetic acid fermentation with <i>Acetobacter pasteurianus</i> SKU1108. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 4549-4561.	1.7	16
14313	Co-evolutionary interactions between host resistance and pathogen avirulence genes in rice-Magnaporthe oryzae pathosystem. <i>Fungal Genetics and Biology</i> , 2018, 115, 9-19.	0.9	15
14314	Novel orthohepeviruses in wild rodents from So Paulo State, Brazil. <i>Virology</i> , 2018, 519, 12-16.	1.1	13
14315	A large-scale phylogeny of Microhylidae inferred from a combined dataset of 121 genes and 427 taxa. <i>Molecular Phylogenetics and Evolution</i> , 2018, 126, 85-91.	1.2	35
14316	Molecular phylogeny of <i>Galium</i> L. of the tribe Rubieae (Rubiaceae) – Emphasis on Chinese species and recognition of a new genus <i>Pseudogalium</i> . <i>Molecular Phylogenetics and Evolution</i> , 2018, 126, 221-232.	1.2	11
14317	Identification of the First Diketomorpholine Biosynthetic Pathway Using FAC-MS Technology. <i>ACS Chemical Biology</i> , 2018, 13, 1142-1147.	1.6	30
14318	Wild birds in Chile Harbor diverse avian influenza A viruses. <i>Emerging Microbes and Infections</i> , 2018, 7, 1-4.	3.0	20
14319	UDP-Glucuronic Acid Transport Is Required for Virulence of <i>Cryptococcus neoformans</i> . <i>MBio</i> , 2018, 9, .	1.8	15
14320	A New Genus of Tapeworm (Cestoda: Onchoproteocephalidea) from Sawfish (Elasmobranchii: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 100	0.3	4
14322	A nation-wide genetic survey revealed a complex population structure of <i>Bemisia tabaci</i> in Pakistan. <i>Acta Tropica</i> , 2018, 183, 119-125.	0.9	27

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14323	Spore morphology and ultrastructure of an <i>Ascosphaera apis</i> strain from the honeybees ( <i>Apis mellifera</i> ). <i>Journal of Microbiology and Biotechnology</i> , 2018, 8, 107-114.	0.8	6
14324	Whole-genome resequencing reveals signatures of selection and timing of duck domestication. <i>GigaScience</i> , 2018, 7, .	3.3	86
14325	Impact of spatial organization on a novel auxotrophic interaction among soil microbes. <i>ISME Journal</i> , 2018, 12, 1443-1456.	4.4	51
14326	Analysis of DNAs associated with coconut foliar decay disease implicates a unique single-stranded DNA virus representing a new taxon. <i>Scientific Reports</i> , 2018, 8, 5698.	1.6	19
14327	LINEs Contribute to the Origins of Middle Bodies of SINEs besides 3' UTR Tails. <i>Genome Biology and Evolution</i> , 2018, 10, 370-379.	1.1	6
14328	A tandem array of UDP-glycosyltransferases from the UGT73C subfamily glycosylate sapogenins, forming a spectrum of mono- and bisdesmosidic saponins. <i>Plant Molecular Biology</i> , 2018, 97, 37-55.	2.0	31
14329	DNA barcoding for specific and sensitive detection of <i>Cuminum cyminum</i> adulteration in <i>Bunium persicum</i> . <i>Phytomedicine</i> , 2018, 50, 178-183.	2.3	32
14330	<i>Geodermatophilus chilensis</i> sp. nov., from soil of the Yungay core-region of the Atacama Desert, Chile. <i>Systematic and Applied Microbiology</i> , 2018, 41, 427-436.	1.2	25
14331	Molecular basis for the folding of $\beta^2$ -helical autotransporter passenger domains. <i>Nature Communications</i> , 2018, 9, 1395.	5.8	18
14332	Novel Hyper Antimony-Oxidizing Bacteria Isolated from Contaminated Mine Soils in China. <i>Geomicrobiology Journal</i> , 2018, 35, 713-720.	1.0	35
14333	HNRNPA1 promotes recognition of splice site decoys by U2AF2 in vivo. <i>Genome Research</i> , 2018, 28, 689-698.	2.4	28
14334	Influence of Parameters in Multiple Sequence Alignment Methods for Protein Sequences. <i>Advances in Intelligent Systems and Computing</i> , 2018, , 183-191.	0.5	0
14335	Pollutants degradation performance and microbial community structure of aerobic granular sludge systems using inoculums adapted at mild and low temperature. <i>Chemosphere</i> , 2018, 204, 431-441.	4.2	31
14336	Analysis of HIV-1 envelope evolution suggests antibody-mediated selection of common epitopes among Chinese former plasma donors from a narrow-source outbreak. <i>Scientific Reports</i> , 2018, 8, 5743.	1.6	3
14337	Morphological and molecular characterisation of <i>Aphelenchoides primadentus</i> n. sp. (Nematoda). <i>Journal of Microbiology and Biotechnology</i> , 2018, 8, 107-114.	0.2	14
14338	Genome-wide comparisons reveal evidence for a species complex in the black-lip pearl oyster <i>Pinctada margaritifera</i> (Bivalvia: Pteriidae). <i>Scientific Reports</i> , 2018, 8, 191.	1.6	7
14339	Comparative analysis of low complexity regions in Plasmodia. <i>Scientific Reports</i> , 2018, 8, 335.	1.6	20
14340	Sweep Dynamics (SD) plots: Computational identification of selective sweeps to monitor the adaptation of influenza A viruses. <i>Scientific Reports</i> , 2018, 8, 373.	1.6	16

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14341	HIV-1 Infection in Cyprus, the Eastern Mediterranean European Frontier: A Densely Sampled Transmission Dynamics Analysis from 1986 to 2012. <i>Scientific Reports</i> , 2018, 8, 1702.	1.6	24
14342	Chloroplast genomes of <i>Byrsonima</i> species (Malpighiaceae): comparative analysis and screening of high divergence sequences. <i>Scientific Reports</i> , 2018, 8, 2210.	1.6	108
14343	VglI3 and the Hippo pathway are regulated in Sertoli cells upon entry and during puberty in Atlantic salmon testis. <i>Scientific Reports</i> , 2018, 8, 1912.	1.6	37
14344	Molecular detection of field predation among larvae of two ladybird beetles is partially predicted from laboratory experiments. <i>Scientific Reports</i> , 2018, 8, 2594.	1.6	13
14345	Origin, evolution, and distribution of the molecular machinery for biosynthesis of sialylated lipooligosaccharide structures in <i>Campylobacter coli</i> . <i>Scientific Reports</i> , 2018, 8, 3028.	1.6	13
14346	To be serrate or pinnate: diverse leaf forms of yarrows ( <i>Achillea</i> ) are linked to differential expression patterns of NAM genes. <i>Annals of Botany</i> , 2018, 121, 255-266.	1.4	5
14347	Genetic and morphometric rediscovery of an extinct land snail on oceanic islands. <i>Journal of Molluscan Studies</i> , 2018, 84, 148-156.	0.4	12
14348	Greatly reduced phylogenetic structure in the cultivated potato clade ( <i>Solanum</i> section) Tj ETQq1 1 0.784314 rgBT /Overlock 10 0.8 16		
14349	Recently identified bee viruses and their impact on bee pollinators. <i>Current Opinion in Insect Science</i> , 2018, 26, 120-129.	2.2	86
14350	Identification of <i>Theileria fuliginosa</i> -like species in <i>Ixodes australiensis</i> ticks from western grey kangaroos ( <i>Macropus fuliginosus</i> ) in Western Australia. <i>Ticks and Tick-borne Diseases</i> , 2018, 9, 632-637.	1.1	6
14351	Metaorganisms in extreme environments: do microbes play a role in organismal adaptation?. <i>Zoology</i> , 2018, 127, 1-19.	0.6	194
14352	Resolving taxonomic ambiguity and cryptic speciation of <i>Hypotrigena</i> species through morphometrics and DNA barcoding. <i>Journal of Apicultural Research</i> , 2018, 57, 354-363.	0.7	13
14353	Bacterial Gall of <i>Loropetalum chinense</i> caused by <i>Pseudomonas amygdali</i> pv. <i>loropetali</i> pv. nov.. <i>Plant Disease</i> , 2018, 102, 799-806.	0.7	7
14354	Multi-heme cytochromes provide a pathway for survival in energy-limited environments. <i>Science Advances</i> , 2018, 4, eaao5682.	4.7	155
14355	Anthropogenic N Deposition Alters the Composition of Expressed Class II Fungal Peroxidases. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	19
14356	Mitogenomes of two neotropical bird species and the multiple independent origin of mitochondrial gene orders in Passeriformes. <i>Molecular Biology Reports</i> , 2018, 45, 279-285.	1.0	24
14357	Two new species of Haplorchoides Chen, 1949 (Digenea: Heterophyidae) infecting an Australian siluriform fish, <i>Neoarius graeffei</i> Kner & Steindachner. <i>Systematic Parasitology</i> , 2018, 95, 201-211.	0.5	8
14358	Does the Mid-Atlantic Ridge affect the distribution of abyssal benthic crustaceans across the Atlantic Ocean?. <i>Deep-Sea Research Part II: Topical Studies in Oceanography</i> , 2018, 148, 91-104.	0.6	37

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14360	An improved method for PCR-based detection and routine monitoring of geosmin-producing cyanobacterial blooms. <i>Water Research</i> , 2018, 136, 34-40.	5.3	20
14361	<i>Rhodolirium andicola</i> : a new renewable source of alkaloids with acetylcholinesterase inhibitory activity, a study from nature to molecular docking. <i>Revista Brasileira De Farmacognosia</i> , 2018, 28, 34-43.	0.6	29
14362	The tegumental allergen-like proteins of <i>Schistosoma mansoni</i> : A biochemical study of SmTAL4-TAL13. <i>Molecular and Biochemical Parasitology</i> , 2018, 221, 14-22.	0.5	11
14363	Unique Biochemical and Sequence Features Enable BluB To Destroy Flavin and Distinguish BluB from the Flavin Monooxygenase Superfamily. <i>Biochemistry</i> , 2018, 57, 1748-1757.	1.2	5
14364	Gene duplicates resolving sexual conflict rapidly evolved essential gametogenesis functions. <i>Nature Ecology and Evolution</i> , 2018, 2, 705-712.	3.4	68
14365	Hologenomic adaptations underlying the evolution of sanguivory in the common vampire bat. <i>Nature Ecology and Evolution</i> , 2018, 2, 659-668.	3.4	124
14366	Oxidative demethylation of algal carbohydrates by cytochrome P450 monooxygenases. <i>Nature Chemical Biology</i> , 2018, 14, 342-344.	3.9	47
14367	Characterization of viral RNA splicing using whole-transcriptome datasets from host species. <i>Scientific Reports</i> , 2018, 8, 3273.	1.6	10
14368	Identifying the inhibition of TIR proteins involved in TLR signalling as an anti-inflammatory strategy. <i>SAR and QSAR in Environmental Research</i> , 2018, 29, 295-318.	1.0	7
14369	Characterization of p57, a Stage-Specific Antigen of <i>Pneumocystis murina</i> . <i>Journal of Infectious Diseases</i> , 2018, 218, 282-290.	1.9	11
14370	Extreme dentition does not prevent diet and tooth diversification within combtooth blennies ( <i>Ovalentaria</i> : <i>Blenniidae</i> ). <i>Evolution; International Journal of Organic Evolution</i> , 2018, 72, 930-943.	1.1	13
14371	Genetic characterization and diversity of circulating influenza A/H1N1pdm09 viruses isolated in Jeddah, Saudi Arabia between 2014 and 2015. <i>Archives of Virology</i> , 2018, 163, 1219-1230.	0.9	7
14372	Comparative study on intestinal bacterial communities of <i>Boleophthalmus pectinirostris</i> and <i>Periophthalmus magnuspinnatus</i> with different sexes and feeding strategies. <i>Annals of Microbiology</i> , 2018, 68, 123-133.	1.1	9
14373	Plastome-wide comparison reveals new SNV resources for the authentication of <i>Dendrobium huoshanense</i> and its corresponding medicinal slice ( <i>Huoshan Fengdou</i> ). <i>Acta Pharmaceutica Sinica B</i> , 2018, 8, 466-477.	5.7	23
14374	Molecular gut-content analysis reveals high frequency of <i>Helicoverpa zea</i> ( <i>Lepidoptera</i> : <i>Noctuidae</i> ) consumption by <i>Orius insidiosus</i> ( <i>Hemiptera</i> : <i>Anthocoridae</i> ) in sweet corn. <i>Biological Control</i> , 2018, 121, 1-7.	1.4	15
14375	Generative Cell Specification Requires Transcription Factors Evolutionarily Conserved in Land Plants. <i>Current Biology</i> , 2018, 28, 479-486.e5.	1.8	87
14376	The hidden lipoproteome of <i>Staphylococcus aureus</i> . <i>International Journal of Medical Microbiology</i> , 2018, 308, 569-581.	1.5	7

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14377	De novo assembly of honey bee RNA viral genomes by tapping into the innate insect antiviral response pathway. <i>Journal of Invertebrate Pathology</i> , 2018, 152, 38-47.	1.5	23
14378	A complex of the blood fluke genus <i>Psettarium</i> (Digenea: Aporocotylidae) infecting tetraodontiform fishes of east Queensland waters. <i>Parasitology International</i> , 2018, 67, 321-340.	0.6	17
14379	Intramembranal disulfide cross-linking elucidates the super-quaternary structure of mammalian CatSpers. <i>Reproductive Biology</i> , 2018, 18, 76-82.	0.9	11
14380	Regulation of Kinase Activity in the <i>Caenorhabditis elegans</i> EGF Receptor, LET-23. <i>Structure</i> , 2018, 26, 270-281.e4.	1.6	5
14381	<i>Bacillus onubensis</i> sp. nov., isolated from the air of two Andalusian caves. <i>Systematic and Applied Microbiology</i> , 2018, 41, 167-172.	1.2	26
14382	<i>Agrobacterium bohemicum</i> sp. nov. isolated from poppy seed wastes in central Bohemia. <i>Systematic and Applied Microbiology</i> , 2018, 41, 184-190.	1.2	14
14383	Atlantic forests to the all Americas: Biogeographical history and divergence times of Neotropical <i>Ficus</i> (Moraceae). <i>Molecular Phylogenetics and Evolution</i> , 2018, 122, 46-58.	1.2	27
14384	Molecular phylogeny of Neotropical rock frogs reveals a long history of vicariant diversification in the Atlantic forest. <i>Molecular Phylogenetics and Evolution</i> , 2018, 122, 142-156.	1.2	30
14385	A novel framework for evaluating the performance of codon usage bias metrics. <i>Journal of the Royal Society Interface</i> , 2018, 15, 20170667.	1.5	9
14386	A fungal mock community control for amplicon sequencing experiments. <i>Molecular Ecology Resources</i> , 2018, 18, 541-556.	2.2	69
14387	A population genetics analysis in clinical isolates of <i>Sporothrix schenckii</i> based on calmodulin and calcium/calmodulin-dependent kinase partial gene sequences. <i>Mycoses</i> , 2018, 61, 383-392.	1.8	10
14388	Organization of the TC and TE cellular DNA regions in <i>Nicotiana otophora</i> and functional analysis of three diverged TE-6b genes. <i>Plant Journal</i> , 2018, 94, 274-287.	2.8	16
14389	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
14390	MtNRLK1, a CLAVATA1-like leucine-rich repeat receptor-like kinase upregulated during nodulation in <i>Medicago truncatula</i> . <i>Scientific Reports</i> , 2018, 8, 2046.	1.6	9
14391	When is a native species invasive? Incurion of a novel predatory marsupial detected using molecular and historical data. <i>Diversity and Distributions</i> , 2018, 24, 831-840.	1.9	23
14392	Retinoic acid signaling and neurogenic niche regulation in the developing peripheral nervous system of the cephalochordate amphioxus. <i>Cellular and Molecular Life Sciences</i> , 2018, 75, 2407-2429.	2.4	16
14393	Nanos genes and their role in development and beyond. <i>Cellular and Molecular Life Sciences</i> , 2018, 75, 1929-1946.	2.4	57
14394	Evaluation of genes involved in Norway lobster ( <i>Nephrops norvegicus</i> ) female sexual maturation using transcriptomic analysis. <i>Hydrobiologia</i> , 2018, 825, 137-158.	1.0	4

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14396	Mitochondrial genome diversity and population structure of two western honey bee subspecies in the Republic of South Africa. <i>Scientific Reports</i> , 2018, 8, 1333.	1.6	23
14397	Divergent and parallel routes of biochemical adaptation in high-altitude passerine birds from the Qinghai-Tibet Plateau. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 1865-1870.	3.3	74
14398	Phylogeography reveals unexpectedly low genetic diversity in a widely distributed species: the case of the freshwater crab <i>Aegla platensis</i> (Decapoda: Anomura). <i>Biological Journal of the Linnean Society</i> , 2018, 123, 578-592.	0.7	7
14399	Genome-wide identification and evolution of TC1/Mariner in the silkworm ( <i>Bombyx mori</i> ) genome. <i>Genes and Genomics</i> , 2018, 40, 485-495.	0.5	8
14400	A Macrophage Colony-Stimulating-Factor-Producing $\hat{\gamma}\hat{\delta}$ T Cell Subset Prevents Malarial Parasitemic Recurrence. <i>Immunity</i> , 2018, 48, 350-363.e7.	6.6	105
14401	Microbial ecology of full-scale wastewater treatment systems in the Polar Arctic Circle: Archaea, Bacteria and Fungi. <i>Scientific Reports</i> , 2018, 8, 2208.	1.6	57
14402	Hidden in the Arabian Mountains: Multilocus phylogeny reveals cryptic diversity in the endemic <i>Omanosaura</i> lizards. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2018, 56, 395-407.	0.6	13
14403	microRNA-210 participates in regulating RIG-I signaling pathway via targeting DUBA in miuiy croaker after poly(I:C) stimulation. <i>Fish and Shellfish Immunology</i> , 2018, 77, 1-7.	1.6	10
14404	Management of the American cockroach's oothecae: The potential of entomopathogenic fungi control. <i>Journal of Invertebrate Pathology</i> , 2018, 153, 30-34.	1.5	5
14405	Gene architecture and expression analyses provide insights into the role of glutathione peroxidases (GPXs) in bread wheat ( <i>Triticum aestivum</i> L.). <i>Journal of Plant Physiology</i> , 2018, 223, 19-31.	1.6	39
14406	Two different <i>R</i> gene loci co-evolved with <i>Avr2</i> of <i>Phytophthora infestans</i> and confer distinct resistance specificities in potato. <i>Studies in Mycology</i> , 2018, 89, 105-115.	4.5	49
14407	Codon usage variation of Zika virus: The potential roles of NS2B and NS4A in its global pandemic. <i>Virus Research</i> , 2018, 247, 71-83.	1.1	7
14408	Different Bioactive Neuropeptides are Expressed in Two Sub-Classes of GABAergic RME Nerve Ring Motoneurons in <i>Ascaris suum</i> . <i>ACS Chemical Neuroscience</i> , 2018, 9, 2025-2040.	1.7	6
14409	Clonal polymorphism and high heterozygosity in the celibate genome of the Amazon molly. <i>Nature Ecology and Evolution</i> , 2018, 2, 669-679.	3.4	117
14410	Culture-independent discovery of the malacidins as calcium-dependent antibiotics with activity against multidrug-resistant Gram-positive pathogens. <i>Nature Microbiology</i> , 2018, 3, 415-422.	5.9	338
14411	RAB GTPases in the Basal Land Plant <i>Marchantia polymorpha</i> . <i>Plant and Cell Physiology</i> , 2018, 59, 850-861.	1.5	26
14412	Discovery of Viruses and Virus-Like Pathogens in Pistachio using High-Throughput Sequencing. <i>Plant Disease</i> , 2018, 102, 1419-1425.	0.7	50

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14414	Structural basis for the interaction between the cell polarity proteins Par3 and Par6. <i>Science Signaling</i> , 2018, 11, .	1.6	31
14415	RNA-Interference Pathways Display High Rates of Adaptive Protein Evolution in Multiple Invertebrates. <i>Genetics</i> , 2018, 208, 1585-1599.	1.2	53
14416	<i>Abditibacterium utsteinense</i> sp. nov., the first cultivated member of candidate phylum FBP, isolated from ice-free Antarctic soil samples. <i>Systematic and Applied Microbiology</i> , 2018, 41, 279-290.	1.2	58
14417	Novel global effector mining from the transcriptome of early life stages of the soybean cyst nematode <i>Heterodera glycines</i> . <i>Scientific Reports</i> , 2018, 8, 2505.	1.6	31
14418	Interacting-heads motif has been conserved as a mechanism of myosin II inhibition since before the origin of animals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E1991-E2000.	3.3	70
14419	Diverse <i>Legionella</i> -like Bacteria Associated with Testate Amoebae of the Genus <i>Arcella</i> (Arcellinida). <i>Trends in Microbiology</i> , 2018, 26, 107-115.	0.8	7
14420	The Birth and Demise of the IS <i>Apl1</i> - <i>mcr-1</i> -IS <i>Apl1</i> Composite Transposon: the Vehicle for Transferable Colistin Resistance. <i>MBio</i> , 2018, 9, .	1.8	103
14421	From laboratory to point of entry: development and implementation of a loop-mediated isothermal amplification (LAMP)-based genetic identification system to prevent introduction of quarantine insect species. <i>Pest Management Science</i> , 2018, 74, 1504-1512.	1.7	55
14422	Virological and pathological characterization of an avian H1N1 influenza A virus. <i>Archives of Virology</i> , 2018, 163, 1153-1162.	0.9	6
14423	A heterogeneous human immunodeficiency virus-like particle (VLP) formulation produced by a novel vector system. <i>Npj Vaccines</i> , 2018, 3, 2.	2.9	17
14424	Crystal structure of thermospermine synthase from <i>Medicago truncatula</i> and substrate discriminatory features of plant aminopropyltransferases. <i>Biochemical Journal</i> , 2018, 475, 787-802.	1.7	16
14425	Evolutionary history and systematics of <i>Campylocentrum</i> (Orchidaceae: Vandaeae: Angraecinae): a phylogenetic and biogeographical approach. <i>Botanical Journal of the Linnean Society</i> , 2018, 186, 158-178.	0.8	20
14426	Comparative Genomics of <i>Tenacibaculum dicentrarchi</i> and <i>Tenacibaculum finnmarkense</i> -Highlights Intricate Evolution of Fish-Pathogenic Species. <i>Genome Biology and Evolution</i> , 2018, 10, 452-457.	1.1	36
14427	Modular domain swapping among the bacterial cytotoxic necrotizing factor (CNF) family for efficient cargo delivery into mammalian cells. <i>Journal of Biological Chemistry</i> , 2018, 293, 3860-3870.	1.6	9
14428	Molecular Phylogeny of the Grassland Leafhopper Tribe Hecalini (Hemiptera: Cicadellidae). <i>Trends in Microbiology</i> , 2018, 26, 107-115.	1.3	3
14429	Evolutionary diversification of galactinol synthases in Rosaceae: adaptive roles of galactinol and raffinose during apple bud dormancy. <i>Journal of Experimental Botany</i> , 2018, 69, 1247-1259.	2.4	33
14430	Phylogeny and species delineation in the marine diatom <i>Pseudo-nitzschia</i> (Bacillariophyta) using <i>cox1</i> , <i>LSU</i> , and <i>ITS2</i> <i>rRNA</i> genes: A perspective in character evolution. <i>Journal of Phycology</i> , 2018, 54, 234-248.	1.0	37

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14432	Potato Mop-Top Virus Co-Optes the Stress Sensor HIPP26 for Long-Distance Movement. <i>Plant Physiology</i> , 2018, 176, 2052-2070.	2.3	49
14433	Laimaphelenchus suberensis sp. nov. associated with Quercus suber in Portugal. <i>European Journal of Plant Pathology</i> , 2018, 150, 747-758.	0.8	7
14434	Lytic xylan oxidases from wood-decay fungi unlock biomass degradation. <i>Nature Chemical Biology</i> , 2018, 14, 306-310.	3.9	269
14435	Evolving <i>doublesex</i> expression correlates with the origin and diversification of male sexual ornaments in the <i>Drosophila immigrans</i> species group. <i>Evolution &amp; Development</i> , 2018, 20, 78-88.	1.1	16
14436	Grass and maize vegetation systems restore saline-sodic soils in the Songnen Plain of northeast China. <i>Land Degradation and Development</i> , 2018, 29, 1107-1119.	1.8	48
14437	Transcriptomic insight into pathogenicity-associated factors of <i>Conidiobolus obscurus</i> , an obligate aphid-pathogenic fungus belonging to Entomophthoromycota. <i>Pest Management Science</i> , 2018, 74, 1677-1686.	1.7	12
14438	Complete genome sequence and construction of an infectious full-length cDNA clone of a German isolate of celery mosaic virus. <i>Archives of Virology</i> , 2018, 163, 1107-1111.	0.9	5
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14440	Practical implications of erythromycin resistance gene diversity on surveillance and monitoring of resistance. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	12
14441	A Fast and Reliable Real-time PCR Method for Detection of Ten Animal Species in Meat Products. <i>Journal of Food Science</i> , 2018, 83, 258-265.	1.5	20
14442	Patterns of diversity, endemism and specialization in the root symbiont communities of alder species on the island of Corsica. <i>New Phytologist</i> , 2018, 219, 336-349.	3.5	8
14443	Isolation and characterization of a heterologously expressed bacterial laccase from the anaerobe <i>Geobacter metallireducens</i> . <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 2425-2439.	1.7	26
14444	Evidence for a complex of emergent polioviruses affecting pepper worldwide. <i>Archives of Virology</i> , 2018, 163, 1171-1178.	0.9	15
14445	<i>Corynebacterium furnierii</i> sp. nov., isolated from the female genital tract of a patient with bacterial vaginosis. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 1165-1174.	0.7	15
14446	A naturally occurring epiallele associates with leaf senescence and local climate adaptation in <i>Arabidopsis</i> accessions. <i>Nature Communications</i> , 2018, 9, 460.	5.8	72
14447	Differential depth distribution of microbial function and putative symbionts through sediment-hosted aquifers in the deep terrestrial subsurface. <i>Nature Microbiology</i> , 2018, 3, 328-336.	5.9	227
14448	Adaptation of commensal proliferating <i>Escherichia coli</i> to the intestinal tract of young children with cystic fibrosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 1605-1610.	3.3	41



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14450	The solute transport profile of two Aza-guanine transporters from the Honey bee pathogen <i>Paenibacillus larvae</i> . <i>FEMS Microbiology Letters</i> , 2018, 365, .	0.7	3
14451	Diversity of Translation Initiation Mechanisms across Bacterial Species Is Driven by Environmental Conditions and Growth Demands. <i>Molecular Biology and Evolution</i> , 2018, 35, 582-592.	3.5	24
14452	A novel family of tyrosine integrases encoded by the temperate pleolipovirus SNJ2. <i>Nucleic Acids Research</i> , 2018, 46, 2521-2536.	6.5	30
14453	A Revision of <i>Philander</i> (Marsupialia: Didelphidae), Part 1: <i>P. quica</i> , <i>P. canus</i> , and a New Species from Amazonia. <i>American Museum Novitates</i> , 2018, 3891, 1-70.	0.2	59
14454	A Perfect Match Genomic Landscape Provides a Unified Framework for the Precise Detection of Variation in Natural and Synthetic Haploid Genomes. <i>Genetics</i> , 2018, 208, 1631-1641.	1.2	5
14455	Ancient Diversification of Three-Finger Toxins in <i>Micrurus</i> Coral Snakes. <i>Journal of Molecular Evolution</i> , 2018, 86, 58-67.	0.8	30
14456	Complete plastid genome of critically endangered plant <i>Prangos trifida</i> (Apiaceae: Apioideae). <i>Conservation Genetics Resources</i> , 2018, 10, 847-849.	0.4	5
14457	Morphological, chemical, and molecular analyses differentiate populations of the subterranean nesting stingless bee <i>Mourella caerulea</i> (Apidae: Meliponini). <i>Apidologie</i> , 2018, 49, 367-377.	0.9	12
14458	Unraveling Allosteric Mechanisms of Enzymatic Catalysis with an Evolutionary Analysis of Residue-Residue Contact Dynamical Changes. <i>ACS Catalysis</i> , 2018, 8, 2375-2384.	5.5	18
14459	The non-monotypic status of the neotropical fish genus <i>Hemiodontichthys</i> (Siluriformes, Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 3 and Analysis, 2018, 29, 1224-1230.	0.7	7
14460	Phylogeography of <i>Orinus</i> (Poaceae), a dominant grass genus on the Qinghai-Tibet Plateau. <i>Botanical Journal of the Linnean Society</i> , 2018, 186, 202-223.	0.8	18
14461	Interference with Clp protease impairs carotenoid accumulation during tomato fruit ripening. <i>Journal of Experimental Botany</i> , 2018, 69, 1557-1568.	2.4	58
14462	Dating phototrophic microbial lineages with reticulate gene histories. <i>Geobiology</i> , 2018, 16, 179-189.	1.1	80
14463	A primordial and reversible TCA cycle in a facultatively chemolithoautotrophic thermophile. <i>Science</i> , 2018, 359, 559-563.	6.0	155
14464	In search of a meaningful classification for Amazonian marmosets: Should dwarf marmosets be considered <i>Mico</i> congenetics?. <i>Zoologica Scripta</i> , 2018, 47, 133-143.	0.7	9
14465	Phylodynamics of classical swine fever virus with emphasis on Ecuadorian strains. <i>Transboundary and Emerging Diseases</i> , 2018, 65, 782-790.	1.3	12
14466	Does the Genetic Feature of the Chinese Tree Shrew ( <i>Tupaia belangeri chinensis</i> ) Support Its Potential as a Viable Model for Alzheimer's Disease Research?. <i>Journal of Alzheimer's Disease</i> , 2018, 61, 1015-1028.	1.2	25

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14467	First record of <i>Erysiphe quercicola</i> (Ascomycota: Erysiphales) on species of <i>Quercus</i> subgenus <i>Cyclobalanopsis</i> (evergreen oaks, Fagaceae). <i>Mycoscience</i> , 2018, 59, 105-109.	0.3	7
14468	The genome sequence of the soft-rot fungus <i>Penicillium purpurogenum</i> reveals a high gene dosage for lignocellulolytic enzymes. <i>Mycology</i> , 2018, 9, 59-69.	2.0	12
14469	DNA barcoding for species identification in deep-sea clams (Mollusca: Bivalvia: Vesicomidae). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2018, 29, 1165-1173.	0.7	3
14470	The complete plastome of macaw palm [ <i>Acrocomia aculeata</i> (Jacq.) Lodd. ex Mart.] and extensive molecular analyses of the evolution of plastid genes in <i>Arecaceae</i> . <i>Planta</i> , 2018, 247, 1011-1030.	1.6	38
14471	Cloning and functional characterization of a p-coumaroyl quinate/shikimate 3- $\alpha$ -hydroxylase from potato ( <i>Solanum tuberosum</i> ). <i>Biochemical and Biophysical Research Communications</i> , 2018, 496, 462-467.	1.0	16
14472	Genome-wide comparative analysis of papain-like cysteine protease family genes in castor bean and physic nut. <i>Scientific Reports</i> , 2018, 8, 331.	1.6	28
14473	Deeply-sourced formate fuels sulfate reducers but not methanogens at Lost City hydrothermal field. <i>Scientific Reports</i> , 2018, 8, 755.	1.6	81
14474	The Genomes of Four <i>Meyerozyma caribbica</i> Isolates and Novel Insights into the <i>Meyerozyma guilliermondii</i> Species Complex. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 755-759.	0.8	20
14475	The mechanism of glycosphingolipid degradation revealed by a GALC-SapA complex structure. <i>Nature Communications</i> , 2018, 9, 151.	5.8	37
14476	Novel endogenous simian retroviral integrations in Vero cells: implications for quality control of a human vaccine cell substrate. <i>Scientific Reports</i> , 2018, 8, 644.	1.6	21
14477	The reconstruction of 2,631 draft metagenome-assembled genomes from the global oceans. <i>Scientific Data</i> , 2018, 5, 170203.	2.4	449
14478	Circumscription and phylogeny of the <i>Lepidostromatales</i> ( <i>Lichenized Basidiomycota</i> ) following discovery of new species from China and Africa. <i>Mycologia</i> , 2017, 109, 730-748.	0.8	10
14479	Integrative taxonomy of the neotropical genus <i>Omalonyx</i> (Elasmognatha: Succineidae). <i>Zoologica Scripta</i> , 2018, 47, 174-186.	0.7	7
14480	Molecular analysis of anthocyanin biosynthesis pathway genes and their differential expression in mango peel. <i>Genome</i> , 2018, 61, 157-166.	0.9	32
14481	Identification and genetic characterization of polyomaviruses in estrildid and fringillid finches. <i>Archives of Virology</i> , 2018, 163, 895-909.	0.9	9
14482	A case of biodiversity overestimation in the Balkan <i>Belgrandiella</i> A. J. Wagner, 1927 (Caenogastropoda: Hydrobiidae): molecular divergence not paralleled by high morphological variation. <i>Journal of Natural History</i> , 2018, 52, 323-344.	0.2	26
14483	Anaerobic 4-hydroxyproline utilization: Discovery of a new glycyl radical enzyme in the human gut microbiome uncovers a widespread microbial metabolic activity. <i>Gut Microbes</i> , 2018, 9, 1-16.	4.3	30
14484	The Effect of Nonreversibility on Inferring Rooted Phylogenies. <i>Molecular Biology and Evolution</i> , 2018, 35, 984-1002.	3.5	12

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14485	NHLRC2 variants identified in patients with fibrosis, neurodegeneration, and cerebral angiomas (FINCA): characterisation of a novel cerebropulmonary disease. <i>Acta Neuropathologica</i> , 2018, 135, 727-742.	3.9	21
14486	Next generation sequencing reveals widespread trypanosome diversity and polyparasitism in marsupials from Western Australia. <i>International Journal for Parasitology: Parasites and Wildlife</i> , 2018, 7, 58-67.	0.6	28
14487	Growing old, yet staying young: The role of telomeres in bats' exceptional longevity. <i>Science Advances</i> , 2018, 4, eaao0926.	4.7	120
14488	Investigation of Agonist Recognition and Channel Properties in a Flatworm Glutamate-Gated Chloride Channel. <i>Biochemistry</i> , 2018, 57, 1360-1368.	1.2	2
14489	Natural and Vaccine-Induced Acquisition of Cross-Reactive IgG-Inhibiting ICAM-1-Specific Binding of a <i>Plasmodium falciparum</i> PfEMP1 Subtype Associated Specifically with Cerebral Malaria. <i>Infection and Immunity</i> , 2018, 86, .	1.0	23
14490	<i>Amycolatopsis vastitatis</i> sp. nov., an isolate from a high altitude subsurface soil on Cerro Chajnantor, northern Chile. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 1523-1533.	0.7	16
14491	Expansion of the concept of the Opistholebetinae Fukui, 1929 (Digenea: Opecoelidae Ozaki, 1925), with <i>Magnosimum brooksae</i> n. g., n. sp. from <i>Tripodichthys angustifrons</i> (Hollard) (Tetraodontiformes: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.5	6
14492	The complete chloroplast genome of the green algae <i>Hariotina reticulata</i> (Scenedesmaceae,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 5	0.5	6
14493	Whole Mitochondrial Genomic and Y-Chromosomal Phylogenies of Burmese Long-Tailed Macaque ( <i>Macaca fascicularis aurea</i> ) Suggest Ancient Hybridization between <i>fascicularis</i> and <i>sinica</i> Species Groups. <i>Journal of Heredity</i> , 2018, 109, 360-371.	1.0	20
14494	Draft genome sequence of ramie, <i>Boehmeria nivea</i> (L.) Gaudich. <i>Molecular Ecology Resources</i> , 2018, 18, 639-645.	2.2	46
14495	In vitro susceptibility to ST-246 and Cidofovir corroborates the phylogenetic separation of Brazilian <i>Vaccinia</i> virus into two clades. <i>Antiviral Research</i> , 2018, 152, 36-44.	1.9	4
14496	Molecular phylogeny and biogeographic distribution of pheretimoid earthworms (clitellata:) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 5	1.4	15
14497	Soil metagenome-derived 3-hydroxypalmitic acid methyl ester hydrolases suppress extracellular polysaccharide production in <i>Ralstonia solanacearum</i> . <i>Journal of Biotechnology</i> , 2018, 270, 30-38.	1.9	11
14498	Genomic comparison between members of the <i>Salinibacteraceae</i> family, and description of a new species of <i>Salinibacter</i> ( <i>Salinibacter altiplanensis</i> sp. nov.) isolated from high altitude hypersaline environments of the Argentinian Altiplano. <i>Systematic and Applied Microbiology</i> , 2018, 41, 198-212.	1.2	29
14499	Potential for re-emergence of wheat stem rust in the United Kingdom. <i>Communications Biology</i> , 2018, 1, 13.	2.0	107
14500	<i>Mytella strigata</i> (Bivalvia: Mytilidae): an alien mussel recently introduced to Singapore and spreading rapidly. <i>Molluscan Research</i> , 2018, 38, 170-186.	0.2	30
14501	Accumulation and Dissolution of Magnetite Crystals in a Magnetically Responsive Ciliate. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	17
14502	Identification and characterization of homeobox ( <i>Hox</i> ) genes and conservation of the single <i>Hox</i> cluster (324.6Åkb) in the water flea <i>Daphnia magna</i> . <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2018, 330, 76-82.	0.6	12

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14503	Two species of <i>Phyllodistomum</i> Braun, 1899 (Trematoda: Gorgoderidae) from Moreton Bay, Australia. <i>Systematic Parasitology</i> , 2018, 95, 325-336.	0.5	7
14504	Virtual Genome Walking across the 32â€‰Gb <i>Ambystoma mexicanum</i> genome; assembling gene models and intronic sequence. <i>Scientific Reports</i> , 2018, 8, 618.	1.6	9
14505	Genome and secretome analysis of <i>Pochonia chlamydosporia</i> provide new insight into egg-parasitic mechanisms. <i>Scientific Reports</i> , 2018, 8, 1123.	1.6	20
14506	Mitochondrial DNA suggests cryptic speciation in <i>Prodiplosis longifila</i> (Diptera: Tj ETQq1 1 0.784314 rgBT /Overlock Entomological Research, 2018, 108, 739-749.	0.5	8
14507	Species delimitation of <i>Melia dubia</i> Cav. from <i>Melia azedarach</i> L. complex based on DNA barcoding. <i>Botany</i> , 2018, 96, 329-336.	0.5	14
14508	Identification of epistatic mutations and insights into the evolution of the influenza virus using a mass-based protein phylogenetic approach. <i>Molecular Phylogenetics and Evolution</i> , 2018, 121, 132-138.	1.2	18
14509	Comprehensive list of SUMO targets in <i>Caenorhabditis elegans</i> and its implication for evolutionary conservation of SUMO signaling. <i>Scientific Reports</i> , 2018, 8, 1139.	1.6	18
14510	Blocking Zika virus vertical transmission. <i>Scientific Reports</i> , 2018, 8, 1218.	1.6	55
14511	First report of gummy stem blight caused by <i>Stagonosporopsis cucurbitacearum</i> on cantaloupe in Thailand. <i>Canadian Journal of Plant Pathology</i> , 2018, 40, 306-311.	0.8	15
14512	Altered chemomechanical coupling causes impaired motility of the kinesin-4 motors KIF27 and KIF7. <i>Journal of Cell Biology</i> , 2018, 217, 1319-1334.	2.3	25
14513	Latitudinal variation in genome size in crustaceans. <i>Biological Journal of the Linnean Society</i> , 2018, 123, 348-359.	0.7	24
14514	Machine Learning Leveraging Genomes from Metagenomes Identifies Influential Antibiotic Resistance Genes in the Infant Gut Microbiome. <i>MSystems</i> , 2018, 3, .	1.7	68
14515	Morphometric, molecular and histopathologic description of hepatic infection by <i>Orthosplanchnus arcticus</i> (Trematoda: Digenea: Brachycladiidae) in ringed seals ( <i>Pusa hispida</i> ) from Northwest Greenland. <i>Polar Biology</i> , 2018, 41, 1019-1025.	0.5	2
14516	Genomes of 13 domesticated and wild rice relatives highlight genetic conservation, turnover and innovation across the genus <i>Oryza</i> . <i>Nature Genetics</i> , 2018, 50, 285-296.	9.4	413
14517	Evolutionary history of carbon monoxide dehydrogenase/acetyl-CoA synthase, one of the oldest enzymatic complexes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E1166-E1173.	3.3	160
14518	Three gene phylogeny of the Thoreaales (Rhodophyta) reveals high species diversity. <i>Journal of Phycology</i> , 2018, 54, 159-170.	1.0	10
14519	Fungal networks shape dynamics of bacterial dispersal and community assembly in cheese rind microbiomes. <i>Nature Communications</i> , 2018, 9, 336.	5.8	93
14520	Evolutionary Genetics of Cytoplasmic Incompatibility Genes <i>cifA</i> and <i>cifB</i> in Prophage WO of <i>Wolbachia</i> . <i>Genome Biology and Evolution</i> , 2018, 10, 434-451.	1.1	143

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14521	A new species of shrimp of the genus <i>Urocaridella</i> Borradaile, 1915 (Decapoda: Caridea: Palaemonidae) from Papua New Guinea. <i>Journal of Crustacean Biology</i> , 2018, 38, 206-214.	0.3	4
14522	Polymorphic characters in the reconstruction of the phylogeny of geoemydid turtles. <i>Zoological Journal of the Linnean Society</i> , 2018, 184, 896-918.	1.0	15
14523	A major lineage of non-tailed dsDNA viruses as unrecognized killers of marine bacteria. <i>Nature</i> , 2018, 554, 118-122.	13.7	160
14524	Within-island diversification underlies parachuting frog ( <i>Rhacophorus</i> ) species accumulation on the Sunda Shelf. <i>Journal of Biogeography</i> , 2018, 45, 929-940.	1.4	23
14525	Amphioxus SYCP1: a case of retrogene replacement and co-option of regulatory elements adjacent to the ParaHox cluster. <i>Development Genes and Evolution</i> , 2018, 228, 13-30.	0.4	1
14526	Detection and analysis of mycovirus-related RNA viruses from grape powdery mildew fungus <i>Erysiphe necator</i> . <i>Archives of Virology</i> , 2018, 163, 1019-1030.	0.9	24
14527	Naming the chaos: generic redelimitation in Schismatoglottideae (Araceae). <i>Webbia</i> , 2018, 73, S1-S100.	0.1	15
14528	HPViewer: sensitive and specific genotyping of human papillomavirus in metagenomic DNA. <i>Bioinformatics</i> , 2018, 34, 1986-1995.	1.8	17
14529	<i>Candidatus</i> <i>Neoehrlichia chilensis</i> sp. nov.: Molecular detection and characterization of a novel Anaplasmataceae in wild rodents from Valdivia, southern Chile. <i>Transboundary and Emerging Diseases</i> , 2018, 65, 357-362.	1.3	21
14530	Intraring allostery controls the function and assembly of a heterooligomeric class II chaperonin. <i>FASEB Journal</i> , 2018, 32, 2223-2234.	0.2	1
14531	Proton-pumping rhodopsins are abundantly expressed by microbial eukaryotes in a high-Arctic fjord. <i>Environmental Microbiology</i> , 2018, 20, 890-902.	1.8	14
14532	Examination of gene repertoires and physiological responses to iron and light limitation in Southern Ocean diatoms. <i>Polar Biology</i> , 2018, 41, 679-696.	0.5	28
14533	A seminested PCR assay for detection and typing of human papillomavirus based on E1 gene sequences. <i>Diagnostic Microbiology and Infectious Disease</i> , 2018, 91, 20-26.	0.8	2
14534	New World spittlebugs (Hemiptera: Cercopidae: Ischnorhininae): Dated molecular phylogeny, classification, and evolution of aposomatic coloration. <i>Molecular Phylogenetics and Evolution</i> , 2018, 120, 321-334.	1.2	27
14535	The pomegranate ( <i>Punica granatum</i> L.) genome provides insights into fruit quality and ovule developmental biology. <i>Plant Biotechnology Journal</i> , 2018, 16, 1363-1374.	4.1	115
14536	Enzyme Activities at Different Stages of Plant Biomass Decomposition in Three Species of Fungus-Growing Termites. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	31
14537	Identification of Bacterial Species That Can Utilize Fructose-Asparagine. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	15
14538	De novo transcriptome analyses reveals putative pathway genes involved in biosynthesis and regulation of camptothecin in <i>Nothapodytes nimmoniana</i> (Graham) Mabb.. <i>Plant Molecular Biology</i> , 2018, 96, 197-215.	2.0	41

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14539	Erysiphe azerbaijanica and E.Âlinderae : Two new powdery mildew species (Erysiphales) belonging to the Microsphaera lineage of Erysiphe. Mycoscience, 2018, 59, 181-187.	0.3	8
14540	Reclassification of Lamprotula rochechouartii as Margaritifera rochechouartii comb. nov. (Bivalvia: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 26 phylogenomics of Unionoida. Molecular Phylogenetics and Evolution, 2018, 120, 297-306.	1.2	24
14541	Isolation and biochemical characterisation of two thermophilic green algal species- Asterarcys quadricellulare and Chlorella sorokiniana, which are tolerant to high levels of carbon dioxide and nitric oxide. Algal Research, 2018, 30, 28-37.	2.4	71
14542	Entrapped by the uneven central and Middle Eastern terrains: Genetic status of populations of Hirudo orientalis (Annelida, Clitellata, Hirudinida) with a phylogenetic review of the genus Hirudo. Molecular Phylogenetics and Evolution, 2018, 121, 52-60.	1.2	3
14543	A novel Ehrlichia species in blood and Ixodes ornithorhynchi ticks from platypuses (Ornithorhynchus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 26	1.1	23
14544	A Novel Real-Time Genome Comparison Method Using Discrete Wavelet Transform. Journal of Computational Biology, 2018, 25, 405-416.	0.8	6
14545	Whole-genome sequencing reveals the extent of heterozygosity in a preferentially self-fertilizing hermaphroditic vertebrate. Genome, 2018, 61, 241-247.	0.9	15
14546	Bioinformatic Approaches for Comparative Analysis of Viruses. Methods in Molecular Biology, 2018, 1704, 401-417.	0.4	1
14547	Pan-Genome Storage and Analysis Techniques. Methods in Molecular Biology, 2018, 1704, 29-53.	0.4	24
14548	Phylogenomics. Methods in Molecular Biology, 2018, 1704, 103-187.	0.4	15
14549	Morphology and molecular phylogeny of Holostichides terrae nov. spec. (Ciliophora: Spirotrichea) with discussion on the possible non-monophyly of Holostichides. European Journal of Protistology, 2018, 62, 69-78.	0.5	13
14550	Widespread Whole Genome Duplications Contribute to Genome Complexity and Species Diversity in Angiosperms. Molecular Plant, 2018, 11, 414-428.	3.9	251
14551	Morphophylogenetic study revealed that Erysiphe gracilis (powdery mildew of evergreen oaks,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 26	0.3	12
14552	Libanicoccus massiliensis gen. nov., sp. nov., a new bacterium isolated from human stool. New Microbes and New Infections, 2018, 21, 63-71.	0.8	17
14553	Noncontiguous finished genome sequence and description of Mediterranea massiliensis gen. nov., sp. nov., a new member of the Bacteroidaceae family isolated from human colon. New Microbes and New Infections, 2018, 21, 105-116.	0.8	7
14554	Microfouling development on artificial substrates deployed in the central Red Sea. Oceanologia, 2018, 60, 219-231.	1.1	28
14555	Engineering PTEN-L for Cell-Mediated Delivery. Molecular Therapy - Methods and Clinical Development, 2018, 9, 12-22.	1.8	10
14556	A New Classification of the Dictyostelids. Protist, 2018, 169, 1-28.	0.6	52

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14557	Parendoziomonas haliclona gen. nov. sp. nov. isolated from a marine sponge of the genus Haliclona and description of the family Endoziomonadaceae fam. nov. comprising the genera Endoziomonas, Parendoziomonas, and Kistimonas. Systematic and Applied Microbiology, 2018, 41, 73-84.	1.2	48
14558	Molecular characterization and potential sources of aqueous humor bacterial contamination during phacoemulsification with intraocular lens implantation in dogs. Veterinary Microbiology, 2018, 213, 95-101.	0.8	3
14559	Microbial community of a gasworks aquifer and identification of nitrate-reducing Azoarcus and Georgfuchsia as key players in BTEX degradation. Water Research, 2018, 132, 146-157.	5.3	55
14560	Aquatic long-distance dispersal and vicariance shape the evolution of an ostracod species complex (Crustacea) in four major Brazilian floodplains. Molecular Phylogenetics and Evolution, 2018, 121, 86-97.	1.2	11
14561	Blood flukes Cardicola parvus and C. laruei (Trematoda: Aporocotylidae): life cycles and cryptic infection in spotted seatrout, Cynoscion nebulosus (Teleost: Sciaenidae). Parasitology International, 2018, 67, 150-158.	0.6	15
14562	Molecular characterization and expression analysis of the Na <sup>+</sup> /H <sup>+</sup> exchanger gene family in Medicago truncatula. Functional and Integrative Genomics, 2018, 18, 141-153.	1.4	29
14563	Identification of (R)-selective l-lysine aminotransferases by exploring evolutionary sequence space. Enzyme and Microbial Technology, 2018, 110, 46-52.	1.6	10
14564	Reciprocal Regulation of the TOR Kinase and ABA Receptor Balances Plant Growth and Stress Response. Molecular Cell, 2018, 69, 100-112.e6.	4.5	385
14565	Phylogenetics and geography of speciation in New World Halichoeres wrasses. Molecular Phylogenetics and Evolution, 2018, 121, 35-45.	1.2	18
14566	Leaf spot on cattleya orchid caused by <i>Neoscytalidium orchidacearum</i> in Thailand. Canadian Journal of Plant Pathology, 2018, 40, 109-114.	0.8	11
14567	Individual- and Species-Specific Skin Microbiomes in Three Different Estrildid Finch Species Revealed by 16S Amplicon Sequencing. Microbial Ecology, 2018, 76, 518-529.	1.4	29
14568	Potential recycling of thaumarchaeotal lipids by DPANN Archaea in seasonally hypoxic surface marine sediments. Organic Geochemistry, 2018, 119, 101-109.	0.9	26
14569	Prevalence of mixed genotype hepatitis C virus infections in the UK as determined by genotype-specific PCR and deep sequencing. Journal of Viral Hepatitis, 2018, 25, 524-534.	1.0	24
14570	Genetic and molecular basis of the immune system in the brachiopod Lingula anatina. Developmental and Comparative Immunology, 2018, 82, 7-30.	1.0	31
14571	Morphological, biometrical and molecular characterization of <i>Archaeopsylla erinacei</i> (Bouché, 1835). Bulletin of Entomological Research, 2018, 108, 726-738.	0.5	10
14572	High-throughput analysis of anammox bacteria in wetland and dryland soils along the altitudinal gradient in Qinghai-Tibet Plateau. MicrobiologyOpen, 2018, 7, e00556.	1.2	21
14573	A single amino acid residue regulates the substrate affinity and specificity of indoleamine 2,3-dioxygenase. Archives of Biochemistry and Biophysics, 2018, 640, 1-9.	1.4	7
14574	Assessment of glycerol usage by five different purple non-sulfur bacterial strains for bioplastic production. Journal of Environmental Chemical Engineering, 2018, 6, 616-622.	3.3	21

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14575	Genomic resources and comparative analyses of two economical penaeid shrimp species, <i>Marsupenaeus japonicus</i> and <i>Penaeus monodon</i> . <i>Marine Genomics</i> , 2018, 39, 22-25.	0.4	57
14576	Novel Kunitz-like Peptides Discovered in the Zoanthid <i>Palythoa caribaeorum</i> through Transcriptome Sequencing. <i>Journal of Proteome Research</i> , 2018, 17, 891-902.	1.8	22
14577	<i>Alternaria malicola</i> sp. nov., a New Pathogen Causing Fruit Spot on Apple in China. <i>Plant Disease</i> , 2018, 102, 1273-1282.	0.7	12
14578	The transmission dynamics and diversity of human metapneumovirus in Peru. <i>Influenza and Other Respiratory Viruses</i> , 2018, 12, 508-513.	1.5	6
14579	Phylogeny and a new tribal classification of Opiliaceae (Santalales) based on molecular and morphological evidence. <i>Journal of Systematics and Evolution</i> , 2018, 56, 56-66.	1.6	7
14580	Stable isotope analysis of micronekton around Hawaii reveals suspended particles are an important nutritional source in the lower mesopelagic and upper bathypelagic zones. <i>Limnology and Oceanography</i> , 2018, 63, 1168-1180.	1.6	55
14581	Corticosteroid treatment is associated with increased filamentous fungal burden in allergic fungal disease. <i>Journal of Allergy and Clinical Immunology</i> , 2018, 142, 407-414.	1.5	76
14582	Phylogenetic analyses of Japanese golden chanterelles and a new species description, <i>Cantharellus anzutake</i> sp. nov.. <i>Mycoscience</i> , 2018, 59, 153-165.	0.3	16
14583	Direct sequencing of the white spot syndrome virus from Brazil: Genome assembly and new insights on phylogeny. <i>Virus Research</i> , 2018, 245, 52-61.	1.1	9
14584	The Bioactive Protein-Ligand Conformation of GluN2C-Selective Positive Allosteric Modulators Bound to the NMDA Receptor. <i>Molecular Pharmacology</i> , 2018, 93, 141-156.	1.0	18
14585	Ancient duplications and functional divergence in the interferon regulatory factors of vertebrates provide insights into the evolution of vertebrate immune systems. <i>Developmental and Comparative Immunology</i> , 2018, 81, 324-333.	1.0	13
14586	Deep-sea Entoprocta from the Sea of Okhotsk and the adjacent open Pacific abyssal area: New species and new taxa of host animals. <i>Deep-Sea Research Part II: Topical Studies in Oceanography</i> , 2018, 154, 87-98.	0.6	7
14587	Characteristics of a PHD Finger Subtype. <i>Biochemistry</i> , 2018, 57, 525-539.	1.2	11
14588	Dynamics of widespread foot-and-mouth disease virus serotypes A, O and Asia in southern Asia: A Bayesian phylogenetic perspective. <i>Transboundary and Emerging Diseases</i> , 2018, 65, 696-710.	1.3	16
14589	Resculpting the binding pocket of APC superfamily LeuT-fold amino acid transporters. <i>Cellular and Molecular Life Sciences</i> , 2018, 75, 921-938.	2.4	21
14590	Riverscape genetics identifies speckled dace ( <i>Rhinichthys osculus</i> ) cryptic diversity in the Klamath-Trinity Basin. <i>Conservation Genetics</i> , 2018, 19, 111-127.	0.8	5
14591	L. donovani XPRT: Molecular characterization and evaluation of inhibitors. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2018, 1866, 426-441.	1.1	13
14592	A clustering package for nucleotide sequences using Laplacian Eigenmaps and Gaussian Mixture Model. <i>Computers in Biology and Medicine</i> , 2018, 93, 66-74.	3.9	10



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14593	Characterization of <i>Campylobacter jejuni</i> and <i>Campylobacter coli</i> Broiler Isolates by Whole-Genome Sequencing. <i>Foodborne Pathogens and Disease</i> , 2018, 15, 145-152.	0.8	35
14594	Integration of Contact Tracing and Phylogenetics in an Investigation of Acute HIV Infection. Sexually Transmitted Diseases, 2018, 45, 222-228.	0.8	19
14595	Conserved non-AUG uORFs revealed by a novel regression analysis of ribosome profiling data. <i>Genome Research</i> , 2018, 28, 214-222.	2.4	93
14596	Coalescent species delimitation of a Sumatran parachuting frog. <i>Zoologica Scripta</i> , 2018, 47, 33-43.	0.7	4
14597	Morphoanatomical characters in the Nidularioid Complex (Bromeliaceae: Bromelioideae) from a phylogenetic perspective. <i>Flora: Morphology, Distribution, Functional Ecology of Plants</i> , 2018, 239, 111-121.	0.6	5
14598	ALKALs are in vivo ligands for ALK family receptor tyrosine kinases in the neural crest and derived cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E630-E638.	3.3	68
14599	PLAZA 4.0: an integrative resource for functional, evolutionary and comparative plant genomics. <i>Nucleic Acids Research</i> , 2018, 46, D1190-D1196.	6.5	460
14600	Genome-enabled metabolic reconstruction of dominant chemosynthetic colonizers in deep-sea massive sulfide deposits. <i>Environmental Microbiology</i> , 2018, 20, 862-877.	1.8	41
14601	Trait-specific processes of convergence and conservatism shape ecomorphological evolution in ground-dwelling squirrels. <i>Evolution; International Journal of Organic Evolution</i> , 2018, 72, 473-489.	1.1	22
14602	Phylogenetic placement of <i>Yunnanopilia</i> (Opiliaceae) inferred from molecular and morphological data. <i>Journal of Systematics and Evolution</i> , 2018, 56, 48-55.	1.6	1
14603	Role of cytochrome P450 2B sequence variation and gene copy number in facilitating dietary specialization in mammalian herbivores. <i>Molecular Ecology</i> , 2018, 27, 723-736.	2.0	17
14604	Mutations in <i>Escherichia coli</i> Polyphosphate Kinase That Lead to Dramatically Increased <i>In Vivo</i> Polyphosphate Levels. <i>Journal of Bacteriology</i> , 2018, 200, .	1.0	37
14605	Genomic and phenotypic characterization of an atypical <i>Aeromonas salmonicida</i> strain isolated from a lumpfish and producing unusual granular structures. <i>Journal of Fish Diseases</i> , 2018, 41, 673-681.	0.9	10
14606	Phylogenetic Affinities of Indian Apple Snails: An Insight into the Tibetan Tectonic Terranes. <i>Proceedings of the Zoological Society</i> , 2018, 71, 194-201.	0.4	0
14607	Cyanobacterial photosynthesis under sulfidic conditions: insights from the isolate <i>Leptolyngbya</i> sp. strain hensonii. <i>ISME Journal</i> , 2018, 12, 568-584.	4.4	50
14608	Modulation of BACE1 Activity by Chemically Modified Aptamers. <i>ChemBioChem</i> , 2018, 19, 754-763.	1.3	23
14609	Tracing the introduction history of the invasive swimming crab <i>Charybdis hellerii</i> (A. Milne-Edwards). <i>Biological Invasions</i> , 2018, 20, 1771-1798.	1.2	17
14610	Genome-based classification of micromonosporae with a focus on their biotechnological and ecological potential. <i>Scientific Reports</i> , 2018, 8, 525.	1.6	102

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14612	The MEROPS database of proteolytic enzymes, their substrates and inhibitors in 2017 and a comparison with peptidases in the PANTHER database. <i>Nucleic Acids Research</i> , 2018, 46, D624-D632.	6.5	1,234
14613	Coproheme decarboxylases - Phylogenetic prediction versus biochemical experiments. <i>Archives of Biochemistry and Biophysics</i> , 2018, 640, 27-36.	1.4	30
14614	Adding injury to infection: The relationship between injury status and genetic diversity of <i>Theileria</i> infecting plains zebra, <i>Equus quagga</i> . <i>Infection, Genetics and Evolution</i> , 2018, 58, 269-278.	1.0	3
14615	Classification and evolution of human papillomavirus genome variants: Alpha-5 (HPV26, 51, 69, 82), Alpha-6 (HPV30, 53, 56, 66), Alpha-11 (HPV34, 73), Alpha-13 (HPV54) and Alpha-3 (HPV61). <i>Virology</i> , 2018, 516, 86-101.	1.1	35
14616	Evolution of the growth hormone, prolactin, prolactin 2 and somatolactin family. <i>General and Comparative Endocrinology</i> , 2018, 264, 94-112.	0.8	45
14617	Characterizing protein conformations by correlation analysis of coarse-grained contact matrices. <i>Journal of Chemical Physics</i> , 2018, 148, 025101.	1.2	9
14618	Gone with the trees: Phylogeography of <i>Rhodiola</i> sect. <i>Trifida</i> (Crassulaceae) reveals multiple refugia on the Qinghai-Tibetan Plateau. <i>Molecular Phylogenetics and Evolution</i> , 2018, 121, 110-120.	1.2	33
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14620	Redescription of <i>Tintinnopsis everta</i> Kofoid and Campbell 1929 (Alveolata, Ciliophora). <i>Journal of Eukaryotic Microbiology</i> , 2018, 65, 484-504.	0.8	12
14621	Emergence of Double- and Triple-Gene Reassortant G1P[8] Rotaviruses Possessing a DS-1-Like Backbone after Rotavirus Vaccine Introduction in Malawi. <i>Journal of Virology</i> , 2018, 92, .	1.5	61
14622	Improved Algorithmic Complexity for the 3SEQ Recombination Detection Algorithm. <i>Molecular Biology and Evolution</i> , 2018, 35, 247-251.	3.5	139
14623	Glucose-Induced Trophic Shift in an Endosymbiont Dinoflagellate with Physiological and Molecular Consequences. <i>Plant Physiology</i> , 2018, 176, 1793-1807.	2.3	32
14624	Noncontiguous finished genome sequence of <i>Megasphaera</i> sp. ASD88, isolated from faeces of a child with autism spectrum disorder. <i>New Microbes and New Infections</i> , 2018, 22, 13-16.	0.8	5
14625	Phylogenomics offers resolution of major tunicate relationships. <i>Molecular Phylogenetics and Evolution</i> , 2018, 121, 166-173.	1.2	56
14626	TarHunter, a tool for predicting conserved microRNA targets and target mimics in plants. <i>Bioinformatics</i> , 2018, 34, 1574-1576.	1.8	29
14627	iUUCD 2.0: an update with rich annotations for ubiquitin and ubiquitin-like conjugations. <i>Nucleic Acids Research</i> , 2018, 46, D447-D453.	6.5	57
14628	Morphological and Molecular Redefinition of <i>Euplotes platystoma</i> Dragesco & Dragesco, 1986 and <i>Aspidisca lynceus</i> (Müller, 1773) Ehrenberg, 1859, with Reconsideration of a Well-Known <i>Euplotes</i> Ciliate, <i>Euplotes harpa</i> Stein, 1859 (Ciliophora, Euplotida). <i>Journal of Eukaryotic Microbiology</i> , 2018, 65, 531-543.	0.8	14

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14630	Functional traits can improve our understanding of niche- and dispersal-based processes. <i>Oecologia</i> , 2018, 186, 783-792.	0.9	16
14631	Genomic diversity and distribution of <i>Bifidobacterium longum</i> subsp. <i>longum</i> across the human lifespan. <i>Scientific Reports</i> , 2018, 8, 85.	1.6	99
14632	Taxonomic status of some geofrutex members of Vanguerieae (Rubiaceae): notes on <i>Eriosemopsis</i> and <i>Pygmaeothamnus</i> and the description of a new genus <i>Bridsonia</i> . <i>Botanical Journal of the Linnean Society</i> , 2018, 186, 47-65.	0.8	3
14633	Biosynthesis of bioactive diterpenoids in the medicinal plant <i>Vitex agnus-castus</i> . <i>Plant Journal</i> , 2018, 93, 943-958.	2.8	68
14634	Positive diversity-functioning relationships in model communities of methanotrophic bacteria. <i>Ecology</i> , 2018, 99, 714-723.	1.5	30
14635	A role for 9-lipoxygenases in maize defense against insect herbivory. <i>Plant Signaling and Behavior</i> , 2018, 13, e1422462.	1.2	44
14636	The phylogeography of the cycad genus <i>Dioon</i> (Zamiaceae) clarifies its Cenozoic expansion and diversification in the Mexican transition zone. <i>Annals of Botany</i> , 2018, 121, 535-548.	1.4	42
14637	A new species of Ampharete (Annelida: Ampharetidae) from the NW Iberian Peninsula, with a synoptic table comparing NE Atlantic species of the genus. <i>Zoological Journal of the Linnean Society</i> , 2018, 183, 526-555.	1.0	9
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14639	Matriclans shape populations: Insights from the Angolan Namib Desert into the maternal genetic history of southern Africa. <i>American Journal of Physical Anthropology</i> , 2018, 165, 518-535.	2.1	22
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14641	Systematics of the genus <i>Oecomys</i> (Sigmodontinae: Oryzomyini): molecular phylogenetic, cytogenetic and morphological approaches reveal cryptic species. <i>Zoological Journal of the Linnean Society</i> , 2018, 184, 182-210.	1.0	31
14642	PeachVar-DB: A Curated Collection of Genetic Variations for the Interactive Analysis of Peach Genome Data. <i>Plant and Cell Physiology</i> , 2018, 59, e2-e2.	1.5	12
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14644	Genomic and Biochemical Characterization of <i>Acinetobacter</i> Podophage Petty Reveals a Novel Lysis Mechanism and Tail-Associated Depolymerase Activity. <i>Journal of Virology</i> , 2018, 92, .	1.5	65
14645	<i>Vibrio coralliirubri</i> sp. nov., a new species isolated from mucus of red coral ( <i>Corallium rubrum</i> ) collected at Procida island, Italy. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 1105-1115.	0.7	18
14646	The origins of diversity in ancient landscapes: Deep phylogeographic structuring in a pseudoscorpion ( <i>Pseudotyranochthoniidae</i> : <i>Pseudotyranochthonius</i> ) reflects Plio-Pleistocene climate fluctuations. <i>Zoologischer Anzeiger</i> , 2018, 273, 112-123.	0.4	26

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14648	Roosting ecology of Stenodermatinae bats (Phyllostomidae): evolution of foliage roosting and correlated phenotypes. <i>Mammal Review</i> , 2018, 48, 75-89.	2.2	31
14649	Human Bocavirus: Detection, Quantification and Molecular Characterization in Sewage and Surface Waters in Uruguay. <i>Food and Environmental Virology</i> , 2018, 10, 193-200.	1.5	9
14650	Molecular taxonomy and subgeneric classification of tapeworms of the genus <i>Moniezia</i> Blanchard, 1891 (Cestoda, Anoplocephalidae) in northern cervids ( <i>Alces</i> and <i>Rangifer</i> ). <i>Parasitology International</i> , 2018, 67, 218-224.	0.6	14
14651	<sc>GPS</sc>it: An automated method for evolutionary analysis of nonculturable ciliated microeukaryotes. <i>Molecular Ecology Resources</i> , 2018, 18, 700-713.	2.2	36
14652	Analyses of separate and concatenated <i>cox1</i> and 18S rRNA gene sequences indicate that the bat piroplasm <i>Babesia vesperuginis</i> is phylogenetically close to <i>Cytauxzoon felis</i> and the "prototheilerid" <i>Babesia conradae</i> . <i>Acta Veterinaria Hungarica</i> , 2018, 66, 107-115.	0.2	9
14653	Marine Leech Anticoagulant Diversity and Evolution. <i>Journal of Parasitology</i> , 2018, 104, 210-220.	0.3	14
14654	Species delimitation and sex associations in the bee genus <i>Thygater</i> , with the aid of molecular data, and the description of a new species. <i>Apidologie</i> , 2018, 49, 484-496.	0.9	9
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14656	Gut microbiomes of wild great apes fluctuate seasonally in response to diet. <i>Nature Communications</i> , 2018, 9, 1786.	5.8	192
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14659	Missing enzymes in the biosynthesis of the anticancer drug vinblastine in Madagascar periwinkle. <i>Science</i> , 2018, 360, 1235-1239.	6.0	279
14660	Quantifying the Evolutionary Conservation of Genes Encoding Multidrug Efflux Pumps in the ESKAPE Pathogens To Identify Antimicrobial Drug Targets. <i>MSystems</i> , 2018, 3, .	1.7	20
14661	Antigenic cartography of H1N1 influenza viruses using sequence-based antigenic distance calculation. <i>BMC Bioinformatics</i> , 2018, 19, 51.	1.2	39
14662	BpWrapper: BioPerl-based sequence and tree utilities for rapid prototyping of bioinformatics pipelines. <i>BMC Bioinformatics</i> , 2018, 19, 76.	1.2	11
14663	Evolution of CYP2J19, a gene involved in colour vision and red coloration in birds: positive selection in the face of conservation and pleiotropy. <i>BMC Evolutionary Biology</i> , 2018, 18, 22.	3.2	25
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14667	New insights into the phylogenetics and population structure of the prairie falcon ( <i>Falco mexicanus</i> ). <i>BMC Genomics</i> , 2018, 19, 233.	1.2	25
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14670	The Antarctic sea ice alga <i>Chlamydomonas</i> sp. ICE-L provides insights into adaptive patterns of chloroplast evolution. <i>BMC Plant Biology</i> , 2018, 18, 53.	1.6	22
14671	Vast diversity of prokaryotic virus genomes encoding double jelly-roll major capsid proteins uncovered by genomic and metagenomic sequence analysis. <i>Virology Journal</i> , 2018, 15, 67.	1.4	65
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14675	Analysis of lineage-specific Alu subfamilies in the genome of the olive baboon, <i>Papio anubis</i> . <i>Mobile DNA</i> , 2018, 9, 10.	1.3	10
14676	Expression of <i>meis</i> and <i>hoxa11</i> in dipnoan and teleost fins provides new insights into the evolution of vertebrate appendages. <i>EvoDevo</i> , 2018, 9, 11.	1.3	5
14677	“Candidatus <i>Paraporphyromonas polyenzymogenes</i> ” encodes multi-modular cellulases linked to the type IX secretion system. <i>Microbiome</i> , 2018, 6, 44.	4.9	32
14678	The genomic underpinnings of eukaryotic virus taxonomy: creating a sequence-based framework for family-level virus classification. <i>Microbiome</i> , 2018, 6, 38.	4.9	70
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14680	Comparative transcriptome reveal the potential adaptive evolutionary genes in <i>Andrias davidianus</i> . <i>Hereditas</i> , 2018, 155, 18.	0.5	4
14681	Quantitative trait loci associated with trichomes in the <i>Solanum galapagense</i> accession LA1401. <i>Genetic Resources and Crop Evolution</i> , 2018, 65, 1671-1685.	0.8	12
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14684	Structural Implications of Mutations Conferring Rifampin Resistance in <i>Mycobacterium leprae</i> . <i>Scientific Reports</i> , 2018, 8, 5016.	1.6	41
14685	The <i>Phytophthora cactorum</i> genome provides insights into the adaptation to host defense compounds and fungicides. <i>Scientific Reports</i> , 2018, 8, 6534.	1.6	52
14686	Analysis of <i>Theileria orientalis</i> draft genome sequences reveals potential species-level divergence of the Ikeda, Chitose and Buffeli genotypes. <i>BMC Genomics</i> , 2018, 19, 298.	1.2	24
14687	Glycoside hydrolase gene transcription by <i>Alicyclobacillus acidocaldarius</i> during growth on wheat arabinoxylan and monosaccharides: a proposed xylan hydrolysis mechanism. <i>Biotechnology for Biofuels</i> , 2018, 11, 110.	6.2	5
14688	TREE2FASTA: a flexible Perl script for batch extraction of FASTA sequences from exploratory phylogenetic trees. <i>BMC Research Notes</i> , 2018, 11, 164.	0.6	10
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14693	Molecular identification of <i>Sarcocystis lutrae</i> (Apicomplexa: Sarcocystidae) in muscles of five species of the family Mustelidae. <i>Parasitology Research</i> , 2018, 117, 1989-1993.	0.6	6
14694	Paralytic shellfish toxin producing <i>Aphanizomenon gracile</i> strains isolated from Lake Iznik, Turkey. <i>Toxicon</i> , 2018, 148, 132-142.	0.8	8
14695	Ancient DNA study reveals HLA susceptibility locus for leprosy in medieval Europeans. <i>Nature Communications</i> , 2018, 9, 1569.	5.8	67
14696	Incongruence in molecular species delimitation schemes: What to do when adding more data is difficult. <i>Molecular Ecology</i> , 2018, 27, 2397-2413.	2.0	24
14697	The evolutionary impact of intragenic <i>FliA</i> promoters in proteobacteria. <i>Molecular Microbiology</i> , 2018, 108, 361-378.	1.2	14
14698	Molecular Mechanisms for Species Differences in Organic Anion Transporter 1, OAT1: Implications for Renal Drug Toxicity. <i>Molecular Pharmacology</i> , 2018, 94, 689-699.	1.0	40
14699	A new strategy to infer circularity applied to four new complete frog mitogenomes. <i>Ecology and Evolution</i> , 2018, 8, 4011-4018.	0.8	15
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14702	Host-mediated RNAi of a Notch-like receptor gene in <i>Meloidogyne incognita</i> induces nematode resistance. <i>Parasitology</i> , 2018, 145, 1896-1906.	0.7	5
14703	The genetic architecture of floral traits in the woody plant <i>Prunus mume</i> . <i>Nature Communications</i> , 2018, 9, 1702.	5.8	73
14704	Comparative Transcriptomics in Two Bivalve Species Offers Different Perspectives on the Evolution of Sex-Biased Genes. <i>Genome Biology and Evolution</i> , 2018, 10, 1389-1402.	1.1	17
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14707	First Ultrastructural and Molecular Phylogenetic Evidence from the Blastogregarines, an Early Branching Lineage of Plesiomorphic Apicomplexa. <i>Protist</i> , 2018, 169, 697-726.	0.6	14
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14709	Molecular identification and characterization of endophytes from uncultivated barley. <i>Mycologia</i> , 2018, 110, 453-472.	0.8	7
14710	Microbial Community Composition in a Simultaneous Nitrification and Denitrification Bioreactor for Domestic Wastewater Treatment. <i>IOP Conference Series: Earth and Environmental Science</i> , 2018, 112, 012007.	0.2	4
14711	Evidence for Allopolyploid Speciation in <i>Nymphoides</i> (Menyanthaceae). <i>Systematic Botany</i> , 2018, 43, 117-129.	0.2	10
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14714	Molecular phylogeny of Banjo catfishes (Ostariophysi: Siluriformes: Aspredinidae): A continental radiation in South American freshwaters. <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 459-467.	1.2	10
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14716	Plastid Transcript Editing across Dinoflagellate Lineages Shows Lineage-Specific Application but Conserved Trends. <i>Genome Biology and Evolution</i> , 2018, 10, 1019-1038.	1.1	22
14717	Structural and functional roles of dynamically correlated residues in thymidylate kinase. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 341-354.	1.1	8
14718	Evidence for intragenic recombination and selective sweep in an effector gene of <i>Phytophthora infestans</i> . <i>Evolutionary Applications</i> , 2018, 11, 1342-1353.	1.5	34

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14719	Bacterial Community in Water and Air of Two Sub-Alpine Lakes in Taiwan. <i>Microbes and Environments</i> , 2018, 33, 120-126.	0.7	17
14720	Does reproductive isolation reflect the segregation of color forms in <i>Spiranthes sinensis</i> (Pers.) Ames complex (Orchidaceae) in the Chinese Himalayas?. <i>Ecology and Evolution</i> , 2018, 8, 5455-5469.	0.8	19
14721	ShRNA-mediated knock-down of CXCL8 inhibits tumor growth in colorectal liver metastasis. <i>Biochemical and Biophysical Research Communications</i> , 2018, 500, 731-737.	1.0	34
14722	Molecular data on the CO1 and beta fibrinogen gene in the evolutionary relationships of the mastiff bat (Chiroptera, Molossidae, Molossus). <i>Data in Brief</i> , 2018, 18, 1609-1613.	0.5	6
14723	Complete genome sequence of <i>Bacillus velezensis</i> QST713: A biocontrol agent that protects <i>Agaricus bisporus</i> crops against the green mould disease. <i>Journal of Biotechnology</i> , 2018, 278, 10-19.	1.9	67
14724	Gymnosperms on the EDGE. <i>Scientific Reports</i> , 2018, 8, 6053.	1.6	75
14725	Taxonomic Repositioning of <i>Xanthomonas campestris</i> pv. <i>viticola</i> (Nayudu 1972) Dye 1978 as <i>Xanthomonas citri</i> pv. <i>viticola</i> (Nayudu 1972) Dye 1978 comb. nov. and Emendation of the Description of <i>Xanthomonas citri</i> pv. <i>anacardii</i> to Include Pigmented Isolates Pathogenic to Cashew Plant. <i>Phytopathology</i> , 2018, 108, 1143-1153.	1.1	33
14726	Structural insight into industrially relevant glucoamylases: flexible positions of starch-binding domains. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 463-470.	1.1	12
14727	Tree nut allergies: Allergen homology, cross-reactivity, and implications for therapy. <i>Clinical and Experimental Allergy</i> , 2018, 48, 762-772.	1.4	64
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14730	A New Species of <i>Telipogon</i> (Orchidaceae) from Mexico and its Phylogenetic Position Among Mesoamerican Species. <i>Systematic Botany</i> , 2018, 43, 9-16.	0.2	0
14731	Molecular and morphological data validate the new combination of <i>Lysurus sphaerocephalum</i> from Argentina, with some additional records on Phallales (Agaricomycetes). <i>Mycologia</i> , 2018, 110, 419-433.	0.8	5
14732	Comparative genomic analysis of the <i>Hyphochytrium catenoides</i> . <i>Open Biology</i> , 2018, 8, 170184.	1.5	31
14733	Identification of Novel Gammaherpesviruses in a South American Fur Seal ( <i>Arctocephalus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 182	0.3	12
14734	Characterisation of major histocompatibility complex class I transcripts in an Australian dragon lizard. <i>Developmental and Comparative Immunology</i> , 2018, 84, 164-171.	1.0	3
14735	Robust <i>Frankia</i> phylogeny, species delineation and intraspecies diversity based on Multi-Locus Sequence Analysis (MLSA) and Single-Locus Strain Typing (SLST) adapted to a large sample size. <i>Systematic and Applied Microbiology</i> , 2018, 41, 311-323.	1.2	29
14736	Large-scale sequence analysis reveals novel human-adaptive markers in PB2 segment of seasonal influenza A viruses. <i>Emerging Microbes and Infections</i> , 2018, 7, 1-12.	3.0	13



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14738	The Role of Trehalose 6-Phosphate in Crop Yield and Resilience. <i>Plant Physiology</i> , 2018, 177, 12-23.	2.3	114
14739	Pliocene–Pleistocene ecological niche evolution shapes the phylogeography of a Mediterranean plant group. <i>Molecular Ecology</i> , 2018, 27, 1696-1713.	2.0	25
14740	Mutations in the CDS and promoter of BjuA07.CLV1 cause a multilocular trait in <i>Brassica juncea</i> . <i>Scientific Reports</i> , 2018, 8, 5339.	1.6	29
14741	<i>Paecilomyces</i> Rot: A New Apple Disease. <i>Plant Disease</i> , 2018, 102, 1581-1587.	0.7	15
14742	Ophiostomatoid Fungi Associated with the Four-Eyed Fir Bark Beetle on the Territory of Russia. <i>Russian Journal of Biological Invasions</i> , 2018, 9, 63-74.	0.2	13
14743	<i>Streptomyces carminius</i> sp. nov., a novel actinomycete isolated from <i>Sophora alopecuroides</i> in Xinjiang, China. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 1807-1814.	0.7	7
14744	Horizontal gene transfer constrains the timing of methanogen evolution. <i>Nature Ecology and Evolution</i> , 2018, 2, 897-903.	3.4	109
14745	Mutations in Mitochondrial DNA From Pancreatic Ductal Adenocarcinomas Associate With Survival Times of Patients and Accumulate as Tumors Progress. <i>Gastroenterology</i> , 2018, 154, 1620-1624.e5.	0.6	27
14746	Activity and diversity of methane-oxidizing bacteria along a Norwegian sub-Arctic glacier forefield. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	13
14747	Leeches from Chiapas, Mexico, with a New Species of <i>Erpobdella</i> (Hirudinida: Erpobdellidae). <i>American Museum Novitates</i> , 2018, 3895, 1-15.	0.2	7
14748	The phylogenetic position of <i>Choerodonocola</i> Cribb, 2005 (Digenea: Opecoelidae) with a partial life-cycle for a new species from the blue-barred parrotfish <i>Scarus ghobban</i> Forsskål (Scaridae) in Moreton Bay, Australia. <i>Systematic Parasitology</i> , 2018, 95, 337-352.	0.5	9
14749	Two new species of helicosporous hyphomycetes from Taiwan. <i>Mycological Progress</i> , 2018, 17, 557-569.	0.5	11
14750	A High-Throughput Mutational Scan of an Intrinsically Disordered Acidic Transcriptional Activation Domain. <i>Cell Systems</i> , 2018, 6, 444-455.e6.	2.9	135
14751	Cas13d Is a Compact RNA-Targeting Type VI CRISPR Effector Positively Modulated by a WYL-Domain-Containing Accessory Protein. <i>Molecular Cell</i> , 2018, 70, 327-339.e5.	4.5	356
14752	Phylogenetic analysis of trophic niche evolution reveals a latitudinal herbivory gradient in Clupeoidei (herrings, anchovies, and allies). <i>Molecular Phylogenetics and Evolution</i> , 2018, 124, 151-161.	1.2	37
14753	Phylogeny and biogeography of the African burrowing snake subfamily Aparallactinae (Squamata: Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	1.2	32
14754	Sensitive and frequent identification of high avidity neo-epitope-specific CD8 + T cells in immunotherapy-naïve ovarian cancer. <i>Nature Communications</i> , 2018, 9, 1092.	5.8	122

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14756	SCOTCH: subtype A coreceptor tropism classification in HIV-1. Bioinformatics, 2018, 34, 2575-2580.	1.8	15
14757	New species and a molecular dating analysis of Vetulina Schmidt, 1879 (Porifera: Demospongiae). Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 Society, 2018, 184, 585-604.	1.0	8
14758	The bud midge <i>Pterodiplosis floricola</i> in citrus crops in Colombia. Entomologia Experimentalis Et Applicata, 2018, 166, 204-214.	0.7	2
14759	Molecular phylogeny, systematics, and revision of the type species of <i>Lobomonas</i> , <i>L. afrancei</i> (Volvocales, Chlorophyta) and closely related taxa. Journal of Phycology, 2018, 54, 198-214.	1.0	4
14760	Pleistocene North African genomes link Near Eastern and sub-Saharan African human populations. Science, 2018, 360, 548-552.	6.0	142
14761	The crystal structure of methanol dehydrogenase, a quinoprotein from the marine methylotrophic bacterium <i>Methylophaga aminisulfidivorans</i> MPT. Journal of Microbiology, 2018, 56, 246-254.	1.3	13
14762	Combinatorial inhibition of PTPN12-regulated receptors leads to a broadly effective therapeutic strategy in triple-negative breast cancer. Nature Medicine, 2018, 24, 505-511.	15.2	47
14763	U-Index, a dataset and an impact metric for informatics tools and databases. Scientific Data, 2018, 5, 180043.	2.4	7
14764	Cooption of an appendage-patterning gene cassette in the head segmentation of arachnids. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E3491-E3500.	3.3	36
14765	Gene Co-occurrence Networks Reflect Bacteriophage Ecology and Evolution. MBio, 2018, 9, .	1.8	41
14766	Interaction of N-terminal peptide analogues of the Na <sup>+</sup> ,K <sup>+</sup> -ATPase with membranes. Biochimica Et Biophysica Acta - Biomembranes, 2018, 1860, 1282-1291.	1.4	26
14767	Extremely Divergent Haplotypes in Two Toxin Gene Complexes Encode Alternative Venom Types within Rattlesnake Species. Current Biology, 2018, 28, 1016-1026.e4.	1.8	41
14768	In-host microevolution of <i>Aspergillus fumigatus</i> : A phenotypic and genotypic analysis. Fungal Genetics and Biology, 2018, 113, 1-13.	0.9	80
14769	Effect of phosphate nutrition on growth, physiology and phosphate transporter expression of cucumber seedlings. Plant Physiology and Biochemistry, 2018, 127, 211-222.	2.8	15
14770	One or many? Molecular versus morphological diversity in the aplousobranchian Chaetoderma nitidulum Lovén, 1844 (Mollusca: Caudofoveata). Journal of Molluscan Studies, 2018, 84, 113-131.	0.4	6
14771	New Macrostylidae (Isopoda) from the Northwest Pacific Basin described by means of integrative taxonomy with reference to geographical barriers in the abyss. Zoological Journal of the Linnean Society, 2018, 182, 549-603.	1.0	20
14772	Trophic specialization drives morphological evolution in sea snakes. Royal Society Open Science, 2018, 5, 172141.	1.1	34

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14773	Metagenomic analysis of bat guano samples revealed the presence of viruses potentially carried by insects, among others by <i>Apis mellifera</i> in Hungary. <i>Acta Veterinaria Hungarica</i> , 2018, 66, 151-161.	0.2	6
14774	Bacterial Alkaloid Biosynthesis: Structural Diversity via a Minimalistic Nonribosomal Peptide Synthetase. <i>Cell Chemical Biology</i> , 2018, 25, 659-665.e9.	2.5	24
14775	Deconstructing the evolutionary complexity between rust fungi (Pucciniales) and their plant hosts. <i>Studies in Mycology</i> , 2018, 89, 143-152.	4.5	101
14776	Genome-wide identification of natural RNA aptamers in prokaryotes and eukaryotes. <i>Nature Communications</i> , 2018, 9, 1289.	5.8	37
14777	Diversity of airborne <i>Cladosporium</i> species isolated from agricultural environments of northern Argentinean Patagonia: molecular characterization and plant pathogenicity. <i>Aerobiologia</i> , 2018, 34, 227-239.	0.7	9
14778	Functional analysis RaZIP1 transporter of the ZIP family from the ectomycorrhizal Zn-accumulating <i>Russula atropurpurea</i> . <i>BioMetals</i> , 2018, 31, 255-266.	1.8	13
14779	Discovery of 4-((N-(2-(dimethylamino)ethyl)acrylamido)methyl)-N-(4-methyl-3-((4-(pyridin-3-yl)pyrimidin-2-yl)amino)phenyl)benzamide (CHMFL-PDGFR-159) as a highly selective type II PDGFR $\alpha/\beta$ kinase inhibitor for PDGFR $\alpha/\beta$ driving chronic eosinophilic leukemia. <i>European Journal of Medicinal Chemistry</i> , 2018, 150, 366-384.	2.6	16
14780	Structural model, functional modulation by ivermectin and tissue localization of <i>Haemonchus contortus</i> P-glycoprotein-13. <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2018, 8, 145-157.	1.4	17
14781	Using Chou's general PseAAC to analyze the evolutionary relationship of receptor associated proteins (RAP) with various folding patterns of protein domains. <i>Journal of Theoretical Biology</i> , 2018, 445, 62-74.	0.8	65
14782	Probing the Phylogenomics and Putative Pathogenicity Genes of <i>Pythium insidiosum</i> by Oomycete Genome Analyses. <i>Scientific Reports</i> , 2018, 8, 4135.	1.6	35
14783	A survey of Type III restriction-modification systems reveals numerous, novel epigenetic regulators controlling phase-variable regulons; phasevarions. <i>Nucleic Acids Research</i> , 2018, 46, 3532-3542.	6.5	43
14784	<i>Serratia proteamaculans</i> Strain AGR96X Encodes an Antifeeding Prophage (Tailocin) with Activity against Grass Grub ( <i>Costelytra giveni</i> ) and Manuka Beetle ( <i>Pyronota</i> Species) Larvae. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	27
14785	Biochemical and structural characterization of a novel cold-active esterase-like protein from the psychrophilic yeast <i>Glaciozyma antarctica</i> . <i>Extremophiles</i> , 2018, 22, 607-616.	0.9	24
14786	The wheat TabZIP2 transcription factor is activated by the nutrient starvation-responsive SnRK3/CIPK protein kinase. <i>Plant Molecular Biology</i> , 2018, 96, 543-561.	2.0	23
14787	Ligand Binding Site Structure Influences the Evolution of Protein Complex Function and Topology. <i>Cell Reports</i> , 2018, 22, 3265-3276.	2.9	18
14788	A new species of the deep-sea spongicolid genus <i>Spongicoloides</i> (Crustacea, Decapoda, Stenopodidea) and a new species of the glass sponge genus <i>Corbitella</i> (Hexactinellida, Lyssacinosa, Euplectellidae) from a seamount near the Mariana Trench, with a novel commensal relationship between the two genera. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> . 2018. 135. 88-107.	0.6	11
14789	Using mock communities of arbuscular mycorrhizal fungi to evaluate fidelity associated with Illumina sequencing. <i>Fungal Ecology</i> , 2018, 33, 52-64.	0.7	33
14790	The Dimethylsulfoniopropionate (DMSP) Lyase and Lyase-Like Cupin Family Consists of <i>Bona Fide</i> DMSP lyases as Well as Other Enzymes with Unknown Function. <i>Biochemistry</i> , 2018, 57, 3364-3377.	1.2	22

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14791	An evolutionary hotspot defines functional differences between CRYPTOCHROMES. <i>Nature Communications</i> , 2018, 9, 1138.	5.8	72
14792	Phylogenetic analysis of the CDGSH iron-sulfur binding domain reveals its ancient origin. <i>Scientific Reports</i> , 2018, 8, 4840.	1.6	14
14793	New Threats from H7N9 Influenza Virus: Spread and Evolution of High- and Low-Pathogenicity Variants with High Genomic Diversity in Wave Five. <i>Journal of Virology</i> , 2018, 92, .	1.5	92
14794	Identification and characterization of two novel Gammapapillomavirus genomes in skin of an immunosuppressed Epidermodysplasia Verruciformis patient. <i>Virus Research</i> , 2018, 249, 66-68.	1.1	6
14795	The genomic and functional landscapes of developmental plasticity in the American cockroach. <i>Nature Communications</i> , 2018, 9, 1008.	5.8	113
14796	Phylogenetic relationships in <i>Bulbostylis</i> (Abildgaardieae: Cyperaceae) inferred from nuclear and plastid DNA sequence data. <i>Systematics and Biodiversity</i> , 2018, 16, 441-452.	0.5	7
14797	Variation Across Mitochondrial Gene Trees Provides Evidence for Systematic Error: How Much Gene Tree Variation Is Biological?. <i>Systematic Biology</i> , 2018, 67, 847-860.	2.7	51
14798	Dating the Species Network: Allopolyploidy and Repetitive DNA Evolution in American Daisies ( <i>Melampodium</i> sect. <i>Melampodium</i> , Asteraceae). <i>Systematic Biology</i> , 2018, 67, 1010-1024.	2.7	54
14799	Recent radiation and dispersal of an ancient lineage: The case of <i>Fouquieria</i> (Fouquieriaceae, Ericales) in North American deserts. <i>Molecular Phylogenetics and Evolution</i> , 2018, 126, 92-104.	1.2	19
14800	Formal description of <i>Mycobacterium neglectum</i> sp. nov. and <i>Mycobacterium palauense</i> sp. nov., rapidly growing actinobacteria. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 1209-1223.	0.7	12
14801	Molecular phylogeny of glacial relict species: a case of freshwater Valvatidae molluscs (Mollusca: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 3	1.0	10
14802	Diversity and phylogenetic relationships of North Atlantic <i>Laonice</i> Malmgren, 1867 (Spionidae,) Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.3	9
14803	Phylogenetic analysis of cnidarian peroxiredoxins and stress-responsive expression in the estuarine sea anemone <i>Nematostella vectensis</i> . <i>Comparative Biochemistry and Physiology Part A, Molecular &amp; Integrative Physiology</i> , 2018, 221, 32-43.	0.8	8
14804	Promotion of <i>Lotus tenuis</i> in the Flooding Pampa (Argentina) increases the soil fungal diversity. <i>Fungal Ecology</i> , 2018, 33, 80-91.	0.7	10
14805	Characterization of a $\beta$ 2 adrenergic receptor protein precursor in the European eel ( <i>Anguilla anguilla</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 T	1.1	1
14806	Genome-wide analysis of the MADS-box gene family in polyploid cotton ( <i>Gossypium hirsutum</i> ) and in its diploid parental species ( <i>Gossypium arboreum</i> and <i>Gossypium raimondii</i> ). <i>Plant Physiology and Biochemistry</i> , 2018, 127, 169-184.	2.8	30
14807	Isolation and characterization of pathogenic leptospire associated with cattle. <i>Veterinary Microbiology</i> , 2018, 218, 25-30.	0.8	41
14808	Phylogenetic positions of seven poorly known species of <i>Ferula</i> (Apiaceae) with remarks on the phylogenetic utility of the plastid <i>trnH-psbA</i> , <i>trnS-trnG</i> , and <i>atpB-rbcL</i> intergenic spacers. <i>Systematics and Biodiversity</i> , 2018, 16, 428-440.	0.5	6

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14809	Clonal spread of vanA <i>Enterococcus faecium</i> sequence type 203 in Bulgarian hospitals. <i>Infectious Diseases</i> , 2018, 50, 718-721.	1.4	5
14810	Generalized Bootstrap Supports for Phylogenetic Analyses of Protein Sequences Incorporating Alignment Uncertainty. <i>Systematic Biology</i> , 2018, 67, 997-1009.	2.7	12
14811	Evolutionary and expression analyses reveal a pattern of ancient duplications and functional specializations in the diversification of the Downstream of Kinase (DOK) genes. <i>Developmental and Comparative Immunology</i> , 2018, 84, 193-198.	1.0	2
14812	Interrogation of Benzomalvin Biosynthesis Using Fungal Artificial Chromosomes with Metabolomic Scoring (FAC-MS): Discovery of a Benzodiazepine Synthase Activity. <i>Biochemistry</i> , 2018, 57, 3237-3243.	1.2	19
14813	Evolutionary origins and diversification of testis-specific short histone H2A variants in mammals. <i>Genome Research</i> , 2018, 28, 460-473.	2.4	46
14814	Multiplexed Isothermal Amplification Based Diagnostic Platform to Detect Zika, Chikungunya, and Dengue 1. <i>Journal of Visualized Experiments</i> , 2018, , .	0.2	8
14815	Effects of the Tanaka Line on the genetic structure of <i>Bombax ceiba</i> (Malvaceae) in dry-hot valley areas of southwest China. <i>Ecology and Evolution</i> , 2018, 8, 3599-3608.	0.8	17
14816	<i>Disperis tomaszii</i> (Orchidaceae, Orchidoideae), a new species from Cameroon. <i>Plant Systematics and Evolution</i> , 2018, 304, 231-243.	0.3	0
14817	Comparative genomic analysis of fungal TPP-riboswitches. <i>Fungal Genetics and Biology</i> , 2018, 114, 34-41.	0.9	12
14818	Community structure and distribution of benthic cyanobacteria in Antarctic lacustrine microbial mats. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	18
14819	Genome Reports: Contracted Genes and Dwarfed Plastome in Mycoheterotrophic <i>Sciaphila thaidanica</i> (Triuridaceae, Pandanales). <i>Genome Biology and Evolution</i> , 2018, 10, 976-981.	1.1	17
14820	Unexpected diversity in the mobilome of a <i>Pseudomonas aeruginosa</i> strain isolated from a dental unit waterline revealed by SMRT Sequencing. <i>Genome</i> , 2018, 61, 359-365.	0.9	2
14821	An <i>Aspergillus aculateus</i> strain was capable of producing agriculturally useful nanoparticles via bioremediation of iron ore tailings. <i>Journal of Environmental Management</i> , 2018, 215, 100-107.	3.8	21
14822	Interaction of rs316019 variants of SLC22A2 with metformin and other drugs- an in silico analysis. <i>Journal of Genetic Engineering and Biotechnology</i> , 2018, 16, 769-775.	1.5	9
14823	Taitaia, a novel lichenicolous fungus in tropical montane forests in Kenya (East Africa). <i>Lichenologist</i> , 2018, 50, 173-184.	0.5	13
14824	Major changes in the composition of a Southern Ocean bacterial community in response to diatom-derived dissolved organic matter. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	25
14825	Innovative assembly strategy contributes to understanding the evolution and conservation genetics of the endangered <i>Solenodon paradoxus</i> from the island of Hispaniola. <i>GigaScience</i> , 2018, 7, .	3.3	12
14826	Horizontal Gene Transfer Building Prokaryote Genomes: Genes Related to Exchange Between Cell and Environment are Frequently Transferred. <i>Journal of Molecular Evolution</i> , 2018, 86, 190-203.	0.8	20

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14827	Two monorchiid species from the freckled goatfish, <i>Upeneus tragula</i> Richardson (Perciformes: Tj ETQqO 0 0 rgBT /Overlock 10 Tf 50 74). 2018, 95, 353-365.	0.5	12
14828	Elucidating the substrate specificities of acyl-lipid thioesterases from diverse plant taxa. <i>Plant Physiology and Biochemistry</i> , 2018, 127, 104-118.	2.8	7
14829	Dynamic root exudate chemistry and microbial substrate preferences drive patterns in rhizosphere microbial community assembly. <i>Nature Microbiology</i> , 2018, 3, 470-480.	5.9	1,268
14830	An optically controlled probe identifies lipid-gating fenestrations within the TRPC3 channel. <i>Nature Chemical Biology</i> , 2018, 14, 396-404.	3.9	85
14831	Discovery of enzymes for toluene synthesis from anoxic microbial communities. <i>Nature Chemical Biology</i> , 2018, 14, 451-457.	3.9	47
14832	Lifting the blue-headed veil – integrative taxonomy of the <i>Acanthocercus atricollis</i> species complex (Squamata: Agamidae). <i>Journal of Natural History</i> , 2018, 52, 771-817.	0.2	5
14833	Genomic Changes Associated with the Evolutionary Transitions of Nostoc to a Plant Symbiont. <i>Molecular Biology and Evolution</i> , 2018, 35, 1160-1175.	3.5	54
14834	Variations on a theme: evolution of the phage-shock-protein system in Actinobacteria. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 753-760.	0.7	7
14835	Changes in the soil bacterial community structure and enzyme activities after intercrop mulch with cover crop for eight years in an orchard. <i>European Journal of Soil Biology</i> , 2018, 86, 34-41.	1.4	81
14836	Revised classification of the righteye flounders (Teleostei: Pleuronectidae) based on multilocus phylogeny with complete taxon sampling. <i>Molecular Phylogenetics and Evolution</i> , 2018, 125, 147-162.	1.2	26
14837	Significant association of SNP polymorphism in the tilapia <i>enhancer of polycomb homolog 1</i> gene with salt tolerance. <i>Aquaculture Research</i> , 2018, 49, 1690-1698.	0.9	7
14838	The modules of <i>trans</i> -acyltransferase assembly lines redefined with a central acyl carrier protein. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 664-675.	1.5	49
14839	Microbiota of lutefisk, a Nordic traditional cod dish with a high pH. <i>Food Control</i> , 2018, 90, 312-316.	2.8	10
14840	Genetic diversity of begomoviruses in Pakistan captured through a vector based survey. <i>Microbial Pathogenesis</i> , 2018, 118, 91-97.	1.3	17
14841	Isolation and identification of burn wound superbugs by molecular technique and their susceptibility to silver nanoparticles. <i>IOP Conference Series: Materials Science and Engineering</i> , 2018, 310, 012146.	0.3	0
14842	Draft genome analysis provides insights into the fiber yield, crude protein biosynthesis, and vegetative growth of domesticated ramie ( <i>Boehmeria nivea</i> L. Gaud). <i>DNA Research</i> , 2018, 25, 173-181.	1.5	32
14843	Chikungunya Outbreak in Kedougou, Southeastern Senegal in 2009–2010. <i>Open Forum Infectious Diseases</i> , 2018, 5, ofx259.	0.4	24
14844	Adaptive evolution to a high purine and fat diet of carnivorans revealed by gut microbiomes and host genomes. <i>Environmental Microbiology</i> , 2018, 20, 1711-1722.	1.8	61

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14845	Allegory of a cave crustacean: systematic and biogeographic reality of <i>Halosbaena</i> (Peracarida: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 74 1185-1202.	0.3	19
14846	<i>Acricoactis brachyacontis</i> sp. nov. from Adak Island, Alaska, represents a new genus and family of metridioidean sea anemone (Anthozoa: Hexacorallia: Actiniaria). <i>Marine Biodiversity</i> , 2018, 48, 1583-1590.	0.3	3
14847	A Characteristic-Based Framework for Multiple Sequence Aligners. <i>IEEE Transactions on Cybernetics</i> , 2018, 48, 41-51.	6.2	14
14848	Genetic variations and population structure in three populations of beardless barb, <i>Cyclocheilichthys apogon</i> (Valenciennes, 1842) inferred from mitochondrial cytochrome b sequences. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2018, 29, 82-90.	0.7	3
14849	Isolation and Identification of Halophilic and Halotolerant Bacteria From Badab-e Surt Travertine Spring, Kiasar, Iran, and Investigation of Calcite Biomineralization Induction. <i>Geomicrobiology Journal</i> , 2018, 35, 64-73.	1.0	6
14850	Identifying selectively important amino acid positions associated with alternative habitat environments in fish mitochondrial genomes. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2018, 29, 511-524.	0.7	4
14851	The complete description of larval stages of the lobster shrimp <i>Leonardsaxius amurensis</i> (Kobjakova,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 Association of the United Kingdom, 2018, 98, 1435-1453.	0.4	3
14852	Genome-wide analysis identifies chickpea ( <i>Cicer arietinum</i> ) heat stress transcription factors (Hsfs) responsive to heat stress at the pod development stage. <i>Journal of Plant Research</i> , 2018, 131, 525-542.	1.2	32
14853	The phylogeny of Galerucinae (Coleoptera: Chrysomelidae) and the performance of mitochondrial genomes in phylogenetic inference compared to nuclear <i>scp</i> rRNA <i>scp</i> genes. <i>Cladistics</i> , 2018, 34, 113-130.	1.5	62
14854	What actually is <i>Vriesea</i> ? A total evidence approach in a polyphyletic genus of Tillandsioideae (Bromeliaceae, Poales). <i>Cladistics</i> , 2018, 34, 181-199.	1.5	34
14855	Morphological and genetic analyses of the first record of longrakered trevally, <i>Ulua mentalis</i> (Perciformes: Carangidae) and of the pinjalo snapper, <i>Pinjalo pinjalo</i> (Perciformes: Lutjanidae) in the Odisha coast, Bay of Bengal. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2018, 29, 552-560.	0.7	6
14856	Lineage Diversity and Size Disparity in Musteloidea: Testing Patterns of Adaptive Radiation Using Molecular and Fossil-Based Methods. <i>Systematic Biology</i> , 2018, 67, 127-144.	2.7	75
14857	African histoplasmosis: new clinical and microbiological insights. <i>Medical Mycology</i> , 2018, 56, 51-59.	0.3	21
14858	Mitogenomic analysis in European brown hare ( <i>Lepus europaeus</i> ) proposes genetic and functional differentiation between the distinct lineages. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2018, 29, 353-360.	0.7	11
14859	Systematic Studies of the Genus <i>Aegialomys</i> Weksler et al., 2006 (Rodentia: Cricetidae: Sigmodontinae): Geographic Variation, Species Delimitation, and Biogeography. <i>Journal of Mammalian Evolution</i> , 2018, 25, 71-118.	1.0	15
14860	<i>In silico</i> prediction of drug resistance due to S247R mutation of Influenza H1N1 neuraminidase protein. <i>Journal of Biomolecular Structure and Dynamics</i> , 2018, 36, 966-980.	2.0	17
14861	The discovery of the virulence gene <i>ToxA</i> in the wheat and barley pathogen <i>Bipolaris sorokiniana</i> . <i>Molecular Plant Pathology</i> , 2018, 19, 432-439.	2.0	122
14862	Optimal data partitioning, multispecies coalescent and Bayesian concordance analyses resolve early divergences of the grape family (Vitaceae). <i>Cladistics</i> , 2018, 34, 57-77.	1.5	44

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14863	Clustering Categorical Data via Ensembling Dissimilarity Matrices. <i>Journal of Computational and Graphical Statistics</i> , 2018, 27, 195-208.	0.9	12
14864	Distribution extension of <i>Ateles chamek</i> (Humboldt 1812) in the southwestern Brazilian Amazon: identification by visual evidence and fecal DNA. <i>Mammalia</i> , 2018, 82, 173-177.	0.3	0
14865	Efficient Quartet Representations of Trees and Applications to Supertree and Summary Methods. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 1010-1015.	1.9	5
14866	Morphology and molecular phylogeny of the marine gregarine parasite <i>Selenidium oshoroense</i> n. sp. (Gregarina, Apicomplexa) isolated from a Northwest Pacific <i>Hydrozoa ezoensis</i> Okuda 1934 (Serpulidae, Polychaeta). <i>Marine Biodiversity</i> , 2018, 48, 1489-1498.	0.3	3
14867	Phylogeny and systematics of Aphroditiformia. <i>Cladistics</i> , 2018, 34, 225-259.	1.5	42
14868	Evaluation of eDNA for groundwater invertebrate detection and monitoring: a case study with endangered <i>Stygobromus</i> (Amphipoda: Crangonyctidae). <i>Conservation Genetics Resources</i> , 2018, 10, 247-257.	0.4	55
14869	Biological Data Analysis Program (BDAP): a multitasking biological sequence analysis program. <i>Neural Computing and Applications</i> , 2018, 30, 1493-1501.	3.2	2
14870	Structure and expression of sulfatase and sulfatase modifying factor genes in the diamondback moth, <i>Plutella xylostella</i> . <i>Insect Science</i> , 2018, 25, 946-958.	1.5	8
14871	Morphology and Molecular Phylogeny of a New Hypotrich Ciliate, <i>Pseudourostyla guizhouensis</i> sp. nov. from Southern China, with Notes on a Chinese Population of <i>Hemicycliostyla franzi</i> (Foissner, 1987) Paiva et al., 2012 (Ciliophora, Hypotricha). <i>Journal of Eukaryotic Microbiology</i> , 2018, 65, 132-142.	0.8	11
14872	Metagenomic-based impact study of transgenic grapevine rootstock on its associated virome and soil bacteriome. <i>Plant Biotechnology Journal</i> , 2018, 16, 208-220.	4.1	31
14873	Evolution of the receptors for growth hormone, prolactin, erythropoietin and thrombopoietin in relation to the vertebrate tetraploidizations. <i>General and Comparative Endocrinology</i> , 2018, 257, 143-160.	0.8	26
14874	Phylogenetic and expression analysis of the magnesium transporter family in pear, and functional verification of <i>PbrMGT7</i> in pear pollen. <i>Journal of Horticultural Science and Biotechnology</i> , 2018, 93, 51-63.	0.9	14
14875	The origin of king crabs: hermit crab ancestry under the magnifying glass. <i>Zoological Journal of the Linnean Society</i> , 2018, 182, 300-318.	1.0	17
14876	The Identification of Araliaceae Species by ITS2 Genetic Barcoding and Pollen Morphology. <i>Planta Medica</i> , 2018, 84, 42-48.	0.7	4
14877	Genetic divergence between colonies of Flesh-footed Shearwater <i>Ardenna carneipes</i> exhibiting different foraging strategies. <i>Conservation Genetics</i> , 2018, 19, 27-41.	0.8	11
14878	Looks can be deceiving: species delimitation reveals hidden diversity in the freshwater crab <i>Aegla longirostri</i> (Decapoda: Anomura). <i>Zoological Journal of the Linnean Society</i> , 2018, 182, 24-37.	1.0	18
14879	Poor genetic differentiation but clear cytoform divergence among cryptic species in <i>Simulium damnosum</i> complex (Siphonaptera: Simuliidae). <i>Systematic Entomology</i> , 2018, 43, 123-135.	1.7	3
14880	Recovery of <i>Bacillus mycoides</i> , <i>B. pseudomycoides</i> and <i>Aeromonas hydrophila</i> from common carp ( <i>Cyprinus carpio</i> ) and rainbow trout ( <i>Oncorhynchus mykiss</i> ) with gill disease. <i>Journal of Fish Diseases</i> , 2018, 41, 125-129.	0.9	12



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14881	Planting accelerates restoration of tropical forest but assembly mechanisms appear insensitive to initial composition. <i>Journal of Applied Ecology</i> , 2018, 55, 986-996.	1.9	22
14882	Assessing the effectiveness of mitochondrial COI and 16S rRNA genes for DNA barcoding of farmland spiders in China. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2018, 29, 695-702.	0.7	12
14883	Cardioprotective mitochondrial binding by hexokinase I is induced by a hyperoxic acute thermal insult in the rainbow trout ( <i>Oncorhynchus mykiss</i> ). <i>Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology</i> , 2018, 224, 45-52.	0.7	4
14884	Characterization of <i>Erysipelothrix</i> sp. isolates causing systemic disease in ornamental fish. <i>Journal of Fish Diseases</i> , 2018, 41, 49-60.	0.9	31
14885	Wolbachia in the Genus <i>Bicyclus</i> : a Forgotten Player. <i>Microbial Ecology</i> , 2018, 75, 255-263.	1.4	14
14886	Multiobjective characteristic-based framework for very-large multiple sequence alignment. <i>Applied Soft Computing Journal</i> , 2018, 69, 719-736.	4.1	3
14887	Spatiotemporal evolutionary epidemiology of H5N1 highly pathogenic avian influenza in West Africa and Nigeria, 2006-2015. <i>Transboundary and Emerging Diseases</i> , 2018, 65, e70-e82.	1.3	15
14888	Interactive comparison and remediation of collections of macromolecular structures. <i>Protein Science</i> , 2018, 27, 182-194.	3.1	13
14889	Molecular Phylogeny and Surface Morphology of <i>Thiriolia hyperdolphinae</i> n. sp. and <i>Cephaloidophora oradareae</i> n. sp. (Gregarinasina, Apicomplexa) Isolated from a Deep Sea <i>Oradarea</i> sp. (Amphipoda) in the West Pacific. <i>Journal of Eukaryotic Microbiology</i> , 2018, 65, 372-381.	0.8	4
14890	DNA barcodes and morphology reveal unrecognized species in Chironomidae (Diptera). <i>Insect Systematics and Evolution</i> , 2018, 49, 329-398.	0.2	40
14891	Genomic Analysis of <i>Bacillus</i> sp. Strain B25, a Biocontrol Agent of Maize Pathogen <i>Fusarium verticillioides</i> . <i>Current Microbiology</i> , 2018, 75, 247-255.	1.0	40
14892	Complete genome sequence of two tomato-infecting begomoviruses in Venezuela: evidence of a putative novel species and a novel recombinant strain. <i>Archives of Virology</i> , 2018, 163, 555-558.	0.9	5
14893	Genome-wide identification of 31 cytochrome P450 (CYP) genes in the freshwater rotifer <i>Brachionus calyciflorus</i> and analysis of their benzo[ <i>a</i> ]pyrene-induced expression patterns. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2018, 25, 26-33.	0.4	5
14894	Expression profile of <i>Rhipicephalus microplus</i> vitellogenin receptor during oogenesis. <i>Ticks and Tick-borne Diseases</i> , 2018, 9, 72-81.	1.1	30
14895	Genetic diversity and comparison of diagnostic tests for characterization of foot-and-mouth disease virus strains from Pakistan 2008–2012. <i>Transboundary and Emerging Diseases</i> , 2018, 65, 534-546.	1.3	13
14896	Evaluation of inter-individual differences in gut bacterial isoflavone bioactivation in humans by PCR-based targeting of genes involved in equol formation. <i>Journal of Applied Microbiology</i> , 2018, 124, 220-231.	1.4	13
14897	<i>NAC1</i> , a main regulator of phenylalanine biosynthesis and utilization in maritime pine. <i>Plant Biotechnology Journal</i> , 2018, 16, 1094-1104.	4.1	29
14898	The Enigmatic Genome of an Obligate Ancient <i>Spiroplasma</i> Symbiont in a Hadal Holothurian. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	38

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14900	IntPred: a structure-based predictor of protein-protein interaction sites. <i>Bioinformatics</i> , 2018, 34, 223-229.	1.8	59
14901	Highly Expressed Genes Are Preferentially Co-Opted for C4 Photosynthesis. <i>Molecular Biology and Evolution</i> , 2018, 35, 94-106.	3.5	57
14902	Targeted Enrichment of Large Gene Families for Phylogenetic Inference: Phylogeny and Molecular Evolution of Photosynthesis Genes in the Portulugo Clade (Caryophyllales). <i>Systematic Biology</i> , 2018, 67, 367-383.	2.7	46
14903	Genomic population structure and conservation of the red listed <i>Carabus arcensis</i> (Coleoptera: Carabidae) in island-mainland habitats of Northern Europe. <i>Insect Conservation and Diversity</i> , 2018, 11, 255-266.	1.4	8
14904	Influence of the geography of speciation on current patterns of coral reef fish biodiversity across the Indo-Pacific. <i>Ecography</i> , 2018, 41, 1295-1306.	2.1	20
14905	Origin and evolution of chloroplast group I introns in lichen algae. <i>Journal of Phycology</i> , 2018, 54, 66-78.	1.0	4
14906	A new subarctic strain of <i>Tetrademus obliquus</i> part I: identification and fatty acid profiling. <i>Journal of Applied Phycology</i> , 2018, 30, 2737-2750.	1.5	17
14907	Impact of tree priors in species delimitation and phylogenetics of the genus <i>Oligoryzomys</i> (Rodentia). <i>Tj ETQq0 0 0,rgBT /Overlock 10 TF</i>	1.2	19
14908	Resolving a phylogenetic hypothesis for parrots: implications from systematics to conservation. <i>Emu</i> , 2018, 118, 7-21.	0.2	45
14909	<i>Elainella</i> gen. nov.: a new tropical cyanobacterium characterized using a complex genomic approach. <i>European Journal of Phycology</i> , 2018, 53, 39-51.	0.9	27
14910	The <i>Linum usitatissimum</i> L. plastome reveals atypical structural evolution, new editing sites, and the phylogenetic position of Linaceae within Malpighiales. <i>Plant Cell Reports</i> , 2018, 37, 307-328.	2.8	43
14911	Cloning and characterization of a monoterpene synthase gene from flowers of <i>Camelina sativa</i> . <i>Planta</i> , 2018, 247, 443-457.	1.6	8
14912	Discovery and validation of species-specific diagnostic SNP markers for the endangered San Diego fairy shrimp ( <i>Branchinecta sandiegonensis</i> ) and the versatile fairy shrimp ( <i>Branchinecta lindahli</i> ). <i>Conservation Genetics Resources</i> , 2018, 10, 897-905.	0.4	1
14913	Evolution of equine influenza viruses (H3N8) during a Brazilian outbreak, 2015. <i>Brazilian Journal of Microbiology</i> , 2018, 49, 336-346.	0.8	12
14914	Scorpion envenoming in Morona Santiago, Amazonian Ecuador: Molecular phylogenetics confirms involvement of the <i>Tityus obscurus</i> group. <i>Acta Tropica</i> , 2018, 178, 1-9.	0.9	12
14915	Targeted sequencing of clade-specific markers from skin microbiomes for forensic human identification. <i>Forensic Science International: Genetics</i> , 2018, 32, 50-61.	1.6	69
14916	A phylogenetic and morphological overview of sections <i>Bohusia</i> , <i>Sanguinolenti</i> , and allied sections within <i>Agaricus</i> subg. <i>Pseudochitonina</i> with three new species from France, Iran, and Portugal. <i>Fungal Biology</i> , 2018, 122, 34-51.	1.1	8

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14917	Molecular changes in vitellogenin gene of <i>Spodoptera exigua</i> after long-time exposure to cadmium –“ Toxic side effect or microevolution?. <i>Ecotoxicology and Environmental Safety</i> , 2018, 147, 461-470.	2.9	21
14918	Evaluating methods for phylogenomic analyses, and a new phylogeny for a major frog clade (Hylloidea) based on 2214 loci. <i>Molecular Phylogenetics and Evolution</i> , 2018, 119, 128-143.	1.2	63
14919	An Efficient, Large-Scale Survey of Hepatitis C Viremia in the Democratic Republic of the Congo Using Dried Blood Spots. <i>Clinical Infectious Diseases</i> , 2018, 66, 254-260.	2.9	19
14920	A Gene Family Coding for Salivary Proteins (SHOT) of the Polyphagous Spider Mite <i>Tetranychus urticae</i> Exhibits Fast Host-Dependent Transcriptional Plasticity. <i>Molecular Plant-Microbe Interactions</i> , 2018, 31, 112-124.	1.4	29
14921	A cerato-plantanin protein SsCP1 targets plant PR1 and contributes to virulence of <i>Sclerotinia sclerotiorum</i> . <i>New Phytologist</i> , 2018, 217, 739-755.	3.5	211
14922	Mitochondrial phylogenomics and genome rearrangements in the barklice (Insecta: Psocodea). <i>Molecular Phylogenetics and Evolution</i> , 2018, 119, 118-127.	1.2	44
14923	Genome sequencing and comparative genomics reveal the potential pathogenic mechanism of <i>Cercospora sojina</i> Hara on soybean. <i>DNA Research</i> , 2018, 25, 25-37.	1.5	16
14924	Abundance and Multilocus Sequence Analysis of <i>Vibrio</i> Bacteria Associated with Diseased Elkhorn Coral ( <i>Acropora palmata</i> ) of the Florida Keys. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	23
14925	Review of the <i>Chromis xanthurus</i> species group (Perciformes: Pomacentridae), with description of a new species. <i>Ichthyological Research</i> , 2018, 65, 177-191.	0.5	1
14926	Genealogical and niche modeling analyses reveal recent expansion and limited genetic divergence in the <i>Formicivora serrana</i> complex (Passeriformes: Thamnophilidae). <i>Journal of Ornithology</i> , 2018, 159, 79-92.	0.5	2
14927	Spatial and Temporal Scales of Range Expansion in Wild <i>Phaseolus vulgaris</i> . <i>Molecular Biology and Evolution</i> , 2018, 35, 119-131.	3.5	76
14928	Microevolution of the VQ gene family in six species of <i>Fragaria</i> . <i>Genome</i> , 2018, 61, 49-57.	0.9	13
14929	Gastrointestinal distribution of chicken gastrin-cholecystokinin family transcript expression and response to short-term nutritive state. <i>General and Comparative Endocrinology</i> , 2018, 255, 64-70.	0.8	15
14930	Life on the Edge: A Comparative Study of Ecophysiological Adaptations of Frogs to Tropical Semiarid Environments. <i>Physiological and Biochemical Zoology</i> , 2018, 91, 740-756.	0.6	12
14931	Comparative Genomic Analyses of <i>Clavibacter michiganensis</i> subsp. <i>insidiosus</i> and Pathogenicity on <i>Medicago truncatula</i> . <i>Phytopathology</i> , 2018, 108, 172-185.	1.1	15
14932	Comparative genomics reveals cotton-specific virulence factors in flexible genomic regions in <i>Verticillium dahliae</i> and evidence of horizontal gene transfer from <i>Fusarium</i> . <i>New Phytologist</i> , 2018, 217, 756-770.	3.5	91
14933	Spider™s venom phospholipases D: A structural review. <i>International Journal of Biological Macromolecules</i> , 2018, 107, 1054-1065.	3.6	16
14934	Phylogenomics and species delimitation of a complex radiation of Neotropical suboscine birds ( <i>Pachyrhamphus</i> ). <i>Molecular Phylogenetics and Evolution</i> , 2018, 118, 204-221.	1.2	39

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14935	Phylogeny, biogeography and character evolution in the tribe Desmodieae (Fabaceae: Papilionoideae), with special emphasis on the New Caledonian endemic genera. <i>Molecular Phylogenetics and Evolution</i> , 2018, 118, 108-121.	1.2	19
14936	Phylogenomic support for evolutionary relationships of New World direct-developing frogs (Anura): Tj ETQq1 1 0.784314 rgBT /Overlo	1.2	74
14937	Bioengineered AAV Capsids with Combined High Human Liver Transduction In Vivo and Unique Humoral Seroreactivity. <i>Molecular Therapy</i> , 2018, 26, 289-303.	3.7	130
14938	Acclimation to extremely high ammonia levels in continuous biomethanation process and the associated microbial community dynamics. <i>Bioresource Technology</i> , 2018, 247, 616-623.	4.8	133
14939	More evolution underground: Accelerated mitochondrial substitution rate in Australian burrowing freshwater crayfishes (Decapoda: Parastacidae). <i>Molecular Phylogenetics and Evolution</i> , 2018, 118, 88-98.	1.2	19
14940	Microbial sequence typing in the genomic era. <i>Infection, Genetics and Evolution</i> , 2018, 63, 346-359.	1.0	50
14941	<i>Galleria mellonella</i> as an infection model to investigate virulence of <i>Vibrio parahaemolyticus</i> . <i>Virulence</i> , 2018, 9, 197-207.	1.8	43
14942	Independent pseudogenization of CYP2J19 in penguins, owls and kiwis implicates gene in red carotenoid synthesis. <i>Molecular Phylogenetics and Evolution</i> , 2018, 118, 47-53.	1.2	22
14943	Geographic isolation and elevational gradients promote diversification in an endemic shrew on Sulawesi. <i>Molecular Phylogenetics and Evolution</i> , 2018, 118, 306-317.	1.2	16
14944	Focusing the diversity of <i>Gardnerella vaginalis</i> through the lens of ecotypes. <i>Evolutionary Applications</i> , 2018, 11, 312-324.	1.5	34
14945	T cell receptor alpha variable 12 bias in the immunodominant response to Yellow fever virus. <i>European Journal of Immunology</i> , 2018, 48, 258-272.	1.6	44
14946	Exon-based phylogenomics strengthens the phylogeny of Neotropical cichlids and identifies remaining conflicting clades (Cichliformes: Cichlidae: Cichlinae). <i>Molecular Phylogenetics and Evolution</i> , 2018, 118, 232-243.	1.2	44
14947	Fungal Olecranon Bursitis in an Immunocompetent Patient by <i>Knoxdaviesia dimorphospora</i> sp. nov.: Case Report and Review. <i>Mycopathologia</i> , 2018, 183, 407-415.	1.3	2
14948	Development of a novel myconanominating approach for the recovery of agriculturally important elements from jarosite waste. <i>Journal of Environmental Sciences</i> , 2018, 67, 356-367.	3.2	12
14949	Full-Genome Sequence of Porcine Circovirus type 3 recovered from serum of sows with stillbirths in Brazil. <i>Transboundary and Emerging Diseases</i> , 2018, 65, 5-9.	1.3	114
14950	Use of Comparative Genomics-Based Markers for Discrimination of Host Specificity in <i>Fusarium oxysporum</i> . <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	62
14951	A Trichosporonales genome tree based on 27 haploid and three evolutionarily conserved "natural" hybrid genomes. <i>Yeast</i> , 2018, 35, 99-111.	0.8	21
14952	Roles of Retinoic Acid Signaling in Shaping the Neuronal Architecture of the Developing Amphioxus Nervous System. <i>Molecular Neurobiology</i> , 2018, 55, 5210-5229.	1.9	17

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14953	Methanogenic Paraffin Biodegradation: Alkylsuccinate Synthase Gene Quantification and Dicarboxylic Acid Production. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	21
14954	Plantaricyclin A, a Novel Circular Bacteriocin Produced by <i>Lactobacillus plantarum</i> NI326: Purification, Characterization, and Heterologous Production. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	64
14955	Genetic analysis of Japanese and American specimens of <i>Scirpus hattorianus</i> suggests its introduction from North America. <i>Journal of Plant Research</i> , 2018, 131, 91-97.	1.2	4
14956	Molecular phylogeny and biogeography of the Westâ€Palaeartic <i>Velia</i> (Heteroptera: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 17	1.7	10
14957	Transcriptome mining for phylogenetic markers in a recently radiated genus of tropical plants ( <i>Renealmia</i> L.f., Zingiberaceae). <i>Molecular Phylogenetics and Evolution</i> , 2018, 119, 13-24.	1.2	13
14958	A New Subspecies of <i>Oxytricha granulifera</i> (Hypotrichia: Oxytrichidae) from Mexico, with Notes on its Morphogenesis and Phylogenetic Position. <i>Journal of Eukaryotic Microbiology</i> , 2018, 65, 357-371.	0.8	16
14959	A Tyrosine-Based Trafficking Motif of the Tegument Protein pUL71 Is Crucial for Human Cytomegalovirus Secondary Envelopment. <i>Journal of Virology</i> , 2018, 92, .	1.5	30
14960	A molecular phylogeny of East African <i>Amytta</i> (Orthoptera: Tettigoniidae, Meconematinae) with data on their cytogenetics. <i>Systematic Entomology</i> , 2018, 43, 239-249.	1.7	7
14961	<i>Coniella lustricola</i> , a new species from submerged detritus. <i>Mycological Progress</i> , 2018, 17, 191-203.	0.5	8
14962	Genome-wide identification and analysis of the growth-regulating factor family in tobacco () Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 30 33	1.0	33
14963	Reprint of: Disentangling drivers of plant endemism and diversification in the European Alps - a phylogenetic and spatially explicit approach. <i>Perspectives in Plant Ecology, Evolution and Systematics</i> , 2018, 30, 31-40.	1.1	7
14964	Complete genome sequence of datura leaf curl virus, a novel begomovirus infecting <i>Datura innoxia</i> in Sudan, related to begomoviruses causing tomato yellow leaf curl disease. <i>Archives of Virology</i> , 2018, 163, 273-275.	0.9	4
14965	A comprehensive phylogeny of the genus <i>Kurixalus</i> (Rhacophoridae, Anura) sheds light on the geographical range evolution of frilled swamp treefrogs. <i>Molecular Phylogenetics and Evolution</i> , 2018, 121, 224-232.	1.2	18
14966	Discovery of a Potentially New Subfamily of ELFV Dehydrogenases Effective for Arginine Deamination by Enzyme Mining. <i>Biotechnology Journal</i> , 2018, 13, 1700305.	1.8	2
14967	New insights into the molecular phylogeny and taxonomy of mormyrids (Osteoglossiformes,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 187 2018, 56, 61-76.	0.6	8
14968	Discovery of the first maize-infecting mastrevirus in the Americas using a vector-enabled metagenomics approach. <i>Archives of Virology</i> , 2018, 163, 263-267.	0.9	14
14969	Convergent adaptive evolution in marginal environments: unloading transposable elements as a common strategy among mangrove genomes. <i>New Phytologist</i> , 2018, 217, 428-438.	3.5	69
14970	One-third of the plastid genes evolved under positive selection in PACMAD grasses. <i>Planta</i> , 2018, 247, 255-266.	1.6	99

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14971	Genetic diversity of potato virus Y (PVY): sequence analyses reveal ten novel PVY recombinant structures. <i>Archives of Virology</i> , 2018, 163, 23-32.	0.9	47
14972	Genome Characterization of Oleaginous <i>Aspergillus oryzae</i> BCC7051: A Potential Fungal-Based Platform for Lipid Production. <i>Current Microbiology</i> , 2018, 75, 57-70.	1.0	30
14973	DNA metabarcoding of airborne pollen: new protocols for improved taxonomic identification of environmental samples. <i>Aerobiologia</i> , 2018, 34, 63-74.	0.7	39
14974	Origin and phylogeography of African savannah elephants ( <i>Loxodonta africana</i> ) in Kruger and nearby parks in southern Africa. <i>Conservation Genetics</i> , 2018, 19, 155-167.	0.8	8
14975	Evidence of the supercomplex organization of photosystem II and light-harvesting complexes in <i>Nannochloropsis granulata</i> . <i>Photosynthesis Research</i> , 2018, 136, 49-61.	1.6	13
14976	Higher DNA insert fragment sizes improve mitogenomic assemblies from metagenomic pyrosequencing datasets: an example using Limenitidinae butterflies (Lepidoptera, Nymphalidae). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2018, 29, 840-845.	0.7	8
14977	Heavy metal tolerance traits of filamentous fungi isolated from gold and gemstone mining sites. <i>Brazilian Journal of Microbiology</i> , 2018, 49, 29-37.	0.8	150
14978	Mitochondrial genomes of the Pacific sierra mackerel <i>Scomberomorus sierra</i> and the Monterey Spanish mackerel <i>Scomberomorus concolor</i> (Perciformes, Scombridae). <i>Conservation Genetics Resources</i> , 2018, 10, 471-474.	0.4	1
14979	The complete plastid genome of <i>Carmichaelia australis</i> R. Br. (Leguminosae: Papilionoideae). <i>Conservation Genetics Resources</i> , 2018, 10, 519-521.	0.4	1
14980	The roles of mucus-forming mucins, peritrophins and peritrophins with mucin domains in the insect midgut. <i>Insect Molecular Biology</i> , 2018, 27, 46-60.	1.0	48
14981	Phylogenetic analysis and revision of subfamily classification of Belostomatidae genera (Insecta: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 3	1.0	19
14982	Multilocus phylogeny and species delimitation within the genus <i>Glaucocyteris</i> (Chiroptera, Tj ETQq1 1 0.784314 rgBT /Overlock Democratic Republic of the Congo. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2018, 56, 1-22.	0.6	22
14983	Systematics of the <i>Culex coronator</i> complex (Diptera: Culicidae): morphological and molecular assessment. <i>Zoological Journal of the Linnean Society</i> , 2018, 182, 735-757.	1.0	8
14984	The mitogenomic phylogeny of the Elasmobranchii (Chondrichthyes). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2018, 29, 867-878.	0.7	30
14985	Genetic and morphological discrimination of three species of ninespined stickleback <i>Pungitius</i> spp. (Teleostei, Gasterosteidae) in France with the revalidation of <i>Pungitius vulgaris</i> (Mauduyt, 1848). <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2018, 56, 77-101.	0.6	10
14986	A novel grablovirus from non-cultivated grapevine ( <i>Vitis</i> sp.) in North America. <i>Archives of Virology</i> , 2018, 163, 259-262.	0.9	23
14987	Relationships between residue Voronoi volume and sequence conservation in proteins. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2018, 1866, 379-386.	1.1	1
14988	A multilocus phylogeny of the genus <i>Sarcohyala</i> (Anura: Hylidae), and an investigation of species boundaries using statistical species delimitation. <i>Molecular Phylogenetics and Evolution</i> , 2018, 118, 184-193.	1.2	14

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14989	Coexistence of two novel resistance plasmids, <i>bla</i> <sub>KPC-2</sub> -carrying p14057A and <i>tetA</i> (A)-carrying p14057B, in <i>Pseudomonas aeruginosa</i> . <i>Virulence</i> , 2018, 9, 306-311.	1.8	18
14990	Gut histology, immunology and the intestinal microbiota of rainbow trout, <i>Oncorhynchus mykiss</i> (Walbaum), fed process variants of soybean meal. <i>Aquaculture Research</i> , 2018, 49, 492-504.	0.9	41
14991	Inducible microRNA-122 modulates RIG-I signaling pathway via targeting DAK in miyu croaker after poly(I:C) stimulation. <i>Developmental and Comparative Immunology</i> , 2018, 78, 52-60.	1.0	20
14992	Ecological and genomic profiling of anaerobic methane-oxidizing archaea in a deep granitic environment. <i>ISME Journal</i> , 2018, 12, 31-47.	4.4	59
14993	Exploring the interaction between <i>Mycobacterium tuberculosis</i> enolase and human plasminogen using computational methods and experimental techniques. <i>Journal of Cellular Biochemistry</i> , 2018, 119, 2408-2417.	1.2	15
14994	Clustal Omega for making accurate alignments of many protein sequences. <i>Protein Science</i> , 2018, 27, 135-145.	3.1	1,286
14995	Minimal requirements for reverse polymerization and tRNA repair by tRNA <sup>His</sup> guanylyltransferase. <i>RNA Biology</i> , 2018, 15, 614-622.	1.5	9
14996	Implementing a web-based introductory bioinformatics course for non-bioinformaticians that incorporates practical exercises. <i>Biochemistry and Molecular Biology Education</i> , 2018, 46, 31-38.	0.5	7
14997	In Vivo Selection of a Computationally Designed SCHEMA AAV Library Yields a Novel Variant for Infection of Adult Neural Stem Cells in the SVZ. <i>Molecular Therapy</i> , 2018, 26, 304-319.	3.7	72
14998	Does multigenerational exposure to hormetic concentrations of imidacloprid precondition aphids for increased insecticide tolerance?. <i>Pest Management Science</i> , 2018, 74, 314-322.	1.7	31
14999	Mitochondrial recovery from shotgun metagenome sequencing enabling phylogenetic analysis of the common thresher shark ( <i>Alopias vulpinus</i> ). <i>Meta Gene</i> , 2018, 15, 10-15.	0.3	11
15000	A dynamic microbial community with high functional redundancy inhabits the cold, oxic subseafloor aquifer. <i>ISME Journal</i> , 2018, 12, 1-16.	4.4	148
15001	Discovering the silk road: Nuclear and mitochondrial sequence data resolve the phylogenetic relationships among theraphosid spider subfamilies. <i>Molecular Phylogenetics and Evolution</i> , 2018, 119, 63-70.	1.2	35
15002	Three new species of <i>Gyrodactylus</i> von Nordmann, 1832 described from <i>Goodea atripinnis</i> (Pisces): <i>Tj ETQq1 1 0.784314 rgBT /Overl</i> 2018, 117, 139-150.	0.6	13
15003	<i>Phoma destructiva</i> causing blight of tomato plants: a new fungal threat for tomato plantations in Brazil?. <i>Tropical Plant Pathology</i> , 2018, 43, 257-262.	0.8	6
15004	Next generation sequencing elucidates cacao badnavirus diversity and reveals the existence of more than ten viral species. <i>Virus Research</i> , 2018, 244, 235-251.	1.1	39
15005	Discovery of an old, archipelago-wide, endemic radiation of Philippine snakes. <i>Molecular Phylogenetics and Evolution</i> , 2018, 119, 144-150.	1.2	14
15006	Genic simple sequence repeat markers for measuring genetic diversity in a native food crop: a case study of Australian <i>Kunzea pomifera</i> F.Muell. (muntries). <i>Genetic Resources and Crop Evolution</i> , 2018, 65, 917-937.	0.8	1

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15007	Molecular characterization of faba bean necrotic yellows viruses in Tunisia. Archives of Virology, 2018, 163, 687-694.	0.9	16
15008	Revision of Podocotyloides Yamaguti, 1934 (Digenea: Opecoelidae), resurrection of Pedunculacetabulum Yamaguti, 1934 and the naming of a cryptic opecoelid species. Systematic Parasitology, 2018, 95, 1-31.	0.5	31
15009	How many pygmy marmoset ( <i>Cebuella</i> Gray, 1870) species are there? A taxonomic re-appraisal based on new molecular evidence. Molecular Phylogenetics and Evolution, 2018, 120, 170-182.	1.2	23
15010	Prospects on the evolutionary mitogenomics of plants: A case study on the olive family (Oleaceae). Molecular Ecology Resources, 2018, 18, 407-423.	2.2	49
15011	The striking polyphyly of <i>Suiriri</i> : Convergent evolution and social mimicry in two cryptic Neotropical birds. Journal of Zoological Systematics and Evolutionary Research, 2018, 56, 270-279.	0.6	8
15012	Pleistocene climatic changes drive diversification across a tropical savanna. Molecular Ecology, 2018, 27, 520-532.	2.0	31
15013	High-throughput sequencing of the chloroplast and mitochondrion of <i>Chlamydomonas reinhardtii</i> to generate improved <i>de novo</i> assemblies, analyze expression patterns and transcript speciation, and evaluate diversity among laboratory strains and wild isolates. Plant Journal, 2018, 93, 545-565.	2.8	90
15014	Deciphering signature of selection affecting beef quality traits in Angus cattle. Genes and Genomics, 2018, 40, 63-75.	0.5	27
15015	Fungal communities associated with species of <i>Fraxinus</i> tolerant to ash dieback, and their potential for biological control. Fungal Biology, 2018, 122, 110-120.	1.1	54
15016	A new <i>Rhizopogon</i> species associated with <i>Pinus amamiana</i> in Japan. Mycoscience, 2018, 59, 176-180.	0.3	4
15017	PDB-wide identification of biological assemblies from conserved quaternary structure geometry. Nature Methods, 2018, 15, 67-72.	9.0	69
15018	Comparative epigenomics reveals evolution of duplicated genes in potato and tomato. Plant Journal, 2018, 93, 460-471.	2.8	33
15019	Structural variations in wheat HKT1;5 underpin differences in Na <sup>+</sup> transport capacity. Cellular and Molecular Life Sciences, 2018, 75, 1133-1144.	2.4	45
15020	Astakines in arthropods—phylogeny and gene structure. Developmental and Comparative Immunology, 2018, 81, 141-151.	1.0	10
15021	Sex determination and differentiation genes in a functional hermaphrodite scallop, <i>Nodipecten subnodosus</i> . Marine Genomics, 2018, 37, 161-175.	0.4	16
15022	Three new records of powdery mildews found in Mexico with one genus and one new species proposed. Mycoscience, 2018, 59, 1-7.	0.3	25
15023	Characterization of a New Tymovirus Causing Stunting and Chlorotic Mosaic in Naranjilla ( <i>Solanum</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.7	6
15024	DNA mismatch repair proteins MLH1 and PMS2 can be imported to the nucleus by a classical nuclear import pathway. Biochimie, 2018, 146, 87-96.	1.3	18



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15025	Quantifying the Survival of Multiple <i>Salmonella enterica</i> Serovars In Vivo via Massively Parallel Whole-Genome Sequencing To Predict Zoonotic Risk. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	13
15026	Nutrient-Colimited <i>Trichodesmium</i> as a Nitrogen Source or Sink in a Future Ocean. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	28
15027	On the Early Evolution of Catabolic Pathways: A Comparative Genomics Approach. I. The Cases of Glucose, Ribose, and the Nucleobases Catabolic Routes. <i>Journal of Molecular Evolution</i> , 2018, 86, 27-46.	0.8	9
15028	Phylogenomic detection and functional prediction of genes potentially important for plant meiosis. <i>Gene</i> , 2018, 643, 83-97.	1.0	4
15029	<i>Phyllactinia fraxinicola</i> , another Asian fungal pathogen on <i>Fraxinus excelsior</i> (common ash) introduced to Europe?. <i>Mycoscience</i> , 2018, 59, 85-88.	0.3	3
15030	Systematics and phylogeography of the widely distributed African skink <i>Trachylepis varia</i> species complex. <i>Molecular Phylogenetics and Evolution</i> , 2018, 120, 103-117.	1.2	11
15031	Evolutionary dynamism in bryophytes: Phylogenomic inferences confirm rapid radiation in the moss family Funariaceae. <i>Molecular Phylogenetics and Evolution</i> , 2018, 120, 240-247.	1.2	33
15032	Metabolic versatility of small archaea <i>Micrarchaeota</i> and <i>Parvarchaeota</i> . <i>ISME Journal</i> , 2018, 12, 756-775.	4.4	91
15033	Evolutionary conservation and functional divergence of the LFK gene family play important roles in the photoperiodic flowering pathway of land plants. <i>Heredity</i> , 2018, 120, 310-328.	1.2	13
15034	Phylogeny and the colourful history of jewel bugs (Insecta: Hemiptera: Scutelleridae). <i>Cladistics</i> , 2018, 34, 502-516.	1.5	15
15035	Homeodomain-interacting protein kinase phosphorylates the <i>Drosophila</i> Paired box protein 6 (Pax6) homologues Twin of eyeless and Eyeless. <i>Insect Molecular Biology</i> , 2018, 27, 198-211.	1.0	10
15036	Cell-Type Transcriptomes of the Multicellular Green Alga <i>Volvox carterii</i> Yield Insights into the Evolutionary Origins of Germ and Somatic Differentiation Programs. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 531-550.	0.8	29
15037	Phylogeny of <i>Campyloneurum</i> (Polypodiaceae). <i>International Journal of Plant Sciences</i> , 2018, 179, 36-49.	0.6	10
15038	Comparative genomics reveals the presence of putative toxin-antitoxin system in <i>Wolbachia</i> genomes. <i>Molecular Genetics and Genomics</i> , 2018, 293, 525-540.	1.0	12
15039	Diversity and biogeography of frogs in the genus <i>Amnirana</i> (Anura: Ranidae) across sub-Saharan Africa. <i>Molecular Phylogenetics and Evolution</i> , 2018, 120, 274-285.	1.2	29
15040	Rapid allopolyploid radiation of moonwort ferns ( <i>Botrychium</i> ; <i>Ophioglossaceae</i> ) revealed by PacBio sequencing of homologous and homeologous nuclear regions. <i>Molecular Phylogenetics and Evolution</i> , 2018, 120, 342-353.	1.2	60
15041	First insights into the solenogaster diversity of the Sea of Okhotsk with the description of a new species of <i>Kruppomenia</i> (Simrothiellidae, Cavibelonia). <i>Deep-Sea Research Part II: Topical Studies in Oceanography</i> , 2018, 154, 214-229.	0.6	7
15042	Conservation of Specificity in Two Low-Specificity Proteins. <i>Biochemistry</i> , 2018, 57, 684-695.	1.2	16

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15043	A new species of antbird (Passeriformes: Thamnophilidae) from the Cordillera Azul, San Martín, Peru. <i>Auk</i> , 2018, 135, 114-126.	0.7	8
15044	Subtilisin inhibitor like protein pLPI-1™ from leaves of pigeonpea ( <i>Cajanus cajan</i> , cv. BSMR 736) exhibits inhibition against <i>Helicoverpa armigera</i> gut proteinases. <i>3 Biotech</i> , 2018, 8, 19.	1.1	2
15045	Functional divergence and comparative in silico study of Cas4 proteins of DUF83 class. <i>Journal of Molecular Recognition</i> , 2018, 31, e2694.	1.1	0
15046	Progressive loss of hybrid histidine kinase genes during the evolution of budding yeasts ( <i>Saccharomycotina</i> ). <i>Current Genetics</i> , 2018, 64, 841-851.	0.8	7
15047	Network analysis of pseudogene-gene relationships: from pseudogene evolution to their functional potentials. , 2018, , .		5
15048	Genome Assembly and Annotation of the Medicinal Plant <i>Calotropis gigantea</i> , a Producer of Anticancer and Antimalarial Cardenolides. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 385-391.	0.8	38
15049	Genome characterization of an Argentinean isolate of alfalfa leaf curl virus. <i>Archives of Virology</i> , 2018, 163, 799-803.	0.9	16
15050	<i>Helicoverpa</i> -inducible Thioredoxin h from <i>Cicer arietinum</i> : structural modeling and potential targets. <i>International Journal of Biological Macromolecules</i> , 2018, 109, 231-243.	3.6	13
15051	A Completely Reimplemented MPI Bioinformatics Toolkit with a New HHpred Server at its Core. <i>Journal of Molecular Biology</i> , 2018, 430, 2237-2243.	2.0	1,956
15052	Vacuolar Trafficking Protein VPS38 Is Dispensable for Autophagy. <i>Plant Physiology</i> , 2018, 176, 1559-1572.	2.3	34
15053	A novel Chromatiales bacterium is a potential sulfide oxidizer in multiple orders of marine sponges. <i>Environmental Microbiology</i> , 2018, 20, 800-814.	1.8	27
15054	Identification of opossums <i>Didelphis aurita</i> (Wied-Neuweid, 1826) as a definitive host of <i>Sarcocystis falcatula</i> -like sporocysts. <i>Parasitology Research</i> , 2018, 117, 213-223.	0.6	14
15055	Species limits in the Morelet's Alligator lizard ( <i>Anguinae: Gerrhonotinae</i> ). <i>Molecular Phylogenetics and Evolution</i> , 2018, 120, 16-27.	1.2	10
15056	Cryptic diversity in <i>Rhampholeon boulengeri</i> (Sauria: Chamaeleonidae), a pygmy chameleon from the Albertine Rift biodiversity hotspot. <i>Molecular Phylogenetics and Evolution</i> , 2018, 122, 125-141.	1.2	17
15057	Monophyly of the species of <i>Hepatozoon</i> (Adeleorina: Hepatozoidae) parasitizing (African) anurans, with the description of three new species from hyperoliid frogs in South Africa. <i>Parasitology</i> , 2018, 145, 1039-1050.	0.7	24
15058	Diversity, systematics, and evolution of Cynodonteae inflorescences (Chloridoideae " Poaceae). <i>Systematics and Biodiversity</i> , 2018, 16, 245-259.	0.5	5
15059	The complete genome sequence of a third distinct baculovirus isolated from the true armyworm, <i>Mythimna unipuncta</i> , contains two copies of the lef-7 gene. <i>Virus Genes</i> , 2018, 54, 297-310.	0.7	14
15060	Dynamic correlations between microbiota succession and flavor development involved in the ripening of Kazak artisanal cheese. <i>Food Research International</i> , 2018, 105, 733-742.	2.9	88

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15061	Ossicaulis yunnanensis sp. nov. (Lyophyllaceae, Agaricales) from southwestern China. Mycoscience, 2018, 59, 33-37.	0.3	11
15062	Two large deletions extending beyond either end of the RHD gene and their red cell phenotypes. Journal of Human Genetics, 2018, 63, 27-35.	1.1	13
15063	Rice <i>TSV3</i> Encoding Obg-Like GTPase Protein Is Essential for Chloroplast Development During the Early Leaf Stage Under Cold Stress. G3: Genes, Genomes, Genetics, 2018, 8, 253-263.	0.8	15
15064	Actin genes and their expression in pacific white shrimp, <i>Litopenaeus vannamei</i> . Molecular Genetics and Genomics, 2018, 293, 479-493.	1.0	12
15065	Delimitation of evolutionary units in Cuvier's dwarf caiman, <i>Paleosuchus palpebrosus</i> (Cuvier, 1807): insights from conservation of a broadly distributed species. Conservation Genetics, 2018, 19, 599-610.	0.8	34
15066	<i>Desoria trispinata</i> (MacGillivray, 1896), a promising model Collembola species to study biological invasions in soil communities. Pedobiologia, 2018, 67, 45-56.	0.5	2
15067	The enigmatic SAR202 cluster up close: shedding light on a globally distributed dark ocean lineage involved in sulfur cycling. ISME Journal, 2018, 12, 655-668.	4.4	101
15068	Oligomannosidic glycans at Asn-110 are essential for secretion of human diamine oxidase. Journal of Biological Chemistry, 2018, 293, 1070-1087.	1.6	9
15069	Auxin enhances grafting success in <i>Carya cathayensis</i> (Chinese hickory). Planta, 2018, 247, 761-772.	1.6	20
15070	Modelling studies determining the mode of action of anthelmintics inhibiting <i>in vitro</i> trehalose-6-phosphate phosphatase (TPP) of <i>Anisakis simplex</i> s.l. Experimental Parasitology, 2018, 184, 46-56.	0.5	9
15071	<i>Leveillula buddlejae</i> sp. nov., a new species with an asexual morph resembling phylogenetically basal Phyllactinia species. Mycoscience, 2018, 59, 71-74.	0.3	2
15072	Coelomycetous <i>Dothideomycetes</i> with emphasis on the families <i>Cucurbitariaceae</i> and <i>Didymellaceae</i> . Studies in Mycology, 2018, 90, 1-69.	4.5	129
15073	Evolutionary history of the cobalamin-independent methionine synthase gene family across the land plants. Molecular Phylogenetics and Evolution, 2018, 120, 33-42.	1.2	8
15074	Structure-based analysis of Clot as a thioredoxin-related protein of 14 kDa in <i>Drosophila</i> experimental and computational approaches. Biotechnology and Applied Biochemistry, 2018, 65, 338-345.	1.4	2
15075	<i>Streptomyces sediminis</i> sp. nov. isolated from crater lake sediment. Antonie Van Leeuwenhoek, 2018, 111, 493-500.	0.7	23
15076	Distribution and Phylogeny of Microsymbionts Associated with Cowpea ( <i>Vigna unguiculata</i> ) Nodulation in Three Agroecological Regions of Mozambique. Applied and Environmental Microbiology, 2018, 84, .	1.4	51
15077	An ultraprocessive, accurate reverse transcriptase encoded by a metazoan group II intron. Rna, 2018, 24, 183-195.	1.6	69
15078	A transposition-active <i>Phyllostachys edulis</i> long terminal repeat (LTR) retrotransposon. Journal of Plant Research, 2018, 131, 203-210.	1.2	13

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15079	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
15080	Tracking wetland community evolution using Diptera taxonomic, functional and phylogenetic structure. <i>Insect Conservation and Diversity</i> , 2018, 11, 276-293.	1.4	8
15081	<i>De novo</i> assembly of the zucchini genome reveals a whole-genome duplication associated with the origin of the <i>Cucurbita</i> genus. <i>Plant Biotechnology Journal</i> , 2018, 16, 1161-1171.	4.1	160
15082	Pectin methylesterase inhibitor (PMEI) family can be related to male sterility in Chinese cabbage ( <i>Brassica rapa</i> ssp. <i>pekinensis</i> ). <i>Molecular Genetics and Genomics</i> , 2018, 293, 343-357.	1.0	21
15083	Bioelectrogenesis with microbial fuel cells (MFCs) using the microalga <i>Chlorella vulgaris</i> and bacterial communities. <i>Electronic Journal of Biotechnology</i> , 2018, 31, 34-43.	1.2	60
15084	A Y161F Hemagglutinin Substitution Increases Thermostability and Improves Yields of 2009 H1N1 Influenza A Virus in Cells. <i>Journal of Virology</i> , 2018, 92, .	1.5	21
15085	Description of <i>Deinococcus populi</i> sp. nov. from the trunk surface of a Japanese aspen tree. <i>Archives of Microbiology</i> , 2018, 200, 291-297.	1.0	3
15086	Identification of an anellovirus and genomoviruses in ixodid ticks. <i>Virus Genes</i> , 2018, 54, 155-159.	0.7	17
15087	Characterization of a <i>Heterobasidion irregulare</i> endo- $\alpha$ -chondroitinase that mediate growth on pectin. <i>Journal of Phytopathology</i> , 2018, 166, 34-43.	0.5	1
15088	A new aerobic chemolithoautotrophic arsenic oxidizing microorganism isolated from a high Andean watershed. <i>Biodegradation</i> , 2018, 29, 59-69.	1.5	20
15089	Genome-wide investigation of transcription factors provides insights into transcriptional regulation in <i>Plutella xylostella</i> . <i>Molecular Genetics and Genomics</i> , 2018, 293, 435-449.	1.0	8
15090	Characterization of a novel single-stranded RNA mycovirus related to invertebrate viruses from the plant pathogen <i>Verticillium dahliae</i> . <i>Archives of Virology</i> , 2018, 163, 771-776.	0.9	14
15091	High-throughput sequencing of kDNA amplicons for the analysis of <i>Leishmania</i> minicircles and identification of Neotropical species. <i>Parasitology</i> , 2018, 145, 585-594.	0.7	23
15092	Carbon Amendments Alter Microbial Community Structure and Net Mercury Methylation Potential in Sediments. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	38
15093	Classification of G-protein coupled receptors based on a rich generation of convolutional neural network, N-gram transformation and multiple sequence alignments. <i>Amino Acids</i> , 2018, 50, 255-266.	1.2	8
15094	<i>Kribbella podocarpi</i> sp. nov., isolated from the leaves of a yellowwood tree ( <i>Podocarpus latifolius</i> ). <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 875-882.	0.7	13
15095	Differential RNA Sequencing Implicates Sulfide as the Master Regulator of S <sup>0</sup> Metabolism in <i>Chlorobaculum tepidum</i> and Other Green Sulfur Bacteria. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	2
15096	Whole-Genome Characterization of <i>Bacillus cereus</i> Associated with Specific Disease Manifestations. <i>Infection and Immunity</i> , 2018, 86, .	1.0	11

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15097	Curvularia malina causes a foliar disease on hybrid Bermuda grass in China. European Journal of Plant Pathology, 2018, 151, 557-562.	0.8	2
15098	Lignin and cellulose synthesis and antioxidative defense mechanisms are affected by light quality in Brachypodium distachyon. Plant Cell, Tissue and Organ Culture, 2018, 133, 1-14.	1.2	20
15099	Evolution of vomeronasal receptor 1 (V1R) genes in the common marmoset (Callithrix jacchus). Gene, 2018, 642, 343-353.	1.0	22
15100	Monorchis lewisi n. sp. (Trematoda: Monorchidae) from the surf bream, Acanthopagrus australis (Sparidae), in Moreton Bay, Australia. Journal of Helminthology, 2018, 92, 100-108.	0.4	16
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15373	Discovery and annotation of a novel transposable element family in <i>Gossypium</i> . <i>BMC Plant Biology</i> , 2018, 18, 307.	1.6	6
15374	Pairwise Alignment, Multiple Alignment, and BLAST. <i>Learning Materials in Biosciences</i> , 2018, , 51-79.	0.2	0
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15414	The illusion of rarity in an epibenthic jellyfish: facts and artefacts in the distribution of <i>Tesserogastria musculosa</i> (Hydrozoa, Ptychogastriidae). <i>Helgoland Marine Research</i> , 2018, 72, .	1.3	2
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15438	The genome of common long-arm octopus <i>Octopus minor</i> . <i>GigaScience</i> , 2018, 7, .	3.3	43
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15443	Patterns of chromosomal evolution in the florally diverse Andean clade <i>Lochrominae</i> (Solanaceae). <i>Perspectives in Plant Ecology, Evolution and Systematics</i> , 2018, 35, 31-43.	1.1	13
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15446	Heterobucephalopsine and prosorhynchine trematodes (Digenea: Bucephalidae) from teleost fishes of Moreton Bay, Queensland, Australia, with the description of two new species. <i>Systematic Parasitology</i> , 2018, 95, 783-806.	0.5	6
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15448	Transcriptional recording by CRISPR spacer acquisition from RNA. <i>Nature</i> , 2018, 562, 380-385.	13.7	117
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15453	Characterization of dog serum virome from Northeastern Brazil. <i>Virology</i> , 2018, 525, 192-199.	1.1	21
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15455	Phylogeny of Hesionidae (Aciculata, Annelida), with four new species from deep-sea eastern Pacific methane seeps, and resolution of the affinity of <i>Hesiolyra</i> . <i>Invertebrate Systematics</i> , 2018, 32, 1050.	0.5	15
15456	Unveiling the RNA virosphere associated with marine microorganisms. <i>Molecular Ecology Resources</i> , 2018, 18, 1444-1455.	2.2	59
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15459	The rare orange-red colored <i>Euphorbia pulcherrima</i> cultivar "Harvest Orange"™ shows a nonsense mutation in a flavonoid 3-O-methyltransferase allele expressed in the bracts. <i>BMC Plant Biology</i> , 2018, 18, 216.	1.6	16
15460	A structural investigation of NRZ mediated apoptosis regulation in zebrafish. <i>Cell Death and Disease</i> , 2018, 9, 967.	2.7	8
15461	Acquired cancer resistance to combination immunotherapy from transcriptional loss of class I HLA. <i>Nature Communications</i> , 2018, 9, 3868.	5.8	211
15462	Strain-level diversity drives alternative community types in millimetre-scale granular biofilms. <i>Nature Microbiology</i> , 2018, 3, 1295-1303.	5.9	93
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15465	Molecular comparisons of native range collections of <i>Gadirtha fusca</i> , a potential biological control agent of Chinese tallotree. <i>Biocontrol Science and Technology</i> , 2018, 28, 796-804.	0.5	2
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15468	A novel divergent group of Ostreid herpesvirus 1 Var variants associated with a mortality event in Pacific oyster spat in Normandy (France) in 2016. <i>Journal of Fish Diseases</i> , 2018, 41, 1759-1769.	0.9	21
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15474	Botulinum Neurotoxin-Producing Bacteria. Isn't It Time that We Called a Species a Species?. <i>MBio</i> , 2018, 9, .	1.8	40
15475	Impact of selected amino acids of HP0377 ( <i>Helicobacter pylori</i> thiol oxidoreductase) on its functioning as a CcmG (cytochrome c maturation) protein and Dsb (disulfide bond) isomerase. <i>PLoS ONE</i> , 2018, 13, e0195358.	1.1	5

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15477	Fungal-type carbohydrate binding modules from the coccolithophore <i>Emiliana huxleyi</i> show binding affinity to cellulose and chitin. <i>PLoS ONE</i> , 2018, 13, e0197875.	1.1	6
15478	A re-evaluation of subtidal <i>Lithophyllum</i> species (Corallinales, Rhodophyta) from North Carolina, USA, and the proposal of <i>L. searlesii</i> sp. nov. <i>Phycologia</i> , 2018, 57, 318-330.	0.6	28
15479	A Mechanism for Genome Size Reduction Following Genomic Rearrangements. <i>Frontiers in Genetics</i> , 2018, 9, 454.	1.1	23
15480	Identification and full-genome characterization of novel circoviruses in masked palm civets ( <i>Paguma</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 TF	1.1	11
15481	Rifamycin congeners kanglemycins are active against rifampicin-resistant bacteria via a distinct mechanism. <i>Nature Communications</i> , 2018, 9, 4147.	5.8	57
15482	Dead or alive? Sexual conflict and lethal copulatory interactions in long-jawed <i>Tetragnatha</i> spiders. <i>Behavioral Ecology</i> , 2018, , .	1.0	1
15483	Phylogenetic position of the extinct blue antelope, <i>Hippotragus leucophaeus</i> (Pallas, 1766) (Bovidae:) Tj ETQq1 1 0.784314 rgBT /Overlock 10 TF 2018, 182, 225-235.	1.0	9
15484	Environmental pH modulates transcriptomic responses in the fungus <i>Fusarium</i> sp. associated with KSHB <i>Euwallacea</i> sp. near <i>forficatus</i> . <i>BMC Genomics</i> , 2018, 19, 721.	1.2	15
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15486	Detection of the carbapenemase gene blaVIM-5 in members of the <i>Pseudomonas putida</i> group isolated from polluted Nigerian wetlands. <i>Scientific Reports</i> , 2018, 8, 15116.	1.6	20
15487	Respiratory chain Complex I of unparalleled divergence in diplomonads. <i>Journal of Biological Chemistry</i> , 2018, 293, 16043-16056.	1.6	18
15488	Description and genetic variation of a distinct species of <i>Potyvirus</i> infecting saffron ( <i>Crocus sativus</i> L.) plants in major production regions in Iran. <i>Annals of Applied Biology</i> , 2018, 173, 233-242.	1.3	10
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15490	Genome hypermobility by lateral transduction. <i>Science</i> , 2018, 362, 207-212.	6.0	187
15491	Exploring malaria vector diversity on the Amazon Frontier. <i>Malaria Journal</i> , 2018, 17, 342.	0.8	26
15492	Domain architecture of BAF250a reveals the ARID and ARM-repeat domains with implication in function and assembly of the BAF remodeling complex. <i>PLoS ONE</i> , 2018, 13, e0205267.	1.1	19
15493	A comprehensive and integrative re-description of <i>Synchaeta oblonga</i> and its relationship to <i>Synchaeta tremula</i> , <i>Synchaeta rufina</i> and <i>Synchaeta littoralis</i> (Rotifera: Monogononta). <i>Organisms Diversity and Evolution</i> , 2018, 18, 407-423.	0.7	5

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15495	Genome-Wide Identification and Characterization of wALOG Family Genes Involved in Branch Meristem Development of Branching Head Wheat. <i>Genes</i> , 2018, 9, 510.	1.0	8
15496	Monocot plastid phylogenomics, timeline, net rates of species diversification, the power of multi-gene analyses, and a functional model for the origin of monocots. <i>American Journal of Botany</i> , 2018, 105, 1888-1910.	0.8	161
15497	Comparative genomic analysis of pyrene-degrading <i>Mycobacterium</i> species: Genomic islands and ring-hydroxylating dioxygenases involved in pyrene degradation. <i>Journal of Microbiology</i> , 2018, 56, 798-804.	1.3	20
15498	Biotite: a unifying open source computational biology framework in Python. <i>BMC Bioinformatics</i> , 2018, 19, 346.	1.2	67
15499	Microbiota stability in healthy individuals after single-dose lactulose challenge—a randomized controlled study. <i>PLoS ONE</i> , 2018, 13, e0206214.	1.1	18
15500	A Workflow for Predicting MicroRNAs Targets via Accessibility in Flavivirus Genomes. <i>Lecture Notes in Computer Science</i> , 2018, , 124-132.	1.0	1
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15504	DNA barcode data reveal biogeographic trends in Arctic non-biting midges. <i>Genome</i> , 2018, 61, 787-796.	0.9	14
15505	Field studies reveal a close relative of <i>C. elegans</i> thrives in the fresh figs of <i>Ficus septica</i> and disperses on its <i>Ceratosolen</i> pollinating wasps. <i>BMC Ecology</i> , 2018, 18, 26.	3.0	21
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15634	High-resolution ISR amplicon sequencing reveals personalized oral microbiome. <i>Microbiome</i> , 2018, 6, 153.	4.9	32
15635	Sequence analysis of the cDNA encoding for SpCTX: a lethal factor from scorpionfish venom ( <i>Scorpaena plumieri</i> ). <i>Journal of Venomous Animals and Toxins Including Tropical Diseases</i> , 2018, 24, 24.	0.8	4
15636	Identifying genetic diversity of O antigens in <i>Aeromonas hydrophila</i> for molecular serotype detection. <i>PLoS ONE</i> , 2018, 13, e0203445.	1.1	8
15637	De novo transcriptome analysis of the egg parasitoid <i>Trichogramma chilonis</i> Ishii (Hymenoptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 1 0.4 3	0.4	3
15638	Two new species of the genus <i>Metaxonchium</i> Coomans & Nair 1975 (Nematoda, Dorylaimida), Tj ETQq1 1 0.784314 rgBT /Overlock 0.4 3 <i>Zoologischer Anzeiger</i> , 2018, 277, 1-11.	0.4	3

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15640	Molecular Characterization of <i>Trypanosoma cruzi</i> in Infected <i>Meccus pallidipennis</i> in the Southern Region of the State of Mexico, Mexico. <i>Vector-Borne and Zoonotic Diseases</i> , 2018, 18, 683-689.	0.6	6
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15645	First record of <i>Culex</i> ( <i>Culex</i> ) <i>bidens</i> (Diptera: Culicidae) in Colombia: Taxonomic and epidemiological implications. <i>Acta Tropica</i> , 2018, 188, 251-257.	0.9	3
15646	Proline provides site-specific flexibility for in vivo collagen. <i>Scientific Reports</i> , 2018, 8, 13809.	1.6	40
15647	Evolution of Spore Morphology in the Blechnaceae. <i>International Journal of Plant Sciences</i> , 2018, 179, 712-729.	0.6	12
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15649	Metagenomic analysis with strain-level resolution reveals fine-scale variation in the human pregnancy microbiome. <i>Genome Research</i> , 2018, 28, 1467-1480.	2.4	117
15650	Systematic Identification and Classification of $\beta$ -Lactamases Based on Sequence Similarity Criteria: $\beta$ -Lactamase Annotation. <i>Evolutionary Bioinformatics</i> , 2018, 14, 117693431879735.	0.6	15
15651	Pulmonary fungal granulomas and fibrinous pneumonia caused by different hypocrealean fungi in reptiles. <i>Veterinary Microbiology</i> , 2018, 225, 58-63.	0.8	8
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15654	Diverse Bacteria Utilize Alginate Within the Microbiome of the Giant Kelp <i>Macrocystis pyrifera</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 1914.	1.5	38
15655	Full-Genome Characterization and Genetic Evolution of West African Isolates of Bagaza Virus. <i>Viruses</i> , 2018, 10, 193.	1.5	5
15656	Three-Finger Toxin Diversification in the Venoms of Cat-Eye Snakes (Colubridae: <i>Boiga</i> ). <i>Journal of Molecular Evolution</i> , 2018, 86, 531-545.	0.8	14

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15658	Successive domain rearrangements underlie the evolution of a regulatory module controlled by a small interfering peptide. <i>Molecular Biology and Evolution</i> , 2018, 35, 2873-2885.	3.5	16
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15660	<i>DSH5</i> , a dihydrosphingosine C4 hydroxylase gene family member, shows spatially restricted expression in rice and is lethal when expressed ectopically. <i>Genes and Genetic Systems</i> , 2018, 93, 135-142.	0.2	0
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15663	Development and characterization of stable anaerobic thermophilic methanogenic microbiomes fermenting switchgrass at decreasing residence times. <i>Biotechnology for Biofuels</i> , 2018, 11, 243.	6.2	37
15664	MYBA From Blueberry ( <i>Vaccinium</i> Section <i>Cyanococcus</i> ) Is a Subgroup 6 Type R2R3MYB Transcription Factor That Activates Anthocyanin Production. <i>Frontiers in Plant Science</i> , 2018, 9, 1300.	1.7	55
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15670	Phylogenomic analysis unravels evolution of yellow fever virus within hosts. <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006738.	1.3	24
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15676	Tracing HIV-1 strains that imprint broadly neutralizing antibody responses. <i>Nature</i> , 2018, 561, 406-410.	13.7	47
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15678	Population genetic structure of banana corm weevil <i>Cosmopolites sordidus</i> (Germar) in India. <i>Journal of Asia-Pacific Entomology</i> , 2018, 21, 1222-1232.	0.4	2
15679	Synergistic inhibition of anaerobic ammonium oxidation (anammox) activity by phenol and thiocyanate. <i>Chemosphere</i> , 2018, 213, 498-506.	4.2	29
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15684	Global Transcriptome Analyses Reveal Differentially Expressed Genes of Six Organs and Putative Genes Involved in (Iso)flavonoid Biosynthesis in <i>Belamcanda chinensis</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 1160.	1.7	9
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15696	Application of microbial fuel cell technology for wastewater treatment and electricity generation under Nordic countries climate conditions: Study of performance and microbial communities. <i>Bioresource Technology</i> , 2018, 270, 1-10.	4.8	16
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15708	A Solvent-Free Approach for Converting Cellulose Waste into Volatile Organic Compounds with Endophytic Fungi. <i>Journal of Fungi</i> (Basel, Switzerland), 2018, 4, 102.	1.5	8
15709	Bioinformatic analysis of Chinese hamster ovary host cell protein lipases. <i>AIChE Journal</i> , 2018, 64, 4247-4254.	1.8	6
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15711	Order-level fern plastome phylogenomics: new insights from Hymenophyllales. <i>American Journal of Botany</i> , 2018, 105, 1545-1555.	0.8	30

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15713	Comparative analysis of mitochondrial genomes of the superfamily Grylloidea (Insecta, Orthoptera) reveals phylogenetic distribution of gene rearrangements. <i>International Journal of Biological Macromolecules</i> , 2018, 120, 1048-1054.	3.6	11
15714	Can we identify the Mexican hairless dog in the archaeological record? Morphological and genetic insights from Tizayuca, Basin of Mexico. <i>Journal of Archaeological Science</i> , 2018, 98, 128-136.	1.2	4
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15720	Faster Evolving Primate Genes Are More Likely to Duplicate. <i>Molecular Biology and Evolution</i> , 2018, 35, 107-118.	3.5	38
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15723	The opium poppy genome and morphinan production. <i>Science</i> , 2018, 362, 343-347.	6.0	225
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15726	Phylogenetic relationships in Malesian Pacific <i>Piper</i> (Piperaceae) and their implications for systematics. <i>Taxon</i> , 2018, 67, 693-724.	0.4	15
15727	Untangling the generic boundaries in tribe Marrubieae (Lamiaceae: Lamioideae) using nuclear and plastid DNA sequences. <i>Taxon</i> , 2018, 67, 770-783.	0.4	13
15728	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
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15730	<i>Pseudomonas aeruginosa</i> utilizes host polyunsaturated phosphatidylethanolamines to trigger theft-ferroptosis in bronchial epithelium. <i>Journal of Clinical Investigation</i> , 2018, 128, 4639-4653.	3.9	159
15731	Identification and characterization of WUSCHEL-related homeobox (WOX) gene family in economically important orchid species <i>Phalaenopsis equestris</i> and <i>Dendrobium catenatum</i> . <i>Plant Gene</i> , 2018, 14, 37-45.	1.4	7
15732	Further polyphyly of pinnotheroid crabs: the molecular phylogenetic position of the polychaete-associated Aphanodactylidae. <i>Invertebrate Systematics</i> , 2018, 32, 92.	0.5	18
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15735	New species of <i>Cloacina</i> von Linstow, 1898 (Nematoda: Strongyloidea) parasitic in the stomachs of wallaroos, <i>Osphranter</i> spp. (Marsupialia: Macropodidae) from northern Australia. <i>Systematic Parasitology</i> , 2018, 95, 527-542.	0.5	5
15736	New contributions to <i>Gruberia lanceolata</i> (Gruber, 1884) Kahl, 1932 based on analyses of multiple populations and genes (Ciliophora, Heterotrichea, Gruberiidae). <i>European Journal of Protistology</i> , 2018, 65, 16-30.	0.5	10
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15738	Amazonian bird's nest fungi (Basidiomycota): Current knowledge and novelties on <i>Cyathus</i> species. <i>Mycoscience</i> , 2018, 59, 331-342.	0.3	13
15739	A Hybrid Flow for Multiple Sequence Alignment with a BLASTn Based Pairwise Alignment Processor. , 2018, , .		0
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15741	Adaptive genomic evolution of opsins reveals that early mammals flourished in nocturnal environments. <i>BMC Genomics</i> , 2018, 19, 121.	1.2	22
15742	Genomic Variation Among and Within Six <i>Juglans</i> Species. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2153-2165.	0.8	73
15743	Identification of transposons near predicted lncRNA and mRNA pools of <i>Prunus mume</i> using an integrative transposable element database constructed from Rosaceae plant genomes. <i>Molecular Genetics and Genomics</i> , 2018, 293, 1301-1316.	1.0	3
15744	The <i>Crambe abyssinica</i> plastome: Brassicaceae phylogenomic analysis, evolution of RNA editing sites, hotspot and microsatellite characterization of the tribe Brassiceae. <i>Gene</i> , 2018, 671, 36-49.	1.0	15
15745	A new species and a new record of <i>Helicomyces</i> from Taiwan. <i>Mycoscience</i> , 2018, 59, 433-440.	0.3	7
15746	Morphology and molecular phylogeny of <i>Brasiliomyces malachrae</i> , a unique powdery mildew distributed in Central and South America. <i>Mycoscience</i> , 2018, 59, 461-466.	0.3	8
15747	Characterization of Papaya ringspot virus isolates infecting transgenic papaya 'Huanong No.1' in South China. <i>Scientific Reports</i> , 2018, 8, 8206.	1.6	16



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15749	Species composition, functional and phylogenetic distances correlate with success of invasive <i>Chromolaena odorata</i> in an experimental test. <i>Ecology Letters</i> , 2018, 21, 1211-1220.	3.0	40
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15751	How small an island? Speciation by endemic mammals ( <i>Apomys</i> , Muridae) on an oceanic Philippine island. <i>Journal of Biogeography</i> , 2018, 45, 1675-1687.	1.4	13
15752	Constant conflict between <i>Gypsy</i> LTR retrotransposons and CHH methylation within a stress-adapted mangrove genome. <i>New Phytologist</i> , 2018, 220, 922-935.	3.5	31
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15755	Worms that suck: Phylogenetic analysis of Hirudinea solidifies the position of Acanthobdellida and necessitates the dissolution of Rhynchobdellida. <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 129-134.	1.2	61
15756	Complete genome sequences of three novel cycloviruses identified in a dragonfly (Odonata): Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 422	0.9	4
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15758	Systematics and historical biogeography of the <i>Aphanius dispar</i> species group (Teleostei): Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 34	0.6	41
15759	Identification of Plant Virus Receptor Candidates in the Stylets of Their Aphid Vectors. <i>Journal of Virology</i> , 2018, 92, .	1.5	53
15760	The kinetoplast DNA of the Australian trypanosome, <i>Trypanosoma copemani</i> , shares features with <i>Trypanosoma cruzi</i> and <i>Trypanosoma lewisi</i> . <i>International Journal for Parasitology</i> , 2018, 48, 691-700.	1.3	13
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15764	Systematic prediction of genes functionally linked to CRISPR-Cas systems by gene neighborhood analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E5307-E5316.	3.3	138
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15772	A new microsporidium, <i>Apotasporea heleios</i> n. g., n. sp., from the Riverine grass shrimp <i>Palaemonetes paludosus</i> (Decapoda: Caridea: Palaemonidae). <i>Journal of Invertebrate Pathology</i> , 2018, 157, 125-135.	1.5	12
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15775	Oral yeast colonization in patients with primary and secondary Sjögren's syndrome. <i>Oral Diseases</i> , 2018, 24, 1367-1378.	1.5	11
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15777	Evolutionary analyses of Sindbis virus strains isolated from mosquitoes in Kenya. <i>Archives of Virology</i> , 2018, 163, 2465-2469.	0.9	12
15778	Assembly of a complete genome sequence for <i>Gemmata obscuriglobus</i> reveals a novel prokaryotic rRNA operon gene architecture. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 2095-2105.	0.7	4
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15781	Identification and distribution of microsymbionts associated with soybean nodulation in Mozambican soils. <i>Systematic and Applied Microbiology</i> , 2018, 41, 506-515.	1.2	21
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15797	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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15801	<i>Wolbachia</i> enhances insect-specific flavivirus infection in <i>Aedes aegypti</i> mosquitoes. <i>Ecology and Evolution</i> , 2018, 8, 5441-5454.	0.8	35

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15803	Jizanpeptins, Cyanobacterial Protease Inhibitors from a <i>Symploca</i> sp. Cyanobacterium Collected in the Red Sea. <i>Journal of Natural Products</i> , 2018, 81, 1417-1425.	1.5	17
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15807	Identifying RNA splicing factors using IFT genes in <i>Chlamydomonas reinhardtii</i> . <i>Open Biology</i> , 2018, 8, 170211.	1.5	10
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15810	Description of <i>Mediterraneibacter massiliensis</i> , gen. nov., sp. nov., a new genus isolated from the gut microbiota of an obese patient and reclassification of <i>Ruminococcus faecis</i> , <i>Ruminococcus lactaris</i> , <i>Ruminococcus torques</i> , <i>Ruminococcus gnavus</i> and <i>Clostridium glycyrrhizinilyticum</i> as <i>Mediterraneibacter faecis</i> comb. nov., <i>Mediterraneibacter lactaris</i> comb. nov., <i>Mediterraneibacter torques</i> comb. nov., <i>Mediterraneibacter gnavus</i> comb. nov. and <i>Mediterraneibacter glycyrrhizinilyticus</i> comb. nov. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 2107-2128.	0.7	87
15811	<i>Lepocreadiidae</i> Odhner, 1905 and <i>Aephhnidiogenidae</i> Yamaguti, 1934 (Digenea: Lepocreadioidea) of fishes from Moreton Bay, Queensland, Australia, with the erection of a new family and genus. <i>Systematic Parasitology</i> , 2018, 95, 479-498.	0.5	29
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15813	Ancient acquisition of algalinate utilization loci by human gut microbiota. <i>Scientific Reports</i> , 2018, 8, 8075.	1.6	38
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15853	Fern genomes elucidate land plant evolution and cyanobacterial symbioses. <i>Nature Plants</i> , 2018, 4, 460-472.	4.7	391
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15857	Isolation by marine barriers and climate explain areas of endemism in an island rodent. <i>Journal of Biogeography</i> , 2018, 45, 2053-2066.	1.4	12
15858	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
15859	<i>Batriscydrmaenus</i> Parker and Owens, New Genus, and Convergent Evolution of a "Reductive" Ecomorph in Socially Symbiotic Pselaphinae (Coleoptera: Staphylinidae). <i>The Coleopterists Bulletin</i> , 2018, 72, 219.	0.1	8
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15863	Generic assignment of <i>Leuciscus kurui</i> Bogutskaya from the upper Tigris drainage, and a replacement name for <i>Alburnus kurui</i> Mangit & Yerli (Teleostei: Leuciscidae). <i>Zootaxa</i> , 2018, 4410, 113-135.	0.2	16
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15866	GRAM domain proteins specialize functionally distinct ER-PM contact sites in human cells. <i>ELife</i> , 2018, 7, .	2.8	96
15867	Phylogenetic Analysis of Pigeon Paramyxoviruses Type-1 Identified in Mourning Collared-doves ( <i>Streptopelia decipiens</i> ) in Namibia, Africa. <i>Journal of Wildlife Diseases</i> , 2018, 54, 601-606.	0.3	4
15868	The genome of tapeworm <i>Taenia multiceps</i> sheds light on understanding parasitic mechanism and control of coenurosis disease. <i>DNA Research</i> , 2018, 25, 499-510.	1.5	36
15869	Transcriptional and Translational Landscape of Equine Torovirus. <i>Journal of Virology</i> , 2018, 92, .	1.5	24
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15882	High-throughput sequencing of the mitochondrial genomes from archived fish scales: an example of the endangered putative species flock of Sevan trout <i>Salmo ischchan</i> . <i>Hydrobiologia</i> , 2018, 822, 217-228.	1.0	14
15883	<i>Herpobasidium filicinum</i> (Eocronartiaceae, Platyglloeales) occurs on <i>Dennstaedtia wilfordii</i> (Dennstaedtiaceae) in Japan. <i>Mycoscience</i> , 2018, 59, 443-448.	0.3	3
15884	Whole genome comparison of <i>Aspergillus flavus</i> L-morphotype strain NRRL 3357 (type) and S-morphotype strain AF70. <i>PLoS ONE</i> , 2018, 13, e0199169.	1.1	27
15885	Annotation, classification, genomic organization and expression of the <i>Vitis vinifera</i> CYPome. <i>PLoS ONE</i> , 2018, 13, e0199902.	1.1	11
15886	Two new species of <i>Bacciger</i> Nicoll, 1914 (Trematoda: Faustulidae) in species of <i>Herklotsichthys</i> Whitley (Clupeidae) from Queensland waters. <i>Systematic Parasitology</i> , 2018, 95, 645-654.	0.5	6
15887	<i>HEAT INDUCIBLE LIPASE1</i> Remodels Chloroplastic Monogalactosyldiacylglycerol by Liberating $\pm$ -Linolenic Acid in <i>Arabidopsis</i> Leaves under Heat Stress. <i>Plant Cell</i> , 2018, 30, 1887-1905.	3.1	71
15888	Genetic population structure of the convict surgeonfish <i>Acanthurus triostegus</i> : a phylogeographic reassessment across its range. <i>Journal of Fish Biology</i> , 2018, 93, 597-608.	0.7	6
15889	<i>Candidatus Nitrosotenuis aquarius</i> , an Ammonia-Oxidizing Archaeon from a Freshwater Aquarium Biofilter. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	36
15890	Methyl-CpG-binding (SmMBD2/3) and chromobox (SmCBX) proteins are required for neoblast proliferation and oviposition in the parasitic blood fluke <i>Schistosoma mansoni</i> . <i>PLoS Pathogens</i> , 2018, 14, e1007107.	2.1	16
15891	Elucidating Allosteric Communications in Proteins with Difference Contact Network Analysis. <i>Journal of Chemical Information and Modeling</i> , 2018, 58, 1325-1330.	2.5	36



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15892	Duplication of a Pks gene cluster and subsequent functional diversification facilitate environmental adaptation in <i>Metarhizium</i> species. <i>PLoS Genetics</i> , 2018, 14, e1007472.	1.5	34
15893	Single-cell RNA-seq reveals hidden transcriptional variation in malaria parasites. <i>ELife</i> , 2018, 7, .	2.8	171
15894	The CLAVATA receptor FASCIATED EAR2 responds to distinct CLE peptides by signaling through two downstream effectors. <i>ELife</i> , 2018, 7, .	2.8	69
15895	<scp>DNA</scp> 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
15896	A streamlined cohesin apparatus is sufficient for mitosis and meiosis in the protist <i>Tetrahymena</i> . <i>Chromosoma</i> , 2018, 127, 421-435.	1.0	11
15897	De Novo Sequencing of a <i>Sparassis latifolia</i> Genome and Its Associated Comparative Analyses. <i>Canadian Journal of Infectious Diseases and Medical Microbiology</i> , 2018, 2018, 1-12.	0.7	9
15898	Double-digest <scp>RAD</scp>seq loci using standard Illumina indexes improve deep and shallow phylogenetic resolution of <i>Lophodermium</i>, a widespread fungal endophyte of pine needles. <i>Ecology and Evolution</i> , 2018, 8, 6638-6651.	0.8	14
15899	Concurrent Duplication of <i>Drosophila</i> Cid and Cenp-C Genes Resulted in Accelerated Evolution and Male Germline-Biased Expression of the New Copies. <i>Journal of Molecular Evolution</i> , 2018, 86, 353-364.	0.8	7
15900	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
15901	Discrimination of <i>Anopheles</i> species of the <i>Arribalzagia</i> Series in Colombia using a multilocus approach. <i>Infection, Genetics and Evolution</i> , 2018, 64, 76-84.	1.0	4
15902	Morphological and molecular evidence support a new endophytic fungus, <i>Chaetomella endophytica</i> from Japan. <i>Mycoscience</i> , 2018, 59, 473-478.	0.3	3
15903	Phylogenetics of <i>Camelina</i> Crantz. (Brassicaceae) and insights on the origin of gold-of-pleasure ( <i>Camelina sativa</i> ). <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 834-842.	1.2	55
15904	Genomic insights into the mitochondria of 11 eastern North American species of <i>Cladonia</i>. <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 508-512.	0.2	10
15905	Investigation of viable taxa in the deep terrestrial biosphere suggests high rates of nutrient recycling. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	29
15906	High-quality assembly of the reference genome for scarlet sage, <i>Salvia splendens</i> , an economically important ornamental plant. <i>GigaScience</i> , 2018, 7, .	3.3	49
15907	A hybrid solver for protein multiple sequence alignment problem. <i>Journal of Bioinformatics and Computational Biology</i> , 2018, 16, 1850015.	0.3	3
15908	Genetic manipulation of <i>Leishmania donovani</i> threonyl tRNA synthetase facilitates its exploration as a potential therapeutic target. <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006575.	1.3	12
15909	Extensive intraspecific gene order and gene structural variations between Mo17 and other maize genomes. <i>Nature Genetics</i> , 2018, 50, 1289-1295.	9.4	335

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15910	The role of progenesis in the diversification of the interstitial annelid lineage Psammodrillidae. <i>Invertebrate Systematics</i> , 2018, 32, 774.	0.5	15
15911	The role of biogeographical barriers and bridges in determining divergent lineages in <i>Ficus</i> (Moraceae). <i>Botanical Journal of the Linnean Society</i> , 2018, 187, 594-613.	0.8	15
15912	Î²-Klotho deficiency shifts the gut-liver bile acid axis and induces hepatic alterations in mice. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2018, 315, E833-E847.	1.8	13
15913	Deciphering the molecular determinants of cholinergic anthelmintic sensitivity in nematodes: When novel functional validation approaches highlight major differences between the model <i>Caenorhabditis elegans</i> and parasitic species. <i>PLoS Pathogens</i> , 2018, 14, e1006996.	2.1	55
15914	Antiproliferative and Antimicrobial Activities of Secondary Metabolites and Phylogenetic Study of Endophytic <i>Trichoderma</i> Species From <i>Vinca</i> Plants. <i>Frontiers in Microbiology</i> , 2018, 9, 1484.	1.5	64
15915	<i>Arabidopsis</i> Kunitz Trypsin Inhibitors in Defense Against Spider Mites. <i>Frontiers in Plant Science</i> , 2018, 9, 986.	1.7	47
15916	Comparison of the Anion Inhibition Profiles of the Î±-CA Isoforms (SpiCA1, SpiCA2 and SpiCA3) from the Scleractinian Coral <i>Stylophora pistillata</i> . <i>International Journal of Molecular Sciences</i> , 2018, 19, 2128.	1.8	10
15917	Barcoding and morphometry to identify and assess genetic population differentiation and size variability in loliginid squid paralarvae from NE Atlantic (Spain). <i>Marine Biology</i> , 2018, 165, 1.	0.7	9
15918	<i>Lasiodiplodia hormozganensis</i> causing basal stem rot on <i>Ricinus communis</i> in Brazil. <i>Australasian Plant Disease Notes</i> , 2018, 13, 1.	0.4	10
15919	Genomic variation of introduced <i>Salvinia minima</i> in southeastern United States. <i>Aquatic Botany</i> , 2018, 151, 38-42.	0.8	4
15920	Molecular systematics of the digenean community parasitising the cerithiid gastropod <i>Clypeomorus batillariaeformis</i> Habe & Kusage on the Great Barrier Reef. <i>Parasitology International</i> , 2018, 67, 722-735.	0.6	16
15921	<i>Trigonocephalotrema</i> (Digenea : Haplospalchnidae), a new genus for trematodes parasitising fishes of two Indo-West Pacific acanthurid genera. <i>Invertebrate Systematics</i> , 2018, 32, 759.	0.5	8
15922	Molecular Adaptations for Sensing and Securing Prey and Insight into Amniote Genome Diversity from the Garter Snake Genome. <i>Genome Biology and Evolution</i> , 2018, 10, 2110-2129.	1.1	72
15923	A Tangled Web: Origins of Reproductive Parasitism. <i>Genome Biology and Evolution</i> , 2018, 10, 2292-2309.	1.1	47
15924	Analyses of nervous system patterning genes in the tardigrade <i>Hypsibius exemplaris</i> illuminate the evolution of panarthropod brains. <i>EvoDevo</i> , 2018, 9, 19.	1.3	16
15925	Emerging Coxsackievirus A6 Causing Hand, Foot and Mouth Disease, Vietnam. <i>Emerging Infectious Diseases</i> , 2018, 24, 654-662.	2.0	60
15926	Multiple Kinases Can Phosphorylate the N-Terminal Sequences of Mitochondrial Proteins in <i>Arabidopsis thaliana</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 982.	1.7	10
15927	New Insights in Biocontrol Strategy against <i>Cephalcia tannourinensis</i> , the Principal Insect Defoliator of Lebanese Cedars. <i>Forest Science</i> , 2018, 64, 383-391.	0.5	2

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15928	Checklist of decapods (Crustacea) from the coast of the São Paulo state (Brazil) supported by integrative molecular and morphological data: I. Infraorder Caridea: families Hippolytidae, Lysmatidae, Ogyrididae, Processidae and Thoridae. <i>Zootaxa</i> , 2018, 4370, 76.	0.2	18
15929	Genome sequence and effectorome of <i>Moniliophthora perniciosa</i> and <i>Moniliophthora roreri</i> subpopulations. <i>BMC Genomics</i> , 2018, 19, 509.	1.2	18
15930	Draft genome sequence of <i>Annulohyphoxylon stygium</i> , <i>Aspergillus mulundensis</i> , <i>Berkeleyomyces basicola</i> (syn. <i>Thielaviopsis basicola</i> ), <i>Ceratocystis smalleyi</i> , two <i>Cercospora beticola</i> strains, <i>Coleophoma cylindrospora</i> , <i>Fusarium fracticaudum</i> , <i>Phialophora</i> cf. <i>hyalina</i> , and <i>Morchella septimelata</i> . <i>IMA Fungus</i> , 2018, 9, 199-223.	1.7	37
15931	Building a toolbox of protein scaffolds for future immobilization of biocatalysts. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 8373-8388.	1.7	33
15932	Intergeneric relationships in the <i>Gorteria</i> clade of <i>Arctotideae-Gorteriinae</i> (Asteraceae), with description of a new genus, <i>Roessleria</i> . <i>South African Journal of Botany</i> , 2018, 118, 216-231.	1.2	0
15933	Acquisition of MACPF domain-encoding genes is the main contributor to LPS glycan diversity in gut <i>Bacteroides</i> species. <i>ISME Journal</i> , 2018, 12, 2919-2928.	4.4	17
15934	Investigation of recombination-intense viral groups and their genes in the Earth's virome. <i>Scientific Reports</i> , 2018, 8, 11496.	1.6	14
15935	Within-Genome Shine-Dalgarno Sequences Are Not Selected for Function. <i>Molecular Biology and Evolution</i> , 2018, 35, 2487-2498.	3.5	16
15936	The Bits Between Proteins. , 2018, , .		1
15937	Distinctive characters of <i>Nostoc</i> genomes in cyanolichens. <i>BMC Genomics</i> , 2018, 19, 434.	1.2	30
15938	Multiple massive domestication and recent amplification of <i>Kolobok</i> superfamily transposons in the clawed frog <i>Xenopus</i> . <i>Zoological Letters</i> , 2018, 4, 17.	0.7	0
15939	Data on the <i>Amphidinium carterae</i> Dn241EHU isolation and morphological and molecular characterization. <i>Data in Brief</i> , 2018, 20, 1-5.	0.5	7
15940	Genome wide identification of taste receptor genes in common carp ( <i>Cyprinus carpio</i> ) and phylogenetic analysis in teleost. <i>Gene</i> , 2018, 678, 65-72.	1.0	12
15941	Characterization and Genome Analysis of a Phthalate Esters-Degrading Strain <i>Sphingobium yanoikuyae</i> SHJ. <i>BioMed Research International</i> , 2018, 2018, 1-8.	0.9	15
15942	New genomic data and analyses challenge the traditional vision of animal epithelium evolution. <i>BMC Genomics</i> , 2018, 19, 393.	1.2	50
15943	Molecular characterization and differential expression suggested diverse functions of P-type II Ca <sup>2+</sup> ATPases in <i>Triticum aestivum</i> L. <i>BMC Genomics</i> , 2018, 19, 389.	1.2	39
15944	A new Aura virus isolate in Brazil shows segment duplication in the variable region of the nsP3 gene. <i>Parasites and Vectors</i> , 2018, 11, 321.	1.0	3
15945	Hematobin is a novel immunomodulatory protein from the saliva of the horn fly <i>Haematobia irritans</i> that inhibits the inflammatory response in murine macrophages. <i>Parasites and Vectors</i> , 2018, 11, 435.	1.0	8

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15947	Genome-wide identification and analysis of the ALTERNATIVE OXIDASE gene family in diploid and hexaploid wheat. <i>PLoS ONE</i> , 2018, 13, e0201439.	1.1	8
15948	Genome-Wide Identification of NBS-Encoding Resistance Genes in Sunflower ( <i>Helianthus annuus</i> L.). <i>Genes</i> , 2018, 9, 384.	1.0	45
15949	A High-Quality, Long-Read De Novo Genome Assembly to Aid Conservation of Hawaii's Last Remaining Crow Species. <i>Genes</i> , 2018, 9, 393.	1.0	22
15950	Laboulbeniales hyperparasites (Fungi, Ascomycota) of bat flies: Independent origins and host associations. <i>Ecology and Evolution</i> , 2018, 8, 8396-8418.	0.8	16
15951	Studying the Evolution of Histone Variants Using Phylogeny. <i>Methods in Molecular Biology</i> , 2018, 1832, 273-291.	0.4	6
15952	Diversity and characterization of cultivable oleaginous yeasts isolated from mangrove forests. <i>World Journal of Microbiology and Biotechnology</i> , 2018, 34, 125.	1.7	13
15953	Individual components of paired typical NLR immune receptors are regulated by distinct E3 ligases. <i>Nature Plants</i> , 2018, 4, 699-710.	4.7	43
15954	Ovine keratome: identification, localisation and genomic organisation of keratin and keratin-associated proteins. <i>Animal Genetics</i> , 2018, 49, 361-370.	0.6	3
15955	Characterization of Bathyarchaeota genomes assembled from metagenomes of biofilms residing in mesophilic and thermophilic biogas reactors. <i>Biotechnology for Biofuels</i> , 2018, 11, 167.	6.2	38
15956	Solution scattering study of the <i>Bacillus subtilis</i> PgdS enzyme involved in poly- $\gamma$ -glutamic acids degradation. <i>PLoS ONE</i> , 2018, 13, e0195355.	1.1	2
15957	The Complete Mitogenome of <i>Falco amurensis</i> (Falconiformes, Falconidae), and a Comparative Analysis of Genus <i>Falco</i> . <i>Zoological Science</i> , 2018, 35, 367.	0.3	6
15958	Evolutionary pathways to NS5A inhibitor resistance in genotype 1 hepatitis C virus. <i>Antiviral Research</i> , 2018, 158, 45-51.	1.9	3
15959	Rapid evolutionary dynamics of pepper mild mottle virus. <i>Virus Research</i> , 2018, 256, 96-99.	1.1	7
15960	Speciation patterns in complex subterranean environments: a case study using short-tailed whipscorpions (Schizomida: Hubbardiidae). <i>Biological Journal of the Linnean Society</i> , 2018, 125, 355-367.	0.7	16
15961	The endemic Cladophorales (Ulvophyceae) of ancient Lake Baikal represent a monophyletic group of very closely related but morphologically diverse species. <i>Journal of Phycology</i> , 2018, 54, 616-629.	1.0	12
15962	<i>luxR</i> Homolog-Linked Biosynthetic Gene Clusters in Proteobacteria. <i>MSystems</i> , 2018, 3, .	1.7	25
15963	Determinants of the cytosolic turnover of mitochondrial intermembrane space proteins. <i>BMC Biology</i> , 2018, 16, 66.	1.7	45

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15965	Molecular Markers Associated With Chemical Analysis: A Powerful Tool for Quality Control Assessment of Copalchi Medicinal Plant Complex. <i>Frontiers in Pharmacology</i> , 2018, 9, 666.	1.6	12
15966	Silencing the Odorant Binding Protein RferOBP1768 Reduces the Strong Preference of Palm Weevil for the Major Aggregation Pheromone Compound Ferrugineol. <i>Frontiers in Physiology</i> , 2018, 9, 252.	1.3	33
15967	Molecular Epidemiology of Bacterial Wilt in the Madagascar Highlands Caused by Andean (Phylotype) Tj ETQq1 1 0.784314 rgBT /Ove... <i>Frontiers in Plant Science</i> , 2017, 8, 2258.	1.7	35
15968	Non-parent of Origin Expression of Numerous Effector Genes Indicates a Role of Gene Regulation in Host Adaption of the Hybrid Triticale Powdery Mildew Pathogen. <i>Frontiers in Plant Science</i> , 2018, 9, 49.	1.7	33
15969	Structure and Distribution of Centromeric Retrotransposons at Diploid and Allotetraploid Coffea Centromeric and Pericentromeric Regions. <i>Frontiers in Plant Science</i> , 2018, 9, 175.	1.7	31
15970	Gene Duplication and Transference of Function in the paleoAP3 Lineage of Floral Organ Identity Genes. <i>Frontiers in Plant Science</i> , 2018, 9, 334.	1.7	13
15971	Phylogenetic and CRISPR/Cas9 Studies in Deciphering the Evolutionary Trajectory and Phenotypic Impacts of Rice ERECTA Genes. <i>Frontiers in Plant Science</i> , 2018, 9, 473.	1.7	33
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15975	Chloroplastic Serine Hydroxymethyltransferase From Medicago truncatula: A Structural Characterization. <i>Frontiers in Plant Science</i> , 2018, 9, 584.	1.7	18
15976	Genome Size, Molecular Phylogeny, and Evolutionary History of the Tribe Aquilarieae (Thymelaeaceae), the Natural Source of Agarwood. <i>Frontiers in Plant Science</i> , 2018, 9, 712.	1.7	19
15977	Genomic Analysis of 48 Paenibacillus larvae Bacteriophages. <i>Viruses</i> , 2018, 10, 377.	1.5	26
15978	Bioinformatic Tools to Study the Soil Microorganisms: An In Silico Approach for Sustainable Agriculture. , 2018, , 169-182.		22
15979	A comparative computational genomics of Ebola Virus Disease strains: In-silico Insight for Ebola control. <i>Informatics in Medicine Unlocked</i> , 2018, 12, 106-119.	1.9	15
15980	Gene exchange drives the ecological success of a multi-host bacterial pathogen. <i>Nature Ecology and Evolution</i> , 2018, 2, 1468-1478.	3.4	156
15981	Viromic Analysis of Wastewater Input to a River Catchment Reveals a Diverse Assemblage of RNA Viruses. <i>MSystems</i> , 2018, 3, .	1.7	59

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15982	Description of <i>Crassolabium costaricense</i> sp. n. (Nematoda: Dorylaimida: Dorylaimidae) from Costa Rica. <i>Nematology</i> , 2018, 20, 1007-1014.	0.2	1
15983	Conserved phylogenetic distribution and limited antibiotic resistance of class 1 integrons revealed by assessing the bacterial genome and plasmid collection. <i>Microbiome</i> , 2018, 6, 130.	4.9	83
15984	Detection of <i>mcr-1</i> Plasmids in <i>Enterobacteriaceae</i> Isolates From Human Specimens: Comparison With Those in <i>Escherichia coli</i> Isolates From Livestock in Korea. <i>Annals of Laboratory Medicine</i> , 2018, 38, 555-562.	1.2	23
15985	Polymorphic sites preferentially avoid co-evolving residues in MHC class I proteins. <i>PLoS Computational Biology</i> , 2018, 14, e1006188.	1.5	6
15986	Evolution of DNMT2 in drosophilids: Evidence for positive and purifying selection and insights into new protein (pathways) interactions. <i>Genetics and Molecular Biology</i> , 2018, 41, 215-234.	0.6	14
15987	A benchmarking study on virtual ligand screening against homology models of human GPCRs. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 978-989.	1.5	13
15988	In Silico Methods to Predict Disease-Resistance Candidate Genes in Plants. , 2018, , 91-106.		0
15989	Reemergence of H3N8 Equine Influenza A virus in Chile, 2018. <i>Transboundary and Emerging Diseases</i> , 2018, 65, 1408-1415.	1.3	11
15990	Haplotype diversity in mitochondrial DNA reveals the multiple origins of Tibetan horse. <i>PLoS ONE</i> , 2018, 13, e0201564.	1.1	7
15991	Description of a new species of <i>Moenkhausia</i> (Characiformes: Characidae) from the upper Paraguay basin, Central Brazil, with comments on its phylogenetic relationships. <i>Neotropical Ichthyology</i> , 2018, 16, .	0.5	4
15992	Revealing Unexplored Sequence-Function Space Using Sequence Similarity Networks. <i>Biochemistry</i> , 2018, 57, 4651-4662.	1.2	58
15993	Plasmid and chromosomal integration of four novel bla <sub>IMP</sub> -carrying transposons from <i>Pseudomonas aeruginosa</i> , <i>Klebsiella pneumoniae</i> and an <i>Enterobacter</i> sp.. <i>Journal of Antimicrobial Chemotherapy</i> , 2018, 73, 3005-3015.	1.3	41
15994	The effects of contemporary selection and dispersal limitation on the community assembly of acidophilic microalgae. <i>Journal of Phycology</i> , 2018, 54, 720-733.	1.0	18
15995	A Diverse Range of Human Gut Bacteria Have the Potential To Metabolize the Dietary Component Gallic Acid. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	20
15996	The genomic impact of historical hybridization with massive mitochondrial DNA introgression. <i>Genome Biology</i> , 2018, 19, 91.	3.8	71
15997	Genome-Wide Identification and Characterization of WD40 Protein Genes in the Silkworm, <i>Bombyx mori</i> . <i>International Journal of Molecular Sciences</i> , 2018, 19, 527.	1.8	17
15998	<i>Pectobacterium atrosepticum</i> Phage vB_PatP_CB5: A Member of the Proposed Genus <i>Phimunavirus</i> <sup>™</sup> . <i>Viruses</i> , 2018, 10, 394.	1.5	21
15999	Complete genome sequences of two gemycircularviruses associated with non-cultivated plants in Brazil. <i>Archives of Virology</i> , 2018, 163, 3163-3166.	0.9	8

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16001	Modelling of polyhydroxyalkanoate synthase from <i>Aquitalea</i> sp. USM4 suggests a novel mechanism for polymer elongation. International Journal of Biological Macromolecules, 2018, 119, 438-445.	3.6	8
16002	<i>Fuscidea lightfootii</i> and <i>F. pusilla</i> (Fuscideaceae, Umbilicariomycetidae.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.5	4
16003	Pan-genome analyses of 24 <i>Shewanella</i> strains re-emphasize the diversification of their functions yet evolutionary dynamics of metal-reducing pathway. Biotechnology for Biofuels, 2018, 11, 193.	6.2	59
16004	Unexpected invasion of miniature inverted-repeat transposable elements in viral genomes. Mobile DNA, 2018, 9, 19.	1.3	20
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16006	Local Repressor AcrR Regulates AcrAB Efflux Pump Required for Biofilm Formation and Virulence in <i>Acinetobacter nosocomialis</i> . Frontiers in Cellular and Infection Microbiology, 2018, 8, 270.	1.8	27
16007	A genome-wide diversity study of grapevine <i>rupestris</i> stem pitting-associated virus. Archives of Virology, 2018, 163, 3105-3111.	0.9	29
16008	Residue coevolution reveals functionally important intramolecular interactions in formamidopyrimidine-DNA glycosylase. DNA Repair, 2018, 69, 24-33.	1.3	2
16009	Divergent evolution and clade-specific duplications of the Insulin-like Receptor in malacostracan crustaceans. General and Comparative Endocrinology, 2018, 268, 34-39.	0.8	9
16010	Evolution, Diversification, and Biogeography of Grasshoppers (Orthoptera: Acrididae). Insect Systematics and Diversity, 2018, 2, .	0.7	48
16011	Patterns of genomic site inheritance in HIV-1M inter-subtype recombinants delineate the most likely genomic sites of subtype-specific adaptation. Virus Evolution, 2018, 4, vey015.	2.2	3
16012	Evidence for involvement of a <i>transformer</i> paralogue in sex determination of the wasp <i>Leptopilina clavipes</i> . Insect Molecular Biology, 2018, 27, 780-795.	1.0	12
16013	Characterization of naturally occurring, new and persistent subclinical foot-and-mouth disease virus infection in vaccinated Asian buffalo in Islamabad Capital Territory, Pakistan. Transboundary and Emerging Diseases, 2018, 65, 1836-1850.	1.3	39
16014	Comparative transcriptomics reveals shared gene expression changes during independent evolutionary origins of stem and hypocotyl/root tubers in Brassica (Brassicaceae). PLoS ONE, 2018, 13, e0197166.	1.1	16
16015	Morphological and phylogenetic characterization of a novel <i>Unicauda</i> species, infecting the kidney of <i>Astyanax altiparanae</i> (Teleostei: Characidae) in Brazil. Acta Parasitologica, 2018, 63, 495-503.	0.4	4
16016	In silico characterization and expression profiling of the diacylglycerol acyltransferase gene family (DGAT1, DGAT2, DGAT3 and WS/DGAT) from oil palm, <i>Elaeis guineensis</i> . Plant Science, 2018, 275, 84-96.	1.7	37
16017	Trypanosomal mitochondrial intermediate peptidase does not behave as a classical mitochondrial processing peptidase. PLoS ONE, 2018, 13, e0196474.	1.1	9

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16019	Genome-Wide Characterization and Expression Analyses of <i>Pleurotus ostreatus</i> MYB Transcription Factors during Developmental Stages and under Heat Stress Based on de novo Sequenced Genome. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2052.	1.8	36
16020	Phylogenetic relationships of living and fossil African papionins: Combined evidence from morphology and molecules. <i>Journal of Human Evolution</i> , 2018, 123, 35-51.	1.3	22
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16159	Bioinformatics and Translation Initiation. , 2018, , 173-195.		0
16160	Bioinformatics and Translation Elongation. , 2018, , 197-238.		1
16161	CRISPR/Cas9-based heritable targeted mutagenesis in <i>Thermobia domestica</i> : A genetic tool in an apterygote development model of wing evolution. Arthropod Structure and Development, 2018, 47, 362-369.	0.8	11

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16163	A multifunctional human monoclonal neutralizing antibody that targets a unique conserved epitope on influenza HA. <i>Nature Communications</i> , 2018, 9, 2669.	5.8	67
16164	Bioelectric-calcineurin signaling module regulates allometric growth and size of the zebrafish fin. <i>Scientific Reports</i> , 2018, 8, 10391.	1.6	42
16165	The phylogenetic placement of Australian Linderniaceae and implications for generic taxonomy. <i>Australian Systematic Botany</i> , 2018, 31, 241.	0.3	5
16166	Sequences of Circadian Clock Proteins in the Nudibranch Molluscs <i>Hermissenda crassicornis</i> , <i>Melibe leonina</i> , and <i>Tritonia diomedea</i> . <i>Biological Bulletin</i> , 2018, 234, 207-218.	0.7	20
16167	Rad52-Rad51 association is essential to protect Rad51 filaments against Srs2, but facultative for filament formation. <i>ELife</i> , 2018, 7, .	2.8	19
16168	Protein Isoelectric Point and <i>Helicobacter pylori</i> . , 2018, , 397-412.		0
16169	Fundamentals of Proteomics. , 2018, , 421-436.		0
16170	A new species of <i>Wallinia</i> Pearse, 1920 (Digenea: Allocreadiidae) collected from <i>Astyanax fasciatus</i> (Cuvier, 1819) and <i>A. lacustris</i> Lucena and Soares, 2016 (Characiformes: Characidae) in Brazil based on morphology and DNA sequences. <i>Parasitology Research</i> , 2018, 117, 2847-2854.	0.6	11
16171	Grapevine virus T is relatively widespread in Slovakia and Czech Republic and genetically diverse. <i>Virus Genes</i> , 2018, 54, 737-741.	0.7	11
16172	The phylogeny of the genus <i>Indoplanorbis</i> (Gastropoda, Planorbidae) from Africa and the French West Indies. <i>Zoologica Scripta</i> , 2018, 47, 558-564.	0.7	8
16173	Sympatric Parasites Have Similar Host-Associated, but Asynchronous, Patterns of Diversification. <i>American Naturalist</i> , 2018, 192, E106-E119.	1.0	10
16174	The potential colonization histories of <i>Opsariichthys bidens</i> (Cyprinidae) in China using Bayesian binary MCMC analysis. <i>Gene</i> , 2018, 676, 1-8.	1.0	7
16175	Molecular phylogeny unveils hidden diversity of hillstream loaches (Cypriniformes: Cobitoidea) in the northern Western Ghats of India. <i>Meta Gene</i> , 2018, 17, 237-248.	0.3	6
16176	<i>Caridina susuroflabra</i> Richard & Clark, 2009 is a junior synonym of the widespread <i>Caridina africana</i> Kingsley, 1882 (Decapoda, Atyidae). <i>Crustaceana</i> , 2018, 91, 243-249.	0.1	0
16177	Chikungunya virus: genomic microevolution in Eastern India and its in-silico epitope prediction. <i>3 Biotech</i> , 2018, 8, 318.	1.1	8
16178	Prevalence and molecular variability of Apple chlorotic leaf spot virus capsid protein genes in Lithuania. <i>Journal of Plant Diseases and Protection</i> , 2018, 125, 389-396.	1.6	3
16179	Species delimitation and mitogenome phylogenetics in the subterranean genus <i>Pseudoniphargus</i> (Crustacea: Amphipoda). <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 988-999.	1.2	25



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16181	Translational Control through Differential Ribosome Pausing during Amino Acid Limitation in Mammalian Cells. <i>Molecular Cell</i> , 2018, 71, 229-243.e11.	4.5	123
16182	Squamate reptiles challenge paradigms of genomic repeat element evolution set by birds and mammals. <i>Nature Communications</i> , 2018, 9, 2774.	5.8	101
16183	Competitive organelle-specific adaptors recruit Vps13 to membrane contact sites. <i>Journal of Cell Biology</i> , 2018, 217, 3593-3607.	2.3	122
16184	Silica bodies in leaves of neotropical Podostemaceae: taxonomic and phylogenetic perspectives. <i>Annals of Botany</i> , 2018, 122, 1187-1201.	1.4	6
16185	Exon-Capture-Based Phylogeny and Diversification of the Venomous Gastropods (Neogastropoda). <i>Trends in Ecology and Evolution</i> , 2018, 33, 143-151.	3.5	46
16186	Morphological and Genetic Identification of <i>Pseudo-nitzschia</i> H. Peragallo, 1900 (Bacillariophyta) from the Sea of Japan. <i>Russian Journal of Marine Biology</i> , 2018, 44, 192-201.	0.2	5
16187	Fine metagenomic profile of the Mediterranean stratified and mixed water columns revealed by assembly and recruitment. <i>Microbiome</i> , 2018, 6, 128.	4.9	95
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16189	Comparative Analysis of CRISPR Loci Found in <i>Streptomyces</i> Genome Sequences. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2018, 10, 848-853.	2.2	2
16190	A novel species of <i>Diaporthe</i> causing leaf spot in <i>Pachira glabra</i> . <i>Tropical Plant Pathology</i> , 2018, 43, 460-467.	0.8	8
16191	Isolation of high-CO <sub>2</sub> -acclimated <i>Micractinium</i> sp. strains from eutrophic reservoir water. <i>Algal Research</i> , 2018, 34, 126-133.	2.4	8
16192	Linking serpentization, hyperalkaline mineral waters and abiotic methane production in continental peridotites: an integrated hydrogeological-bio-geochemical model from the Cabeço de Vide CH <sub>4</sub> -rich aquifer (Portugal). <i>Applied Geochemistry</i> , 2018, 96, 287-301.	1.4	15
16193	Mitochondrial genomes of the South American frogs <i>Eupsophus vertebralis</i> and <i>E. emiliopugini</i> (Neobatrachia: Alsodidae) and their phylogenetic relationships. <i>Journal of Genomics</i> , 2018, 6, 98-102.	0.6	5
16194	Computational characterization of the binding mode between oncoprotein EtsA and DNA repair enzymes. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 1055-1063.	1.5	4
16195	<i>Ceratocystis cacaofunesta</i> genome analysis reveals a large expansion of extracellular phosphatidylinositol-specific phospholipase-C genes (PI-PLC). <i>BMC Genomics</i> , 2018, 19, 58.	1.2	19
16196	Comparative genomics of the miniature wasp and pest control agent <i>Trichogramma pretiosum</i> . <i>BMC Biology</i> , 2018, 16, 54.	1.7	57
16197	Increasing the economic value of lignocellulosic stillage through medium-chain fatty acid production. <i>Biotechnology for Biofuels</i> , 2018, 11, 200.	6.2	99

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16199	Bioactivity Assessment of Indian Origin Mangrove Actinobacteria against <i>Candida albicans</i> . <i>Marine Drugs</i> , 2018, 16, 60.	2.2	15
16200	Diagnostic accuracy of digital RNA quantification versus real-time PCR for the detection of respiratory syncytial virus in nasopharyngeal aspirates from children with acute respiratory infection. <i>Journal of Clinical Virology</i> , 2018, 106, 34-40.	1.6	15
16201	Co-expression of squalene epoxidases with triterpene cyclases boosts production of triterpenoids in plants and yeast. <i>Metabolic Engineering</i> , 2018, 49, 1-12.	3.6	38
16202	HIV-1 Transmission Clustering and Phylodynamics Highlight the Important Role of Young Men Who Have Sex with Men. <i>AIDS Research and Human Retroviruses</i> , 2018, 34, 879-888.	0.5	27
16203	<i>MtNODULE ROOT1</i> and <i>MtNODULE ROOT2</i> Are Essential for Indeterminate Nodule Identity. <i>Plant Physiology</i> , 2018, 178, 295-316.	2.3	40
16204	Assessing the Likelihood of Gene Flow From Sugarcane ( <i>Saccharum</i> Hybrids) to Wild Relatives in South Africa. <i>Frontiers in Bioengineering and Biotechnology</i> , 2018, 6, 72.	2.0	6
16205	High quality draft genome sequence of <i>Mycoplasma testudineum</i> strain BH29T, isolated from the respiratory tract of a desert tortoise. <i>Standards in Genomic Sciences</i> , 2018, 13, 9.	1.5	3
16206	Comparative transcriptome analyses of three medicinal <i>Forsythia</i> species and prediction of candidate genes involved in secondary metabolisms. <i>Journal of Natural Medicines</i> , 2018, 72, 867-881.	1.1	15
16207	A Tandem Amino Acid Residue Motif in Guard Cell SLAC1 Anion Channel of Grasses Allows for the Control of Stomatal Aperture by Nitrate. <i>Current Biology</i> , 2018, 28, 1370-1379.e5.	1.8	46
16208	Phylogenetic analyses and in-seedling expression of ammonium and nitrate transporters in wheat. <i>Scientific Reports</i> , 2018, 8, 7082.	1.6	26
16209	Complete genome sequence of bacteriophage Deep-Purple, a novel member of the family Siphoviridae infecting <i>Bacillus cereus</i> . <i>Archives of Virology</i> , 2018, 163, 2555-2559.	0.9	6
16210	Identification of two isoforms of Pop in the domestic silkworm, <i>Bombyx mori</i> : Cloning, characterization and expression analysis. <i>Gene</i> , 2018, 667, 101-111.	1.0	5
16211	Acyl-CoA-binding protein family members in laticifers are possibly involved in lipid and latex metabolism of <i>Hevea brasiliensis</i> (the Para rubber tree). <i>BMC Genomics</i> , 2018, 19, 5.	1.2	8
16212	Global analysis of prokaryotic tRNA-derived cyclodipeptide biosynthesis. <i>BMC Genomics</i> , 2018, 19, 45.	1.2	35
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16214	Computational analysis of the receptor binding specificity of novel influenza A/H7N9 viruses. <i>BMC Genomics</i> , 2018, 19, 88.	1.2	8
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16217	Alphasatellitidae: a new family with two subfamilies for the classification of geminivirus- and nanovirus-associated alphasatellites. Archives of Virology, 2018, 163, 2587-2600.	0.9	133
16218	Genomic expansion of magnetotactic bacteria reveals an early common origin of magnetotaxis with lineage-specific evolution. ISME Journal, 2018, 12, 1508-1519.	4.4	103
16219	MALDI-TOF MS for identification of <i>Tsukamurella</i> species: <i>Tsukamurella tyrosinosolvens</i> as the predominant species associated with ocular infections. Emerging Microbes and Infections, 2018, 7, 1-11.	3.0	24
16220	Discovery and functional characterisation of a luqin-type neuropeptide signalling system in a deuterostome. Scientific Reports, 2018, 8, 7220.	1.6	34
16221	Uncovering the evolutionary history of neo-XY sex chromosomes in the grasshopper <i>Ronderosia bergii</i> (Orthoptera, Melanoplinae) through satellite DNA analysis. BMC Evolutionary Biology, 2018, 18, 2.	3.2	13
16222	Phylogenomics of the olive tree ( <i>Olea europaea</i> ) reveals the relative contribution of ancient allo- and autopolyploidization events. BMC Biology, 2018, 16, 15.	1.7	30
16223	Global sequence diversity of the lactate dehydrogenase gene in <i>Plasmodium falciparum</i> . Malaria Journal, 2018, 17, 16.	0.8	13
16224	Structural patterns of selection and diversity for <i>Plasmodium vivax</i> antigens DBP and AMA1. Malaria Journal, 2018, 17, 183.	0.8	10
16225	Reconstruction of a replication-competent ancestral murine endogenous retrovirus-L. Retrovirology, 2018, 15, 34.	0.9	11
16226	Identification and genome analysis of tomato chlorotic spot virus and dsRNA viruses from coinfecting vegetables in the Dominican Republic by high-throughput sequencing. Virology Journal, 2018, 15, 24.	1.4	7
16227	SACCHARIS: an automated pipeline to streamline discovery of carbohydrate active enzyme activities within polyspecific families and de novo sequence datasets. Biotechnology for Biofuels, 2018, 11, 27.	6.2	52
16228	Comparative genomics analysis of triatomines reveals common first line and inducible immunity-related genes and the absence of Imd canonical components among hemimetabolous arthropods. Parasites and Vectors, 2018, 11, 48.	1.0	53
16229	Identification and genetic characterization of <i>Sarcocystis arctica</i> and <i>Sarcocystis lutrae</i> in red foxes ( <i>Vulpes vulpes</i> ) from Baltic States and Spain. Parasites and Vectors, 2018, 11, 173.	1.0	21
16230	In-depth resistome analysis by targeted metagenomics. Microbiome, 2018, 6, 11.	4.9	115
16231	Metagenomic investigation of vestimentiferan tubeworm endosymbionts from Mid-Cayman Rise reveals new insights into metabolism and diversity. Microbiome, 2018, 6, 19.	4.9	32
16232	Phylogenomics and barcoding of <i>Panax</i> : toward the identification of ginseng species. BMC Evolutionary Biology, 2018, 18, 44.	3.2	45
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16235	Blood-feeding, susceptibility to infection with Schmallenberg virus and phylogenetics of <i>Culicoides</i> (Diptera: Ceratopogonidae) from the United Kingdom. <i>Parasites and Vectors</i> , 2018, 11, 116.	1.0	18
16236	Occurrence and distribution of <i>Giardia</i> species in wild rodents in Germany. <i>Parasites and Vectors</i> , 2018, 11, 213.	1.0	36
16237	Molecular and morphological characterisation of <i>Pharyngostromylus kappa</i> Mawson, 1965 (Nematoda: Strongylida) from Australian macropodid marsupials with the description of a new species, <i>P. patriciae</i> n. sp.. <i>Parasites and Vectors</i> , 2018, 11, 271.	1.0	1
16238	High-quality draft genome of the methanotroph <i>Methylovulum psychrotolerans</i> Str. HV10-M2 isolated from plant material at a high-altitude environment. <i>Standards in Genomic Sciences</i> , 2018, 13, 10.	1.5	5
16239	Survey of Grapevine Pinot gris virus in certified grapevine stocks in Ukraine. <i>European Journal of Plant Pathology</i> , 2018, 152, 555-560.	0.8	11
16240	Notes on powdery mildews (Erysiphales) in Thailand VI. <i>Phyllactinia</i> and <i>Leveillula</i> . <i>Mycological Progress</i> , 2018, 17, 701-718.	0.5	7
16241	Genetic diversity of human sapovirus across the Americas. <i>Journal of Clinical Virology</i> , 2018, 104, 65-72.	1.6	45
16242	Transoceanic Stepping-stones between Cretaceous waterfalls? The enigmatic biogeography of pantropical <i>Oocyclus</i> cascade beetles. <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 416-428.	1.2	15
16243	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
16244	Comparative Population Genomics Analysis of the Mammalian Fungal Pathogen <i>Pneumocystis</i> . <i>MBio</i> , 2018, 9, .	1.8	23
16245	Molecular Phylogeny of <i>Astragalus</i> sect. <i>Ammodendron</i> (Fabaceae) Inferred from Chloroplast <i>ycf1</i> Gene. <i>Annales Botanici Fennici</i> , 2018, 55, 75-82.	0.0	20
16246	Potential forensic biogeographic application of diatom colony consistency analysis employing pyrosequencing profiles of the 18S rDNA V7 region. <i>International Journal of Legal Medicine</i> , 2018, 132, 1611-1620.	1.2	9
16247	Next-generation sequencing library preparation method for identification of RNA viruses on the Ion Torrent Sequencing Platform. <i>Virus Genes</i> , 2018, 54, 536-542.	0.7	5
16248	Generation of a novel next-generation sequencing-based method for the isolation of new human papillomavirus types. <i>Virology</i> , 2018, 520, 1-10.	1.1	25
16249	Different rearing conditions alter gut microbiota composition and host physiology in Shaoxing ducks. <i>Scientific Reports</i> , 2018, 8, 7387.	1.6	38
16250	A genomic evaluation of taxonomic trends through time in coast horned lizards (genus <i>Phrynosoma</i> )	2.0	14
16251	Novel Maltogenic Amylase CoMA from <i>Corallococcus</i> sp. Strain EGB Catalyzes the Conversion of Maltooligosaccharides and Soluble Starch to Maltose. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	24

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16253	Involvement of aquaporin NIP1;1 in the contrasting tolerance response to root hypoxia in <i>Prunus</i> rootstocks. <i>Journal of Plant Physiology</i> , 2018, 228, 19-28.	1.6	7
16254	Comparative transcriptomics gives insights into the evolution of parasitism in <i>Strongyloides</i> nematodes at the genus, subclade and species level. <i>Scientific Reports</i> , 2018, 8, 5192.	1.6	24
16255	A thin ice layer segregates two distinct fungal communities in Antarctic brines from Tarn Flat (Northern Victoria Land). <i>Scientific Reports</i> , 2018, 8, 6582.	1.6	21
16256	Microbial community analysis and biodeterioration of waterlogged archaeological wood from the Nanhai No. 1 shipwreck during storage. <i>Scientific Reports</i> , 2018, 8, 7170.	1.6	30
16257	A double helical motif in OCIAD2 is essential for its localization, interactions and STAT3 activation. <i>Scientific Reports</i> , 2018, 8, 7362.	1.6	26
16258	Anaerobic carbon monoxide metabolism by <i>Pleomorphomonas carboxyditropha</i> sp. nov., a new mesophilic hydrogenogenic carboxydrotroph. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	18
16259	Profiling microbial strains in urban environments using metagenomic sequencing data. <i>Biology Direct</i> , 2018, 13, 9.	1.9	29
16260	Microbial diversity and ecotoxicity of sediments 3Âyears after the Jiaozhou Bay oil spill. <i>AMB Express</i> , 2018, 8, 79.	1.4	19
16261	Multilevel social structure and diet shape the gut microbiota of the gelada monkey, the only grazing primate. <i>Microbiome</i> , 2018, 6, 84.	4.9	56
16262	Complete genome sequence of "Thiodictyon syntrophicum" sp. nov. strain Cad16T, a photolithoautotrophic purple sulfur bacterium isolated from the alpine meromictic Lake Cadagno. <i>Standards in Genomic Sciences</i> , 2018, 13, 14.	1.5	12
16263	Phylogenetics of Datureae (Solanaceae), including description of the new genus <i>Trompettia</i> and re"circumscription of the tribe. <i>Taxon</i> , 2018, 67, 359-375.	0.4	15
16264	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
16265	Complete chloroplast genome sequence of the red silk cotton tree ( <i>Bombax ceiba</i> ). <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 315-316.	0.2	5
16266	The complete mitochondrial genome of <i>Bombax ceiba</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 313-314.	0.2	1
16267	Whole-genome de novo sequencing reveals unique genes that contributed to the adaptive evolution of the Mikado pheasant. <i>GigaScience</i> , 2018, 7, .	3.3	21
16268	First Complete Genome Sequence of Pepper mild mottle virus from Chili Pepper in the United States. <i>Genome Announcements</i> , 2018, 6, .	0.8	7
16269	Characterization of photosynthetic ferredoxin from the Antarctic alga <i>Chlamydomonas</i> sp. <i>UWO</i> 241 reveals novel features of cold adaptation. <i>New Phytologist</i> , 2018, 219, 588-604.	3.5	25

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16270	Distribution of gene segments of the pandemic A(H1N1) 2009 virus lineage in pig populations. <i>Transboundary and Emerging Diseases</i> , 2018, 65, 1502-1513.	1.3	5
16271	Integrative taxonomy reveals a new genus and new species of Philosciidae (Crustacea: Isopoda): <i>Tj ETQq1 1 0.784314 rgBT /Overlock</i>	0.4	11
16272	Development of hypobranchial muscles with special reference to the evolution of the vertebrate neck. <i>Zoological Letters</i> , 2018, 4, 5.	0.7	14
16273	NvERTx: A gene expression database to compare embryogenesis and regeneration in the sea anemone <i>Nematostella vectensis</i> . <i>Development (Cambridge)</i> , 2018, 145, .	1.2	47
16274	Peculiar genes for thermostable bifunctional catalase-peroxidases in <i>Chaetomium thermophilum</i> and their molecular evolution. <i>Gene</i> , 2018, 666, 83-91.	1.0	2
16275	Morphological and mitochondrial DNA data reshuffle the taxonomy of the genera <i>Atopochetus</i> Attems, <i>Litostrophus</i> Chamberlin and <i>Tonkinbolus</i> Verhoeff (Diplopoda: Spirobolida: Pachybolidae), with descriptions of nine new species. <i>Invertebrate Systematics</i> , 2018, 32, 159.	0.5	12
16276	A bipartite periplasmic receptor–diguanylate cyclase pair (XAC2383–XAC2382) in the bacterium <i>Xanthomonas citri</i> . <i>Journal of Biological Chemistry</i> , 2018, 293, 10767-10781.	1.6	2
16277	The first horse herders and the impact of early Bronze Age steppe expansions into Asia. <i>Science</i> , 2018, 360, .	6.0	262
16278	Human-Associated Lachnospiraceae Genetic Markers Improve Detection of Fecal Pollution Sources in Urban Waters. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	58
16279	Molecular systematics of sturgeon nucleocytoplasmic large DNA viruses. <i>Molecular Phylogenetics and Evolution</i> , 2018, 128, 26-37.	1.2	18
16280	Targeted Structure–Activity Analysis of Endochin-like Quinolones Reveals Potent Qi and Qo Site Inhibitors of <i>Toxoplasma gondii</i> and <i>Plasmodium falciparum</i> Cytochrome <i>bc1</i> and Identifies ELQ-400 as a Remarkably Effective Compound against Acute Experimental Toxoplasmosis. <i>ACS Infectious Diseases</i> , 2018, 4, 1574-1584.	1.8	32
16281	Comparative transcriptomics provides insight into the molecular basis of species diversification of section <i>Trigonopodia</i> ( <i>Cypridium</i> ) on the Qinghai-Tibetan Plateau. <i>Scientific Reports</i> , 2018, 8, 11640.	1.6	11
16282	Next-generation sequence data demonstrate several pathogenic bee viruses in Middle East and African honey bee subspecies ( <i>Apis mellifera syriaca</i> , <i>Apis mellifera intermissa</i> ) as well as their cohabiting pathogenic mites ( <i>Varroa destructor</i> ). <i>Virus Genes</i> , 2018, 54, 694-705.	0.7	7
16283	Evolutionary analysis and structural characterization of <i>Aquilaria sinensis</i> sesquiterpene synthase in agarwood formation: A computational study. <i>Journal of Theoretical Biology</i> , 2018, 456, 249-260.	0.8	4
16284	Allosteric mechanisms underlie GPCR signaling to SH3-domain proteins through arrestin. <i>Nature Chemical Biology</i> , 2018, 14, 876-886.	3.9	50
16285	Genome Analyses of the Microalga <i>Picochlorum</i> Provide Insights into the Evolution of Thermotolerance in the Green Lineage. <i>Genome Biology and Evolution</i> , 2018, 10, 2347-2365.	1.1	36
16286	Transcriptomic and proteomic responses of the oceanic diatom <i>Pseudo-nitzschia granii</i> to iron limitation. <i>Environmental Microbiology</i> , 2018, 20, 3109-3126.	1.8	39
16287	Comparison of metaheuristics to measure gene effects on phylogenetic supports and topologies. <i>BMC Bioinformatics</i> , 2018, 19, 218.	1.2	1

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16288	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
16289	Oral consumption of cinnamon enhances the expression of immunity and lipid absorption genes in the small intestinal epithelium and alters the gut microbiota in normal mice. <i>Journal of Functional Foods</i> , 2018, 49, 96-104.	1.6	3
16290	Integrated genomic and fossil evidence illuminates life's early evolution and eukaryote origin. <i>Nature Ecology and Evolution</i> , 2018, 2, 1556-1562.	3.4	274
16291	Genetic Variation of the Pathogen Causing Impatiens Downy Mildew Predating and Including Twenty-first Century Epidemics on <i>Impatiens walleriana</i> . <i>Plant Disease</i> , 2018, 102, 2411-2420.	0.7	17
16292	Resource stability and geographic isolation are associated with genome divergence in western Palearctic crossbills. <i>Journal of Evolutionary Biology</i> , 2018, 31, 1715-1731.	0.8	11
16293	DNA Sequence Variation among Conspecific Accessions of the Legume <i>Coursetia caribaea</i> Reveals Geographically Localized Clades Here Ranked as Species. <i>Systematic Botany</i> , 2018, 43, 664-675.	0.2	20
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16323	A consensus secondary structure of ITS2 for the diatom Order Cymatosirales (Mediophyceae,) Tj ETQq1 1 0.784314 rgBT /Overlock 1011 <i>Molecular Phylogenetics and Evolution</i> , 2018, 129, 117-129.	1.2	9



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16331	Molecular, physiological and phylogenetic traits of Lactococcus 936-type phages from distinct dairy environments. <i>Scientific Reports</i> , 2018, 8, 12540.	1.6	13
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16343	The chromosome-level genome assemblies of two rattans ( <i>Calamus simplicifolius</i> and <i>Daemonorops</i> ) Tj ETQq1 1 0.784314 rgBT /Ove 3.3 28	3.3	28
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16358	Impact of transposable elements on genome structure and evolution in bread wheat. <i>Genome Biology</i> , 2018, 19, 103.	3.8	226
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16362	Iron-Sulfur Cluster Biosynthesis in Algae with Complex Plastids. <i>Genome Biology and Evolution</i> , 2018, 10, 2061-2071.	1.1	9
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16364	CTCF maintains regulatory homeostasis of cancer pathways. <i>Genome Biology</i> , 2018, 19, 106.	3.8	38
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16366	New Biological Insights Into How Deforestation in Amazonia Affects Soil Microbial Communities Using Metagenomics and Metagenome-Assembled Genomes. <i>Frontiers in Microbiology</i> , 2018, 9, 1635.	1.5	51
16367	Diversity and Applications of Endophytic Actinobacteria of Plants in Special and Other Ecological Niches. <i>Frontiers in Microbiology</i> , 2018, 9, 1767.	1.5	155
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16380	Testing the utility of DNA barcodes and a preliminary phylogenetic framework for Chinese freshwater mussels ( <i>Bivalvia: Unionidae</i> ) from the middle and lower Yangtze River. <i>PLoS ONE</i> , 2018, 13, e0200956.	1.1	20
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16383	Distribution and population structure of endobacteria in arbuscular mycorrhizal fungi at North Atlantic dunes. <i>ISME Journal</i> , 2018, 12, 3001-3013.	4.4	15
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16387	The structure of the ubiquitin-like modifier FAT10 reveals an alternative targeting mechanism for proteasomal degradation. <i>Nature Communications</i> , 2018, 9, 3321.	5.8	25
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16393	Phylogenetic analysis and a review of the history of the accidental phytoplankter, <i>Phaeodactylum tricornutum</i> Bohlin ( <i>Bacillariophyta</i> ). <i>PLoS ONE</i> , 2018, 13, e0196744.	1.1	17
16394	Species Tree Estimation using ddRADseq Data from Historical Specimens Confirms the Monophyly of Highly Disjunct Species of <i>Chloropyron</i> ( <i>Orobanchaceae</i> ). <i>Systematic Botany</i> , 2018, 43, 701-708.	0.2	6
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16398	Antimicrobial and Cytotoxic Properties of Bioactive Metabolites Produced by <i>Streptomyces cavourensis</i> YBQ59 Isolated from <i>Cinnamomum cassia</i> Prels in Yen Bai Province of Vietnam. <i>Current Microbiology</i> , 2018, 75, 1247-1255.	1.0	39
16399	Phylogeny, ecology and taxonomy of systemic pathogens and their relatives in Ajellomycetaceae (Onygenales): <i>Blastomyces</i> , <i>Emergomyces</i> , <i>Emmonsia</i> , <i>Emmonsiiellopsis</i> . <i>Fungal Diversity</i> , 2018, 90, 245-291.	4.7	71
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16403	Prevalence and Genetic Diversity of Grabloviruses in Free-Living <i>Vitis</i> spp.. <i>Plant Disease</i> , 2018, 102, 2308-2316.	0.7	20
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16407	Emergence and Evolution of Novel Reassortant Influenza A Viruses in Canines in Southern China. <i>MBio</i> , 2018, 9, .	1.8	41
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16409	Isolation and sequence analysis of a novel rhesus macaque foamy virus isolate with a serotype-1-like env. <i>Archives of Virology</i> , 2018, 163, 2507-2512.	0.9	5
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16412	High Gut Microbiota Diversity Provides Lower Resistance against Infection by an Intestinal Parasite in Bumblebees. <i>American Naturalist</i> , 2018, 192, 131-141.	1.0	28
16413	The Family of Two-Component Systems That Regulate Hydrocarbon Degradation Pathways. , 2018, , 201-220.		0
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16416	Improved de novo genome assembly and analysis of the Chinese cucurbit <i>Siraitia grosvenorii</i> , also known as monk fruit or luo-han-guo. GigaScience, 2018, 7, .	3.3	32
16417	Divergent Allele Advantage at Human MHC Genes: Signatures of Past and Ongoing Selection. Molecular Biology and Evolution, 2018, 35, 2145-2158.	3.5	128
16418	Functional characterization of CYP4G11, a highly conserved enzyme in the western honey bee <i>Apis mellifera</i> . Insect Molecular Biology, 2018, 27, 661-674.	1.0	33
16419	White seed color in common bean ( <i>Phaseolus vulgaris</i> ) results from convergent evolution in the <i>P</i> ( <i>pigment</i> ) gene. New Phytologist, 2018, 219, 1112-1123.	3.5	77
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16518	Identification and Molecular Characterization of Recombinant Potato Virus Y (PVY) in Potato from South Korea, PVY <sup>NTN</sup> Strain. <i>Plant Disease</i> , 2019, 103, 137-142.	0.7	14
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16528	The Sanguicolous Apostome <i>Metacollinia luciensis</i> Jankowski 1980 (Colliniidae, Apostomatia). <i>Microbiology</i> , 2019, 66, 140-146.	0.8	7
16529	The plant hormone auxin directs timing of xylem development by inhibition of secondary cell wall deposition through repression of secondary wall NAC domain transcription factors. <i>Physiologia Plantarum</i> , 2019, 165, 673-689.	2.6	54
16530	Free alignment classification of dikarya fungi using some machine learning methods. <i>Neural Computing and Applications</i> , 2019, 31, 6995-7016.	3.2	10
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16540	Inference of Horizontal Gene Transfer: Gaining Insights Into Evolution via Lateral Acquisition of Genetic Material. , 2019, , 953-964.		2
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16706	Almond ( <i>Prunus dulcis</i> ) Allergen Pru du 8, the First Member of a New Family of Food Allergens. <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 8626-8631.	2.4	15
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16729	Methane-fuelled biofilms predominantly composed of methanotrophic ANME-1 in Arctic gas hydrate-related sediments. <i>Scientific Reports</i> , 2019, 9, 9725.	1.6	33
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16733	Integrative analysis reveals evolutionary patterns and potential functions of SWEET transporters in Euphorbiaceae. <i>International Journal of Biological Macromolecules</i> , 2019, 139, 1-11.	3.6	29
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16990	The PATRIC Bioinformatics Resource Center: expanding data and analysis capabilities. <i>Nucleic Acids Research</i> , 2020, 48, D606-D612.	6.5	552
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17013	Kalign 3: multiple sequence alignment of large datasets. <i>Bioinformatics</i> , 2020, 36, 1928-1929.	1.8	83
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17037	Genome-wide identification of ABC transporters in monogeneans. <i>Molecular and Biochemical Parasitology</i> , 2019, 234, 111234.	0.5	9
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17254	Unraveling the functional role of the orphan solute carrier, SLC22A24 in the transport of steroid conjugates through metabolomic and genome-wide association studies. <i>PLoS Genetics</i> , 2019, 15, e1008208.	1.5	23
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17262	Morphological and Molecular Characterization of <i>Zanthoxylum zanthoxyloides</i> ( <i>Rutaceae</i> ) from Burkina Faso. <i>Plants</i> , 2019, 8, 353.	1.6	9

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17264	Evolutionary dynamics of lineage 2 West Nile virus in Europe, 2004–2018: Phylogeny, selection pressure and phylogeography. <i>Molecular Phylogenetics and Evolution</i> , 2019, 141, 106617.	1.2	30
17265	Three novel <i>Ambrosia</i> <i>Fusarium</i> Clade species producing clavate macroconidia known ( <i>F.</i> ) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5</i> <i>Euwallacea</i> spp. (Coleoptera: Scolytinae) on woody hosts. <i>Mycologia</i> , 2019, 111, 919-935.	0.8	30
17266	MYB Gene Family in Potato ( <i>Solanum tuberosum</i> L.): Genome-Wide Identification of Hormone-Responsive Reveals Their Potential Functions in Growth and Development. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4847.	1.8	74
17267	Current Progress of Avian Vaccines Against West Nile Virus. <i>Vaccines</i> , 2019, 7, 126.	2.1	13
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17269	Effect of diversity in gp41 membrane proximal external region of primary HIV-1 Indian subtype C sequences on interaction with broadly neutralizing antibodies 4E10 and 10E8. <i>Virus Research</i> , 2019, 273, 197763.	1.1	6
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17273	Water stress affects the frequency of Firmicutes, Clostridiales and <i>Lysobacter</i> in rhizosphere soils of greenhouse grape. <i>Agricultural Water Management</i> , 2019, 226, 105776.	2.4	35
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17279	Fast and accurate genome comparison using genome images: The Extended Natural Vector Method. <i>Molecular Phylogenetics and Evolution</i> , 2019, 141, 106633.	1.2	9
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17285	Chromosome number diversity in Asian <i>Cryptocercus</i> (Blattodea, Cryptocercidae) and implications for karyotype evolution and geographic distribution on the Western Sichuan Plateau. <i>Systematics and Biodiversity</i> , 2019, 17, 594-608.	0.5	4
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17290	Haplotype-resolved genomes of geminivirus-resistant and geminivirus-susceptible African cassava cultivars. <i>BMC Biology</i> , 2019, 17, 75.	1.7	42
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17298	A comparative analysis of complete plastid genomes from <i>Prangos fedtschenkoi</i> and <i>Prangos lipskyi</i> (Apiaceae). <i>Ecology and Evolution</i> , 2019, 9, 364-377.	0.8	13

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17301	Immunological MHC supertypes and allelic expression: how low is the functional MHC diversity in free-ranging Namibian cheetahs?. <i>Conservation Genetics</i> , 2019, 20, 65-80.	0.8	13
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17305	Penaeid shrimp genome provides insights into benthic adaptation and frequent molting. <i>Nature Communications</i> , 2019, 10, 356.	5.8	328
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17312	Genome sequence of <i>Malania oleifera</i> , a tree with great value for nervonic acid production. <i>GigaScience</i> , 2019, 8, .	3.3	36
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17314	Unexpected phylogenetic relationships within the world's largest limbless skink species ( <i>Acontias</i> ) Tj ETQq1 1 0.784314 rgBT /Overl <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2019, 57, 445-460.	0.6	3
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17328	Babesial infection in the Madagascan flying fox, <i>Pteropus rufus</i> Geoffroy, 1803. <i>Parasites and Vectors</i> , 2019, 12, 51.	1.0	14
17329	Atlantic West <i>Ophiothrix</i> spp. in the scope of integrative taxonomy: Confirming the existence of <i>Ophiothrix trinidadensis</i> Tommasi, 1970. <i>PLoS ONE</i> , 2019, 14, e0210331.	1.1	11
17330	Archaea dominate the microbial community in an ecosystem with low-to-moderate temperature and extreme acidity. <i>Microbiome</i> , 2019, 7, 11.	4.9	58
17331	Transcriptional Reprogramming of Rice Cells by <i>Xanthomonas oryzae</i> TALEs. <i>Frontiers in Plant Science</i> , 2019, 10, 162.	1.7	38
17332	Biostimulation of carbonate precipitation process in soil for copper immobilization. <i>Journal of Hazardous Materials</i> , 2019, 368, 705-713.	6.5	88
17333	<i>Leishmania</i> cytochrome b gene sequence polymorphisms in southern Iran: relationships with different cutaneous clinical manifestations. <i>BMC Infectious Diseases</i> , 2019, 19, 98.	1.3	9
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17336	Molecular evolution of the <i>semenogelin 1</i> and <i>2</i> and mating system in gibbons. <i>American Journal of Physical Anthropology</i> , 2019, 168, 364-369.	2.1	4
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17339	Function and Evolution of Nematode RNAi Pathways. <i>Non-coding RNA</i> , 2019, 5, 8.	1.3	49
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17342	MIPS: Functional dynamics in evolutionary pathways of plant kingdom. <i>Genomics</i> , 2019, 111, 1929-1945.	1.3	17
17343	Genetic Diversity and Gene Family Expansions in Members of the Genus <i>Entamoeba</i> . <i>Genome Biology and Evolution</i> , 2019, 11, 688-705.	1.1	22
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17347	Endemic, endangered and evolutionarily significant: cryptic lineages in Seychelles' frogs ( <i>Anura</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	0.7	11
17348	The control of endopolygalacturonase expression by the sugarcane RAV transcription factor during aerenchyma formation. <i>Journal of Experimental Botany</i> , 2019, 70, 497-506.	2.4	24
17349	Origin of Gibberellin-Dependent Transcriptional Regulation by Molecular Exploitation of a Transactivation Domain in DELLA Proteins. <i>Molecular Biology and Evolution</i> , 2019, 36, 908-918.	3.5	38
17350	Gene annotation errors are common in the mammalian mitochondrial genomes database. <i>BMC Genomics</i> , 2019, 20, 73.	1.2	28
17351	Analysis of a new begomovirus unveils a composite element conserved in the CP gene promoters of several Geminiviridae genera: Clues to comprehend the complex regulation of late genes. <i>PLoS ONE</i> , 2019, 14, e0210485.	1.1	16
17352	Whole-genome sequence of the bovine blood fluke <i>Schistosoma bovis</i> supports interspecific hybridization with <i>S. haematobium</i> . <i>PLoS Pathogens</i> , 2019, 15, e1007513.	2.1	49

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17355	Unraveling the Developmental and Genetic Mechanisms Underpinning Floral Architecture in Proteaceae. <i>Frontiers in Plant Science</i> , 2019, 10, 18.	1.7	17
17356	Lectin Sequence Distribution in QTLs from Rice ( <i>Oryza sativa</i> ) Suggest A Role in Morphological Traits and Stress Responses. <i>International Journal of Molecular Sciences</i> , 2019, 20, 437.	1.8	9
17357	Identification and Characterization of Mitogen-Activated Protein Kinase (MAPK) Genes in Sunflower ( <i>Helianthus annuus</i> L.). <i>Plants</i> , 2019, 8, 28.	1.6	21
17358	Species delimitation and genetic structure of two endemic <i>Magnolia</i> species (section <i>Magnolia</i> ); Tj ETQq1 1 0.784314 rgBT /Overlock 12	0.5	12
17359	Bioremediation of petroleum-contaminated soil enhanced by aged refuse. <i>Chemosphere</i> , 2019, 222, 98-105.	4.2	41
17360	Identification and expression profiling of microRNAs in <i>Hymenolepis</i> . <i>International Journal for Parasitology</i> , 2019, 49, 211-223.	1.3	13
17361	Metabolic diversity within the globally abundant Marine Group II Euryarchaea offers insight into ecological patterns. <i>Nature Communications</i> , 2019, 10, 271.	5.8	66
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17363	An Extension of the Kimura Two-Parameter Model to the Natural Evolutionary Process. <i>Journal of Molecular Evolution</i> , 2019, 87, 60-67.	0.8	46
17364	The complete mitogenome of a South African cryptic species of tadpole shrimp within the <i>Triops granarius</i> (Lucas, 1864) species group. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 455-456.	0.2	3
17365	Syndromic survey and molecular analysis of influenza viruses at the human–swine interface in two West African cosmopolitan cities suggest the possibility of bidirectional interspecies transmission. <i>Zoonoses and Public Health</i> , 2019, 66, 232-247.	0.9	7
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17367	Comparative metagenomic analyses of a high-altitude Himalayan geothermal spring revealed temperature-constrained habitat-specific microbial community and metabolic dynamics. <i>Archives of Microbiology</i> , 2019, 201, 377-388.	1.0	12
17368	Bayesian phylogenetic analysis of the influenza-A virus genomes isolated in Tunisia, and determination of potential recombination events. <i>Molecular Phylogenetics and Evolution</i> , 2019, 134, 253-268.	1.2	6
17369	Hydrogen-based metabolism as an ancestral trait in lineages sibling to the Cyanobacteria. <i>Nature Communications</i> , 2019, 10, 463.	5.8	87
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17372	Genomic Signals of Adaptation towards Mutualism and Sociality in Two Ambrosia Beetle Complexes. <i>Life</i> , 2019, 9, 2.	1.1	5
17373	A <i>Piscibacillus</i> sp. Isolated from A Soda Lake Exhibits Anticancer Activity Against Breast Cancer MDA-MB-231 Cells. <i>Microorganisms</i> , 2019, 7, 34.	1.6	19
17374	Fungal Endophyte Communities of Three Agricultural Important Grass Species Differ in Their Response Towards Management Regimes. <i>Microorganisms</i> , 2019, 7, 37.	1.6	14
17375	Heterologous expression and characterization of a new galactose-binding lectin from <i>Bauhinia forficata</i> with antiproliferative activity. <i>International Journal of Biological Macromolecules</i> , 2019, 128, 877-884.	3.6	10
17376	Evolution of salivary glue genes in <i>Drosophila</i> species. <i>BMC Evolutionary Biology</i> , 2019, 19, 36.	3.2	14
17377	Genome-wide identification and expression analysis of expansin gene family in common wheat ( <i>Triticum aestivum</i> L.). <i>BMC Genomics</i> , 2019, 20, 101.	1.2	67
17378	Assessing phylogenetic information to reveal uncertainty in historical data: An example using Goodeinae (Teleostei: Cyprinodontiformes: Goodeidae). <i>Molecular Phylogenetics and Evolution</i> , 2019, 134, 282-290.	1.2	6
17379	The flagellin of candidate live biotherapeutic <i>Enterococcus gallinarum</i> MRx0518 is a potent immunostimulant. <i>Scientific Reports</i> , 2019, 9, 801.	1.6	34
17380	Phylogeography of HIV-1 suggests that Ugandan fishing communities are a sink for, not a source of, virus from general populations. <i>Scientific Reports</i> , 2019, 9, 1051.	1.6	43
17381	Phylogenetic and morphological analyses of the mycoparasitic genus <i>Piptocephalis</i> . <i>Mycologia</i> , 2019, 111, 54-68.	0.8	9
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17383	Methanotrophy, Methylophony, the Human Body, and Disease. , 2019, , 1-20.		1
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17387	The landscape of transposable elements and satellite DNAs in the genome of a dioecious plant spinach ( <i>Spinacia oleracea</i> L.). <i>Mobile DNA</i> , 2019, 10, 3.	1.3	37
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17491	Genetic variation and relationships among Afrotropical species of <i>Myotis</i> (Chiroptera:) <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 30</i>	0.6	16
17492	<i>Bacillus thuringiensis</i> Cry1Da_7 and Cry1B.868 Protein Interactions with Novel Receptors Allow Control of Resistant Fall Armyworms, <i>Spodoptera frugiperda</i> (J.E. Smith). <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	33
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17515	First Report of Integrative Conjugative Elements in <i>Riemerella anatipestifer</i> Isolates From Ducks in China. <i>Frontiers in Veterinary Science</i> , 2019, 6, 128.	0.9	10

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17520	The acidocalcisome inositol-1,4,5-trisphosphate receptor of <i>Trypanosoma brucei</i> is stimulated by luminal polyphosphate hydrolysis products. <i>Journal of Biological Chemistry</i> , 2019, 294, 10628-10637.	1.6	15
17521	Revision of freshwater shrimps belonging to <i>Caridina weberi</i> complex (Crustacea: Decapoda: Tj ETQq1 1 0.784314 rgBT /Overl... 815-847.	0.2	1
17522	Chromosomal and Genomic Dynamics of Satellite DNAs in Characidae (Characiformes, Teleostei) Species. <i>Zebrafish</i> , 2019, 16, 408-414.	0.5	2
17523	Ancient complement and lineage-specific evolution of the Sec7 ARF GEF proteins in eukaryotes. <i>Molecular Biology of the Cell</i> , 2019, 30, 1846-1863.	0.9	21
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17526	MHCSeqNet: a deep neural network model for universal MHC binding prediction. <i>BMC Bioinformatics</i> , 2019, 20, 270.	1.2	56
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17529	Rapid divergence, molecular evolution, and morphological diversification of coastal host-parasite systems from southern Brazil. <i>Parasitology</i> , 2019, 146, 1313-1332.	0.7	3
17530	Transcript expression profiling in two contrasting cultivars and molecular cloning of a SKP-1 like gene, a component of SCF-ubiquitin proteasome system from mungbean <i>Vigna radiata</i> L.. <i>Scientific Reports</i> , 2019, 9, 8103.	1.6	8
17531	Exploiting orthology and de novo transcriptome assembly to refine target sequence information. <i>BMC Medical Genomics</i> , 2019, 12, 69.	0.7	2
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17571	Characterization of <i>Colletotrichum</i> Species Causing Anthracnose of Pomegranate in the Southeastern United States. <i>Plant Disease</i> , 2019, 103, 2771-2780.	0.7	20
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17589	A novel metabarcoding approach to investigate <i>Fusarium</i> species composition in soil and plant samples. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	25
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17603	Mediterranean grassland soil Câ€“N compound turnover is dependent on rainfall and depth, and is mediated by genomically divergent microorganisms. <i>Nature Microbiology</i> , 2019, 4, 1356-1367.	5.9	170
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17640	The Microbiome of Temporal Arteries. <i>Pathogens and Immunity</i> , 2019, 4, 21.	1.4	19
17641	The first complete mitochondrial genomes of snow sheep ( <i>Ovis nivicola</i> ) and thinhorn sheep ( <i>Ovis dalli</i> ) and their phylogenetic implications for the genus <i>Ovis</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1332-1333.	0.2	5

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17785	Dicyemida and Orthonectida: Two Stories of Body Plan Simplification. <i>Frontiers in Genetics</i> , 2019, 10, 443.	1.1	37

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17793	The SMC5/6 Complex Subunit NSE4A Is Involved in DNA Damage Repair and Seed Development. <i>Plant Cell</i> , 2019, 31, 1579-1597.	3.1	27
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17796	Divergent Axin and GSK-3 paralogs in the beta-catenin destruction complexes of tapeworms. <i>Development Genes and Evolution</i> , 2019, 229, 89-102.	0.4	9
17797	Genome characterization of three <i>Alstroemeria</i> necrotic streak orthotospovirus (ANSV) isolates naturally infecting bell pepper ( <i>Capsicum annuum</i> ) in Antioquia (Colombia). <i>Tropical Plant Pathology</i> , 2019, 44, 326-334.	0.8	2
17798	Exploring safety of food truck products in a developed country. <i>International Journal of Hospitality Management</i> , 2019, 81, 150-158.	5.3	17
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17800	A brainstorm on the systematics of <i>Turnera</i> (Turneraceae, Malpighiales) caused by insights from molecular phylogenetics and morphological evolution. <i>Molecular Phylogenetics and Evolution</i> , 2019, 137, 44-63.	1.2	11
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17802	Bacterial Metabolism of C1 Sulfur Compounds. , 2019, , 421-463.		2
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17805	Bacterial communities of <i>Aphis gossypii</i> and <i>Myzus persicae</i> (Hemiptera: Aphididae) from pepper crops ( <i>Capsicum</i> sp.). <i>Scientific Reports</i> , 2019, 9, 5766.	1.6	22
17806	Topology Dictates Evolution of Regulatory Cysteines in a Family of Viral Oncoproteins. <i>Molecular Biology and Evolution</i> , 2019, 36, 1521-1532.	3.5	6
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17810	Classification and monomer-by-monomer annotation dataset of suprachromosomal family 1 alpha satellite higher-order repeats in hg38 human genome assembly. <i>Data in Brief</i> , 2019, 24, 103708.	0.5	27
17811	Transcriptome analyses of <i>Paris polyphylla</i> var. <i>chinensis</i> , <i>Ypsilandra thibetica</i> , and <i>Polygonatum kingianum</i> characterize their steroidal saponin biosynthesis pathway. <i>FÄ–toterapÄ–Äç</i> , 2019, 135, 52-63.	1.1	20
17812	Genome Evolution of the Obligate Endosymbiont <i>Buchnera aphidicola</i> . <i>Molecular Biology and Evolution</i> , 2019, 36, 1481-1489.	3.5	85
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17814	Subtype classification and functional annotation of L1Md retrotransposon promoters. <i>Mobile DNA</i> , 2019, 10, 14.	1.3	18
17815	Unprecedented bacterial community richness in soybean nodules vary with cultivar and water status. <i>Microbiome</i> , 2019, 7, 63.	4.9	51
17816	How integrative taxonomy can save a species from extinction: The supposedly extinct mouse opossum <i>Cryptonanus ignitus</i> (Diaz, Flores and Barquez, 2000) is a synonym of the living <i>C. chacoensis</i> (Tate, 1908). <i>Systematic Zoology</i> , 2019, 68, 107-116.	0.8	10
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17818	Functional coupling in the evolution of suction feeding and gill ventilation of sculpins (Perciformes: <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5</i>	0.9	9
17819	Zinc Excess Induces a Hypoxia-Like Response by Inhibiting Cysteine Oxidases in Poplar Roots. <i>Plant Physiology</i> , 2019, 180, 1614-1628.	2.3	19
17820	The genome of cowpea ( <i>Vigna unguiculata</i> [L.] Walp.). <i>Plant Journal</i> , 2019, 98, 767-782.	2.8	264
17821	Dating Whole Genome Duplication in <i>Ceratopteris thalictroides</i> and Potential Adaptive Values of Retained Gene Duplicates. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1926.	1.8	11

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17823	Population genetic structure of native Iranian population of <i>Apis mellifera meda</i> based on intergenic region and COX2 gene of mtDNA. <i>Insectes Sociaux</i> , 2019, 66, 413-424.	0.7	5
17824	New insights into phospholipases in oat ( <i>Avena sativa</i> ) from bioinformatic analysis. <i>International Journal of Biological Macromolecules</i> , 2019, 133, 804-810.	3.6	0
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17826	Phylogeography of the Recent Expansion of <i>Helicoverpa armigera</i> (Lepidoptera: Noctuidae) in South America and the Caribbean Basin. <i>Annals of the Entomological Society of America</i> , 2019, 112, 388-401.	1.3	23
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17833	Sexual Dichromatism Drives Diversification within a Major Radiation of African Amphibians. <i>Systematic Biology</i> , 2019, 68, 859-875.	2.7	41
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17835	Complete genome sequence of bile-isolated <i>Enterococcus avium</i> strain 352. <i>Gut Pathogens</i> , 2019, 11, 16.	1.6	12
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17837	Genome-informed <i>Bradyrhizobium</i> taxonomy: where to from here?. <i>Systematic and Applied Microbiology</i> , 2019, 42, 427-439.	1.2	62
17838	Human Immunodeficiency Virus Type 1 Phylodynamics to Detect and Characterize Active Transmission Clusters in North Carolina. <i>Journal of Infectious Diseases</i> , 2020, 221, 1321-1330.	1.9	19
17839	Agricultural Origins of a Highly Persistent Lineage of Vancomycin-Resistant <i>Enterococcus faecalis</i> in New Zealand. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	11

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17841	Tandem-genotypes: robust detection of tandem repeat expansions from long DNA reads. <i>Genome Biology</i> , 2019, 20, 58.	3.8	103
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17843	Between Spines and Molecules: A Total Evidence Phylogeny of the Brazilian Endemic Genus <i>Encholirium</i> (Pitcairnioideae, Bromeliaceae). <i>Systematic Botany</i> , 2019, 44, 14-25.	0.2	5
17844	A New Prevalent Densovirus Discovered in Acari. Insight from Metagenomics in Viral Communities Associated with Two-Spotted Mite ( <i>Tetranychus urticae</i> ) Populations. <i>Viruses</i> , 2019, 11, 233.	1.5	19
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17846	Genomic analysis of ant domatia-associated melanized fungi (Chaetothyriales, Ascomycota). <i>Mycological Progress</i> , 2019, 18, 541-552.	0.5	17
17847	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
17848	Inadvertent Paralog Inclusion Drives Artifactual Topologies and Timetree Estimates in Phylogenomics. <i>Molecular Biology and Evolution</i> , 2019, 36, 1344-1356.	3.5	56
17849	Chicken Organic Anion-Transporting Polypeptide 1A2, a Novel Avian Hepatitis E Virus (HEV) ORF2-Interacting Protein, Is Involved in Avian HEV Infection. <i>Journal of Virology</i> , 2019, 93, .	1.5	5
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17852	Four new monorchiids from the golden trevally, <i>Gnathanodon speciosus</i> (Forssk.) (Perciformes: Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	0.5	13
17853	<i>Sarcocystis</i> species identification in the moose ( <i>Alces alces</i> ) from the Baltic States. <i>Parasitology Research</i> , 2019, 118, 1601-1608.	0.6	19
17854	<i>Masenia nkomatiensis</i> n. sp. (Digenea: Cephalogonimidae) from <i>Clarias gariepinus</i> (Burchell) (Clariidae) in Incomati Basin, Mozambique. <i>Systematic Parasitology</i> , 2019, 96, 311-326.	0.5	8
17855	Complete genome of DENV2 isolated from mosquitoes in Mexico. <i>Infection, Genetics and Evolution</i> , 2019, 71, 98-107.	1.0	1
17856	Genomic analysis of methicillin-resistant <i>Staphylococcus aureus</i> isolated from poultry and occupational farm workers in Umgungundlovu District, South Africa. <i>Science of the Total Environment</i> , 2019, 670, 704-716.	3.9	33
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17859	Lysosomal targeting of the ABC transporter TAPL is determined by membrane-localized charged residues. <i>Journal of Biological Chemistry</i> , 2019, 294, 7308-7323.	1.6	15
17860	Emergence of a Thrombospondin Superfamily at the Origin of Metazoans. <i>Molecular Biology and Evolution</i> , 2019, 36, 1220-1238.	3.5	5
17861	Characteristics Associated With Human Immunodeficiency Virus Transmission Networks Involving Adolescent Girls and Young Women in Human Immunodeficiency Virus Prevention Trials Network 068 Study. <i>Sexually Transmitted Diseases</i> , 2019, 46, e46-e49.	0.8	1
17862	PRX9 and PRX40 Are Extensin Peroxidases Essential for Maintaining Tapetum and Microspore Cell Wall Integrity during Arabidopsis Anther Development. <i>Plant Cell</i> , 2019, 31, 848-861.	3.1	56
17863	Phylogenetic relationships of Pakistan <i>Gelidium</i> (Gelidiales, Rhodophyta) species with recognition of <i>Gelidium pakistanicum</i> stat. nov. <i>Botanica Marina</i> , 2019, 62, 141-147.	0.6	5
17864	Discrete Wavelet Packet Transform Based Discriminant Analysis for Whole Genome Sequences. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2019, 18, .	0.2	2
17865	Human-Origin Influenza A(H3N2) Reassortant Viruses in Swine, Southeast Mexico. <i>Emerging Infectious Diseases</i> , 2019, 25, 691-700.	2.0	18
17866	Strong selection of the TLR2 coding region among the Lagomorpha suggests an evolutionary history that differs from other mammals. <i>Immunogenetics</i> , 2019, 71, 437-443.	1.2	9
17867	Development of a highly specific co-dominant marker for genotyping the Ph-3 (tomato late blight) Tj ETQq1 1 0.784314 rgBT <sub>4</sub> /Overlook	1.0	
17868	A novel Australian flying-fox retrovirus shares an evolutionary ancestor with Koala, Gibbon and <i>Melomys gamma</i> -retroviruses. <i>Virus Genes</i> , 2019, 55, 421-424.	0.7	10
17869	A novel species and a new combination of <i>Daldinia</i> from Ban Hua Thung community forest in the northern part of Thailand. <i>Mycological Progress</i> , 2019, 18, 553-564.	0.5	8
17870	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
17871	Taxonomy and toxicity of <i>Prorocentrum</i> from Perhentian Islands (Malaysia), with a description of a non-toxic species <i>Prorocentrum malayense</i> sp. nov. (Dinophyceae). <i>Harmful Algae</i> , 2019, 83, 95-108.	2.2	22
17872	Detection and characterisation of canine astrovirus, canine parvovirus and canine papillomavirus in puppies using next generation sequencing. <i>Scientific Reports</i> , 2019, 9, 4602.	1.6	15
17873	Conservation of ethanol fermentation and its regulation in land plants. <i>Journal of Experimental Botany</i> , 2019, 70, 1815-1827.	2.4	51
17874	Analysis of a flagellar filament cap mutant reveals that HtrA serine protease degrades unfolded flagellin protein in the periplasm of <i>Borrelia burgdorferi</i> . <i>Molecular Microbiology</i> , 2019, 111, 1652-1670.	1.2	18
17875	A New Species of Dwarf Channa (Teleostei: Channidae) from Meghalaya, Northeast India. <i>Copeia</i> , 2019, 107, 61.	1.4	8

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17877	Latitudinal patterns in phylogenetic and functional diversity of Diptera in temperate bogs. <i>Canadian Entomologist</i> , 2019, 151, 187-208.	0.4	1
17878	“Genome skimming” with the MinION hand-held sequencer identifies CITES-listed shark species in India’s exports market. <i>Scientific Reports</i> , 2019, 9, 4476.	1.6	45
17879	Genome of <i>Crucihimalaya himalaica</i> , a close relative of <i>Arabidopsis</i> , shows ecological adaptation to high altitude. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 7137-7146.	3.3	108
17880	Alterations of the Mice Gut Microbiome via <i>Schistosoma japonicum</i> Ova-Induced Granuloma. <i>Frontiers in Microbiology</i> , 2019, 10, 352.	1.5	63
17881	Structures in multiple conformations reveal distinct transition metal and proton pathways in an Nrap transporter. <i>ELife</i> , 2019, 8, .	2.8	50
17882	Sensitivity to the two peptide bacteriocin plantaricin EF is dependent on CorC, a membrane-bound, magnesium/cobalt efflux protein. <i>MicrobiologyOpen</i> , 2019, 8, e827.	1.2	17
17883	Mini-review an insect-specific system for terrestrialization: Laccase-mediated cuticle formation. <i>Insect Biochemistry and Molecular Biology</i> , 2019, 108, 61-70.	1.2	41
17884	First successful isolation of <i>Entoloma clypeatum</i> species complex from basidiospores. <i>Mycoscience</i> , 2019, 60, 221-227.	0.3	3
17885	OsNAC-like transcription factor involved in regulating seed-storage protein content at different stages of grain filling in rice under aerobic conditions. <i>Journal of Genetics</i> , 2019, 98, 1.	0.4	9
17886	Establishment of monokaryotic and dikaryotic isolates of Hedgehog mushrooms ( <i>Hydnum repandum</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tt	0.8	8
17887	Molecular phylogeny of the ghost knifefishes (Gymnotiformes: Apterontidae). <i>Molecular Phylogenetics and Evolution</i> , 2019, 135, 297-307.	1.2	14
17888	Diversified secondary metabolite biosynthesis gene repertoire revealed in symbiotic dinoflagellates. <i>Scientific Reports</i> , 2019, 9, 1204.	1.6	21
17889	Identification and Characterization of a Dominant Sulfolane-Degrading <i>Rhodofera</i> sp. via Stable Isotope Probing Combined with Metagenomics. <i>Scientific Reports</i> , 2019, 9, 3121.	1.6	19
17890	Plant-Pathogenic <i>Agrobacterium tumefaciens</i> Strains Have Diverse Type VI Effector-Immunity Pairs and Vary in In-Planta Competitiveness. <i>Molecular Plant-Microbe Interactions</i> , 2019, 32, 961-971.	1.4	36
17891	Systematic Identification of Pathogenic <i>Streptomyces</i> sp. AMCC400023 That Causes Common Scab and Genomic Analysis of Its Pathogenicity Island. <i>Phytopathology</i> , 2019, 109, 1115-1128.	1.1	11
17892	Functional Characterization of OXYL, A SghC1qDC LacNAc-specific Lectin from The Crinoid Feather Star <i>Anneissia Japonica</i> . <i>Marine Drugs</i> , 2019, 17, 136.	2.2	11
17893	A new species of deep-sea mussel (Bivalvia: Mytilidae: Gigantidas) from the South China Sea: Morphology, phylogenetic position, and gill-associated microbes. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2019, 146, 79-90.	0.6	58

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17895	Movement of juvenile tuna deduced from parasite data. <i>ICES Journal of Marine Science</i> , 2019, 76, 1678-1689.	1.2	12
17896	Virus Genomes from Deep Sea Sediments Expand the Ocean Megavirome and Support Independent Origins of Viral Gigantism. <i>MBio</i> , 2019, 10, .	1.8	85
17897	Evolution of an insect immune barrier through horizontal gene transfer mediated by a parasitic wasp. <i>PLoS Genetics</i> , 2019, 15, e1007998.	1.5	32
17898	Insights Into an Unexplored Component of the Mosquito Repeatome: Distribution and Variability of Viral Sequences Integrated Into the Genome of the Arboviral Vector <i>Aedes albopictus</i> . <i>Frontiers in Genetics</i> , 2019, 10, 93.	1.1	21
17899	Shotgun Metagenomics of a Water Kefir Fermentation Ecosystem Reveals a Novel <i>Oenococcus</i> Species. <i>Frontiers in Microbiology</i> , 2019, 10, 479.	1.5	80
17900	The transcriptome of the veiled chameleon ( <i>Chamaeleo calytratus</i> ): A resource for studying the evolution and development of vertebrates. <i>Developmental Dynamics</i> , 2019, 248, 702-708.	0.8	26
17901	Partial characterization of a divergent isolate of pokeweed mosaic virus from Mississippi. <i>Journal of Plant Pathology</i> , 2019, 101, 1127-1131.	0.6	0
17902	Microbial ecology dynamics of a partial nitrification bioreactor with Polar Arctic Circle activated sludge operating at low temperature. <i>Chemosphere</i> , 2019, 225, 73-82.	4.2	16
17903	Genomics-based diversity analysis of <i>Vanilla</i> species using a <i>Vanilla planifolia</i> draft genome and Genotyping-By-Sequencing. <i>Scientific Reports</i> , 2019, 9, 3416.	1.6	36
17904	Duplication and selection in $\beta$ -ketoacyl-ACP synthase gene lineages in the sexually deceptive <i>Chiloglottis</i> (Orchidaceae). <i>Annals of Botany</i> , 2019, 123, 1053-1066.	1.4	7
17905	Glass confers rhabdomeric photoreceptor identity in <i>Drosophila</i> , but not across all metazoans. <i>EvoDevo</i> , 2019, 10, 4.	1.3	1
17906	<i>Mycena</i> section <i>Sacchariferae</i> : three new species with basal discs from China. <i>Mycological Progress</i> , 2019, 18, 483-493.	0.5	8
17907	Weeds as Potential Inoculum Reservoir for <i>Colletotrichum nymphaeae</i> Causing Strawberry Anthracnose in Iran and Rep-PCR Fingerprinting as Useful Marker to Differentiate <i>C. acutatum</i> Complex on Strawberry. <i>Frontiers in Microbiology</i> , 2019, 10, 129.	1.5	17
17908	A virus-induced gene silencing system for functional genetics in a betalainic species, <i>Amaranthus tricolor</i> (Amaranthaceae). <i>Applications in Plant Sciences</i> , 2019, 7, e01221.	0.8	15
17909	Pck-ing up steam: Widening the salmonid gluconeogenic gene duplication trail. <i>Gene</i> , 2019, 698, 129-140.	1.0	12
17910	Polyurethanases: Three-dimensional structures and molecular dynamics simulations of enzymes that degrade polyurethane. <i>Journal of Molecular Graphics and Modelling</i> , 2019, 89, 82-95.	1.3	23
17911	The influence of Pleistocene glaciations on Chacoan fauna: genetic structure and historical demography of an endemic frog of the South American Gran Chaco. <i>Biological Journal of the Linnean Society</i> , 2019, 126, 404-416.	0.7	11



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17912	Mycobiome Profiles in Breast Milk from Healthy Women Depend on Mode of Delivery, Geographic Location, and Interaction with Bacteria. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	76
17913	Identification of the OXA-48 Carbapenemase Family by Use of Tryptic Peptides and Liquid Chromatography-Tandem Mass Spectrometry. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	1.8	15
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18049	Spatial and temporal variations in species diversity of fish assemblages near a sewage treatment plant in northern Taiwan. <i>Fisheries Science</i> , 2019, 85, 581-590.	0.7	3
18050	Genetic diversity of <i>Streptococcus equi</i> subsp. <i>zoepidemicus</i> isolated from horses. <i>Comparative Immunology, Microbiology and Infectious Diseases</i> , 2019, 65, 7-13.	0.7	8
18051	Molecular structure of sauropsid $\beta$ -keratins from tuatara ( <i>Sphenodon punctatus</i> ). <i>Journal of Structural Biology</i> , 2019, 207, 21-28.	1.3	13
18052	Insights into ecological role of a new deltaproteobacterial order <i>Candidatus</i> Acidulodesulfobacterales by metagenomics and metatranscriptomics. <i>ISME Journal</i> , 2019, 13, 2044-2057.	4.4	112
18053	The mitochondrial genome of a slit limpet <i>Pseudorimula</i> sp. (Vetigastropoda: Lepetodrilidae) from hydrothermal vent on the Southwest Indian Ridge. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1189-1190.	0.2	2
18054	Origin and evolution of papillomavirus (onco)genes and genomes. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20180303.	1.8	37
18055	Genome sequence of the corn leaf aphid ( <i>Rhopalosiphum maidis</i> Fitch). <i>GigaScience</i> , 2019, 8, .	3.3	60



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18056	Phylogeny of the genus <i>Aporcelinus</i> Andr�ssy, 2009 (Nematoda: Dorylaimida: Aporcelaimidae) with description of two new species from Costa Rica. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2019, 57, 240-257.	0.6	2
18057	New Insights into Long Terminal Repeat Retrotransposons in Mulberry Species. <i>Genes</i> , 2019, 10, 285.	1.0	11
18058	Molecular-based assessments of tribal and generic limits and relationships in Rubiaceae (Gentianales): Polyphyly of Pomazoteae and paraphyly of Ophiorrhizeae and <i>Ophiorrhiza</i> . <i>Taxon</i> , 2019, 68, 72-91.	0.4	12
18059	Phylogenetic Studies. <i>Methods in Molecular Biology</i> , 2019, 1971, 9-68.	0.4	4
18060	Colonization of Seeds by Soilborne Fungi: Linking Seed Dormancy-Defense Syndromes, Evolutionary Constraints, and Fungal Traits. , 2019, , 465-481.		0
18061	The reclassification of 37 strains from The Mosonmagyar�r Algal Culture Collection, Hungary, which were previously identified as <i>Anabaena</i> (Cyanobacteria, Nostocaceae). <i>South African Journal of Botany</i> , 2019, 123, 333-340.	1.2	0
18062	Taxonomic insights into the phylogeny of <i>Bacillus badius</i> and proposal for its reclassification to the genus <i>Pseudobacillus</i> as <i>Pseudobacillus badius</i> comb. nov. and reclassification of <i>Bacillus wudalianchiensis</i> Liu et al., 2017 as <i>Pseudobacillus wudalianchiensis</i> comb. nov.. <i>Systematic and Applied Microbiology</i> , 2019, 42, 360-372.	1.2	4
18063	The enzymes OSC1 and CYP716A263 produce a high variety of triterpenoids in the latex of <i>Taraxacum koksaghyz</i> . <i>Scientific Reports</i> , 2019, 9, 5942.	1.6	24
18064	Satellitome landscape analysis of <i>Megaleporinus macrocephalus</i> (Teleostei, Anostomidae) reveals intense accumulation of satellite sequences on the heteromorphic sex chromosome. <i>Scientific Reports</i> , 2019, 9, 5856.	1.6	40
18065	The First Transcriptome Assembly of Yenyuan Stream Salamander ( <i>Batrachuperus yenyuanensis</i> ) Provides Novel Insights into Its Molecular Evolution. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1529.	1.8	7
18066	Molecular and Structural Characterization of MHC Class II $\beta$ Genes Reveals High Diversity in the Cold-Adapted Icefish <i>Chionodraco hamatus</i> . <i>Scientific Reports</i> , 2019, 9, 5523.	1.6	7
18067	A molecular phylogeny of the gastropod family Haminoeidae sensu lato (Heterobranchia: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	0.5	4
18068	A New Tymovirus Isolated From <i>Solanum quitoense</i> : Characterization and Prevalence in Two Solanaceous Crops in Ecuador. <i>Plant Disease</i> , 2019, 103, 2246-2251.	0.7	3
18069	New genera and species from the Equatorial Pacific provide phylogenetic insights into deep-sea Polynoidae (Annelida). <i>Zoological Journal of the Linnean Society</i> , 2019, 185, 555-635.	1.0	32
18070	Resolving the relationships of clams and cockles: dense transcriptome sampling drastically improves the bivalve tree of life. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20182684.	1.2	59
18071	The Distribution of Tryptophan-Dependent Indole-3-Acetic Acid Synthesis Pathways in Bacteria Unraveled by Large-Scale Genomic Analysis. <i>Molecules</i> , 2019, 24, 1411.	1.7	76
18072	First description of two moderately halophilic and psychrotolerant <i>Mycoplasma</i> species isolated from cephalopods and proposal of <i>Mycoplasma marinum</i> sp. nov. and <i>Mycoplasma todarodis</i> sp. nov. <i>Systematic and Applied Microbiology</i> , 2019, 42, 457-467.	1.2	22
18073	ML-DSP: Machine Learning with Digital Signal Processing for ultrafast, accurate, and scalable genome classification at all taxonomic levels. <i>BMC Genomics</i> , 2019, 20, 267.	1.2	42

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18074	Evolution of a novel chimeric maltotriose transporter in <i>Saccharomyces eubayanus</i> from parent proteins unable to perform this function. <i>PLoS Genetics</i> , 2019, 15, e1007786.	1.5	35
18075	Phylogenomics clarifies biogeographic and evolutionary history, and conservation status of West Indian tremblers and thrashers (Aves: Mimidae). <i>Molecular Phylogenetics and Evolution</i> , 2019, 136, 196-205.	1.2	5
18076	Combining Protein and Metabolic Engineering Strategies for High-Level Production of <i>O</i> -Acetylhomoserine in <i>Escherichia coli</i> . <i>ACS Synthetic Biology</i> , 2019, 8, 1153-1167.	1.9	30
18077	Wetland Sediments Host Diverse Microbial Taxa Capable of Cycling Alcohols. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	10
18078	Assessing the Pathogenicity of Two Bacteria Isolated from the Entomopathogenic Nematode <i>Heterorhabditis indica</i> against <i>Galleria mellonella</i> and Some Pest Insects. <i>Insects</i> , 2019, 10, 83.	1.0	5
18079	Analysis of hepatitis B virus-mixed genotype infection by ultra deep pyrosequencing in Sudanese patients, 2015–2016. <i>Infection</i> , 2019, 47, 793-803.	2.3	3
18080	Analyses of 202 plastid genomes elucidate the phylogeny of <i>Solanum</i> section <i>Petota</i> . <i>Scientific Reports</i> , 2019, 9, 4454.	1.6	34
18081	Phylogenetic relationships among tibet <i>Rubus</i> (Rosaceae) species inferred from multiple chloroplast and nuclear DNA sequences. <i>AIP Conference Proceedings</i> , 2019, , .	0.3	2
18082	The mitochondrial genome of common whelk <i>Buccinum undatum</i> (Neogastropoda: Buccinidae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 457-459.	0.2	1
18083	Molecular phylogeny of Paraonidae (Annelida). <i>Molecular Phylogenetics and Evolution</i> , 2019, 136, 1-13.	1.2	11
18084	The genome of the giant <i>Nomura</i> jellyfish sheds light on the early evolution of active predation. <i>BMC Biology</i> , 2019, 17, 28.	1.7	38
18085	Evolution of Mutator transposable elements across eukaryotic diversity. <i>Mobile DNA</i> , 2019, 10, 12.	1.3	32
18086	Evaluation of <i>invA</i> Diversity among <i>Salmonella</i> Species Suggests Why Some Commercially Available Rapid Detection Kits May Fail To Detect Multiple <i>Salmonella</i> Subspecies and Species. <i>Journal of Food Protection</i> , 2019, 82, 710-717.	0.8	13
18087	The speciation history of northern- and southern-sourced <i>Eranthis</i> ( <i>Ranunculaceae</i> ) species on the Korean peninsula and surrounding areas. <i>Ecology and Evolution</i> , 2019, 9, 2907-2919.	0.8	8
18088	The genome of the arapaima ( <i>Arapaima gigas</i> ) provides insights into gigantism, fast growth and chromosomal sex determination system. <i>Scientific Reports</i> , 2019, 9, 5293.	1.6	25
18089	Morphology, phylogeny, and sexual stage of <i>Fusarium caatingaense</i> and <i>Fusarium pernambucanum</i> , new species of the <i>Fusarium incarnatum-equiseti</i> species complex associated with insects in Brazil. <i>Mycologia</i> , 2019, 111, 244-259.	0.8	36
18090	Molecular characterization of laccase genes from the basidiomycete <i>Trametes hirsuta</i> Bm-2 and analysis of the 5' untranslated region (5'UTR). <i>3 Biotech</i> , 2019, 9, 160.	1.1	3
18091	High-throughput methods in aptamer discovery and analysis. <i>Methods in Enzymology</i> , 2019, 621, 329-346.	0.4	8

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18093	Comparative genomics and transcriptomics analysis reveals evolution patterns of selection in the <i>Salix</i> phylogeny. <i>BMC Genomics</i> , 2019, 20, 253.	1.2	9
18094	Variation among human, veterinary and environmental <i>Mycobacterium chelonae-abscessus</i> complex isolates observed using core genome phylogenomic analysis, targeted gene comparison, and anti-microbial susceptibility patterns. <i>PLoS ONE</i> , 2019, 14, e0214274.	1.1	12
18095	Predation on stink bugs (Hemiptera: Pentatomidae) in cotton and soybean agroecosystems. <i>PLoS ONE</i> , 2019, 14, e0214325.	1.1	9
18096	<i>Structural Bioinformatics.</i> , 2019, , 169-199.		14
18097	Comparative study on pattern recognition receptors in non-teleost ray-finned fishes and their evolutionary significance in primitive vertebrates. <i>Science China Life Sciences</i> , 2019, 62, 566-578.	2.3	12
18098	Effective removal of nitrate by denitrification re-enforced with a two-stage anoxic/oxic (A/O) process from a digested piggery wastewater with a low C/N ratio. <i>Journal of Environmental Management</i> , 2019, 240, 19-26.	3.8	31
18099	Diverse single-stranded DNA viruses associated with honey bees ( <i>Apis mellifera</i> ). <i>Infection, Genetics and Evolution</i> , 2019, 71, 179-188.	1.0	31
18100	Redefining the medicago sativa alphapartitiviruses genome sequences. <i>Virus Research</i> , 2019, 265, 156-161.	1.1	12
18101	Dynamic evolutionary history and gene content of sex chromosomes across diverse songbirds. <i>Nature Ecology and Evolution</i> , 2019, 3, 834-844.	3.4	68
18102	Casting light on Asgardarchaeota metabolism in a sunlit microoxic niche. <i>Nature Microbiology</i> , 2019, 4, 1129-1137.	5.9	96
18103	Localized production of defence chemicals by intracellular symbionts of <i>Haliclona</i> sponges. <i>Nature Microbiology</i> , 2019, 4, 1149-1159.	5.9	69
18104	Meta-analysis of fecal metagenomes reveals global microbial signatures that are specific for colorectal cancer. <i>Nature Medicine</i> , 2019, 25, 679-689.	15.2	734
18105	Low pathogenic avian influenza (H7N6) virus causing an outbreak in commercial Turkey farms in Chile. <i>Emerging Microbes and Infections</i> , 2019, 8, 479-485.	3.0	12
18106	Character Evolution and Recircumscription of the Northern Andean <i>Begonia</i> Section <i>Casparya</i> (Begoniaceae). <i>Systematic Botany</i> , 2019, 44, 52-65.	0.2	4
18107	New Insights Into the Polar Lipid Composition of Extremely Halo(alkali)philic Euryarchaea From Hypersaline Lakes. <i>Frontiers in Microbiology</i> , 2019, 10, 377.	1.5	48
18108	Cloning and characterization of a novel aspartate/glutamate racemase from the acorn worm <i>Saccoglossus kowalevskii</i> . <i>Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology</i> , 2019, 232, 87-92.	0.7	4
18109	Systematic study of truffles in the genus <i>Ruhlandiella</i> , with the description of two new species from Patagonia. <i>Mycologia</i> , 2019, 111, 477-492.	0.8	11

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18110	Life in wood: preliminary phylogeny of deep-sea wood-boring bivalves (Xylophagaidae), with descriptions of three new genera and one new species. <i>Journal of Molluscan Studies</i> , 2019, 85, 232-243.	0.4	21
18111	Low coverage sequencing for repetitive DNA analysis in <i>Passiflora edulis</i> Sims: citogenomic characterization of transposable elements and satellite DNA. <i>BMC Genomics</i> , 2019, 20, 262.	1.2	17
18112	Introduction to Bioinformatics. , 2019, , 1-18.		0
18113	Genetic analysis of the endangered Hyacinth Macaw ( <i>Anodorhynchus hyacinthinus</i> ) based on mitochondrial markers: different conservation efforts are required for different populations. <i>Journal of Ornithology</i> , 2019, 160, 711-720.	0.5	4
18114	Secondary structure of the internal transcribed rDNA (ITS) regions of <i>Cosmopolites sordidus</i> (Germar) and <i>Odoiporus longicollis</i> (Olivier): a first report in family Curculionidae. <i>International Journal of Tropical Insect Science</i> , 2019, 39, 53-61.	0.4	0
18115	HIV-1 remission following CCR5 <sup>Δ32</sup> /Δ32 haematopoietic stem-cell transplantation. <i>Nature</i> , 2019, 568, 244-248.	13.7	447
18116	TMK1-mediated auxin signalling regulates differential growth of the apical hook. <i>Nature</i> , 2019, 568, 240-243.	13.7	156
18117	SSS-test: a novel test for detecting positive selection on RNA secondary structure. <i>BMC Bioinformatics</i> , 2019, 20, 151.	1.2	12
18118	Development of <i>Phytomonas lipae</i> sp. n. (Kinetoplastea: Trypanosomatidae) in the true bug <i>Coreus marginatus</i> (Heteroptera: Coreidae) and insights into the evolution of life cycles in the genus <i>Phytomonas</i> . <i>PLoS ONE</i> , 2019, 14, e0214484.	1.1	12
18119	Didymozoids in Muscle of Atlantic Chub Mackerel ( <i>Scomber colias</i> ). <i>Acta Parasitologica</i> , 2019, 64, 308-315.	0.4	1
18120	The Molecular and Structural Basis of O-methylation Reaction in Coumarin Biosynthesis in <i>Peucedanum praeruptorum</i> Dunn. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1533.	1.8	19
18121	Phylogeography of eagle rays of the genus <i>Aetobatus</i> : <i>Aetobatus narinari</i> is restricted to the continental western Atlantic Ocean. <i>Hydrobiologia</i> , 2019, 836, 169-183.	1.0	15
18122	Horizontal gene transfer allowed the emergence of broad host range entomopathogens. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 7982-7989.	3.3	61
18123	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
18124	Sexually Antagonistic Mitonuclear Coevolution in Duplicate Oxidative Phosphorylation Genes. <i>Integrative and Comparative Biology</i> , 2019, 59, 864-874.	0.9	9
18125	The unique photosynthetic apparatus of Pinaceae: analysis of photosynthetic complexes in <i>Picea abies</i> . <i>Journal of Experimental Botany</i> , 2019, 70, 3211-3225.	2.4	21
18126	<i>Rhodnius prolixus</i> : Identification of missing components of the IMD immune signaling pathway and functional characterization of its role in eliminating bacteria. <i>PLoS ONE</i> , 2019, 14, e0214794.	1.1	37
18127	<i>Populus trichocarpa</i> clade A PP2C protein phosphatases: their stress-induced expression patterns, interactions in core abscisic acid signaling, and potential for regulation of growth and development. <i>Plant Molecular Biology</i> , 2019, 100, 303-317.	2.0	17

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18129	Response of a kleptoplastidic foraminifer to heterotrophic starvation: photosynthesis and lipid droplet biogenesis. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	20
18130	Multilocus phylogeny and a new classification for African, Asian and Indian supple and writhing skinks (Scincidae: Lygosominae). <i>Zoological Journal of the Linnean Society</i> , 2019, 186, 1067-1096.	1.0	15
18131	Two forms of phosphomannomutase in gammaproteobacteria: The overlooked membrane-bound form of AlgC is required for twitching motility of <i>Lysobacter enzymogenes</i> . <i>Environmental Microbiology</i> , 2019, 21, 3969-3978.	1.8	2
18132	Genetic structure, phylogeography, and demography of <i>Anadara tuberculosa</i> (Bivalvia) from East Pacific as revealed by mtDNA: Implications to conservation. <i>Ecology and Evolution</i> , 2019, 9, 4392-4402.	0.8	9
18133	Hunting for novel disease resistance genes: observations and opportunities from the Rosaceae. <i>Acta Horticulturae</i> , 2019, , 125-134.	0.1	2
18134	Darkening of the Greenland Ice Sheet: Fungal Abundance and Diversity Are Associated With Algal Bloom. <i>Frontiers in Microbiology</i> , 2019, 10, 557.	1.5	58
18135	Deciphering the Role of a SLOG Superfamily Protein YpsA in Gram-Positive Bacteria. <i>Frontiers in Microbiology</i> , 2019, 10, 623.	1.5	15
18136	Genetic structure analyses of the tomato-infecting crinivirus Tomato chlorosis virus indicates low genetic variability in the p22 gene and evidence of segregation based on sampling location in Brazil. <i>Tropical Plant Pathology</i> , 2019, 44, 292-296.	0.8	3
18137	Phylogenetic inference for the study of within-host HIV-1 dynamics and persistence on antiretroviral therapy. <i>Lancet HIV</i> , 2019, 6, e325-e333.	2.1	7
18138	A species-level phylogeny of <i>Trachylepis</i> (Scincidae: Mabuyinae) provides insight into their reproductive mode evolution. <i>Molecular Phylogenetics and Evolution</i> , 2019, 136, 183-195.	1.2	16
18139	A single application of fertiliser or manure to a cropping field has limited long-term effects on soil microbial communities. <i>Soil Research</i> , 2019, 57, 228.	0.6	7
18140	Conserved peptide vaccine candidates containing multiple Ebola nucleoprotein epitopes display interactions with diverse HLA molecules. <i>Medical Microbiology and Immunology</i> , 2019, 208, 227-238.	2.6	16
18141	A centromere satellite concomitant with extensive karyotypic diversity across the <i>Peromyscus</i> genus defies predictions of molecular drive. <i>Chromosome Research</i> , 2019, 27, 237-252.	1.0	30
18142	Phylogenomic reappraisal of the Neotropical catfish family Loricariidae (Teleostei: Siluriformes) using ultraconserved elements. <i>Molecular Phylogenetics and Evolution</i> , 2019, 135, 148-165.	1.2	71
18143	Four new epiphytic species in the <i>Micarea prasina</i> group from Europe. <i>Lichenologist</i> , 2019, 51, 7-25.	0.5	26
18144	Characterization of the mitochondrial genome of an ancient amphipod <i>Halice</i> sp. MT-2017 (Pardaliscidae) from 10,908 m in the Mariana Trench. <i>Scientific Reports</i> , 2019, 9, 2610.	1.6	16
18145	Structure of SPH (self-incompatibility protein homologue) proteins: a widespread family of small, highly stable, secreted proteins. <i>Biochemical Journal</i> , 2019, 476, 809-826.	1.7	8

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18146	Pathway and Gene Discovery from Natural Hosts and Organisms. <i>Methods in Molecular Biology</i> , 2019, 1927, 1-9.	0.4	1
18147	V1 and V2 Domains of HIV Envelope Contribute to CCR5 Antagonist Resistance. <i>Journal of Virology</i> , 2019, 93, .	1.5	5
18148	Identification and characterization of the first pectin methyltransferase gene discovered in the root lesion nematode <i>Pratylenchus penetrans</i> . <i>PLoS ONE</i> , 2019, 14, e0212540.	1.1	14
18149	Histone H1, the forgotten histone. <i>Epigenomics</i> , 2019, 11, 363-366.	1.0	29
18150	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
18151	Subterranean Clover Stunt Virus Revisited: Detection of Two Missing Genome Components. <i>Viruses</i> , 2019, 11, 138.	1.5	3
18152	Genome organisation and comparative genomics of four novel <i>Wolbachia</i> genome assemblies from Indian <i>Drosophila</i> host. <i>Functional and Integrative Genomics</i> , 2019, 19, 617-632.	1.4	3
18153	Evolution of Base Excision Repair in <i>Entamoeba histolytica</i> is shaped by gene loss, gene duplication, and lateral gene transfer. <i>DNA Repair</i> , 2019, 76, 76-88.	1.3	10
18154	Quantifying population-specific growth in benthic bacterial communities under low oxygen using H218O. <i>ISME Journal</i> , 2019, 13, 1546-1559.	4.4	53
18155	Ideating iDNA: Lessons and limitations from leeches in legacy collections. <i>PLoS ONE</i> , 2019, 14, e0212226.	1.1	14
18156	Origin and evolution of the octoploid strawberry genome. <i>Nature Genetics</i> , 2019, 51, 541-547.	9.4	469
18157	â€C <i>Candidatus Viridilinea mediisalina</i> â€™, a novel phototrophic Chloroflexi bacterium from a Siberian soda lake. <i>FEMS Microbiology Letters</i> , 2019, 366, .	0.7	17
18158	Identification of an active miniature invertedâ€Crepeat transposable element <i><sc>mj</sc>ing</i> in rice. <i>Plant Journal</i> , 2019, 98, 639-653.	2.8	11
18159	Gene Editing of Mouse Embryonic and Epiblast Stem Cells. <i>Methods in Molecular Biology</i> , 2019, 1940, 77-95.	0.4	6
18160	Evolution and a revised nomenclature of P4 ATPases, a eukaryotic family of lipid flippases. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2019, 1861, 1135-1151.	1.4	46
18161	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
18162	<i>Prototheca paracutis</i> sp. nov., a novel oleaginous achlorophyllous microalga isolated from a mangrove forest. <i>Mycoscience</i> , 2019, 60, 165-169.	0.3	11
18163	Phylogeny and distribution of <i>Bradyrhizobium</i> symbionts nodulating cowpea ( <i>Vigna unguiculata</i> L.) Tj ETQq1 1 0.784314 rgBT /Overl and Applied Microbiology, 2019, 42, 403-414.	1.2	22

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18164	Genomic characteristics and pathogenicity of natural recombinant porcine reproductive and respiratory syndrome virus 2 harboring genes of a Korean field strain and VR-2332-like strain. <i>Virology</i> , 2019, 530, 89-98.	1.1	12
18165	Molecular characteristics of a novel recombinant of porcine epidemic diarrhea virus. <i>Archives of Virology</i> , 2019, 164, 1199-1204.	0.9	8
18166	Recurrent speciation of a tomato yellow leaf curl geminivirus in Portugal by recombination. <i>Scientific Reports</i> , 2019, 9, 1332.	1.6	25
18167	Antibodies Against Egg- and Cell-Grown Influenza A(H3N2) Viruses in Adults Hospitalized During the 2017–2018 Influenza Season. <i>Journal of Infectious Diseases</i> , 2019, 219, 1904-1912.	1.9	37
18168	An Insect Counteradaptation against Host Plant Defenses Evolved through Concerted Neofunctionalization. <i>Molecular Biology and Evolution</i> , 2019, 36, 930-941.	3.5	41
18169	“Dorsal”-“Ventral”-Genes Are Part of an Ancient Axial Patterning System: Evidence from <i>Trichoplax adhaerens</i> (Placozoa). <i>Molecular Biology and Evolution</i> , 2019, 36, 966-973.	3.5	26
18170	Evolutionary Relationships Between the Laccase Genes of Polyporales: Orthology-Based Classification of Laccase Isozymes and Functional Insight From <i>Trametes hirsuta</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 152.	1.5	25
18171	Transcriptomics Identifies Modules of Differentially Expressed Genes and Novel Cyclotides in <i>Viola pubescens</i> . <i>Frontiers in Plant Science</i> , 2019, 10, 156.	1.7	12
18172	Genome-wide identification of the Na <sup>+</sup> /H <sup>+</sup> exchanger gene family in <i>Lateolabrax maculatus</i> and its involvement in salinity regulation. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2019, 29, 286-298.	0.4	10
18173	Tracking the origin of two genetic components associated with transposable element bursts in domesticated rice. <i>Nature Communications</i> , 2019, 10, 641.	5.8	34
18174	24-nt reproductive phasiRNAs are broadly present in angiosperms. <i>Nature Communications</i> , 2019, 10, 627.	5.8	106
18175	Mercury methylating microbial communities of boreal forest soils. <i>Scientific Reports</i> , 2019, 9, 518.	1.6	53
18176	<i>Lactobacillus rhamnosus</i> GG reverses mortality of neonatal mice against <i>Salmonella</i> challenge. <i>Toxicology Research</i> , 2019, 8, 361-372.	0.9	15
18177	Phylogenetic analysis of haemagglutinin gene deciphering a new genetically distinct lineage of canine distemper virus circulating among domestic dogs in India. <i>Transboundary and Emerging Diseases</i> , 2019, 66, 1252-1267.	1.3	36
18178	Genomic comparison of facultatively anaerobic and obligatory aerobic <i>Caldibacillus debilis</i> strains GB1 and Tf helps explain physiological differences. <i>Canadian Journal of Microbiology</i> , 2019, 65, 421-428.	0.8	0
18179	Genomic content of a novel yeast species <i>Hanseniaspora gamundiae</i> sp. nov. from fungal stromata (Cyttaria) associated with a unique fermented beverage in Andean Patagonia, Argentina. <i>PLoS ONE</i> , 2019, 14, e0210792.	1.1	37
18180	Exploring the evolution and terrestrialization of scorpions (Arachnida: Scorpiones) with rocks and clocks. <i>Organisms Diversity and Evolution</i> , 2019, 19, 71-86.	0.7	33
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18183	RRMdb—an evolutionary-oriented database of RNA recognition motif sequences. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	1.4	10
18184	Delegating Sex: Differential Gene Expression in Stolonizing Syllids Uncovers the Hormonal Control of Reproduction. <i>Genome Biology and Evolution</i> , 2019, 11, 295-318.	1.1	13
18185	Paleozoic diversification of terrestrial chitin-degrading bacterial lineages. <i>BMC Evolutionary Biology</i> , 2019, 19, 34.	3.2	9
18186	Evolution of the modular, disordered stress proteins known as dehydrins. <i>PLoS ONE</i> , 2019, 14, e0211813.	1.1	28
18187	Absence of adaptive evolution is the main barrier against influenza emergence in horses in Asia despite frequent virus interspecies transmission from wild birds. <i>PLoS Pathogens</i> , 2019, 15, e1007531.	2.1	12
18188	Characteristics of the First Protein Tyrosine Phosphatase with Phytase Activity from a Soil Metagenome. <i>Genes</i> , 2019, 10, 101.	1.0	8
18189	The first chromosome-level genome for a marine mammal as a resource to study ecology and evolution. <i>Molecular Ecology Resources</i> , 2019, 19, 944-956.	2.2	27
18190	Forest giants on different evolutionary branches: Ecomorphological convergence in helicopter damselflies*. <i>Evolution; International Journal of Organic Evolution</i> , 2019, 73, 1045-1054.	1.1	10
18191	Detection of Natural Products and Their Producers in Ocean Sediments. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	33
18192	Genomic insights into neonicotinoid sensitivity in the solitary bee <i>Osmia bicornis</i> . <i>PLoS Genetics</i> , 2019, 15, e1007903.	1.5	68
18193	SALiBASE: A Database of Simulated Protein Alignments. <i>Evolutionary Bioinformatics</i> , 2019, 15, 117693431882108.	0.6	4
18194	A mole rat's gut microbiota suggests selective influence of diet on microbial niche space and evolution. <i>Experimental Biology and Medicine</i> , 2019, 244, 471-483.	1.1	2
18195	Use of genome-scale models to get new insights into the marine actinomycete genus <i>Salinispora</i> . <i>BMC Systems Biology</i> , 2019, 13, 11.	3.0	3
18196	Skmer: assembly-free and alignment-free sample identification using genome skims. <i>Genome Biology</i> , 2019, 20, 34.	3.8	70
18197	Gene duplication and relaxation from selective constraints of GCYC genes correlated with various floral symmetry patterns in Asiatic Gesneriaceae tribe Trichosporeae. <i>PLoS ONE</i> , 2019, 14, e0210054.	1.1	5
18198	Compression of Large Sets of Sequence Data Reveals Fine Diversification of Functional Profiles in Multigene Families of Proteins: A Study for Peptidyl-Prolyl cis/trans Isomerases (PPIase). <i>Biomolecules</i> , 2019, 9, 59.	1.8	2
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18202	MapB, the <i>Brucella suis</i> TamB homologue, is involved in cell envelope biogenesis, cell division and virulence. <i>Scientific Reports</i> , 2019, 9, 2158.	1.6	14
18203	Conodipine-P1-3, the First Phospholipases A2 Characterized from Injected Cone Snail Venom*. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 876a-891.	2.5	7
18204	Extensive Losses of Photosynthesis Genes in the Plastome of a Mycoheterotrophic Orchid, <i>Cyrtosia septentrionalis</i> (Vanilloideae: Orchidaceae). <i>Genome Biology and Evolution</i> , 2019, 11, 565-571.	1.1	30
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18207	Unraveling new molecular players involved in the autoregulation of nodulation in <i>Medicago truncatula</i> . <i>Journal of Experimental Botany</i> , 2019, 70, 1407-1417.	2.4	41
18208	Phylogenomic analysis of cytochrome P450 multigene family and their differential expression analysis in <i>Solanum lycopersicum</i> L. suggested tissue specific promoters. <i>BMC Genomics</i> , 2019, 20, 116.	1.2	40
18209	A tale of two genes: divergent evolutionary fate of haptoglobin and hemopexin in hemoglobinless antarctic icefishes. <i>Journal of Experimental Biology</i> , 2019, 222, .	0.8	8
18210	Unveiling the Kinomes of <i>Leishmania infantum</i> and <i>L. braziliensis</i> Empowers the Discovery of New Kinase Targets and Antileishmanial Compounds. <i>Computational and Structural Biotechnology Journal</i> , 2019, 17, 352-361.	1.9	16
18211	First report of fruit rot on cantaloupe caused by <i>Fusarium equiseti</i> in Thailand. <i>Journal of General Plant Pathology</i> , 2019, 85, 295-300.	0.6	11
18212	Is <i>Nymphaea lotus</i> var. <i>thermalis</i> a Tertiary relict in Europe?. <i>Aquatic Botany</i> , 2019, 155, 1-4.	0.8	4
18213	Molecular phylogenetic relationships among populations of <i>Sagittaria aginashi</i> Makino (Alismataceae) and endemic Chinese species. <i>Journal of Asia-Pacific Biodiversity</i> , 2019, 12, 106-114.	0.2	1
18214	Mitogenomic evidence of close relationships between New Zealand's extinct giant raptors and small-sized Australian sister-taxa. <i>Molecular Phylogenetics and Evolution</i> , 2019, 134, 122-128.	1.2	17
18215	Carboxydrotrophy potential of uncultivated Hydrothermarchaeota from the subseafloor crustal biosphere. <i>ISME Journal</i> , 2019, 13, 1457-1468.	4.4	31
18216	A novel polyketide synthase gene cluster in the plant pathogenic fungus <i>Pseudocercospora fijiensis</i> . <i>PLoS ONE</i> , 2019, 14, e0212229.	1.1	10
18217	Computational and mutational analysis of TatD DNase of <i>Bacillus anthracis</i> . <i>Journal of Cellular Biochemistry</i> , 2019, 120, 11318-11330.	1.2	6

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18219	New lineages and old species: Lineage diversity and regional distribution of <i>Moina</i> (Crustacea: Tj ETQq1 1 0.784314,rgBT /Oygrlock 10	1.2	19
18220	Phosphatidic acid governs natural egress in <i>Toxoplasma gondii</i> via a guanylate cyclase receptor platform. <i>Nature Microbiology</i> , 2019, 4, 420-428.	5.9	94
18221	Combining morphological and molecular data resolves the phylogeny of Squilloidea (Crustacea : Tj ETQq1 1 0.784314,rgBT /Overlock 10	0.5	5
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18225	Altered Gut Microbiota in Chinese Children With Autism Spectrum Disorders. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 40.	1.8	114
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18227	The effect of interventions on the transmission and spread of HIV in South Africa: a phylodynamic analysis. <i>Scientific Reports</i> , 2019, 9, 2640.	1.6	9
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18231	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
18232	Reprogramming of the cambium regulators during adventitious root development upon wounding of storage tap roots in radish ( <i>Raphanus sativus</i> L.). <i>Biology Open</i> , 2019, 8, .	0.6	6
18233	&lt;p&gt;Comparative analysis of KPC-2-encoding chimera plasmids with multi-replicon IncR:Inc<sub>A1763-KPC</sub>:IncN1 or IncFII<sub>A8</sub>:Inc<sub>A1763-KPC</sub>:IncN1&lt;/p&gt;. <i>Infection and Drug Resistance</i> . 2019. Volume 12. 285-296.	1.1	30
18234	Altered Gene Regulatory Networks Are Associated With the Transition From C3 to Crassulacean Acid Metabolism in <i>Erycina</i> (Oncidiinae: Orchidaceae). <i>Frontiers in Plant Science</i> , 2018, 9, 2000.	1.7	30
18235	Usutu Virus Isolated from Rodents in Senegal. <i>Viruses</i> , 2019, 11, 181.	1.5	37

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18239	Genetic diversity and origin of the rare, narrow endemic <i>Asperula crassifolia</i> (Rubiaceae). <i>Plant Systematics and Evolution</i> , 2019, 305, 181-192.	0.3	2
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18244	Glass in the water: Molecular phylogenetics and evolution of Indian glassy perchlets (Teleostei: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 42 0.6	0.6	8
18245	Western Bluetongue virus serotype 3 in Sardinia, diagnosis and characterization. <i>Transboundary and Emerging Diseases</i> , 2019, 66, 1426-1431.	1.3	25
18246	Genome-Wide Identification and Characterization of the ALOG Domain Genes in Rice. <i>International Journal of Genomics</i> , 2019, 2019, 1-13.	0.8	12
18247	Genome-resolved metagenomics of eukaryotic populations during early colonization of premature infants and in hospital rooms. <i>Microbiome</i> , 2019, 7, 26.	4.9	60
18248	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
18249	Haplotype diversity in medically important red scorpion (Scorpiones: Buthidae: <i>Hottentotta tamulus</i> ) from India. <i>Journal of Genetics</i> , 2019, 98, 1.	0.4	3
18250	Recent advances in understanding the replication initiator protein of the ssDNA plant viruses of the family Nanoviridae. <i>VirusDisease</i> , 2019, 30, 22-31.	1.0	10
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18252	Molecular identification and antiviral function of the guanylate-binding protein (GBP) genes in the Chinese tree shrew ( <i>Tupaia belangeri chinesis</i> ). <i>Developmental and Comparative Immunology</i> , 2019, 96, 27-36.	1.0	16
18253	Updated distribution and first description of <i>Scyllarus subarctus</i> (Crustacea: Scyllaridae) decapodid stage. <i>Journal of the Marine Biological Association of the United Kingdom</i> , 2019, 99, 1181-1188.	0.4	5

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18255	Extensive Variations in Diurnal Growth Patterns and Metabolism Among <i>Ulva</i> spp. Strains. <i>Plant Physiology</i> , 2019, 180, 109-123.	2.3	37
18256	<i>Pseudomonas</i> Diversity Within Urban Freshwaters. <i>Frontiers in Microbiology</i> , 2019, 10, 195.	1.5	16
18257	Genome Sequencing of <i>Cladobotryum protrusum</i> Provides Insights into the Evolution and Pathogenic Mechanisms of the Cobweb Disease Pathogen on Cultivated Mushroom. <i>Genes</i> , 2019, 10, 124.	1.0	25
18258	Repeated evolution of a morphological novelty: a phylogenetic analysis of the inflated fruiting calyx in the Physalideae tribe (Solanaceae). <i>American Journal of Botany</i> , 2019, 106, 270-279.	0.8	30
18259	Biochemical characterization of TyrA dehydrogenases from <i>Saccharomyces cerevisiae</i> (Ascomycota) and <i>Pleurotus ostreatus</i> (Basidiomycota). <i>Archives of Biochemistry and Biophysics</i> , 2019, 665, 12-19.	1.4	3
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18261	Isolation and characterization of a novel mycovirus infecting an edible mushroom, <i>Grifola frondosa</i> . <i>Mycoscience</i> , 2019, 60, 211-220.	0.3	15
18262	The Old and the New: Discovery Proteomics Identifies Putative Novel Seminal Fluid Proteins in <i>Drosophila</i> . <i>Molecular and Cellular Proteomics</i> , 2019, 18, S23-S33.	2.5	20
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18266	Teneurin C-Terminal Associated Peptide (TCAP)-1 and Latrophilin Interaction in HEK293 Cells: Evidence for Modulation of Intercellular Adhesion. <i>Frontiers in Endocrinology</i> , 2019, 10, 22.	1.5	19
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18270	Distinct methanotrophic communities exist in habitats with different soil water contents. <i>Soil Biology and Biochemistry</i> , 2019, 132, 143-152.	4.2	65
18271	Analysis of mitochondrial and chloroplast genomes in two volvocine algae: <i>Eudorina elegans</i> and <i>Eudorina cylindrica</i> (Volvocaceae, Chlorophyta). <i>European Journal of Phycology</i> , 2019, 54, 193-205.	0.9	12

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18273	Viral infection detection using metagenomics technology in six poultry farms of eastern China. <i>PLoS ONE</i> , 2019, 14, e0211553.	1.1	8
18274	Replicon-Based Typing of Incl-Complex Plasmids, and Comparative Genomics Analysis of Incl <sup>3</sup> /K1 Plasmids. <i>Frontiers in Microbiology</i> , 2019, 10, 48.	1.5	20
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18279	Auxosporulation in <i>Chaetoceros acadianus</i> sp. nov. (Bacillariophyceae), a new member of the Section <i>Compressa</i> . <i>European Journal of Phycology</i> , 2019, 54, 206-221.	0.9	6
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18281	Isolation and Characterization of Human Gut Bacteria Capable of Extracellular Electron Transport by Electrochemical Techniques. <i>Frontiers in Microbiology</i> , 2018, 9, 3267.	1.5	38
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18284	Virome Diversity Correlates with Intestinal Microbiome Diversity in Adult Monozygotic Twins. <i>Cell Host and Microbe</i> , 2019, 25, 261-272.e5.	5.1	159
18285	The <i>Cedrus</i> -associated truffle <i>Trappeindia himalayensis</i> is a morphologically unique and phylogenetically divergent species of <i>Rhizopogon</i> . <i>Mycologia</i> , 2019, 111, 225-234.	0.8	3
18286	Complete mitochondrial genome of <i>Stichaeus grigorjewi</i> Herzenstein, 1890 (Zoarcales: Stichaeidae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 899-901.	0.2	4
18287	The intestinal environment as an evolutionary adaptation to mouthbrooding in the <i>Astatotilapia burtoni</i> cichlid. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	8
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18297	Establishment, molecular and biological characterization of HCB-514: a novel human cervical cancer cell line. <i>Scientific Reports</i> , 2019, 9, 1913.	1.6	14
18298	Diversity and origin of the genus <i>Lobophora</i> in the Mediterranean Sea including the description of two new species. <i>Phycologia</i> , 2019, 58, 163-168.	0.6	14
18299	Survey on the <i>CRISPR</i> arrays in <i>Lactobacillus helveticus</i> genomes. <i>Letters in Applied Microbiology</i> , 2019, 68, 394-402.	1.0	10
18300	Phototactic tails: Evolution and molecular basis of a novel sensory trait in sea snakes. <i>Molecular Ecology</i> , 2019, 28, 2013-2028.	2.0	15
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18302	Morphological Species of <i>Gloeandromyces</i> ( <i>Ascomycota</i> , <i>Laboulbeniales</i> ) Evaluated Using Single-locus Species Delimitation Methods. <i>Fungal Systematics and Evolution</i> , 2019, 3, 19-34.	0.9	15
18303	Genetic diversity of three <i>Aegla</i> species (Decapoda, Anomura) revealed by AFLP and mtDNA markers. <i>Crustaceana</i> , 2019, 92, 445-462.	0.1	2
18304	<i>Aphelenchoides medicagus</i> n. sp. (Tylenchina: Aphelenchoididae) found in <i>Medicago sativa</i> imported into China from the USA. <i>Nematology</i> , 2019, 21, 709-723.	0.2	4
18305	New observations on <i>Miculenchus</i> Andr�ssy, 1959 (Nematoda: Tylenchidae) with descriptions of two new and one known species from Iran. <i>Nematology</i> , 2019, 21, 937-956.	0.2	3
18306	<i>Lobocriconema iranense</i> (Van den Berg, Eskandari, Tiedt & Karegar, 2010) n. comb. and description of <i>L. nokandense</i> n. sp. (Nematoda: Criconematidae) from Iran. <i>Nematology</i> , 2019, 21, 1043-1061.	0.2	8
18307	Population Genome Sequencing of the Scab Fungal Species <i>Venturia inaequalis</i> , <i>Venturia pirina</i> , <i>Venturia aucupariae</i> and <i>Venturia asperata</i> . <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2405-2414.	0.8	33

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18450	<i>Dactylonectria</i> and <i>Ilyonectria</i> Species Causing Black Foot Disease of Andean Blackberry ( <i>Rubus</i> ) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50 1	0.7	13
18451	Notes, outline and divergence times of Basidiomycota. <i>Fungal Diversity</i> , 2019, 99, 105-367.	4.7	256

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18453	Host-Symbiont Interactions in Deep-Sea Chemosymbiotic Vesicomylid Clams: Insights From Transcriptome Sequencing. <i>Frontiers in Marine Science</i> , 2019, 6, .	1.2	17
18454	PacBio Long-Read Sequencing Reveals the Transcriptomic Complexity and Aux/IAA Gene Evolution in <i>Gnetum</i> (Gnetales). <i>Forests</i> , 2019, 10, 1043.	0.9	6
18455	Identification of a Novel Adeno-like Penguin Circovirus at Cape Crozier (Ross Island, Antarctica). <i>Viruses</i> , 2019, 11, 1088.	1.5	18
18456	Superior cellulolytic activity of <i>Trichoderma guizhouense</i> on raw wheat straw. <i>World Journal of Microbiology and Biotechnology</i> , 2019, 35, 194.	1.7	14
18457	Elucidating the etiology of onion bacterial scale rot in the semi-arid region of Northeastern Brazil. <i>Tropical Plant Pathology</i> , 2019, 44, 494-502.	0.8	4
18458	<i>Trochodendron aralioides</i> , the first chromosome-level draft genome in Trochodendrales and a valuable resource for basal eudicot research. <i>GigaScience</i> , 2019, 8, .	3.3	20
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18461	First Report of Coexistence of Three Different MDR Plasmids, and That of Occurrence of IMP-Encoding Plasmid in <i>Leclercia adecarboxylata</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 2468.	1.5	4
18462	Whole Genome Re-sequencing Reveals Natural Variation and Adaptive Evolution of <i>Phytophthora sojae</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 2792.	1.5	39
18463	Identification, Evolution, and Expression Profiling of Histone Lysine Methylation Moderators in <i>Brassica rapa</i> . <i>Plants</i> , 2019, 8, 526.	1.6	8
18464	The Sequence and a Three-Dimensional Structural Analysis Reveal Substrate Specificity among Snake Venom Phosphodiesterases. <i>Toxins</i> , 2019, 11, 625.	1.5	15
18465	Highly thermostable carboxylic acid reductases generated by ancestral sequence reconstruction. <i>Communications Biology</i> , 2019, 2, 429.	2.0	34
18466	Genomic insights from the first chromosome-scale assemblies of oat ( <i>Avena</i> spp.) diploid species. <i>BMC Biology</i> , 2019, 17, 92.	1.7	58
18467	Incomer, a DD36E family of Tc1/mariner transposons newly discovered in animals. <i>Mobile DNA</i> , 2019, 10, 45.	1.3	22
18468	Multi-drug resistance traits of methicillin-resistant <i>Staphylococcus aureus</i> and other Staphylococcal species from clinical and environmental sources. <i>Journal of Water and Health</i> , 2019, 17, 930-943.	1.1	15
18469	Evidence that cyanobacterial Sll1217 functions analogously to PGRL1 in enhancing PGR5-dependent cyclic electron flow. <i>Nature Communications</i> , 2019, 10, 5299.	5.8	33

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18471	The dynamic proteome of influenza A virus infection identifies M segment splicing as a host range determinant. <i>Nature Communications</i> , 2019, 10, 5518.	5.8	34
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18473	Genomic and phenotypic insights point to diverse ecological strategies by facultative anaerobes obtained from subsurface coal seams. <i>Scientific Reports</i> , 2019, 9, 16186.	1.6	19
18474	The $\hat{\imath}^2$ -oxidation pathway is downregulated during diapause termination in <i>Calanus</i> copepods. <i>Scientific Reports</i> , 2019, 9, 16686.	1.6	13
18475	<i>Serratia liquefaciens</i> FG3 isolated from a metallophyte plant sheds light on the evolution and mechanisms of adaptive traits in extreme environments. <i>Scientific Reports</i> , 2019, 9, 18006.	1.6	10
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18482	Detection and characterization of bacterial endosymbionts in Southeast Asian tephritid fruit fly populations. <i>BMC Microbiology</i> , 2019, 19, 290.	1.3	14
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18487	Endo- $\hat{\imath}^2$ -1,3-glucanase (GH16 Family) from <i>Trichoderma harzianum</i> Participates in Cell Wall Biogenesis but Is Not Essential for Antagonism Against Plant Pathogens. <i>Biomolecules</i> , 2019, 9, 781.	1.8	23



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18491	Phylogenetic position of two species of the <i>Liolaemus elongatus-kriegi</i> Complex and a new northern limit for <i>L. buergeri</i> (Squamata: Liolaemidae). <i>Phyllomedusa</i> , 2019, 18, 115-121.	0.2	1
18492	SimSpliceEvol: alternative splicing-aware simulation of biological sequence evolution. <i>BMC Bioinformatics</i> , 2019, 20, 640.	1.2	3
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18501	Gut Microbiota in Children With Cystic Fibrosis: A Taxonomic and Functional Dysbiosis. <i>Scientific Reports</i> , 2019, 9, 18593.	1.6	84
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18516	<i>cdtA</i> (B), <i>cdtB</i> (C), and a New <i>cdtA</i> -Like Gene, <i>cdtD</i> (E), in <i>Clostridium difficile</i> Strains Recovered across Latin America. Antimicrobial Agents and Chemotherapy, 2019, 64, .	1.4	37
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18555	Is molecular evolution faster in the tropics?. <i>Heredity</i> , 2019, 122, 513-524.	1.2	25
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18563	Draft genome of the cotton aphid <i>Aphis gossypii</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2019, 105, 25-32.	1.2	55
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18576	A new surface gliding species of Chironomidae: An independent invasion of marine environments and its evolutionary implications. <i>Zoologica Scripta</i> , 2019, 48, 81-92.	0.7	9
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18586	Comparative study of cultures and next-generation sequencing in the diagnosis of shoulder prosthetic joint infections. <i>Journal of Shoulder and Elbow Surgery</i> , 2019, 28, 1-8.	1.2	58
18587	Complex patterns of hybridization and introgression across evolutionary timescales in Mexican whiptail lizards ( <i>Aspidoscelis</i> ). <i>Molecular Phylogenetics and Evolution</i> , 2019, 132, 284-295.	1.2	25
18588	Evolutionary history of <i>Manihot carthagenensis</i> (Euphorbiaceae) and allied species in eastern South America. <i>Molecular Phylogenetics and Evolution</i> , 2019, 132, 207-218.	1.2	0
18589	Bacteriome-associated <i>Wolbachia</i> of the parthenogenetic termite <i>Cavitermes tuberosus</i> . <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	16
18590	Genetic diversity of <i>Culicoides</i> species within the <i>Pulicaris</i> complex (Diptera: Ceratopogonidae) in Turkey inferred from mitochondrial COI gene sequences. <i>Acta Tropica</i> , 2019, 190, 380-388.	0.9	8
18591	<i>Schizosaccharomyces pombe</i> contains separate CC- and A-adding tRNA nucleotidyltransferases. <i>Biochemical and Biophysical Research Communications</i> , 2019, 508, 785-790.	1.0	8
18592	Identification of the full 26 cytochrome P450 (CYP) genes and analysis of their expression in response to benzo[ <i>a</i> ]pyrene in the marine rotifer <i>Brachionus rotundiformis</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2019, 29, 185-192.	0.4	6
18593	Distinguishing CPT gene family members and vetting the sequence structure of a putative rubber synthesizing variant in <i>Hevea brasiliensis</i> . <i>Gene</i> , 2019, 689, 183-193.	1.0	5
18594	Prediction and analysis of GH14 family $\alpha$ -amylases in oat seedling extract: Structure and function insights using in silico approaches. <i>International Journal of Biological Macromolecules</i> , 2019, 125, 361-369.	3.6	7
18595	Viral gastroenteritis among children of 0-5 years in Nigeria: Characterization of the first Nigerian aichivirus, recombinant noroviruses and detection of a zoonotic astrovirus. <i>Journal of Clinical Virology</i> , 2019, 111, 4-11.	1.6	35
18596	Phylogenetically diverse endophytic bacteria from desert plants induce transcriptional changes of tissue-specific ion transporters and salinity stress in <i>Arabidopsis thaliana</i> . <i>Plant Science</i> , 2019, 280, 228-240.	1.7	33

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18598	Comparative Analysis of Oomycete Genome Evolution Using the Oomycete Gene Order Browser (OGO). <i>Genome Biology and Evolution</i> , 2019, 11, 189-206.	1.1	17
18599	<i>Pseudofrancisella aestuarii</i> gen. nov., sp. nov., a novel member of the family Francisellaceae isolated from estuarine seawater. <i>Antonie Van Leeuwenhoek</i> , 2019, 112, 877-886.	0.7	12
18600	Classification of microbial transglutaminases by evaluation of evolution trees, sequence motifs, secondary structure topology and conservation of potential catalytic residues. <i>Biochemical and Biophysical Research Communications</i> , 2019, 509, 506-513.	1.0	8
18601	Mapping of dwarfing gene Rht14 in durum wheat and its effect on seedling vigor, internode length and plant height. <i>Crop Journal</i> , 2019, 7, 187-197.	2.3	18
18602	Predicting interspecies transmission of avian influenza virus based on wavelet packet decomposition. <i>Computational Biology and Chemistry</i> , 2019, 78, 455-459.	1.1	6
18603	Disabled insecticidal proteins: A novel tool to understand differences in insect receptor utilization. <i>Insect Biochemistry and Molecular Biology</i> , 2019, 105, 79-88.	1.2	14
18604	Real-time PCR quantification of <i>Fusarium avenaceum</i> in soil and seeds. <i>Journal of Microbiological Methods</i> , 2019, 157, 21-30.	0.7	18
18605	Codon-Optimization of Wild-Type Adeno-Associated Virus Capsid Sequences Enhances DNA Family Shuffling while Conserving Functionality. <i>Molecular Therapy - Methods and Clinical Development</i> , 2019, 12, 71-84.	1.8	22
18606	Whole genome re-sequencing analysis of two tomato genotypes for polymorphism insight in cloned genes and a genetic map construction. <i>Scientia Horticulturae</i> , 2019, 247, 58-66.	1.7	14
18607	Multilocus phylogeography of the brown-spotted pitviper <i>Protobothrops mucrosquamatus</i> (Reptilia: Tj ETQq0 0 0 rgBT /Overlock 10 Tf and Evolution, 2019, 133, 82-91.	1.2	19
18608	Novel genetic code and record-setting AT-richness in the highly reduced plastid genome of the holoparasitic plant <i>Balanophora</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 934-943.	3.3	66
18609	The Previously Unidentified, Divergent Badnavirus Species Cacao red vein-banding virus is Associated with Cacao Swollen Shoot Disease in Nigeria. <i>Plant Disease</i> , 2019, 103, 1302-1308.	0.7	10
18610	Multilocus Characterization, Gene Expression Analysis of Putative Immunodominant Protein Coding Regions, and Development of Recombinase Polymerase Amplification Assay for Detection of <i>Candidatus Phytoplasma Pruni</i> ™ in <i>Prunus avium</i> . <i>Phytopathology</i> , 2019, 109, 983-992.	1.1	8
18611	Differential ratio amplicons ( <i>R</i> <sub>amp</sub> ) for the evaluation of RNA integrity extracted from complex environmental samples. <i>Environmental Microbiology</i> , 2019, 21, 827-844.	1.8	13
18612	Clinical characteristics, rapid identification, molecular epidemiology and antifungal susceptibilities of <i>Talaromyces marneffeii</i> infections in Shenzhen, China. <i>Mycoses</i> , 2019, 62, 450-457.	1.8	7
18613	Expansion and Diversification of MFS Transporters in <i>Kluyveromyces marxianus</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 3330.	1.5	17
18614	On the Typology of Relations. <i>Evolutionary Biology</i> , 2019, 46, 71-89.	0.5	36

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18616	Insights into product release dynamics through structural analyses of thymidylate kinase. <i>International Journal of Biological Macromolecules</i> , 2019, 123, 637-647.	3.6	5
18617	Understanding the transition from water to land: Insights from multi-omic analyses of the perivitelline fluid of apple snail eggs. <i>Journal of Proteomics</i> , 2019, 194, 79-88.	1.2	11
18618	In silico identification and evolutionary analysis of candidate genes involved in the biosynthesis methylproline genes in cyanobacteria strains of Iran. <i>Phytochemistry Letters</i> , 2019, 29, 199-211.	0.6	19
18619	Genome classification improvements based on k-mer intervals in sequences. <i>Genomics</i> , 2019, 111, 1574-1582.	1.3	11
18620	Placing the regionally threatened moss <i>Orthodontium gracile</i> in the big picture – Phylogeny, genome incongruence and anthropogenic dispersal in the order Orthodontiales. <i>Molecular Phylogenetics and Evolution</i> , 2019, 134, 186-199.	1.2	4
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18622	Antidiabetic Potential of Green Seaweed <i>Enteromorpha prolifera</i> Flavonoids Regulating Insulin Signaling Pathway and Gut Microbiota in Type 2 Diabetic Mice. <i>Journal of Food Science</i> , 2019, 84, 165-173.	1.5	105
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18627	Whole-Genome Sequencing for Characterization of Capsule Locus and Prediction of Serogroup of Invasive Meningococcal Isolates. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	1.8	18
18628	Phylogenetic placement of the Peruvian-endemic genus <i>Machaerophorus</i> (Brassicaceae) based on molecular data and implication for its systematics. <i>Plant Systematics and Evolution</i> , 2019, 305, 77-87.	0.3	3
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18630	Gut microbiota dysbiosis correlates with a low-dose PCB126-induced dyslipidemia and non-alcoholic fatty liver disease. <i>Science of the Total Environment</i> , 2019, 653, 274-282.	3.9	65
18631	Overcoming challenges in variant calling: exploring sequence diversity in candidate genes for plant development in perennial ryegrass ( <i>Lolium perenne</i> ). <i>DNA Research</i> , 2019, 26, 1-12.	1.5	14
18632	Structural analysis reveals a pyruvate-binding activator site in the <i>Agrobacterium tumefaciens</i> ADP-glucose pyrophosphorylase. <i>Journal of Biological Chemistry</i> , 2019, 294, 1338-1348.	1.6	11



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18634	Genome-wide identification and characterization of the Dof gene family in cassava ( <i>Manihot</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.8	29
18635	Avocado rhizobacteria emit volatile organic compounds with antifungal activity against <i>Fusarium solani</i> , <i>Fusarium</i> sp. associated with Kuroshio shot hole borer, and <i>Colletotrichum gloeosporioides</i> . <i>Microbiological Research</i> , 2019, 219, 74-83.	2.5	68
18636	Identification of insect-specific flaviviruses in areas of Brazil and Paraguay experiencing endemic arbovirus transmission and the description of a novel flavivirus infecting <i>Sabethes belisarioi</i> . <i>Virology</i> , 2019, 527, 98-106.	1.1	15
18637	The introduced terrestrial slugs <i>Ambigolimax nyctelius</i> (Bourguignat, 1861) and <i>Ambigolimax valentianus</i> (Férussac, 1821) (Gastropoda: Limacidae) in California, with a discussion of taxonomy, systematics, and discovery by citizen science. <i>Journal of Natural History</i> , 2019, 53, 1607-1632.	0.2	15
18638	The Origin and Population History of the Endangered Golden Snub-Nosed Monkey ( <i>Rhinopithecus</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 20	3.5	20
18639	<i>Paecilomyces niveus</i> : Pathogenicity in the Orchard and Sensitivity to Three Fungicides. <i>Plant Disease</i> , 2019, 103, 125-131.	0.7	3
18640	<i>pahE</i> , a Functional Marker Gene for Polycyclic Aromatic Hydrocarbon-Degrading Bacteria. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	46
18641	Heterologous expression and biochemical characterization of a novel cold-active $\alpha$ -amylase from the Antarctic bacteria <i>Pseudoalteromonas</i> sp. 2-3. <i>Protein Expression and Purification</i> , 2019, 155, 78-85.	0.6	22
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18645	Oligopeptide Signaling through TbGPR89 Drives Trypanosome Quorum Sensing. <i>Cell</i> , 2019, 176, 306-317.e16.	13.5	116
18646	Microbial communities in local and transplanted soils along a latitudinal gradient. <i>Catena</i> , 2019, 173, 456-464.	2.2	11
18647	Bovine papillomavirus 24: a novel member of the genus Xipapillomavirus detected in the Amazon region. <i>Archives of Virology</i> , 2019, 164, 637-641.	0.9	8
18648	Complete nitrification: insights into the ecophysiology of comammox <i>Nitrospira</i> . <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 177-189.	1.7	224
18649	Discovery of three RNA viruses using ant transcriptomic datasets. <i>Archives of Virology</i> , 2019, 164, 643-647.	0.9	9
18650	Insights into genes encoding respiratory burst oxidase homologs (RBOHs) in rubber tree ( <i>Hevea</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 31	2.5	31

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18651	Increased evolutionary rates and conserved transcriptional response following allopolyploidization in brown algae. <i>Evolution; International Journal of Organic Evolution</i> , 2019, 73, 59-72.	1.1	11
18652	Efficient mining of natural NADH-utilizing dehydrogenases enables systematic cofactor engineering of lysine synthesis pathway of <i>Corynebacterium glutamicum</i> . <i>Metabolic Engineering</i> , 2019, 52, 77-86.	3.6	44
18653	Implications of introgression for wildlife translocations: the case of North American martens. <i>Conservation Genetics</i> , 2019, 20, 153-166.	0.8	16
18654	Phylogenetic analysis of Alphapapillomavirus based on L1, E6 and E7 regions suggests that carcinogenicity and tissue tropism have appeared multiple times during viral evolution. <i>Infection, Genetics and Evolution</i> , 2019, 67, 210-221.	1.0	2
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18656	PgUGT95B2 preferentially metabolizes flavones/flavonols and has evolved independently from flavone/flavonol UGTs identified in <i>Arabidopsis thaliana</i> . <i>Phytochemistry</i> , 2019, 157, 184-193.	1.4	24
18657	The complete mitochondrial genome of <i>Parasesarma pictum</i> (Brachyura: Grapsoidea: Sesarmidae) and comparison with other Brachyuran crabs. <i>Genomics</i> , 2019, 111, 799-807.	1.3	24
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18661	Herpesvirus infection in marine mammals: A retrospective molecular survey of stranded cetaceans in the Portuguese coastline. <i>Infection, Genetics and Evolution</i> , 2019, 67, 222-233.	1.0	14
18662	Complete Genome Sequence of <i>Massilia oculi</i> sp. nov. CCUG 43427T (=DSM 26321T), the Type Strain of <i>M. oculi</i> , and Comparison with Genome Sequences of Other <i>Massilia</i> Strains. <i>Current Microbiology</i> , 2019, 76, 1082-1086.	1.0	6
18663	The expansion of genes encoding soluble silk components in the greater wax moth, <i>Galleria mellonella</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2019, 106, 28-38.	1.2	17
18664	Core genome phylogenetic analysis of the avian associated <i>Borrelia turdi</i> indicates a close relationship to <i>Borrelia garinii</i> . <i>Molecular Phylogenetics and Evolution</i> , 2019, 131, 93-98.	1.2	13
18665	As Blind as a Bat? Opsin Phylogenetics Illuminates the Evolution of Color Vision in Bats. <i>Molecular Biology and Evolution</i> , 2019, 36, 54-68.	3.5	28
18666	Independent activation of the BoMYB2 gene leading to purple traits in <i>Brassica oleracea</i> . <i>Theoretical and Applied Genetics</i> , 2019, 132, 895-906.	1.8	60
18667	Identification and initial characterization of a new subgroup in the GH3 gene family in woody plants. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2019, 28, 280-290.	0.9	18
18668	Novel herpesviruses in riverine and marine cetaceans from South America. <i>Acta Tropica</i> , 2019, 190, 220-227.	0.9	19

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18670	Molecular characterization of the 2â€²,5â€²-oligoadenylate synthetase family in the Chinese tree shrew ( <i>Tupaia belangeri chinensis</i> ). Cytokine, 2019, 114, 106-114.	1.4	10
18671	Differential expression of heat shock and floral regulatory genes in pseudocarpel initials of mantled female inflorescences from <i>Elaeis guineensis</i> Jacq.. Plant Reproduction, 2019, 32, 167-179.	1.3	1
18672	The genome of â€˜Candidatus Phytoplasma solaniâ€™™ strain SA-1 is highly dynamic and prone to adopting foreign sequences. Systematic and Applied Microbiology, 2019, 42, 117-127.	1.2	53
18673	Insights into the origin and evolution of Peritrichia (Oligohymenophorea, Ciliophora) based on analyses of morphology and phylogenomics. Molecular Phylogenetics and Evolution, 2019, 132, 25-35.	1.2	50
18674	The Kdm/Kmt gene families in the self-fertilizing mangrove rivulus fish, <i>Kryptolebias marmoratus</i> , suggest involvement of histone methylation machinery in development and reproduction. Gene, 2019, 687, 173-187.	1.0	25
18675	Differential evolution of antigenic regions of porcine reproductive and respiratory syndrome virus 1 before and after vaccine introduction. Virus Research, 2019, 260, 12-19.	1.1	16
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18677	On the origin of orphan hybrids between <i>Aquilegia formosa</i> and <i>Aquilegia flavescens</i> . AoB PLANTS, 2019, 11, ply071.	1.2	5
18678	Mechanistic basis of vitamin B12 and cobinamide salvaging by the <i>Vibrio</i> species. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2019, 1867, 140-151.	1.1	10
18679	Profiles of bacterial assemblages from microplastics of tropical coastal environments. Science of the Total Environment, 2019, 655, 313-320.	3.9	130
18680	Importance of routine viral load monitoring: higher levels of resistance at ART failure in Uganda and Lesotho compared with Switzerland. Journal of Antimicrobial Chemotherapy, 2019, 74, 468-472.	1.3	9
18681	Soybean Sudden Death Syndrome Causal Agent <i>Fusarium brasiliense</i> Present in Michigan. Plant Disease, 2019, 103, 1234-1243.	0.7	20
18682	Key amino acid residues of the AGT1 permease required for maltotriose consumption and fermentation by <i>Saccharomyces cerevisiae</i> . Journal of Applied Microbiology, 2019, 126, 580-594.	1.4	13
18683	Fluorescent <i>Pseudomonas</i> and cyclic lipopeptide diversity in the rhizosphere of cocoyam (<sc><i>Xanthosoma sagittifolium</i></sc>). Environmental Microbiology, 2019, 21, 1019-1034.	1.8	32
18684	Mechanisms of cnidocyte development in the moon jellyfish <i>Aurelia</i>. Evolution & Development, 2019, 21, 72-81.	1.1	10
18685	Intragenomic <i>internal transcribed spacer 2</i> variation in a genus of parasitoid wasps (Hymenoptera: Braconidae): implications for accurate species delimitation and phylogenetic analysis. Insect Molecular Biology, 2019, 28, 485-498.	1.0	4
18686	Molecular phylogeny and divergence times of <i>Onosma</i> (Boraginaceae s.s.) based on nrDNA ITS and plastid <i>rpl</i> 32 <i>â€™rn</i>L<sub></sub> (UAG) </sub> and <i>trn</i>H<i>â€™psb</i>A sequences. Nordic Journal of Botany, 2019, 37, e02060.	0.2	19

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18687	Genome wide identification of the trihelix transcription factors and overexpression of <i>Gh_A05G2067</i> ( <i>GTâ€²</i> ), a novel gene contributing to increased drought and salt stresses tolerance in cotton. <i>Physiologia Plantarum</i> , 2019, 167, 447-464.	2.6	57
18688	Diversity, Dynamics, and Distribution of <i>Bdellovibrio</i> and Like Organisms in Perialpine Lakes. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	30
18689	Systematic survey of plant LTR-retrotransposons elucidates phylogenetic relationships of their polyprotein domains and provides a reference for element classification. <i>Mobile DNA</i> , 2019, 10, 1.	1.3	265
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18691	Complete mitochondrial genome of <i>Japalura flaviceps</i> : Deep insights into the phylogeny and gene rearrangements of Agamidae species. <i>International Journal of Biological Macromolecules</i> , 2019, 125, 423-431.	3.6	23
18692	A kiwellin disarms the metabolic activity of a secreted fungal virulence factor. <i>Nature</i> , 2019, 565, 650-653.	13.7	48
18693	Novel Paranannizziopsis species in a Wagler's viper ( <i>Tropidolaemus wagleri</i> ), tentacled snakes ( <i>Erpeton tentaculatum</i> ), and a rhinoceros snake ( <i>Rhynchophis boulengeri</i> ) in a zoological collection. <i>Medical Mycology</i> , 2019, 57, 825-832.	0.3	10
18694	Diversity and distribution of the <i>bmp</i> gene cluster and its Polybrominated products in the genus <i>Pseudoalteromonas</i> . <i>Environmental Microbiology</i> , 2019, 21, 1575-1585.	1.8	15
18695	In love and war: The morphometric and phylogenetic basis of ornamentation, and the evolution of male display behavior, in the livebearer genus <i>Poecilia</i> . <i>Evolution; International Journal of Organic Evolution</i> , 2019, 73, 360-377.	1.1	18
18696	Trophic Specialization Results in Genomic Reduction in Free-Living Marine <i>Idiomarina</i> Bacteria. <i>MBio</i> , 2019, 10, .	1.8	13
18697	Insight into the correlation between biochar amendment and shifts in bacterial community 4 years after a single incorporation in soybean- and maize-planted soils in northeastern China. <i>Canadian Journal of Microbiology</i> , 2019, 65, 353-364.	0.8	8
18698	Sestrin-like protein from <i>Dictyostelium discoideum</i> is involved in autophagy under starvation stress. <i>Microbiological Research</i> , 2019, 220, 61-71.	2.5	12
18699	The HIV gp41 Fusion Protein Inhibits T-Cell Activation through the Lentiviral Lytic Peptide 2 Motif. <i>Biochemistry</i> , 2019, 58, 818-832.	1.2	1
18700	Genetic Structure of <i>Liriomyza trifolii</i> (Diptera: Agromyzidae) Associated With Host Plants From Southeastern Mexico. <i>Environmental Entomology</i> , 2019, 48, 253-262.	0.7	2
18701	Comparative Transcriptomics Reveals Patterns of Adaptive Evolution Associated with Depth and Age Within Marine Rockfishes (Sebastes). <i>Journal of Heredity</i> , 2019, 110, 340-350.	1.0	12
18702	The phylogeny of Ryocalanoidea (Copepoda, Calanoida) based on morphology and a multi-gene analysis with a description of new ryocalanoidean species. <i>Zoological Journal of the Linnean Society</i> , 2019, 185, 925-957.	1.0	7
18703	Gene Encoding a Novel Enzyme of LDH2/MDH2 Family is Lost in Plant and Animal Genomes During Transition to Land. <i>Journal of Molecular Evolution</i> , 2019, 87, 52-59.	0.8	4
18704	Identification of newly settled Caribbean coral recruits by ITS-targeted single-step nested multiplex PCR. <i>Coral Reefs</i> , 2019, 38, 79-92.	0.9	4

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18706	Young colonization history of a widespread sand dollar (Echinodermata; Clypeasteroidea) in western Taiwan. <i>Quaternary International</i> , 2019, 528, 120-129.	0.7	3
18707	<i>Jiangella anatolica</i> sp. nov. isolated from coastal lake soil. <i>Antonie Van Leeuwenhoek</i> , 2019, 112, 887-895.	0.7	6
18708	Transcriptomic analysis related to the flowering of the citrus hybrid <i>Microcitrangemonia</i> . <i>Current Plant Biology</i> , 2019, 18, 100097.	2.3	1
18709	Birth of an order: Comprehensive molecular phylogenetic study excludes <i>Herpomyces</i> (Fungi). <i>Trends in Microbiology</i> , 2019, 27, 50-58.	1.2	27
18710	A cis-acting bidirectional transcription switch controls sexual dimorphism in the liverwort. <i>EMBO Journal</i> , 2019, 38, .	3.5	59
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18713	Niche-directed evolution modulates genome architecture in freshwater Planctomycetes. <i>ISME Journal</i> , 2019, 13, 1056-1071.	4.4	67
18714	The Prodigal Compound: Return of Ribosyl 1,5-Bisphosphate as an Important Player in Metabolism. <i>Microbiology and Molecular Biology Reviews</i> , 2019, 83, .	2.9	2
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18718	Draft Genome Assembly and Population Genetics of an Agricultural Pollinator, the Solitary Alkali Bee ( <i>Halictidae: Nomia melanderi</i> ). <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 625-634.	0.8	19
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18725	Genome-wide identification and comparative analysis of alternative splicing across four legume species. <i>Planta</i> , 2019, 249, 1133-1142.	1.6	16
18726	G418 induces programmed cell death in <i>Acanthamoeba</i> through the elevation of intracellular calcium and cytochrome c translocation. <i>Parasitology Research</i> , 2019, 118, 641-651.	0.6	7
18727	Structure and function prediction of arsenate reductase from <i>Deinococcus indicus</i> DR1. <i>Journal of Molecular Modeling</i> , 2019, 25, 15.	0.8	11
18728	Genome-wide analysis of the Hsf gene family in <i>Brassica oleracea</i> and a comparative analysis of the Hsf gene family in <i>B. oleracea</i> , <i>B. rapa</i> and <i>B. napus</i> . <i>Functional and Integrative Genomics</i> , 2019, 19, 515-531.	1.4	44
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18735	Computational analysis in designing T cell epitopes enriched peptides of Ebola glycoprotein exhibiting strong binding interaction with HLA molecules. <i>Journal of Theoretical Biology</i> , 2019, 465, 34-44.	0.8	19
18736	Impact of planktonic low nucleic acid-content bacteria to bacterial community structure and associated ecological functions in a shallow lake. <i>Science of the Total Environment</i> , 2019, 658, 868-878.	3.9	28
18737	Comparative Proteomic Analysis of Slime from the Striped Pyjama Squid, <i>Sepioloidea lineolata</i> , and the Southern Bottletail Squid, <i>Sepiadarium austrinum</i> (Cephalopoda: Sepiariidae). <i>Journal of Proteome Research</i> , 2019, 18, 890-899.	1.8	4
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18749	The genetic diversity and evolution of diatom-diazotroph associations highlights traits favoring symbiont integration. <i>FEMS Microbiology Letters</i> , 2019, 366, .	0.7	36
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18752	Underestimated and cryptic diversification patterns across Afro-tropical lowland forests. <i>Journal of Biogeography</i> , 2019, 46, 381-391.	1.4	22
18753	Respiratory Selenite Reductase from <i>Bacillus selenitireducens</i> Strain MLS10. <i>Journal of Bacteriology</i> , 2019, 201, .	1.0	37
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18757	Revisiting avian "missing" genes from de novo assembled transcripts. <i>BMC Genomics</i> , 2019, 20, 4.	1.2	36
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18760	Multiple Introductions of Domestic Cat Feline Leukemia Virus in Endangered Florida Panthers <sup>1</sup> . <i>Emerging Infectious Diseases</i> , 2019, 25, 92-101.	2.0	39
18761	Sequencing and Genomic Diversity Analysis of IncHI5 Plasmids. <i>Frontiers in Microbiology</i> , 2018, 9, 3318.	1.5	30
18762	Identification of Novel Potential Inhibitors of Pteridine Reductase 1 in <i>Trypanosoma brucei</i> via Computational Structure-Based Approaches and in Vitro Inhibition Assays. <i>Molecules</i> , 2019, 24, 142.	1.7	21
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18764	Evaluating Statistical Multiple Sequence Alignment in Comparison to Other Alignment Methods on Protein Data Sets. <i>Systematic Biology</i> , 2019, 68, 396-411.	2.7	23
18765	A human subcutaneous infection by <i>Microascus ennothomasiorum</i> sp. nov. <i>Mycoses</i> , 2019, 62, 157-164.	1.8	6
18766	Evolutionary origin of 2A-like sequences in Totiviridae genomes. <i>Virus Research</i> , 2019, 259, 1-9.	1.1	20
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18771	Monitoring of in planta gene expression for xylan degradation and assimilation in the maize pathogen <i>Bipolaris maydis</i> . <i>Mycoscience</i> , 2019, 60, 116-124.	0.3	1
18772	New insights into adaptation and population structure of cork oak using genotyping by sequencing. <i>Global Change Biology</i> , 2019, 25, 337-350.	4.2	48
18773	Molecular authentication of <i>Anthemis deserti</i> Boiss. (Asteraceae) based on ITS2 region of nrDNA gene sequence. <i>Saudi Journal of Biological Sciences</i> , 2019, 26, 155-159.	1.8	2
18774	EncoMPASS: an online database for analyzing structure and symmetry in membrane proteins. <i>Nucleic Acids Research</i> , 2019, 47, D315-D321.	6.5	17
18775	Sex-Biased Dispersal Obscures Species Boundaries in Integrative Species Delimitation Approaches. <i>Systematic Biology</i> , 2019, 68, 441-459.	2.7	21
18776	Genus delimitation, biogeography and diversification of <i>Choristoneura</i> Lederer (Lepidoptera: Tj ETQq1 1 0.784314 rgBT /Over 10	1.7	10



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18778	Effect of temperature on the microflora community composition in the digestive tract of the veined rapa whelk ( <i>Rapana venosa</i> ) revealed by 16S rRNA gene sequencing. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2019, 29, 145-153.	0.4	7
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18785	Genomic and Transcriptomic Basis of <i>Hanseniaspora vineae</i> 's Impact on Flavor Diversity and Wine Quality. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	51
18786	Virulence behavior of uropathogenic <i>Escherichia coli</i> strains in the host model <i>Caenorhabditis elegans</i> . <i>MicrobiologyOpen</i> , 2019, 8, e00756.	1.2	16
18787	Systematics of <i>Onobrychis</i> sect. <i>Heliobrychis</i> (Fabaceae): morphology and molecular phylogeny revisited. <i>Plant Systematics and Evolution</i> , 2019, 305, 33-48.	0.3	5
18788	iEKP2.0: an update with rich annotations for eukaryotic protein kinases, protein phosphatases and proteins containing phosphoprotein-binding domains. <i>Nucleic Acids Research</i> , 2019, 47, D344-D350.	6.5	22
18789	Epidemiology of tick-borne pathogens in the semi-arid and the arid agro-ecological zones of Punjab province, Pakistan. <i>Transboundary and Emerging Diseases</i> , 2019, 66, 526-536.	1.3	49
18790	Identification of superior cellulase secretion phenotypes in haploids derived from natural <i>Saccharomyces cerevisiae</i> isolates. <i>FEMS Yeast Research</i> , 2019, 19, .	1.1	13
18791	PER extended-spectrum $\beta$ -lactamases originate from <i>Pararheinheimera</i> spp. <i>International Journal of Antimicrobial Agents</i> , 2019, 53, 158-164.	1.1	12
18792	Correlates of ecological dominance within <i>Pheidole</i> ants (Hymenoptera: Formicidae). <i>Ecological Entomology</i> , 2019, 44, 163-171.	1.1	10
18793	Differential involvement of the three nuclear estrogen receptors during oogenesis in European sea bass ( <i>Dicentrarchus labrax</i> ). <i>Biology of Reproduction</i> , 2019, 100, 757-772.	1.2	6
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18799	A bacterial DNA repair pathway specific to a natural antibiotic. Molecular Microbiology, 2019, 111, 338-353.	1.2	19
18800	Isolation and Characterization of a Distinct Influenza A Virus from Egyptian Bats. Journal of Virology, 2019, 93, .	1.5	42
18801	Patterns of mutation within an emerging endemic lineage of <i>HEV</i> . Journal of Viral Hepatitis, 2019, 26, 191-198.	1.0	5
18802	Independent evolution of porcine reproductive and respiratory syndrome virus 2 with genetic heterogeneity in antigenic regions of structural proteins in Korea. Archives of Virology, 2019, 164, 213-224.	0.9	10
18803	Isotope discrimination by form IC RubisCO from <i>Ralstonia eutropha</i> and <i>Rhodobacter sphaeroides</i> , metabolically versatile members of <i>Proteobacteria</i> from aquatic and soil habitats. Environmental Microbiology, 2019, 21, 72-80.	1.8	19
18804	No evidence of quantitative signal honesty across species of aposematic burnet moths (Lepidoptera: Tj ETQq1 1 0,784314 rgBT /Ovele	0,8	10
18805	Prophage Diversity of <i>Candidatus</i> <i>Liberibacter asiaticus</i> Strains in California. Phytopathology, 2019, 109, 551-559.	1.1	34
18806	Chitin synthesis and degradation in <i>Lepeophtheirus salmonis</i> : Molecular characterization and gene expression profile during synthesis of a new exoskeleton. Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology, 2019, 227, 123-133.	0.8	13
18807	A Steric Gating Mechanism Dictates the Substrate Specificity of a Rab-GEF. Developmental Cell, 2019, 48, 100-114.e9.	3.1	49
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18809	Cyanate and urea are substrates for nitrification by Thaumarchaeota in the marine environment. Nature Microbiology, 2019, 4, 234-243.	5.9	103
18810	Biogeography of thermophiles and predominance of <i>Thermus scotoductus</i> in domestic water heaters. Extremophiles, 2019, 23, 119-132.	0.9	4
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18812	Unexpected bird-feather mite associations revealed by DNA metabarcoding uncovers a dynamic ecoevolutionary scenario. Molecular Ecology, 2019, 28, 379-390.	2.0	21

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18814	Recent lake expansion triggered the adaptive radiation of freshwater snails in the ancient Lake Biwa. <i>Evolution Letters</i> , 2019, 3, 43-54.	1.6	23
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18816	DNA barcoding of large oak-living cerambycids: diagnostic tool, phylogenetic insights and natural hybridization between <i>Cerambyx cerdo</i> and <i>Cerambyx welensii</i> (Coleoptera: Cerambycidae). <i>Bulletin of Entomological Research</i> , 2019, 109, 583-594.	0.5	16
18817	HIV-1 DNA Is Maintained in Antigen-Specific CD4+ T Cell Subsets in Patients on Long-Term Antiretroviral Therapy Regardless of Recurrent Antigen Exposure. <i>AIDS Research and Human Retroviruses</i> , 2019, 35, 112-120.	0.5	16
18818	Whole-genome sequence of the oriental lung fluke <i>Paragonimus westermani</i> . <i>GigaScience</i> , 2019, 8, .	3.3	29
18819	The draft genomes of five agriculturally important African orphan crops. <i>GigaScience</i> , 2019, 8, .	3.3	108
18820	A polyphasic approach to the delimitation of diatom species: a case study for the genus <i>Pinnularia</i> (Bacillariophyta). <i>Journal of Phycology</i> , 2019, 55, 365-379.	1.0	15
18821	Phylogeography of a widespread lizard complex reflects patterns of both geographic and ecological isolation. <i>Molecular Ecology</i> , 2019, 28, 644-657.	2.0	23
18822	A comparative study of the efficiency of HCV NS3/4A protease drugs against different HCV genotypes using in silico approaches. <i>Life Sciences</i> , 2019, 217, 176-184.	2.0	7
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18825	ARGDIT: a validation and integration toolkit for Antimicrobial Resistance Gene Databases. <i>Bioinformatics</i> , 2019, 35, 2466-2474.	1.8	12
18826	Whole Genome Sequencing detects Inter-Facility Transmission of Carbapenem-resistant <i>Klebsiella pneumoniae</i> . <i>Journal of Infection</i> , 2019, 78, 187-199.	1.7	26
18827	Inner ear development in cyclostomes and evolution of the vertebrate semicircular canals. <i>Nature</i> , 2019, 565, 347-350.	13.7	44
18828	The <i>Suhyomyces</i> clade: from single isolate to multiple species to disintegrating sex loci. <i>FEMS Yeast Research</i> , 2019, 19, .	1.1	10
18829	Outbreak of viral haemorrhagic septicaemia (VHS) in lumpfish ( <i>Cyclopterus lumpus</i> ) in Iceland caused by VHS virus genotype IV. <i>Journal of Fish Diseases</i> , 2019, 42, 47-62.	0.9	28
18830	Human Immunodeficiency Virus (HIV)-1 Transmission Among Persons With Acute HIV-1 Infection in Malawi: Demographic, Behavioral, and Phylogenetic Relationships. <i>Clinical Infectious Diseases</i> , 2019, 69, 853-860.	2.9	3

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18832	CYP76B74 Catalyzes the 3 <sup>β</sup> -Hydroxylation of Geranylhydroquinone in Shikonin Biosynthesis. <i>Plant Physiology</i> , 2019, 179, 402-414.	2.3	33
18833	Diversity in CO <sub>2</sub> -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
18834	Resuscitation of anammox bacteria after >10,000 years of dormancy. <i>ISME Journal</i> , 2019, 13, 1098-1109.	4.4	51
18835	A Novel R2R3-MYB Transcription Factor Contributes to Petal Blotch Formation by Regulating Organ-Specific Expression of <i>PsCHS</i> in Tree Peony ( <i>Paeonia suffruticosa</i> ). <i>Plant and Cell Physiology</i> , 2019, 60, 599-611.	1.5	77
18836	Genome mining reveals uncommon alkylpyrones as type III PKS products from myxobacteria. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2019, 46, 319-334.	1.4	30
18837	Molecular phylogeny and morphology of <i>Elatostema</i> s.l. (Urticaceae): Implications for inter- and infrageneric classifications. <i>Molecular Phylogenetics and Evolution</i> , 2019, 132, 251-264.	1.2	15
18838	Habitat-specificity and diversity of culturable cold-adapted yeasts of a cold-based glacier in the Tianshan Mountains, northwestern China. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 2311-2327.	1.7	12
18839	<i>Nephrocystidium pickii</i> Weissenberg, 1921 belongs to Myxozoa (Cnidaria) but is not conspecific with <i>Myxidium lieberkuehni</i> BÄtschli, 1882 (Myxozoa: Bivalvulida: Variisporina: Myxidiidae): molecular-genetic evidence. <i>Systematic Parasitology</i> , 2019, 96, 15-22.	0.5	1
18840	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
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18842	Phylogeny and acoustic signal evolution of a pure tone song katydid <i>Pseudophyllus titan</i> (Orthoptera: Tettigoniidae) based on the complete mitogenome. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2019, 30, 385-396.	0.7	14
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18845	Continued reassortment of avian H6 influenza viruses from Southern China, 2014–2016. <i>Transboundary and Emerging Diseases</i> , 2019, 66, 592-598.	1.3	19
18846	Identification and comprehensive analysis of the characteristics and roles of leucine-rich repeat receptor-like protein kinase (LRR-RLK) genes in <i>Sedum alfredii</i> Hance responding to cadmium stress. <i>Ecotoxicology and Environmental Safety</i> , 2019, 167, 95-106.	2.9	16
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18848	Identification of Rickettsial Infections ( <i>Rickettsia</i> sp. TH2014) in <i>Ctenocephalides orientis</i> Fleas (Siphonaptera: Pulicidae). <i>Journal of Medical Entomology</i> , 2019, 56, 526-532.	0.9	4

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18855	Expression and characterization of silkworm <i>Bombyx mori</i> 1,2-N-acetylglucosaminyltransferase II, a key enzyme for complex-type N-glycan biosynthesis. <i>Journal of Bioscience and Bioengineering</i> , 2019, 127, 273-280.	1.1	8
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18861	High-Throughput Reconstruction of Ancestral Protein Sequence, Structure, and Molecular Function. <i>Methods in Molecular Biology</i> , 2019, 1851, 135-170.	0.4	15
18862	Evolutionary distribution of deoxynucleoside 5-monophosphate N-glycosidase, DNPH1. <i>Gene</i> , 2019, 683, 1-11.	1.0	3
18863	Prevalence and Genome Characterization of Field Isolates of Sugarcane Mosaic Virus (SCMV) in Nigeria. <i>Plant Disease</i> , 2019, 103, 818-824.	0.7	8
18864	Remarkable morphological variation in the proboscis of <i>Neorhadynorhynchus nudus</i> (Harada, Tj) ETQq1 1 0.784314 rgBT/Overl	0.7	12
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18866	A Hybrid Bio-Inspired Algorithm for Protein Domain Problems. <i>EAI/Springer Innovations in Communication and Computing</i> , 2019, , 291-311.	0.9	1

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18868	Niche and fitness differences determine invasion success and impact in laboratory bacterial communities. <i>ISME Journal</i> , 2019, 13, 402-412.	4.4	64
18869	<sc>DNA</sc> Barcoding as useful tool to identify crop pest flea beetles of Turkey. <i>Journal of Applied Entomology</i> , 2019, 143, 105-117.	0.8	9
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18884	Kleptoplastidic benthic foraminifera from aphotic habitats: insights into assimilation of inorganic C, N and S studied with sub $\epsilon$ cellular resolution. <i>Environmental Microbiology</i> , 2019, 21, 125-141.	1.8	41

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18887	Integrative systematics of <i>Placida cremoniana</i> (Trinchese, 1892) (Gastropoda, Heterobranchia). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 66</i>	0.3	10
18888	Living with a giant parchment tube worm: a description of a new nudibranch species (Gastropoda). <i>Tj ETQq1 1 0.784314 rgBT /Overlock 11</i>	0.3	11
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18900	<i>Metaxonchium toroense</i> n. sp. (Nematoda, Dorylaimida, Belondiridae) from Costa Rica, with the first molecular study of a representative of the genus. <i>Journal of Helminthology</i> , 2019, 93, 100-108.	0.4	4
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18902	Morphological and molecular data support recognition of a new rupicolous species of <i>Pinguicula</i> ( <i>Lentibulariaceae</i> ) from the Iberian Peninsula. <i>Plant Biosystems</i> , 2019, 153, 77-87.	0.8	1

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18917	A review of alignment based similarity measures for web usage mining. <i>Artificial Intelligence Review</i> , 2020, 53, 1529-1551.	9.7	8
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18934	Description of <i>Palleronia rufa</i> sp. nov., a biofilm-forming and AHL-producing Rhodobacteraceae, reclassification of <i>Hwanghaeicola aestuarii</i> as <i>Palleronia aestuarii</i> comb. nov., <i>Maribius pontilimi</i> as <i>Palleronia pontilimi</i> comb. nov., <i>Maribius salinus</i> as <i>Palleronia salina</i> comb. nov., <i>Maribius pelagius</i> as <i>Palleronia pelagia</i> comb. nov. and emended description of the genus <i>Palleronia</i> . <i>Systematic and Applied Microbiology</i> , 2020, 43, 126018.	1.2	29
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18942	Cultivable fungi from deep-sea oil reserves in the Gulf of Mexico: Genetic signatures in response to hydrocarbons. <i>Marine Environmental Research</i> , 2020, 153, 104816.	1.1	23
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18945	Probing the effect of a plus 1bp frameshift mutation in protein-DNA interface of domestication gene, <i>&lt;i&gt;NAMB1&lt;/i&gt;</i> , in wheat. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020, 38, 3633-3647.	2.0	14
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18953	Investigation of a New Typeâ€™...I Baeyerâ€™Villiger Monooxygenase from <i>&lt;i&gt;Amycolatopsis thermoflava&lt;/i&gt;</i> Revealed High Thermodynamic but Limited Kinetic Stability. <i>ChemBioChem</i> , 2020, 21, 971-977.	1.3	6
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18956	The sweet side of venom: Glycosylated prothrombin activating metalloproteases from <i>Dispholidus typus</i> (boomslang) and <i>Thelotornis mossambicanus</i> (twig snake). <i>Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology</i> , 2020, 227, 108625.	1.3	11

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18959	Distribution and evolution of the serine/aspartate racemase family in plants. <i>Phytochemistry</i> , 2020, 169, 112164.	1.4	4
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18969	Multiobjective artificial fish swarm algorithm for multiple sequence alignment. <i>Infor</i> , 2020, 58, 38-59.	0.5	5
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18973	Detection of freshwater mussels ( <i>Sinanodonta</i> spp.) in artificial ponds through environmental DNA: a comparison with traditional hand collection methods. <i>Limnology</i> , 2020, 21, 59-65.	0.8	11
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18981	Identification of Proteolytic Thermophiles from Moinit Coastal Hot-Spring, North Sulawesi, Indonesia. <i>Geomicrobiology Journal</i> , 2020, 37, 50-58.	1.0	10
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18989	Genome sequences of two Antarctic strains of <i>Pseudomonas protekii</i> : insights into adaptation to extreme conditions. <i>Archives of Microbiology</i> , 2020, 202, 447-454.	1.0	5
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19001	Bacterial communities in the solid, liquid, dorsal, and ventral epithelium fractions of yak ( <i>Bos</i> ) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50 4	1.2	43
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19031	Polyphasic identification of three new species in <i>Alternaria</i> section <i>Infectoriae</i> causing human cutaneous infection. <i>Mycoses</i> , 2020, 63, 212-224.	1.8	15
19032	Inhibition of histone acetylation and deacetylation enzymes affects longevity, development, and fecundity in the pea aphid ( <i>Acyrtosiphon pisum</i> ). <i>Archives of Insect Biochemistry and Physiology</i> , 2020, 103, e21614.	0.6	9
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19036	HLA Heterozygote Advantage against HIV-1 Is Driven by Quantitative and Qualitative Differences in HLA Allele-Specific Peptide Presentation. <i>Molecular Biology and Evolution</i> , 2020, 37, 639-650.	3.5	60
19037	Discovery of <i>Arostrilepis</i> tapeworms (Cyclophyllidea: Hymenolepididae) and new insights for parasite species diversity from Eastern North America. <i>Parasitology Research</i> , 2020, 119, 567-585.	0.6	6
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19040	A novel thermal Cas12b from a hot spring bacterium with high target mismatch tolerance and robust DNA cleavage efficiency. <i>International Journal of Biological Macromolecules</i> , 2020, 147, 376-384.	3.6	15
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19042	Evolutionary relationships among bifidobacteria and their hosts and environments. <i>BMC Genomics</i> , 2020, 21, 26.	1.2	26
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19045	A fungal family of lytic polysaccharide monoxygenase-like copper proteins. <i>Nature Chemical Biology</i> , 2020, 16, 345-350.	3.9	63
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19048	An Improved Melon Reference Genome With Single-Molecule Sequencing Uncovers a Recent Burst of Transposable Elements With Potential Impact on Genes. <i>Frontiers in Plant Science</i> , 2019, 10, 1815.	1.7	48
19049	Characterization of Nme5-Like Gene/Protein from the Red Alga <i>Chondrus Crispus</i> . <i>Marine Drugs</i> , 2020, 18, 13.	2.2	5
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19051	Subsurface <i>Stappia</i> : Success Through Defence, Specialisation and Putative Pressure-Dependent Carbon Fixation. <i>Microbial Ecology</i> , 2020, 80, 34-46.	1.4	9
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19054	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
19055	The hallmarks of GSK-3 in morphogenesis and embryonic development metabolism in arthropods. <i>Insect Biochemistry and Molecular Biology</i> , 2020, 118, 103307.	1.2	4
19056	Characterization of <i>Bradyrhizobium</i> strains indigenous to Western Australia and South Africa indicates remarkable genetic diversity and reveals putative new species. <i>Systematic and Applied Microbiology</i> , 2020, 43, 126053.	1.2	16
19057	Phylogenetic placement and the timing of diversification in Australia's endemic <i>Vachellia</i> ( <i>Caesalpinioideae</i> , <i>Mimosoid Clade</i> , <i>Fabaceae</i> ) species. <i>Australian Systematic Botany</i> , 2020, 33, 103.	0.3	4
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19059	Ancient DNA Evidence from China Reveals the Expansion of Pacific Dogs. <i>Molecular Biology and Evolution</i> , 2020, 37, 1462-1469.	3.5	18
19060	An Unexpected Case of <i>Lagochilascariasis</i> : Interdisciplinary Management and Use of 12S and 18S rDNA Analysis. <i>American Journal of the Medical Sciences</i> , 2020, 359, 235-241.	0.4	2
19061	Structural Basis of the Substrate Selectivity of Viperin. <i>Biochemistry</i> , 2020, 59, 652-662.	1.2	28
19062	Defining the landscape of ATP-competitive inhibitor resistance residues in protein kinases. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 92-104.	3.6	30
19063	Prevalence and Phylogenetic Characterization of Hepatitis C Virus Among Indian Men Who Have Sex With Men: Limited Evidence for Sexual Transmission. <i>Journal of Infectious Diseases</i> , 2020, 221, 1875-1883.	1.9	4
19064	Systematic Analysis of Impact of Sampling Regions and Storage Methods on Fecal Gut Microbiome and Metabolome Profiles. <i>MSphere</i> , 2020, 5, .	1.3	37



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19066	Extensive chromosomal rearrangements and rapid evolution of novel effector superfamilies contribute to host adaptation and speciation in the basal ascomycetous fungi. <i>Molecular Plant Pathology</i> , 2020, 21, 330-348.	2.0	22
19067	Prevalence, Pathogenicity, Virulence, Antibiotic Resistance, and Phylogenetic Analysis of Biofilm-Producing <i>Listeria monocytogenes</i> Isolated from Different Ecological Niches in Egypt: Food, Humans, Animals, and Environment. <i>Pathogens</i> , 2020, 9, 5.	1.2	21
19068	Plastome evolution and phylogeny of subtribe Aeridinae (Vandaeae, Orchidaceae). <i>Molecular Phylogenetics and Evolution</i> , 2020, 144, 106721.	1.2	14
19069	A precarious future for distinctive peripheral populations of meadow voles ( <i>Microtus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50,582 Td (p	0.6	11
19070	Complex origins of chloroplast membranes with photosynthetic machineries: multiple transfers of genes from divergent organisms at different times or a single endosymbiotic event?. <i>Journal of Plant Research</i> , 2020, 133, 15-33.	1.2	22
19071	Genomics-driven discovery of the biosynthetic gene cluster of maduramicin and its overproduction in <i>Actinomadura</i> sp. J1-007. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2020, 47, 275-285.	1.4	9
19072	Description of three bacterial strains belonging to the new genus <i>Novipirellula</i> gen. nov., reclassification of <i>Rhodopirellula rosea</i> and <i>Rhodopirellula caenicola</i> and readjustment of the genus threshold of the phylogenetic marker <i>rpoB</i> for Planctomycetaceae. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 1779-1795.	0.7	56
19073	Diversity and Expression Patterns of MADS-Box Genes in <i>Gnetum luofuense</i> —Implications for Functional Diversity and Evolution. <i>Tropical Plant Biology</i> , 2020, 13, 36-49.	1.0	8
19074	Polarity of the ATP binding site of the Na <sup>+</sup> ,K <sup>+</sup> -ATPase, gastric H <sup>+</sup> ,K <sup>+</sup> -ATPase and sarcoplasmic reticulum Ca <sup>2+</sup> -ATPase. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2020, 1862, 183138.	1.4	10
19075	The metagenome-assembled genome of <i>Candidatus Oenococcus aquikefiri</i> from water kefir represents the species <i>Oenococcus siceræ</i> . <i>Food Microbiology</i> , 2020, 88, 103402.	2.1	24
19076	Association of phylogenetic distribution and presence of integrons with multidrug resistance in <i>Escherichia coli</i> clinical isolates from children with diarrhoea. <i>Journal of Infection and Public Health</i> , 2020, 13, 767-772.	1.9	13
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19078	Evolution and molecular epidemiology of polyomaviruses. <i>Infection, Genetics and Evolution</i> , 2020, 79, 104150.	1.0	19
19079	Primer design to assess bacterial degradation of glyphosate and other phosphonates. <i>Journal of Microbiological Methods</i> , 2020, 169, 105814.	0.7	6
19080	Su(var)2-10 and the SUMO Pathway Link piRNA-Guided Target Recognition to Chromatin Silencing. <i>Molecular Cell</i> , 2020, 77, 556-570.e6.	4.5	74
19081	Nuclease and ribonuclease activities in response to salt stress: Identification of PvRNS3, a T2/S-like ribonuclease induced in common bean radicles by salt stress. <i>Plant Physiology and Biochemistry</i> , 2020, 147, 235-241.	2.8	21
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19084	Ultrasmall silica nanoparticles directly ligate the T cell receptor complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 285-291.	3.3	17
19085	First record of <i>Caulerpa lentillifera</i> J. Agardh (Bryopsidales, Chlorophyta) from China. <i>Marine Biology Research</i> , 2020, 16, 44-49.	0.3	3
19086	Reinterpreting the phylogenetic position, systematics and distribution of the Raddia-Sucrea lineage (Poaceae, Olyrinae), with a new monotypic and endangered herbaceous bamboo genus from Brazil. <i>Botanical Journal of the Linnean Society</i> , 2020, 192, 34-60.	0.8	8
19087	Type IV CRISPR-Cas systems are highly diverse and involved in competition between plasmids. <i>Nucleic Acids Research</i> , 2020, 48, 2000-2012.	6.5	128
19088	Convergent evolution leading to the appearance of furanocoumarins in citrus plants. <i>Plant Science</i> , 2020, 292, 110392.	1.7	17
19089	The Melanocortin 4 Receptor p.Ile269Asn Mutation Is Associated with Childhood and Adult Obesity in Mexicans. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2020, 105, e1468-e1477.	1.8	9
19090	Seroprevalence and molecular characterization of foot-and-mouth disease virus in Chad. <i>Veterinary Medicine and Science</i> , 2020, 6, 114-121.	0.6	4
19091	Resolution of the identity of three species of <i>Diplostomum</i> (Digenea: Diplostomidae) parasitising freshwater fishes in South Africa, combining molecular and morphological evidence. <i>International Journal for Parasitology: Parasites and Wildlife</i> , 2020, 11, 50-61.	0.6	16
19092	The out-of-India hypothesis: evidence from an ancient centipede genus, <i>Rhysida</i> (Chilopoda). <i>Journal of the Linnean Society</i> , 2020, 189, 828-861.	1.0	17
19093	Locally acquired infection with <i>Dibothriocephalus nihonkaiense</i> (=Diphyllobothrium nihonkaiense) in France: the importance of molecular diagnosis. <i>Parasitology Research</i> , 2020, 119, 513-518.	0.6	7
19094	<i>Lichenibacterium ramalinae</i> gen. nov., sp. nov., <i>Lichenibacterium minor</i> sp. nov., the first endophytic, beta-carotene producing bacterial representatives from lichen thalli and the proposal of the new family <i>Lichenibacteriaceae</i> within the order <i>Rhizobiales</i> . <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 477-489.	0.7	30
19095	Oxidative stress and the early coevolution of life and biospheric oxygen. , 2020, , 67-85.		6
19096	Single-cell transcriptome sequencing of rumen ciliates provides insight into their molecular adaptations to the anaerobic and carbohydrate-rich rumen microenvironment. <i>Molecular Phylogenetics and Evolution</i> , 2020, 143, 106687.	1.2	14
19097	The other side of the Sahulian coin: biogeography and evolution of Melanesian forest dragons (Agamidae). <i>Biological Journal of the Linnean Society</i> , 2020, 129, 99-113.	0.7	13
19098	The Dundee Resource for Sequence Analysis and Structure Prediction. <i>Protein Science</i> , 2020, 29, 277-297.	3.1	14
19099	Genomic identification and characterization of co-occurring <i>Harveyi</i> clade species following a vibriosis outbreak in Pacific white shrimp, <i>Penaeus (Litopenaeus) vannamei</i> . <i>Aquaculture</i> , 2020, 518, 734628.	1.7	8
19100	Human COBRA 2 vaccine contains two major epitopes that are responsible for eliciting neutralizing antibody responses against heterologous clades of viruses. <i>Vaccine</i> , 2020, 38, 830-839.	1.7	9

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19102	<i>Campylobacter jejuni</i> isolated from poultry meat in Brazil: in silico analysis and genomic features of two strains with different phenotypes of antimicrobial susceptibility. <i>Molecular Biology Reports</i> , 2020, 47, 671-681.	1.0	10
19103	A group of species <i>Psychropotes longicauda</i> (Psychropotidae, Elasipodida, Holothuroidea) from the Kuril-Kamchatka Trench area (North-West Pacific). <i>Progress in Oceanography</i> , 2020, 180, 102222.	1.5	12
19104	Pronocephaloid cercariae (Platyhelminthes: Trematoda) from gastropods of the Queensland coast, Australia. <i>Journal of Helminthology</i> , 2020, 94, e105.	0.4	3
19105	Regulation of the Poly(A) Status of Mitochondrial mRNA by Poly(A)-Specific Ribonuclease Is Conserved among Land Plants. <i>Plant and Cell Physiology</i> , 2020, 61, 470-480.	1.5	7
19106	Geographically isolated Colorado potato beetle mediating distinct defense responses in potato is associated with the alteration of gut microbiota. <i>Journal of Pest Science</i> , 2020, 93, 379-390.	1.9	11
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19113	<i>Wolbachia</i> Endosymbiont of the Horn Fly ( <i>Haematobia irritans irritans</i> ): a Supergroup A Strain with Multiple Horizontally Acquired Cytoplasmic Incompatibility Genes. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	18
19114	Evolutionary superscaffolding and chromosome anchoring to improve <i>Anopheles</i> genome assemblies. <i>BMC Biology</i> , 2020, 18, 1.	1.7	177
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19124	Pinworms of the red howler monkey ( <i>Alouatta seniculus</i> ) in Colombia: Gathering the pieces of the pinworm-primate puzzle. <i>International Journal for Parasitology: Parasites and Wildlife</i> , 2020, 11, 17-28.	0.6	4
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19127	DNA sequence repeats identify numerous Type I restrictionâ€”modification systems that are potential epigenetic regulators controlling phaseâ€”variable regulons; phasevarions. <i>FASEB Journal</i> , 2020, 34, 1038-1051.	0.2	29
19128	<i>Rhodopirellula heiligendammensis</i> sp. nov., <i>Rhodopirellula pilleata</i> sp. nov., and <i>Rhodopirellula solitaria</i> sp. nov. isolated from natural or artificial marine surfaces in Northern Germany and California, USA, and emended description of the genus <i>Rhodopirellula</i> . <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 1737-1750.	0.7	35
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19130	Non-destructive DNA extraction method for identification of <i>Bradysia odoriphaga</i> (Diptera: Sciaridae), a pest of Welsh onion, carrot, and Chinese chive in Japan. <i>Applied Entomology and Zoology</i> , 2020, 55, 181-185.	0.6	1
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19156	Polyphasic characterization of <i>Aspergillus</i> section <i>Flavi</i> isolated from animal feeds in Algeria. <i>Journal of Food Safety</i> , 2020, 40, e12743.	1.1	2
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19158	Evolutionary, gene ontology and physiochemical relationships in LEA proteins of <i>Oryza sativa indica</i> : Detailed computational sequence-based insight. <i>Plant Gene</i> , 2020, 21, 100218.	1.4	2
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19166	Genetic consequences of plant edaphic specialization to solfatara fields: Phylogenetic and population genetic analysis of <i>Carex angustisquama</i> (Cyperaceae). <i>Molecular Ecology</i> , 2020, 29, 3234-3247.	2.0	6
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19169	<i>Vibrio taketomensis</i> sp. nov. by genome taxonomy. <i>Systematic and Applied Microbiology</i> , 2020, 43, 126048.	1.2	17
19170	Genomic and gene expression evidence of nonribosomal peptide and polyketide production among ruminal bacteria: a potential role in niche colonization?. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	9
19171	Unrecognized diversity of a scale worm, <i>Polyeunoa laevis</i> (Annelida: Polynoidae), that feeds on soft coral. <i>Zoologica Scripta</i> , 2020, 49, 236-249.	0.7	4
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19175	Is <i>Pteropyrum</i> a pathway to C4 evolution in Polygonaceae? An integrative approach to the taxonomy and anatomy of <i>Pteropyrum</i> (C3), an immediate relative of <i>Calligonum</i> (C4). <i>Botanical Journal of the Linnean Society</i> , 2020, 192, 369-400.	0.8	11
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19192	Use of whole-genome sequencing in the molecular investigation of care-associated HCoV-OC43 infections in a hematopoietic stem cell transplant unit. <i>Journal of Clinical Virology</i> , 2020, 122, 104206.	1.6	5
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19202	Systematic review of the <i>Chromodoris quadricolor</i> group of East Africa, with descriptions of two new species of the genus <i>Chromodoris</i> Alder & Hancock, 1855 (Heterobranchia). <i>Tj ETQq1 1 0.784814 rgB9 /Overl</i>	1.0	14
19203	<i>Cepaea</i> spp. as a source of <i>Brachylaima mesostoma</i> (Digenea: Brachylaimidae) and <i>Brachylecithum</i> sp. (Digenea: Dicrocoeliidae) larvae in Poland. <i>Parasitology Research</i> , 2020, 119, 145-152.	0.6	7
19204	Characterization and expression analysis of P5CS (P <sup>5</sup> 1-pyrroline-5-carboxylate synthase) gene in two distinct populations of the Atlantic Forest native species <i>Eugenia uniflora</i> L.. <i>Molecular Biology Reports</i> , 2020, 47, 1033-1043.	1.0	7
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19207	Redescriptions of three tintinnine ciliates (Ciliophora: Tintinnina) from coastal waters in China based on lorica features, cell morphology, and rDNA sequence data. <i>European Journal of Protistology</i> , 2020, 72, 125659.	0.5	17
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19213	Classification of intra-genomic helitrons based on features extracted from different orders of FCGS. <i>Informatics in Medicine Unlocked</i> , 2020, 18, 100271.	1.9	4
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19355	<i>Polystoma luohetong</i> n. sp. (Monogenea: Polystomatidae) from <i>Rana chaochiaoensis</i> Liu (Amphibia): Tj ETQq1 1 0.784314 rgBT /Over	0.5	4
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19489	Comparative Genomic Analyses Reveal a Specific Mutation Pattern Between Human Coronavirus SARS-CoV-2 and Bat-CoV RaTG13. <i>Frontiers in Microbiology</i> , 2020, 11, 584717.	1.5	23
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19491	The Phosphoglycerate Kinase (PGK) Gene Family of Maize ( <i>Zea mays</i> var. B73). <i>Plants</i> , 2020, 9, 1639.	1.6	7
19492	Effects of Chemical and Solar Soil-Disinfection Methods on Soil Bacterial Communities. <i>Sustainability</i> , 2020, 12, 9833.	1.6	3
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19507	MOB: Pivotal Conserved Proteins in Cytokinesis, Cell Architecture and Tissue Homeostasis. <i>Biology</i> , 2020, 9, 413.	1.3	10
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19511	Combinatorial Glycomic Analyses to Direct CAZyme Discovery for the Tailored Degradation of Canola Meal Non-Starch Dietary Polysaccharides. <i>Microorganisms</i> , 2020, 8, 1888.	1.6	12
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19514	Morphology, ultrastructure, genomics, and phylogeny of <i>Euplotes vanleeuwenhoekii</i> sp. nov. and its ultra-reduced endosymbiont <i>Candidatus Pinguicoccus supinus</i> sp. nov.. <i>Scientific Reports</i> , 2020, 10, 20311.	1.6	37
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19519	Deformed Wing Virus in Two Widespread Invasive Ants: Geographical Distribution, Prevalence, and Phylogeny. <i>Viruses</i> , 2020, 12, 1309.	1.5	4
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19521	Provenances originate morphological and microbiome variation of <i>Tuber pseudobrumale</i> in southwestern China despite strong genetic consistency. <i>Mycological Progress</i> , 2020, 19, 1545-1558.	0.5	5
19522	Evolutionary and structural analysis of SARS-CoV-2 specific evasion of host immunity. <i>Genes and Immunity</i> , 2020, 21, 409-419.	2.2	37
19523	<i>Vickermania</i> gen. nov., trypanosomatids that use two joined flagella to resist midgut peristaltic flow within the fly host. <i>BMC Biology</i> , 2020, 18, 187.	1.7	17
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19527	A conserved regulator controls asexual sporulation in the fungal pathogen <i>Candida albicans</i> . <i>Nature Communications</i> , 2020, 11, 6224.	5.8	10
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19530	A Rapid Colorimetric Assay for On-Site Authentication of Cephalopod Species. <i>Biosensors</i> , 2020, 10, 190.	2.3	7
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19532	A small UTX stabilization domain of Trr is conserved within mammalian MLL3-4/COMPASS and is sufficient to rescue loss of viability in null animals. <i>Genes and Development</i> , 2020, 34, 1493-1502.	2.7	14
19533	Massive gene presence-absence variation shapes an open pan-genome in the Mediterranean mussel. <i>Genome Biology</i> , 2020, 21, 275.	3.8	105

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19542	Three new species of Synergini wasps from same galls on <i>Lithocarpus glaber</i> (Thunb.) in Hunan, China (Hymenoptera, Cynipidae). <i>Insect Systematics and Evolution</i> , 2020, 51, 551-583.	0.2	5
19543	<i>Aphelenchoides smolae</i> n. sp. (Tylenchina: Aphelenchoididae) found in <i>Lilium orientalis</i> imported into China from The Netherlands. <i>Nematology</i> , 2020, 22, 799-813.	0.2	2
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19546	Molecular analysis reveals a high diversity of <i>Anopheles</i> species in Karama, West Sulawesi, Indonesia. <i>Parasites and Vectors</i> , 2020, 13, 379.	1.0	15
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19548	Insights on Zika virus envelope gene conservation in American outbreaks. <i>Brazilian Journal of Microbiology</i> , 2020, 51, 1601-1605.	0.8	1
19549	The complete chloroplast genome of <i>Isochrysis galbana</i> and comparison with related haptophyte species. <i>Algal Research</i> , 2020, 50, 101989.	2.4	14
19550	Use of chitosan and tannins as alternatives to antibiotics to control mold growth on PDO Pecorino Toscano cheese rind. <i>Food Microbiology</i> , 2020, 92, 103598.	2.1	8
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19558	Comparative Proteomics of Octocoral and Scleractinian Scleractinians and the Evolution of Coral Calcification. <i>Genome Biology and Evolution</i> , 2020, 12, 1623-1635.	1.1	14
19559	Molecular identification of <i>Bactrocera passiflorae</i> (Diptera: Tephritidae): Challenge and solution for DNA barcoding. <i>Journal of Applied Entomology</i> , 2020, 144, 877-884.	0.8	2
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19564	Revalidation of <i>Ogyrides occidentalis</i> (Ortmann, 1893) (Decapoda: Caridea: Ogyrididae) from Brazil based on morphological and mtDNA evidences. <i>Journal of Crustacean Biology</i> , 2020, 40, 627-633.	0.3	2
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19566	Population genetic structure and marker-trait associations in East and West African <i>Striga hermonthica</i> with varying phenotypic response to <i>Fusarium oxysporum</i> f. sp. <i>strigae</i> isolates Foxy2 and FK3. <i>Plant Journal</i> , 2020, 104, 391-402.	2.8	4
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19571	Comparative Genomics of Microbacterium Species to Reveal Diversity, Potential for Secondary Metabolites and Heavy Metal Resistance. <i>Frontiers in Microbiology</i> , 2020, 11, 1869.	1.5	29
19572	Genome-Wide Identification and Functional Characterization of the Heat Shock Factor Family in Eggplant ( <i>Solanum melongena</i> L.) under Abiotic Stress Conditions. <i>Plants</i> , 2020, 9, 915.	1.6	12
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19580	MAGA: A Supervised Method to Detect Motifs From Annotated Groups in Alignments. <i>Evolutionary Bioinformatics</i> , 2020, 16, 117693432091619.	0.6	1
19581	Fungal Planet description sheets: 1042–1111. <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2020, 44, 301-459.	1.6	91
19582	Characteristics of <i>Helicobacter pylori</i> strains isolated from Mauritanian patients. <i>Helicobacter</i> , 2020, 25, e12726.	1.6	1
19583	Genetic characterisation of novel G29P[14] and G10P[11] rotavirus strains from African buffalo. <i>Infection, Genetics and Evolution</i> , 2020, 85, 104463.	1.0	9
19584	Multivariate analysis as a method to evaluate antigenic relationships between BVDV vaccine and field strains. <i>Vaccine</i> , 2020, 38, 5764-5772.	1.7	15
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19586	An evolution-based model for designing choriismate mutase enzymes. <i>Science</i> , 2020, 369, 440-445.	6.0	195
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19590	TickSialoFam (TSFam): A Database That Helps to Classify Tick Salivary Proteins, a Review on Tick Salivary Protein Function and Evolution, With Considerations on the Tick Sialome Switching Phenomenon. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 374.	1.8	41
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19594	Quantification of Cable Bacteria in Marine Sediments via qPCR. <i>Frontiers in Microbiology</i> , 2020, 11, 1506.	1.5	14
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19619	Genomic Characterization and Expression of Juvenile Hormone Esterase-Like Carboxylesterase Genes in Pacific White Shrimp, <i>Litopenaeus vannamei</i> . <i>International Journal of Molecular Sciences</i> , 2020, 21, 5444.	1.8	6
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19623	The Gut Microbiota Communities of Wild Arboreal and Ground-Feeding Tropical Primates Are Affected Differently by Habitat Disturbance. <i>MSystems</i> , 2020, 5, .	1.7	36

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19627	A new cyovirus from the Japanese peppered moth, <i>Biston robustus</i> . <i>Journal of Invertebrate Pathology</i> , 2020, 174, 107417.	1.5	5
19628	A Distinct Motif in a Prokaryotic Small Ras-Like GTPase Highlights Unifying Features of Walker B Motifs in P-Loop NTPases. <i>Journal of Molecular Biology</i> , 2020, 432, 5544-5564.	2.0	14
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19630	A novel community-acquired MRSA clone, USA300-LV/J, uniquely evolved in Japan. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 3131-3134.	1.3	12
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19632	Globally Abundant <i>Candidatus</i> <i>Udaebacter</i> Benefits from Release of Antibiotics in Soil and Potentially Performs Trace Gas Scavenging. <i>MSphere</i> , 2020, 5, .	1.3	32
19633	Biallelic loss-of-function <i>ZFYVE19</i> mutations are associated with congenital hepatic fibrosis, sclerosing cholangiopathy and high-GGT cholestasis. <i>Journal of Medical Genetics</i> , 2021, 58, 514-525.	1.5	16
19634	Distribution, DNA barcoding and genetic diversity of potato cyst nematodes in Indonesia. <i>European Journal of Plant Pathology</i> , 2020, 158, 363-380.	0.8	11
19635	Advances in optical mapping for genomic research. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 2051-2062.	1.9	71
19636	Taxonomic study of nine new <i>Winogradskyella</i> species occurring in the shallow waters of Helgoland Roads, North Sea. Proposal of <i>Winogradskyella schleiferi</i> sp. nov., <i>Winogradskyella costae</i> sp. nov., <i>Winogradskyella helgolandensis</i> sp. nov., <i>Winogradskyella vidalii</i> sp. nov., <i>Winogradskyella forsetii</i> sp. nov., <i>Winogradskyella ludwigii</i> sp. nov., <i>Winogradskyella ursingii</i> sp. nov., <i>Winogradskyella wichelsiae</i> sp. nov., and <i>Candidatus</i> <i>Winogradskyella atlantica</i> sp. nov.. <i>Systematic and Applied Microbiology</i> , 2020, 43, 126128.	1.2	38
19637	Quantification of <i>nosZ</i> genes and transcripts in activated sludge microbiomes with novel group-specific qPCR methods validated with metagenomic analyses. <i>Water Research</i> , 2020, 185, 116261.	5.3	19
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19645	Evolutionary directions of single nucleotide substitutions and structural mutations in the chloroplast genomes of the family Calycanthaceae. <i>BMC Evolutionary Biology</i> , 2020, 20, 96.	3.2	23
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19648	Microbiomes and Specific Symbionts of Social Spiders: Compositional Patterns in Host Species, Populations, and Nests. <i>Frontiers in Microbiology</i> , 2020, 11, 1845.	1.5	20
19649	Cyanobacteria Phylogenetic Studies Reveal Evidence for Polyphyletic Genera from Thermal and Freshwater Habitats. <i>Diversity</i> , 2020, 12, 298.	0.7	17
19650	Fungal Endophytic Community Associated with Guarana ( <i>Paullinia cupana</i> Var. <i>Sorbilis</i> ): Diversity Driver by Genotypes in the Centre of Origin. <i>Journal of Fungi (Basel, Switzerland)</i> , 2020, 6, 123.	1.5	3
19651	New Insight into Antimicrobial Compounds from Food and Marine-Sourced Carnobacterium Species through Phenotype and Genome Analyses. <i>Microorganisms</i> , 2020, 8, 1093.	1.6	9
19652	Characterization and selection of functional yeast strains during sourdough fermentation of different cereal wholegrain flours. <i>Scientific Reports</i> , 2020, 10, 12856.	1.6	36
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19654	Structural and posttranslational analysis of human calcium-binding protein, spermatid-associated 1. <i>Journal of Cellular Biochemistry</i> , 2020, 121, 4945-4958.	1.2	3
19655	Relationships among streptococci from the mitis group, misidentified as <i>Streptococcus pneumoniae</i> . <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2020, 39, 1865-1878.	1.3	7
19656	<i>Pseudohurleytrema yolandae</i> n. sp., the first monorchiid trematode reported from the Triacanthidae (Tetraodontiformes). <i>Systematic Parasitology</i> , 2020, 97, 491-500.	0.5	6
19657	Phylogenetic analysis and geographical distribution of <i>Theileria equi</i> and <i>Babesia caballi</i> sequences from horses residing in Spain. <i>Ticks and Tick-borne Diseases</i> , 2020, 11, 101521.	1.1	6
19658	Convergent evolution of processivity in bacterial and fungal cellulases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 19896-19903.	3.3	31
19659	Integrative taxonomy identifies a new stingray species of the genus <i>Hypanus</i> Rafinesque, 1818 (Dasyatidae, Myliobatiformes), from the Tropical Southwestern Atlantic. <i>Journal of Fish Biology</i> , 2020, 97, 1120-1142.	0.7	20

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19661	Enterococci from Wild Magellanic Penguins ( <i>Spheniscus magellanicus</i> ) as an Indicator of Marine Ecosystem Health and Human Impact. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	5
19662	Evolution of Btr1-D Gene in Diploid Wheat Species of the Genus <i>Triticum</i> L.. <i>Russian Journal of Genetics</i> , 2020, 56, 633-637.	0.2	5
19663	Proposal of <i>Spinulacorpis biforme</i> (Smales, 2014) n. g., n. comb. and the <i>Spinulacorpidae</i> n. fam. to resolve paraphyly of the acanthocephalan family <i>Rhadinorhynchidae</i> L&Auml;he, 1912. <i>Systematic Parasitology</i> , 2020, 97, 477-490.	0.5	5
19664	<i>Thecamoeba foliovenanda</i> n. sp. (Amoebozoa, Discosea, Thecamoebida) – One more case of sibling species among amoebae of the genus <i>Thecamoeba</i> . <i>European Journal of Protistology</i> , 2020, 76, 125716.	0.5	6
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19666	OnfD, an AraC-Type Transcriptional Regulator Encoded by <i>Rhizobium tropici</i> CIAT 899 and Involved in Nod Factor Synthesis and Symbiosis. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	8
19667	Production of carbohydrates, lipids and polyunsaturated fatty acids (PUFA) by the polar marine microalga <i>Chlamydomonas malina</i> RCC2488. <i>Algal Research</i> , 2020, 50, 102016.	2.4	35
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19669	Fungus-growing insects host a distinctive microbiota apparently adapted to the fungiculture environment. <i>Scientific Reports</i> , 2020, 10, 12384.	1.6	31
19670	A new species of <i>Gloeandromyces</i> from Ecuador and Panama revealed by morphology and phylogenetic reconstruction, with a discussion of secondary barcodes in <i>Laboulbeniomycetes</i> taxonomy. <i>Mycologia</i> , 2020, 112, 1192-1202.	0.8	18
19671	Effects of fermented feeds and ginseng polysaccharides on the intestinal morphology and microbiota composition of Xuefeng black-bone chicken. <i>PLoS ONE</i> , 2020, 15, e0237357.	1.1	16
19672	Evaluation of Multifarious Plant Growth Promoting Trials of Yeast Isolated from the Soil of Assam Tea ( <i>Camellia sinensis</i> var. <i>assamica</i> ) Plantations in Northern Thailand. <i>Microorganisms</i> , 2020, 8, 1168.	1.6	25
19673	Hidden diversity in Antarctica: Molecular and morphological evidence of two different species within one of the most conspicuous ascidian species. <i>Ecology and Evolution</i> , 2020, 10, 8127-8143.	0.8	6
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19675	Predicting functional effects of missense variants in voltage-gated sodium and calcium channels. <i>Science Translational Medicine</i> , 2020, 12, .	5.8	84
19676	Influence of the polar light cycle on seasonal dynamics of an Antarctic lake microbial community. <i>Microbiome</i> , 2020, 8, 116.	4.9	32
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19682	Phylogeny and diversification of the gallopheasants (Aves: Galliformes): Testing roles of sexual selection and environmental niche divergence. Zoologica Scripta, 2020, 49, 549-562.	0.7	5
19683	<i>De Novo</i> Assembly of the Northern Cardinal (<i>Cardinalis cardinalis</i>) Genome Reveals Candidate Regulatory Regions for Sexually Dichromatic Red Plumage Coloration. G3: Genes, Genomes, Genetics, 2020, 10, 3541-3548.	0.8	9
19684	Bathy- and mesopelagic annelida from the Arctic Ocean: Description of new, redescription of known and notes on some "cosmopolitan" species. Deep-Sea Research Part I: Oceanographic Research Papers, 2020, 165, 103327.	0.6	5
19685	Mechanism Underlying Anti-Markovnikov Addition in the Reaction of Pentalene Synthase. Biochemistry, 2020, 59, 3271-3283.	1.2	11
19686	A new genus of Bucephalidae Poche, 1907 (Trematoda: Digenea) for three new species infecting the yellowtail pike, Sphyaena obtusata Cuvier (Sphyaenidae), from Moreton Bay, Queensland, Australia. Systematic Parasitology, 2020, 97, 455-476.	0.5	9
19687	The Morphology and Phylogeny of Three Diophrys Ciliates Collected from the Subtropical Waters of China, Including a New Species (Ciliophora; Euplotia). Journal of Ocean University of China, 2020, 19, 975-987.	0.6	3
19688	Expression Evolution of Ancestral XY Gametologs across All Major Groups of Placental Mammals. Genome Biology and Evolution, 2020, 12, 2015-2028.	1.1	13
19689	Three Related Enzymes in Candida albicans Achieve Arginine- and Agmatine-Dependent Metabolism That Is Essential for Growth and Fungal Virulence. MBio, 2020, 11, .	1.8	15
19690	The genus Madurella: Molecular identification and epidemiology in Sudan. PLoS Neglected Tropical Diseases, 2020, 14, e0008420.	1.3	8
19691	Horizontal Transfer and Gene Loss Shaped the Evolution of Alpha-Amylases in Bilaterians. G3: Genes, Genomes, Genetics, 2020, 10, 709-719.	0.8	4
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19693	COVID-19 in health-care workers in three hospitals in the south of the Netherlands: a cross-sectional study. Lancet Infectious Diseases, The, 2020, 20, 1273-1280.	4.6	220
19694	ACDC, a global database of amphibian cytochrome-b sequences using reproducible curation for GenBank records. Scientific Data, 2020, 7, 268.	2.4	7
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19698	Genomic Features and Evolution of the Parapoxvirus during the Past Two Decades. <i>Pathogens</i> , 2020, 9, 888.	1.2	7
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19700	Phylogenetic analysis of two new complete genomes of the hepatitis E virus (HEV) genotype 3 from Thailand. <i>Molecular Biology Reports</i> , 2020, 47, 8657-8668.	1.0	2
19701	Three novel species and a new record of <i>Daldinia</i> (Hypoxylaceae) from Thailand. <i>Mycological Progress</i> , 2020, 19, 1113-1132.	0.5	6
19702	Host plant selection and virus transmission by <i>Rhopalosiphum maidis</i> are conditioned by potyvirus infection in <i>Sorghum bicolor</i> . <i>Arthropod-Plant Interactions</i> , 2020, 14, 811-823.	0.5	7
19703	Transmission of SARS-CoV-2 in South Asian countries: molecular evolutionary model based phylogenetic and mutation analysis. <i>Environmental Sustainability</i> , 2021, 4, 533-541.	1.4	4
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19705	First molecular examination of Vietnamese mudflat snails in the genus <i>Naranjia</i> Golding, Ponder & Byrne, 2007 (Gastropoda: Amphibolidae). <i>Scientific Reports</i> , 2020, 10, 18714.	1.6	1
19707	Global regulatory features of alternative splicing across tissues and within the nervous system of <i>C. elegans</i> . <i>Genome Research</i> , 2020, 30, 1766-1780.	2.4	8
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19709	Structural insight into the substrate specificity of <i>Bombyx mori</i> Î <sup>2</sup> -fructofuranosidase belonging to the glycoside hydrolase family 32. <i>Insect Biochemistry and Molecular Biology</i> , 2020, 127, 103494.	1.2	15
19710	Molecular and functional characterization of somatostatin-type signalling in a deuterostome invertebrate. <i>Open Biology</i> , 2020, 10, 200172.	1.5	26
19711	Vulpeculin: a novel and abundant lipocalin in the urine of the common brushtail possum, <i>Trichosurus vulpecula</i> . <i>Open Biology</i> , 2020, 10, 200218.	1.5	2
19712	Repeated evidence that the accelerated evolution of sperm is associated with their fertilization function. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20201286.	1.2	8
19713	De novo biosynthesis of simple aromatic compounds by an arthropod ( <i>Archezogozetes</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 102 Td (	1.2	4
19714	Amplicon-Based, Next-Generation Sequencing Approaches to Characterize Single Nucleotide Polymorphisms of Orthohantavirus Species. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 565591.	1.8	15

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19717	Genome-Wide Identification of Barley ABC Genes and Their Expression in Response to Abiotic Stress Treatment. <i>Plants</i> , 2020, 9, 1281.	1.6	25
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19719	Molecular Basis of Chemotactile Sensation in Octopus. <i>Cell</i> , 2020, 183, 594-604.e14.	13.5	51
19720	Multiple transcriptome mining coupled with tissue specific molecular cloning and mass spectrometry provide insights into agatoxin-like peptide conservation in decapod crustaceans. <i>General and Comparative Endocrinology</i> , 2020, 299, 113609.	0.8	4
19721	The histone modification H3K4me3 marks functional genes in soybean nodules. <i>Genomics</i> , 2020, 112, 5282-5294.	1.3	8
19722	A Split Methyl Halide Transferase AND Gate That Reports by Synthesizing an Indicator Gas. <i>ACS Synthetic Biology</i> , 2020, 9, 3104-3113.	1.9	10
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19724	Detection of four RNA viruses in commercial and informal potato seed tubers in Antioquia (Colombia). <i>Archives of Phytopathology and Plant Protection</i> , 2020, , 1-22.	0.6	4
19725	Morphological, phylogenetic, and pathogenic analyses of <i>Fusarium andiyazi</i> associated with sugar beet root diseases. <i>Archives of Phytopathology and Plant Protection</i> , 0, , 1-19.	0.6	3
19726	Comparative Genomics Platform and Phylogenetic Analysis of Fungal Laccases and Multi-Copper Oxidases. <i>Mycobiology</i> , 2020, 48, 373-382.	0.6	9
19727	Antigenicity prediction and vaccine recommendation of human influenza virus A (H3N2) using convolutional neural networks. <i>Human Vaccines and Immunotherapeutics</i> , 2020, 16, 2690-2708.	1.4	14
19728	Temporal Changes in Patient-Matched <i>Staphylococcus epidermidis</i> Isolates from Infections: towards Defining a "True" Persistent Infection. <i>Microorganisms</i> , 2020, 8, 1508.	1.6	2
19729	Phylogeny of symbiotic genes reveals symbiobars within legume-nodulating <i>Paraburkholderia</i> species. <i>Systematic and Applied Microbiology</i> , 2020, 43, 126151.	1.2	12
19730	Phylotype-Level Characterization of Complex Communities of Lactobacilli Using a High-Throughput, High-Resolution Phenylalanyl-tRNA Synthetase ( <i>pheS</i> ) Gene Amplicon Sequencing Approach. <i>Applied and Environmental Microbiology</i> , 2020, 87, .	1.4	4
19731	A Heterogeneous Swine Show Circuit Drives Zoonotic Transmission of Influenza A Viruses in the United States. <i>Journal of Virology</i> , 2020, 94, .	1.5	7
19732	Genome-wide study of pineapple ( <i>Ananas comosus</i> L.) bHLH transcription factors indicates that cryptochrome-interacting bHLH2 (AcCIB2) participates in flowering time regulation and abiotic stress response. <i>BMC Genomics</i> , 2020, 21, 735.	1.2	24

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19734	Bacterial genome-wide association study of hyper-virulent pneumococcal serotype 1 identifies genetic variation associated with neurotropism. <i>Communications Biology</i> , 2020, 3, 559.	2.0	11
19735	An Expanded Genetic Code Enables Trimethylamine Metabolism in Human Gut Bacteria. <i>MSystems</i> , 2020, 5, .	1.7	22
19736	Identification and Characterization of a Novel CLCN7 Variant Associated with Osteopetrosis. <i>Genes</i> , 2020, 11, 1242.	1.0	3
19737	The complete mitochondrial genome of large odorous frog, <i>Odorrana graminea</i> (Amphibia: Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50 0 0)	0.2	3
19738	Characterization of Current <i>Fusarium oxysporum</i> f. sp. <i>vasinfectum</i> Isolates from Cotton in the San Joaquin Valley of California and Lower Valley El Paso, Texas. <i>Plant Disease</i> , 2021, 105, 1898-1911.	0.7	20
19739	Bacteriome-Associated Endosymbiotic Bacteria of Nosodendron Tree Sap Beetles (Coleoptera: Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50 0 0)	1.5	8
19740	<i>Streptococcus thermophiles</i> DMST-H2 Promotes Recovery in Mice with Antibiotic-Associated Diarrhea. <i>Microorganisms</i> , 2020, 8, 1650.	1.6	18
19741	Compositional and Functional Comparisons of the Microbiota in the Colostrum and Mature Milk of Dairy Goats. <i>Animals</i> , 2020, 10, 1955.	1.0	9
19742	<i>Streptomyces alkaliterrae</i> sp. nov., isolated from an alkaline soil, and emended descriptions of <i>Streptomyces alkaliphilus</i> , <i>Streptomyces calidiresistens</i> and <i>Streptomyces durbertensis</i> . <i>Systematic and Applied Microbiology</i> , 2020, 43, 126153.	1.2	17
19743	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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19745	Large-Scale Phylogenetic Analysis of Trypanosomatid Adenylate Cyclases Reveals Associations with Extracellular Lifestyle and Host-Pathogen Interplay. <i>Genome Biology and Evolution</i> , 2020, 12, 2403-2416.	1.1	19
19746	Origins and genetic legacy of prehistoric dogs. <i>Science</i> , 2020, 370, 557-564.	6.0	152
19747	Entomopathogenic fungi of the genus <i>Beauveria</i> and their pathogenicity to <i>Ips typographus</i> (Coleoptera: Curculionidae) in the Vitosha National Park, Bulgaria. <i>Journal of Forest Science</i> , 2020, 66, 420-435.	0.5	0
19748	Genomic Characterization of Methicillin-Resistant <i>Staphylococcus aureus</i> (MRSA) by High-Throughput Sequencing in a Tertiary Care Hospital. <i>Genes</i> , 2020, 11, 1219.	1.0	10
19749	Trichome morphology provides phylogenetically informative signal for generic delimitation in tribe Marrubieae (Lamiaceae). <i>Flora: Morphology, Distribution, Functional Ecology of Plants</i> , 2020, 273, 151720.	0.6	2
19750	Inferring the genetic variability in Indian SARS-CoV-2 genomes using consensus of multiple sequence alignment techniques. <i>Infection, Genetics and Evolution</i> , 2020, 85, 104522.	1.0	12

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19752	The Quaternary range dynamics of <i>Noccaea iberidea</i> (Brassicaceae), a typical representative of subalpine/alpine steppe communities of Anatolian mountains. <i>Biological Journal of the Linnean Society</i> , 2020, 131, 986-1001.	0.7	7
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19759	Genome-wide characterization and expression analysis suggested diverse functions of the mechanosensitive channel of small conductance-like (MSL) genes in cereal crops. <i>Scientific Reports</i> , 2020, 10, 16583.	1.6	24
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19766	The entomophagous caterpillar fungus <i>Ophiocordyceps sinensis</i> is consumed by its lepidopteran host as a plant endophyte. <i>Fungal Ecology</i> , 2020, 47, 100989.	0.7	26
19767	Range-wide Phylogeography of a Nivicolous Protist <i>Didymium nivicola</i> Meyl. ( <i>Myxomycetes</i> ). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 107 T</i> 171, 125771.	0.6	12
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19770	The complete mitochondrial genome of the yellowfin shiner, <i>Notropis lutipinnis</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 3185-3187.	0.2	0
19771	Demographic, Environmental, and Phenotypic Change but Genetic Consistency in the Jellyfish <i>Mastigias papua</i> . <i>Biological Bulletin</i> , 2020, 239, 80-94.	0.7	1
19772	Comparison of the gut microbiota in the groundwater amphipod <i>Crangonyx islandicus</i> Svavarsson & Kristjánsson, 2006 (Amphipoda: Crangonyctidae) to biofilms in its spring-source habitat. <i>Journal of Crustacean Biology</i> , 2020, 40, 657-667.	0.3	1
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19774	Can domestic pigeon be a potential carrier of zoonotic <i>Salmonella</i> ? <i>Transboundary and Emerging Diseases</i> , 2021, 68, 2321-2333.	1.3	10
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19788	Quinone perception in plants via leucine-rich-repeat receptor-like kinases. <i>Nature</i> , 2020, 587, 92-97.	13.7	77
19789	<i>Fistulifera alcalina</i> sp. nov. (Naviculales, Stauroneidaceae) a new alkaliphilic diatom species from Lake Okeechobee, Florida (USA). <i>Diatom Research</i> , 2020, 35, 301-311.	0.5	0
19790	Mapping genome variation of SARS-CoV-2 worldwide highlights the impact of COVID-19 super-spreaders. <i>Genome Research</i> , 2020, 30, 1434-1448.	2.4	91
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19792	Curated multiple sequence alignment for the Adenomatous Polyposis Coli (APC) gene and accuracy of in silico pathogenicity predictions. <i>PLoS ONE</i> , 2020, 15, e0233673.	1.1	1
19793	Flexible genes establish widespread bacteriophage pan-genomes in cryoconite hole ecosystems. <i>Nature Communications</i> , 2020, 11, 4403.	5.8	36
19794	Production of Diverse Beauveriolide Analogs in Closely Related Fungi: a Rare Case of Fungal Chemodiversity. <i>MSphere</i> , 2020, 5, .	1.3	12
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19799	American mastodon mitochondrial genomes suggest multiple dispersal events in response to Pleistocene climate oscillations. <i>Nature Communications</i> , 2020, 11, 4048.	5.8	9
19800	A phylogeny for African <i>Pipistrellus</i> species with the description of a new species from West Africa (Mammalia: Chiroptera). <i>Zoological Journal of the Linnean Society</i> , 2021, 191, 548-574.	1.0	8
19801	Use of organic exudates from two polar diatoms by bacterial isolates from the Arctic Ocean. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2020, 378, 20190356.	1.6	8
19802	Mutant and Recombinant Phages Selected from <i>In Vitro</i> Coevolution Conditions Overcome Phage-Resistant <i>Listeria monocytogenes</i> . <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	25
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19808	Evolution of Pelage Luminance in Squirrels (Sciuridae). <i>Frontiers in Ecology and Evolution</i> , 2020, 8, .	1.1	4
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19813	Resurrecting the genus <i>Geomorium</i> : Systematic study of fungi in the genera <i>Underwoodia</i> and <i>Gymnohydnotrya</i> (Pezizales) with the description of three new South American species. <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2020, 44, 98-112.	1.6	6
19814	Decrease of oral microbial diversity might correlate with radiation esophagitis in patients with esophageal cancer undergoing chemoradiation: A pilot study. <i>Precision Radiation Oncology</i> , 2020, 4, 81-88.	0.4	4
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19817	Isolation of Cysteine-Rich Peptides from <i>Citrullus colocynthis</i> . <i>Biomolecules</i> , 2020, 10, 1326.	1.8	6
19818	Spidroin profiling of cribellate spiders provides insight into the evolution of spider prey capture strategies. <i>Scientific Reports</i> , 2020, 10, 15721.	1.6	23
19819	Persistence of Suspected Probiotic Organisms in Preterm Infant Gut Microbiota Weeks After Probiotic Supplementation in the NICU. <i>Frontiers in Microbiology</i> , 2020, 11, 574137.	1.5	20
19820	A Human IgSF Cell-Surface Interactome Reveals a Complex Network of Protein-Protein Interactions. <i>Cell</i> , 2020, 182, 1027-1043.e17.	13.5	57
19821	How parasite exposure and time interact to determine <i>Australapatemon burti</i> (Trematoda: Digenea) infections in second intermediate hosts ( <i>Erpobdella microstoma</i> ) (Hirudinea: Erpodeididae). <i>Experimental Parasitology</i> , 2020, 219, 108002.	0.5	2
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19824	Evidence for the Pleistocene Arc Hypothesis from genome-wide SNPs in a Neotropical dry forest specialist, the Rufous-fronted Thornbird ( <i>Furnariidae</i> : <i>Phacellodomus rufifrons</i> ). <i>Molecular Ecology</i> , 2020, 29, 4457-4472.	2.0	15
19825	Diversity of Sea Star-Associated Densoviruses and Transcribed Endogenous Viral Elements of Densovirus Origin. <i>Journal of Virology</i> , 2020, 95, .	1.5	14
19826	SMRT- and Illumina-based RNA-seq analyses unveil the ginsenoside biosynthesis and transcriptomic complexity in <i>Panax notoginseng</i> . <i>Scientific Reports</i> , 2020, 10, 15310.	1.6	10
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19828	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
19829	<i>Sphingomonas palmae</i> sp. nov. and <i>Sphingomonas gellani</i> sp. nov., endophytically associated phyllosphere bacteria isolated from economically important crop plants. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 1617-1632.	0.7	13
19830	Efficacy of DNA barcode internal transcribed spacer 2 (ITS 2) in phylogenetic study of <i>Alpinia</i> species from Peninsular Malaysia. <i>Physiology and Molecular Biology of Plants</i> , 2020, 26, 1889-1896.	1.4	6
19831	A new species of <i>Lecithostaphylus</i> Odhner, 1911 (Trematoda: Zoogonidae) from the Pacific needlefish, <i>Tylosurus pacificus</i> , off the Pacific coast of Mexico, with a molecular assessment of the phylogenetic position of this genus within the family. <i>Marine Biodiversity</i> , 2020, 50, 1.	0.3	4
19832	Amplification Curve Analysis: Data-Driven Multiplexing Using Real-Time Digital PCR. <i>Analytical Chemistry</i> , 2020, 92, 13134-13143.	3.2	35
19833	High-Level Multiplexing in Digital PCR with Intercalating Dyes by Coupling Real-Time Kinetics and Melting Curve Analysis. <i>Analytical Chemistry</i> , 2020, 92, 14181-14188.	3.2	16
19834	Pre-initiation and elongation structures of full-length La Crosse virus polymerase reveal functionally important conformational changes. <i>Nature Communications</i> , 2020, 11, 3590.	5.8	36
19835	The diversification and lineage-specific expansion of nitric oxide signaling in Placozoa: insights in the evolution of gaseous transmission. <i>Scientific Reports</i> , 2020, 10, 13020.	1.6	37
19836	Targeting SARS-CoV-2 Nsp12/Nsp8 interaction interface with approved and investigational drugs: an <i>in silico</i> structure-based approach. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 918-930.	2.0	23
19837	Genetic and environmental determinants of human TCR repertoire diversity. <i>Immunity and Ageing</i> , 2020, 17, 26.	1.8	42
19838	The Absence of C-5 DNA Methylation in <i>Leishmania donovani</i> Allows DNA Enrichment from Complex Samples. <i>Microorganisms</i> , 2020, 8, 1252.	1.6	9
19839	A Novel Primer Mixture for GH48 Genes: Quantification and Identification of Truly Cellulolytic Bacteria in Biogas Fermenters. <i>Microorganisms</i> , 2020, 8, 1297.	1.6	3
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19843	Viral Metagenomic Profiling of Croatian Bat Population Reveals Sample and Habitat Dependent Diversity. Viruses, 2020, 12, 891.	1.5	20
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19845	Comparative Genomics Underlines Multiple Roles of Profftella, an Obligate Symbiont of Psyllids: Providing Toxins, Vitamins, and Carotenoids. Genome Biology and Evolution, 2020, 12, 1975-1987.	1.1	39
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19847	Diversity of Mosquitoes (Diptera: Culicidae) in the Caatinga Biome, Brazil, from the Widespread to the Endemic. Insects, 2020, 11, 468.	1.0	5
19848	Phylogenetic and Chemotaxonomic Studies Confirm the Affinities of Stromatoneurospora phoenix to the Coprophilous Xylariaceae. Journal of Fungi (Basel, Switzerland), 2020, 6, 144.	1.5	19
19849	Teff Type-I Sourdough to Produce Gluten-Free Muffin. Microorganisms, 2020, 8, 1149.	1.6	10
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19854	A novel BSD domain-containing transcription factor controls vegetative growth, leaf senescence, and fruit quality in tomato. Journal of Experimental Botany, 2020, 71, 6945-6957.	2.4	6
19855	Adaptation and molecular evidence for convergence in decapod crustaceans from deep-sea hydrothermal vent environments. Molecular Ecology, 2020, 29, 3954-3969.	2.0	13
19856	Reengineering biocatalysts: Computational redesign of chondroitinase ABC improves efficacy and stability. Science Advances, 2020, 6, eabc6378.	4.7	28
19857	Improved reference genome of the arboviral vector Aedes albopictus. Genome Biology, 2020, 21, 215.	3.8	65
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19860	Congruence Amidst Discordance between Sequence and Protein-Content Based Phylogenies of Fungi. <i>Journal of Fungi</i> (Basel, Switzerland), 2020, 6, 134.	1.5	1
19861	The complete mitochondrial genome of <i>Tachysurus virgatus</i> (Oshima 1926) (Siluriformes: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.2	0
19862	<i>Salmonella enterica</i> Serovar Typhimurium Temporally Modulates the Enteric Microbiota and Host Responses To Overcome Colonization Resistance in Swine. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	18
19863	A Chromosome-Scale Genome Assembly for the <i>Fusarium oxysporum</i> Strain Fo5176 To Establish a Model <i>Arabidopsis</i> -Fungal Pathosystem. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3549-3555.	0.8	28
19864	Investigating the Role of Translationally Control Tumor Protein in Growth, Development and Differentiation of <i>Dictyostelium discoideum</i> . <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 742.	1.8	3
19865	CoronaVR: A Computational Resource and Analysis of Epitopes and Therapeutics for Severe Acute Respiratory Syndrome Coronavirus-2. <i>Frontiers in Microbiology</i> , 2020, 11, 1858.	1.5	23
19866	Whole-Genome Sequences of Two New <i>Caballeronia</i> Strains Isolated from Cryoturbated Peat Circles of the Permafrost-Affected Eastern European Tundra. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	4
19867	Characterization of black spot resistance in diploid roses with QTL detection, meta-analysis and candidate-gene identification. <i>Theoretical and Applied Genetics</i> , 2020, 133, 3299-3321.	1.8	11
19868	Temporal and spatial pattern of endophytic fungi diversity of <i>Camellia sinensis</i> (cv. Shu Cha Zao). <i>BMC Microbiology</i> , 2020, 20, 270.	1.3	18
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19870	Regional sequence expansion or collapse in heterozygous genome assemblies. <i>PLoS Computational Biology</i> , 2020, 16, e1008104.	1.5	31
19871	Old and Cosmopolite: Molecular Phylogeny of Tropical–Subtropical Kites (Aves: Elaninae) with Taxonomic Implications. <i>Diversity</i> , 2020, 12, 327.	0.7	7
19872	DELLA family duplication events lead to different selective constraints in angiosperms. <i>Genetica</i> , 2020, 148, 243-251.	0.5	2
19873	The genetic basis for PRC1 complex diversity emerged early in animal evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 22880-22889.	3.3	22
19874	Supergene evolution via stepwise duplications and neofunctionalization of a floral-organ identity gene. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 23148-23157.	3.3	42
19875	Wireworm (Coleoptera: Elateridae) genomic analysis reveals putative cryptic species, population structure, and adaptation to pest control. <i>Communications Biology</i> , 2020, 3, 489.	2.0	21
19876	Tracking a voyager: mitochondrial DNA analyses reveal mainland-to-island dispersal of an American crocodile ( <i>Crocodylus acutus</i> ) across the Caribbean. <i>Biological Journal of the Linnean Society</i> , 2020, 131, 647-655.	0.7	3

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19878	Genomic and Pathogenic Characteristics of Virulent Newcastle Disease Virus Isolated from Chicken in Live Bird Markets and Backyard Flocks in Kenya. <i>International Journal of Microbiology</i> , 2020, 2020, 1-11.	0.9	5
19879	The ranging of amino acids substitution matrices of various types in accordance with the alignment accuracy criterion. <i>BMC Bioinformatics</i> , 2020, 21, 294.	1.2	5
19880	Identification of Candidate Auxin Response Factors Involved in Pomegranate Seed Coat Development. <i>Frontiers in Plant Science</i> , 2020, 11, 536530.	1.7	3
19881	New multiplex conventional PCR and quadruplex real-time PCR assays for one-tube detection of <i>Phyllosticta citricarpa</i> , <i>Elsinoë fawcettii</i> , <i>Elsinoë australis</i> , and <i>Pseudocercospora angolensis</i> in Citrus: development and validation. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 9363-9385.	1.7	3
19882	Intestinal Tract Microbe Communities Associated with Horseshoe Crabs from Beibu Gulf, China. <i>Current Microbiology</i> , 2020, 77, 3330-3338.	1.0	12
19883	De Novo Gene Birth, Horizontal Gene Transfer, and Gene Duplication as Sources of New Gene Families Associated with the Origin of Symbiosis in <i>Amanita</i> . <i>Genome Biology and Evolution</i> , 2020, 12, 2168-2182.	1.1	5
19884	Are pangolins scapegoats of the COVID-19 outbreak? CoV transmission and pathology evidence?. <i>Conservation Letters</i> , 2020, 13, e12754.	2.8	17
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19886	Sequence Analysis of Egyptian Foot-and-Mouth Disease Virus Field and Vaccine Strains: Intertypic Recombination and Evidence for Accidental Release of Virulent Virus. <i>Viruses</i> , 2020, 12, 990.	1.5	8
19887	Spread of the invasive shell-boring annelid <i>Polydora websteri</i> (Polychaeta, Spionidae) into naturalised oyster reefs in the European Wadden Sea. <i>Marine Biodiversity</i> , 2020, 50, 1.	0.3	15
19888	Sequence Characterization and Molecular Modeling of Clinically Relevant Variants of the SARS-CoV-2 Main Protease. <i>Biochemistry</i> , 2020, 59, 3741-3756.	1.2	30
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19890	Tek/Tie2 is not required for cardiovascular development in zebrafish. <i>Development (Cambridge)</i> , 2020, 147, .	1.2	14
19891	Large-Scale Cloning and Comparative Analysis of TaNAC Genes in Response to Stripe Rust and Powdery Mildew in Wheat ( <i>Triticum aestivum</i> L.). <i>Genes</i> , 2020, 11, 1073.	1.0	8
19892	Isolation and Characterization of the Novel Bacteriophage AXL3 against <i>Stenotrophomonas maltophilia</i> . <i>International Journal of Molecular Sciences</i> , 2020, 21, 6338.	1.8	21
19894	Efficient rational modification of non-ribosomal peptides by adenylation domain substitution. <i>Nature Communications</i> , 2020, 11, 4554.	5.8	62
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19897	Novel Circoviruses Detected in Feces of Sonoran Felids. <i>Viruses</i> , 2020, 12, 1027.	1.5	13
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19904	Phenotypic characterization and phylogenetic analysis of <i>Pseudomonas syringae</i> strains associated with canker disease on apricot in Iran within the context of the global genetic diversity of the <i>P. syringae</i> complex. <i>European Journal of Plant Pathology</i> , 2020, 158, 545-560.	0.8	0
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19911	Multiheme hydroxylamine oxidoreductases produce NO during ammonia oxidation in methanotrophs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 24459-24463.	3.3	25
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19913	The Effects of Deoxynivalenol on the Ultrastructure of the <i>Sacculus Rotundus</i> and Vermiform Appendix, as Well as the Intestinal Microbiota of Weaned Rabbits. <i>Toxins</i> , 2020, 12, 569.	1.5	13

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19922	Patient-Derived HIV-1 Nef Alleles Reveal Uncoupling of CD4 Downregulation and SERINC5 Antagonism Functions of the Viral Pathogenesis Factor. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2020, 85, e23-e26.	0.9	5
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19927	Insights into HP1a-Chromatin Interactions. <i>Cells</i> , 2020, 9, 1866.	1.8	11
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19931	Identification and characterization of <i>Ageratum</i> yellow vein Malaysia virus (AYVMV) and an associated betasatellite among begomoviruses infecting <i>Solanum lycopersicum</i> in Malaysia. <i>Journal of Applied Genetics</i> , 2020, 61, 619-628.	1.0	1



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19933	The chromosome-level draft genome of <i>Dalbergia odorifera</i> . <i>GigaScience</i> , 2020, 9, .	3.3	21
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19935	Functional variation in phylogen, a phyllody-inducing phytoplasma effector family, attributable to a single amino acid polymorphism. <i>Molecular Plant Pathology</i> , 2020, 21, 1322-1336.	2.0	27
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19939	ARDEP, a Rapid Degenerate Primer Design Pipeline Based on <i>k</i> -mers for Amplicon Microbiome Studies. <i>International Journal of Environmental Research and Public Health</i> , 2020, 17, 5958.	1.2	4
19940	Characterization of two GH5 endoglucanases from termite microbiome using synthetic metagenomics. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 8351-8366.	1.7	10
19941	Broad host range of SARS-CoV-2 predicted by comparative and structural analysis of ACE2 in vertebrates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 22311-22322.	3.3	517
19942	Mitogenome phylogenetics in the genus <i>Palaemon</i> (Crustacea: Decapoda) sheds light on species crypticism in the rockpool shrimp <i>P. elegans</i> . <i>PLoS ONE</i> , 2020, 15, e0237037.	1.1	9
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19945	Complex Internal Microstructure of Feather Follicles on Chicken Skin Promotes the Bacterial Cross-Contamination of Carcasses During the Slaughtering Process. <i>Frontiers in Microbiology</i> , 2020, 11, 571913.	1.5	9
19946	Phylogenetic reconstruction of <i>Ficus</i> subg. <i>Synoecia</i> and its allies (Moraceae), with implications on the origin of the climbing habit. <i>Taxon</i> , 2020, 69, 927-945.	0.4	7
19947	Genome-wide identification and expression analysis of the Citrus malectin domain-containing receptor-like kinases in response to arbuscular mycorrhizal fungi colonization and drought. <i>Horticulture Environment and Biotechnology</i> , 2020, 61, 891-901.	0.7	7
19948	Symbiotic microalgal diversity within lichenicolous lichens and crustose hosts on Iberian Peninsula gypsum biocrusts. <i>Scientific Reports</i> , 2020, 10, 14060.	1.6	20
19949	New Genetic Insights About Hybridization and Population Structure of Hawksbill and Loggerhead Turtles From Brazil. <i>Journal of Heredity</i> , 2020, 111, 444-456.	1.0	13

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19951	Continuous Reassortment of Clade 2.3.4.4 H5N6 Highly Pathogenetic Avian Influenza Viruses Demonstrating High Risk to Public Health. <i>Pathogens</i> , 2020, 9, 670.	1.2	13
19952	SARS-CoV-2 ORF8 and SARS-CoV ORF8ab: Genomic Divergence and Functional Convergence. <i>Pathogens</i> , 2020, 9, 677.	1.2	44
19953	A Genome-Wide Survey of MATE Transporters in Brassicaceae and Unveiling Their Expression Profiles under Abiotic Stress in Rapeseed. <i>Plants</i> , 2020, 9, 1072.	1.6	9
19954	Identification of Circovirus Genome in a Chinstrap Penguin ( <i>Pygoscelis antarcticus</i> ) and Adelie Penguin ( <i>Pygoscelis adeliae</i> ) on the Antarctic Peninsula. <i>Viruses</i> , 2020, 12, 858.	1.5	11
19955	Large freshwater phages with the potential to augment aerobic methane oxidation. <i>Nature Microbiology</i> , 2020, 5, 1504-1515.	5.9	66
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19957	New observations on the sexual and asexual reproductive stages of <i>Staurastrum gracile</i> (Desmidiaceae, Zygnematophyceae). <i>Phycologia</i> , 2020, 59, 409-421.	0.6	2
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19961	Unveiling Viruses Associated with Gastroenteritis Using a Metagenomics Approach. <i>Viruses</i> , 2020, 12, 1432.	1.5	11
19962	The sino-nasal warzone: transcriptomic and genomic studies on sino-nasal aspergillosis in dogs. <i>Npj Biofilms and Microbiomes</i> , 2020, 6, 51.	2.9	3
19963	Resolving the systematics of Richtersiidae by multilocus phylogeny and an integrative redescription of the nominal species for the genus <i>Crenubiotus</i> (Tardigrada). <i>Scientific Reports</i> , 2020, 10, 19418.	1.6	13
19964	Identification and characterization of satellite DNAs in two-toed sloths of the genus <i>Choloepus</i> (Megalonychidae, Xenarthra). <i>Scientific Reports</i> , 2020, 10, 19202.	1.6	8
19965	Persistence of pdm2009-H1N1 internal genes of swine influenza in pigs, Thailand. <i>Scientific Reports</i> , 2020, 10, 19847.	1.6	5
19966	Comparative analyses and structural insights of new class glutathione transferases in <i>Cryptosporidium</i> species. <i>Scientific Reports</i> , 2020, 10, 20370.	1.6	4
19967	Production of the antimicrobial compound tetrabromopyrrole and the <i>Pseudomonas</i> quinolone system precursor, 2-heptyl-4-quinolone, by a novel marine species <i>Pseudoalteromonas galathea</i> sp. nov.. <i>Scientific Reports</i> , 2020, 10, 21630.	1.6	15

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19969	Cascabel: A Scalable and Versatile Amplicon Sequence Data Analysis Pipeline Delivering Reproducible and Documented Results. <i>Frontiers in Genetics</i> , 2020, 11, 489357.	1.1	19
19970	A Chromosome-Level Genome Assembly of the Anglerfish <i>Lophius litulon</i> . <i>Frontiers in Genetics</i> , 2020, 11, 581161.	1.1	2
19971	Piscine Orthoreovirus-1 Isolates Differ in Their Ability to Induce Heart and Skeletal Muscle Inflammation in Atlantic Salmon ( <i>Salmo salar</i> ). <i>Pathogens</i> , 2020, 9, 1050.	1.2	28
19972	Genome sequencing of deep-sea hydrothermal vent snails reveals adaptations to extreme environments. <i>GigaScience</i> , 2020, 9, .	3.3	5
19973	Comparative genomics of <i>Klebsiella michiganensis</i> BD177 and related members of <i>Klebsiella</i> sp. reveal the symbiotic relationship with <i>Bactrocera dorsalis</i> . <i>BMC Genetics</i> , 2020, 21, 138.	2.7	5
19974	Molecular identification of four <i>Sarcocystis</i> species in cattle from Lithuania, including <i>S. hominis</i> , and development of a rapid molecular detection method. <i>Parasites and Vectors</i> , 2020, 13, 610.	1.0	27
19975	Metabolic Contributions of an Alphaproteobacterial Endosymbiont in the Apicomplexan <i>Cardiosporidium cionae</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 580719.	1.5	8
19976	Diversity and Genomic Characterization of a Novel Parvarchaeota Family in Acid Mine Drainage Sediments. <i>Frontiers in Microbiology</i> , 2020, 11, 612257.	1.5	22
19977	Molecular Characterization of <i>Diaporthe</i> Species Associated With Hazelnut Defects. <i>Frontiers in Plant Science</i> , 2020, 11, 611655.	1.7	20
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19980	Identification and Characterization of a New Type III Polyketide Synthase from a Marine Yeast, <i>Naganishia uzbekistanensis</i> . <i>Marine Drugs</i> , 2020, 18, 637.	2.2	4
19981	Biological and Genomic Characterization of a Novel Jumbo Bacteriophage, $\nu$ B_VhaM_pir03 with Broad Host Lytic Activity against <i>Vibrio harveyi</i> . <i>Pathogens</i> , 2020, 9, 1051.	1.2	20
19982	T-cell receptor repertoire of cytomegalovirus-specific cytotoxic T-cells after allogeneic stem cell transplantation. <i>Scientific Reports</i> , 2020, 10, 22218.	1.6	7
19983	Genomics Reveals Widespread Ecological Speciation in Flightless Insects. <i>Systematic Biology</i> , 2021, 70, 863-876.	2.7	18
19984	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
19985	Extended synaptotagmin regulates membrane contact site structure and lipid transfer function <i>in vivo</i> . <i>EMBO Reports</i> , 2020, 21, e50264.	2.0	16

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19987	Cultivation-Independent Analysis of the Bacterial Community Associated With the Calcareous Sponge <i>Clathrina clathrus</i> and Isolation of <i>Poriferisphaera corsica</i> Gen. Nov., Sp. Nov., Belonging to the Barely Studied Class Phycisphaerae in the Phylum Planctomycetes. <i>Frontiers in Microbiology</i> , 2020, 11, 602250.	1.5	23
19988	Functional and Genomic Characterization of <i>Ligilactobacillus salivarius</i> TUCO-L2 Isolated From Lama glama Milk: A Promising Immunobiotic Strain to Combat Infections. <i>Frontiers in Microbiology</i> , 2020, 11, 608752.	1.5	12
19989	Origins and Stepwise Expansion of R2R3-MYB Transcription Factors for the Terrestrial Adaptation of Plants. <i>Frontiers in Plant Science</i> , 2020, 11, 575360.	1.7	11
19990	Distribution of Important Probiotic Genes and Identification of the Biogenic Amines Produced by <i>Lactobacillus acidophilus</i> PNW3. <i>Foods</i> , 2020, 9, 1840.	1.9	5
19991	Evolution of MicroRNA Biogenesis Genes in the Sterlet ( <i>Acipenser ruthenus</i> ) and Other Polyploid Vertebrates. <i>International Journal of Molecular Sciences</i> , 2020, 21, 9562.	1.8	2
19992	Multidisciplinary Analysis of <i>Cystoseira sensu lato</i> (SE Spain) Suggest a Complex Colonization of the Mediterranean. <i>Journal of Marine Science and Engineering</i> , 2020, 8, 961.	1.2	6
19993	<i>Soehngenia longivitae</i> sp. nov., a Fermenting Bacterium Isolated from a Petroleum Reservoir in Azerbaijan, and Emended Description of the Genus <i>Soehngenia</i> . <i>Microorganisms</i> , 2020, 8, 1967.	1.6	14
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19995	Phylogenetic Analysis of Mitogenomic Data Sets Resolves the Relationship of Seven <i>Macropostrongyloides</i> Species from Australian Macropodid and Vombatid Marsupials. <i>Pathogens</i> , 2020, 9, 1042.	1.2	5
19996	Intragenomic Polymorphism of the ITS 1 Region of 35S rRNA Gene in the Group of Grasses with Two-Chromosome Species: Different Genome Composition in Closely Related <i>Zingeria</i> Species. <i>Plants</i> , 2020, 9, 1647.	1.6	7
19997	Genetic Diversity of Rift Valley Fever Strains Circulating in Namibia in 2010 and 2011. <i>Viruses</i> , 2020, 12, 1453.	1.5	4
19998	Cloning of the first cDNA encoding a putative CCRFamide precursor: identification of the brain, eyestalk ganglia, and cardiac ganglion as sites of CCRFamide expression in the American lobster, <i>Homarus americanus</i> . <i>Invertebrate Neuroscience</i> , 2020, 20, 24.	1.8	2
19999	Metapangenomics of the oral microbiome provides insights into habitat adaptation and cultivar diversity. <i>Genome Biology</i> , 2020, 21, 293.	3.8	46
20000	Genomic and physiological mechanisms underlying skin plasticity during water to air transition in an amphibious fish. <i>Journal of Experimental Biology</i> , 2021, 224, .	0.8	10
20001	Resolving the Phylogeny of the Olive Family (Oleaceae): Confronting Information from Organellar and Nuclear Genomes. <i>Genes</i> , 2020, 11, 1508.	1.0	25
20002	Whole Genome Characterization and Evolutionary Analysis of G1P[8] Rotavirus A Strains during the Pre- and Post-Vaccine Periods in Mozambique (2012â€“2017). <i>Pathogens</i> , 2020, 9, 1026.	1.2	4
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20005	Nation-Wide Viral Sequence Analysis of HIV-1 Subtype B Epidemic in 2003–2012 Revealed a Contribution of Men Who Have Sex With Men to the Transmission Cluster Formation and Growth in Japan. <i>Frontiers in Reproductive Health</i> , 2020, 2, .	0.6	2
20006	Exposing the Barcoding Void: An Integrative Approach to Study Snail-Borne Parasites in a One Health Context. <i>Frontiers in Veterinary Science</i> , 2020, 7, 605280.	0.9	10
20007	The evolution of the huntingtin-associated protein 40 (HAP40) in conjunction with huntingtin. <i>BMC Evolutionary Biology</i> , 2020, 20, 162.	3.2	11
20008	Comparative analysis of morabine grasshopper genomes reveals highly abundant transposable elements and rapidly proliferating satellite DNA repeats. <i>BMC Biology</i> , 2020, 18, 199.	1.7	29
20009	Discovery of Novel Biosynthetic Gene Cluster Diversity From a Soil Metagenomic Library. <i>Frontiers in Microbiology</i> , 2020, 11, 585398.	1.5	16
20010	Saccharibacteria as Organic Carbon Sinks in Hydrocarbon-Fueled Communities. <i>Frontiers in Microbiology</i> , 2020, 11, 587782.	1.5	22
20011	Genetic Differentiation and Population Structure of Threatened <i>Prunus africana</i> Kalm. in Western Cameroon Using Molecular Markers. <i>Diversity</i> , 2020, 12, 446.	0.7	1
20012	Indo-Pacific Phylogeography of the Lemon Sponge <i>Leucetta chagosensis</i> . <i>Diversity</i> , 2020, 12, 466.	0.7	3
20013	Genome-wide identification and expression analysis of the CLC gene family in pomegranate ( <i>Punica</i> ) Tj ETQq1 1 0.784314 rgBT /Over 1.6 12	1.6	12
20014	Field Observations and Genetic Characterization of Sheep-Associated Malignant Catarrhal Fever in Egypt, 2018. <i>Veterinary Sciences</i> , 2020, 7, 201.	0.6	1
20015	Cloning and functional characterization of two peptidoglycan recognition protein isoforms (PCR-P-LC) in <i>Bactrocera dorsalis</i> (Diptera: Tephritidae). <i>Journal of Integrative Agriculture</i> , 2020, 19, 3025-3034.	1.7	6
20016	Prevalence of temperate viruses in deep South China Sea and western Pacific Ocean. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2020, 166, 103403.	0.6	4
20017	Succinate dehydrogenase gene as a marker for studying <i>Blastocystis</i> genetic diversity. <i>Heliyon</i> , 2020, 6, e05387.	1.4	4
20018	Molecular screening for rickettsial bacteria and piroplasms in ixodid ticks surveyed from white-tailed deer ( <i>Odocoileus virginianus</i> ) and nilgai antelope ( <i>Boselaphus tragocamelus</i> ) in southern Texas. <i>International Journal for Parasitology: Parasites and Wildlife</i> , 2020, 13, 252-260.	0.6	8
20019	The White-Spotted Bamboo Shark Genome Reveals Chromosome Rearrangements and Fast-Evolving Immune Genes of Cartilaginous Fish. <i>IScience</i> , 2020, 23, 101754.	1.9	36
20020	Assessing oligonucleotide designs from early lab developed PCR diagnostic tests for SARS-CoV-2 using the PCR_strainer pipeline. <i>Journal of Clinical Virology</i> , 2020, 131, 104581.	1.6	13
20021	AAV vectors engineered to target insulin receptor greatly enhance intramuscular gene delivery. <i>Molecular Therapy - Methods and Clinical Development</i> , 2020, 19, 496-506.	1.8	8

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20022	Species integrity, introgression, and genetic variation across a coral reef fish hybrid zone. <i>Ecology and Evolution</i> , 2020, 10, 11998-12014.	0.8	8
20023	Foliar fungal endophyte community structure is independent of phylogenetic relatedness in an Asteraceae common garden. <i>Ecology and Evolution</i> , 2020, 10, 13895-13912.	0.8	10
20024	Downy mildew of lavender caused by <i>Peronospora belbahrii</i> in Israel. <i>Mycological Progress</i> , 2020, 19, 1537-1543.	0.5	4
20025	Assessment of yeasts in tropical peat swamp forests in Thailand. <i>Mycological Progress</i> , 2020, 19, 1559-1573.	0.5	2
20026	Fish complement C8 evolution, functional network analyses, and the theoretical interaction between C8 alpha chain and CD59. <i>Molecular Immunology</i> , 2020, 128, 235-248.	1.0	3
20027	First isolation, <i>in-vivo</i> and genomic characterization of zoonotic variegated squirrel Bornavirus 1 (VSBV-1) isolates. <i>Emerging Microbes and Infections</i> , 2020, 9, 2474-2484.	3.0	3
20028	The relationship between molar morphology and ecology within <i>Neotoma</i> . <i>Journal of Mammalogy</i> , 2020, 101, 1711-1726.	0.6	2
20029	Additions to the genus <i>Gimesia</i> : description of <i>Gimesia alba</i> sp. nov., <i>Gimesia algae</i> sp. nov., <i>Gimesia aquarii</i> sp. nov., <i>Gimesia aquatilis</i> sp. nov., <i>Gimesia fumaroli</i> sp. nov. and <i>Gimesia panarensis</i> sp. nov., isolated from aquatic habitats of the Northern Hemisphere. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 1999-2018.	0.7	41
20030	Genomic RNA Elements Drive Phase Separation of the SARS-CoV-2 Nucleocapsid. <i>Molecular Cell</i> , 2020, 80, 1078-1091.e6.	4.5	255
20031	Genome sequencing and phylogenetic analysis of allotetraploid <i>Salix matsudana</i> Koidz. <i>Horticulture Research</i> , 2020, 7, 201.	2.9	30
20032	The phylogenomics of CRISPR-Cas system and revelation of its features in <i>Salmonella</i> . <i>Scientific Reports</i> , 2020, 10, 21156.	1.6	14
20033	<i>Blattella germanica</i> displays a large arsenal of antimicrobial peptide genes. <i>Scientific Reports</i> , 2020, 10, 21058.	1.6	8
20034	Insights into genomic structure and evolutionary processes of coastal <i>Suaeda</i> species in East Asia using cpDNA, nDNA, and genome-wide SNPs. <i>Scientific Reports</i> , 2020, 10, 20950.	1.6	2
20035	Global emergence and evolutionary dynamics of bluetongue virus. <i>Scientific Reports</i> , 2020, 10, 21677.	1.6	26
20036	Dysbiosis in marine aquaculture revealed through microbiome analysis: reverse ecology for environmental sustainability. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	10
20037	Extent of polymorphism and selection pressure on the <i>Trypanosoma cruzi</i> vaccine candidate antigen Tc24. <i>Evolutionary Applications</i> , 2020, 13, 2663-2672.	1.5	11
20038	Effects of Agricultural Fungicide Use on <i>Aspergillus fumigatus</i> Abundance, Antifungal Susceptibility, and Population Structure. <i>MBio</i> , 2020, 11, .	1.8	33
20039	Yes, we can use it: a formal test on the accuracy of low-pass nanopore long-read sequencing for mitophylogenomics and barcoding research using the Caribbean Aspiny lobster <i>Panulirus argus</i> . <i>BMC Genomics</i> , 2020, 21, 882.	1.2	14

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20041	Intronic tRNAs of mitochondrial origin regulate constitutive and alternative splicing. Genome Biology, 2020, 21, 299.	3.8	6
20042	Bioluminescence in an Undescribed Species of Carnivorous Sponge (Cladorhizidae) From the Deep Sea. Frontiers in Marine Science, 2020, 7, .	1.2	10
20043	Hidden Host Mortality from an Introduced Parasitoid: Conventional and Molecular Evaluation of Non-Target Risk. Insects, 2020, 11, 822.	1.0	9
20044	Leaping into the Unknown World of Sporisorium scitamineum Candidate Effectors. Journal of Fungi (Basel, Switzerland), 2020, 6, 339.	1.5	7
20045	Purification and Characterization of Two Novel Laccases from Peniophora lycii. Journal of Fungi (Basel, Switzerland), 2020, 6, 340.	1.5	12
20046	Occurrence of Methicillin-Resistant Staphylococcus spp. on Brazilian Dairy Farms that Produce Unpasteurized Cheese. Toxins, 2020, 12, 779.	1.5	5
20047	Advances in the Bioinformatics Knowledge of mRNA Polyadenylation in Baculovirus Genes. Viruses, 2020, 12, 1395.	1.5	0
20048	Presence and diversity of Chlamydiae bacteria in Spinturnix myoti, an ectoparasite of bats. Parasite, 2020, 27, 54.	0.8	2
20049	CRISPRCasTyper: Automated Identification, Annotation, and Classification of CRISPR-Cas Loci. CRISPR Journal, 2020, 3, 462-469.	1.4	128
20050	Prokaryotic Community Compositions of the Hypersaline Sediments of Tuz Lake Demonstrated by Cloning and High-Throughput Sequencing. Microbiology, 2020, 89, 756-768.	0.5	10
20051	New view on the organization and evolution of Palaeognathae mitogenomes poses the question on the ancestral gene rearrangement in Aves. BMC Genomics, 2020, 21, 874.	1.2	14
20052	Isolation and Taxonomic Characterization of Novel Haloarchaeal Isolates From Indian Solar Saltern: A Brief Review on Distribution of Bacteriorhodopsins and V-Type ATPases in Haloarchaea. Frontiers in Microbiology, 2020, 11, 554927.	1.5	5
20053	Peronosclerospora australiensis is a synonym of P. maydis, which is widespread on Sumatra, and distinct from the most prevalent Java maize downy mildew pathogen. Mycological Progress, 2020, 19, 1309-1315.	0.5	8
20054	Genomic differences between the new Fusarium oxysporum f. sp. apii (Foa) race 4 on celery, the less virulent Foa races 2 and 3, and the avirulent on celery f. sp. coriandrii. BMC Genomics, 2020, 21, 730.	1.2	12
20055	Integrated omics unveil the secondary metabolic landscape of a basal dinoflagellate. BMC Biology, 2020, 18, 139.	1.7	17
20056	Liver-specific knockdown of ANGPTL8 alters the structure of the gut microbiota in mice. Annals of Microbiology, 2020, 70, .	1.1	0
20057	Horizontal Gene Transfer and Tandem Duplication Shape the Unique CAZyme Complement of the Mycoparasitic Oomycetes Pythium oligandrum and Pythium periplocum. Frontiers in Microbiology, 2020, 11, 581698.	1.5	10

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20058	Zygosaccharomyces rouxii, an Aromatic Yeast Isolated From Chili Sauce, Is Able to Biosynthesize 2-Phenylethanol via the Shikimate or Ehrlich Pathways. <i>Frontiers in Microbiology</i> , 2020, 11, 597454.	1.5	18
20059	Existence of Bov-B LINE Retrotransposons in Snake Lineages Reveals Recent Multiple Horizontal Gene Transfers with Copy Number Variation. <i>Genes</i> , 2020, 11, 1241.	1.0	3
20060	Iron Assimilation during Emerging Infections Caused by Opportunistic Fungi with emphasis on Mucorales and the Development of Antifungal Resistance. <i>Genes</i> , 2020, 11, 1296.	1.0	20
20061	Integrated Analysis of the Transcriptome and Metabolome of Cecropia obtusifolia: A Plant with High Chlorogenic Acid Content Traditionally Used to Treat Diabetes Mellitus. <i>International Journal of Molecular Sciences</i> , 2020, 21, 7572.	1.8	10
20062	Trametinib Induces the Stabilization of a Dual GNAQ p.Gly48Leu- and FGFR4 p.Cys172Gly-Mutated Uveal Melanoma. The Role of Molecular Modelling in Personalized Oncology. <i>International Journal of Molecular Sciences</i> , 2020, 21, 8021.	1.8	3
20063	First Account of Phylogeographic Variation, Larval Characters, and Laboratory Rearing of the Endangered Cobblestone Tiger Beetle <i>Cicindelidia marginipennis</i> , Dejean, 1831 with Observations of Their Natural History. <i>Insects</i> , 2020, 11, 708.	1.0	1
20064	Evaluation of RNA Interference for Control of the Grape Mealybug <i>Pseudococcus maritimus</i> (Hemiptera: Pseudococcidae). <i>Insects</i> , 2020, 11, 739.	1.0	3
20065	Identification and Functional Characterization of a Novel Immunomodulatory Protein From <i>Morchella conica</i> SH. <i>Frontiers in Immunology</i> , 2020, 11, 559770.	2.2	5
20066	Independent Recruitment of Duplicated $\beta$ -Subunit-Coding NAD-ME Genes Aided the Evolution of C4 Photosynthesis in Cleomaceae. <i>Frontiers in Plant Science</i> , 2020, 11, 572080.	1.7	12
20067	Mild heat stress changes the microbiota diversity in the respiratory tract and the cecum of layer-type pullets. <i>Poultry Science</i> , 2020, 99, 7015-7026.	1.5	19
20068	Genome-wide identification of MADS-box gene family in sacred lotus ( <i>Nelumbo nucifera</i> ) identifies a SEPALLATA homolog gene involved in floral development. <i>BMC Plant Biology</i> , 2020, 20, 497.	1.6	23
20069	Open gaps in the evolution of the eukaryotic nucleotide excision repair. <i>DNA Repair</i> , 2020, 95, 102955.	1.3	5
20070	Cartilaginous fish class II genes reveal unprecedented old allelic lineages and confirm the late evolutionary emergence of DM. <i>Molecular Immunology</i> , 2020, 128, 125-138.	1.0	6
20071	Transcriptome Sequencing of the Striped Cucumber Beetle, <i>Acalymma vittatum</i> (F.), Reveals Numerous Sex-Specific Transcripts and Xenobiotic Detoxification Genes. <i>BioTech</i> , 2020, 9, 21.	1.3	7
20072	Slc4 Gene Family in Spotted Sea Bass ( <i>Lateolabrax maculatus</i> ): Structure, Evolution, and Expression Profiling in Response to Alkalinity Stress and Salinity Changes. <i>Genes</i> , 2020, 11, 1271.	1.0	7
20073	Uncovering Unique Green Algae and Cyanobacteria Isolated from Biocrusts in Highly Saline Potash Tailing Pile Habitats, Using an Integrative Approach. <i>Microorganisms</i> , 2020, 8, 1667.	1.6	19
20074	Blood Parasites in Endangered Wildlife-Trypanosomes Discovered during a Survey of Haemoprotozoa from the Tasmanian Devil. <i>Pathogens</i> , 2020, 9, 873.	1.2	8
20075	Symmetric and Asymmetric Components of Shape Variation in the Diatom Genus <i>Frustulia</i> (Bacillariophyta). <i>Symmetry</i> , 2020, 12, 1626.	1.1	2



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20076	Inhabited subsurface wet smectites in the hyperarid core of the Atacama Desert as an analog for the search for life on Mars. <i>Scientific Reports</i> , 2020, 10, 19183.	1.6	21
20077	SARS-CoV-2 mutations and where to find them: an <i>in silico</i> perspective of structural changes and antigenicity of the spike protein. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 3336-3346.	2.0	1
20078	Novel Type V-A CRISPR Effectors Are Active Nucleases with Expanded Targeting Capabilities. <i>CRISPR Journal</i> , 2020, 3, 454-461.	1.4	7
20079	First Isolation of <i>Candida nivariensis</i> , an Emerging Fungal Pathogen, in Kuwait. <i>Medical Principles and Practice</i> , 2021, 30, 80-84.	1.1	4
20080	Whole genome analysis of the koa wilt pathogen ( <i>Fusarium oxysporum</i> f. sp. <i>koa</i> ) and the development of molecular tools for early detection and monitoring. <i>BMC Genomics</i> , 2020, 21, 764.	1.2	11
20081	Coupling Transcriptomics and Behaviour to Unveil the Olfactory System of <i>Spodoptera exigua</i> Larvae. <i>Journal of Chemical Ecology</i> , 2020, 46, 1017-1031.	0.9	13
20082	Discovery of multiple anti-CRISPRs highlights anti-defense gene clustering in mobile genetic elements. <i>Nature Communications</i> , 2020, 11, 5652.	5.8	88
20084	Morphological and molecular characterisation of <i>Aporcelaimellus nigeriensis</i> sp. n. (Dorylaimida: Tj ETQq1 1 0.784314 rgBT /Overlock 1 0.2 3		
20085	Phylogeny of two new phoronematid sponges from the Caroline Seamount and South China Sea. <i>Contributions To Zoology</i> , 2020, 89, 175-187.	0.2	0
20086	Molecular phylogeny and classification of <i>Chelidurella</i> Verhoeff, stat. restit. (Dermaptera: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 0.2 4		
20087	Isolation and Characterization of <i>Bacillus cereus</i> Phage vB_BceP-DLc1 Reveals the Largest Member of the $\lambda$ -Like Phages. <i>Microorganisms</i> , 2020, 8, 1750.	1.6	15
20088	Two new species of <i>Hortiboletus</i> (Boletaceae, Boletales) from China. <i>Mycological Progress</i> , 2020, 19, 1377-1386.	0.5	4
20089	Selection of Immunobiotic <i>Ligilactobacillus salivarius</i> Strains from the Intestinal Tract of Wakame-Fed Pigs: Functional and Genomic Studies. <i>Microorganisms</i> , 2020, 8, 1659.	1.6	21
20090	Comparative Genomics of Pathogenic <i>Clavibacter michiganensis</i> subsp. <i>michiganensis</i> Strains from Chile Reveals Potential Virulence Features for Tomato Plants. <i>Microorganisms</i> , 2020, 8, 1679.	1.6	14
20091	<i>Mycoplasma bovis</i> in Nordic European Countries: Emergence and Dominance of a New Clone. <i>Pathogens</i> , 2020, 9, 875.	1.2	14
20092	Characterization of H3 subtype avian influenza viruses isolated from poultry in Vietnam. <i>Virus Genes</i> , 2020, 56, 712-723.	0.7	3
20093	Molecular characterization of begomovirus- $\beta$ satellite- $\alpha$ satellite complex associated with okra enation leaf curl disease in Northern Sri Lanka. <i>3 Biotech</i> , 2020, 10, 506.	1.1	3
20094	An Oscillating MinD Protein Determines the Cellular Positioning of the Motility Machinery in Archaea. <i>Current Biology</i> , 2020, 30, 4956-4972.e4.	1.8	19

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20095	Heritability of the HIV-1 reservoir size and decay under long-term suppressive ART. <i>Nature Communications</i> , 2020, 11, 5542.	5.8	5
20096	A catalogue of biochemically diverse CRISPR-Cas9 orthologs. <i>Nature Communications</i> , 2020, 11, 5512.	5.8	116
20097	Combinatorial expression of GPCR isoforms affects signalling and drug responses. <i>Nature</i> , 2020, 587, 650-656.	13.7	87
20098	High-quality genome sequence assembly of R.A73 <i>Enterococcus faecium</i> isolated from freshwater fish mucus. <i>BMC Microbiology</i> , 2020, 20, 322.	1.3	3
20099	<i>Caldicellulosiruptor bescii</i> Adheres to Polysaccharides via a Type IV Pilin-Dependent Mechanism. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	3
20100	Phylogenomic Insights into Diversity and Evolution of Nonpathogenic <i>Xanthomonas</i> Strains Associated with Citrus. <i>MSphere</i> , 2020, 5, .	1.3	18
20101	Complete genome sequencing and comparative genomic analyses of <i>Bacillus</i> sp. S3, a novel hyper Sb(III)-oxidizing bacterium. <i>BMC Microbiology</i> , 2020, 20, 106.	1.3	11
20102	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
20103	Shedding light: a phylotranscriptomic perspective illuminates the origin of photosymbiosis in marine bivalves. <i>BMC Evolutionary Biology</i> , 2020, 20, 50.	3.2	11
20104	FLAVI: An Amino Acid Substitution Model for Flaviviruses. <i>Journal of Molecular Evolution</i> , 2020, 88, 445-452.	0.8	8
20105	Cryo-EM Structure of the Fork Protection Complex Bound to CMG at a Replication Fork. <i>Molecular Cell</i> , 2020, 78, 926-940.e13.	4.5	111
20106	Neural remodelling in spiny lobster larvae is characterized by broad neuropeptide suppression. <i>General and Comparative Endocrinology</i> , 2020, 294, 113496.	0.8	3
20107	The first case of microsporidiosis in <i>Paramecium</i> . <i>Parasitology</i> , 2020, 147, 957-971.	0.7	12
20108	A microsporidian impairs <i>Plasmodium falciparum</i> transmission in <i>Anopheles arabiensis</i> mosquitoes. <i>Nature Communications</i> , 2020, 11, 2187.	5.8	62
20109	Targeted analysis of polymorphic loci from low-coverage shotgun sequence data allows accurate genotyping of HLA genes in historical human populations. <i>Scientific Reports</i> , 2020, 10, 7339.	1.6	6
20110	The relationship between cigarette smoking and the tongue microbiome in an East Asian population. <i>Journal of Oral Microbiology</i> , 2020, 12, 1742527.	1.2	18
20111	The Population of <i>Fusarium oxysporum</i> f. sp. <i>lactucae</i> in California and Arizona. <i>Plant Disease</i> , 2020, 104, 1811-1816.	0.7	8
20112	Genomic Evidence for Formate Metabolism by <i>Chloroflexi</i> as the Key to Unlocking Deep Carbon in Lost City Microbial Ecosystems. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	23

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20113	Metagenome Mining Reveals Hidden Genomic Diversity of Pelagimyophages in Aquatic Environments. <i>MSystems</i> , 2020, 5, .	1.7	23
20114	Whole-Genome Sequencing of Mexican Strains of <i>Anaplasma marginale</i> : An Approach to the Causal Agent of Bovine Anaplasmosis. <i>International Journal of Genomics</i> , 2020, 2020, 1-7.	0.8	6
20115	Sequencing and Functional Annotation of the Whole Genome of <i>Shiraia bambusicola</i> . G3: Genes, Genomes, Genetics, 2020, 10, 23-35.	0.8	8
20116	Differential Expression of Putative <i>Ornithodoros turicata</i> Defensins Mediated by Tick Feeding. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 152.	1.8	4
20117	<i>Ctenophthalmus baeticus boisseaorum</i> (Beaucournu, 1968) and <i>Ctenophthalmus apertus allani</i> (Smit,) Tj ETQq0 0 0 rgBT /Overlock 10 molecular characterization. <i>Bulletin of Entomological Research</i> , 2020, 110, 663-676.	0.5	8
20118	The chloroalkaloid (âˆ™)-acutumine is biosynthesized via a Fe(II)- and 2-oxoglutarate-dependent halogenase in <i>Menispermaceae</i> plants. <i>Nature Communications</i> , 2020, 11, 1867.	5.8	37
20119	Experimental assembly reveals ecological drift as a major driver of root nodule bacterial diversity in a woody legume crop. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	13
20120	Delineation of a Subgroup of the Genus <i>Paraburkholderia</i> , Including <i>P.Âtterrae</i> DSM 17804T, <i>P.Âhospita</i> DSM 17164T, and Four Soil-Isolated Fungiphiles, Reveals Remarkable Genomic and Ecological Featuresâ€”Proposal for the Definition of a <i>P.Âhospita</i> Species Cluster. <i>Genome Biology and Evolution</i> , 2020, 12, 325-344.	1.1	12
20121	Polymorphisms in human immunoglobulin heavy chain variable genes and their upstream regions. <i>Nucleic Acids Research</i> , 2020, 48, 5499-5510.	6.5	31
20122	A new begomovirus isolated from a potyvirus-infected bean plant causes asymptomatic infections in bean and <i>N. benthamiana</i> . <i>Archives of Virology</i> , 2020, 165, 1659-1665.	0.9	9
20123	A Paleogenomic Reconstruction of the Deep Population History of the Andes. <i>Cell</i> , 2020, 181, 1131-1145.e21.	13.5	69
20124	The strains of bioluminescent bacteria isolated from the White Sea finfishes: genera <i>Photobacterium</i> , <i>Aliivibrio</i> , <i>Vibrio</i> , <i>Shewanella</i> , and first luminous <i>Kosakonia</i> . <i>Journal of Photochemistry and Photobiology B: Biology</i> , 2020, 208, 111895.	1.7	11
20125	Implications of plastome evolution in the true lilies (monocot order Liliales). <i>Molecular Phylogenetics and Evolution</i> , 2020, 148, 106818.	1.2	23
20126	A high-quality reference genome of wild <i>Cannabis sativa</i> . <i>Horticulture Research</i> , 2020, 7, 73.	2.9	73
20127	Structural and biochemical characterization of the exopolysaccharide deacetylase Agd3 required for <i>Aspergillus fumigatus</i> biofilm formation. <i>Nature Communications</i> , 2020, 11, 2450.	5.8	38
20128	The Role of European Starlings ( <i>Sturnus vulgaris</i> ) in the Dissemination of Multidrug-Resistant <i>Escherichia coli</i> among Concentrated Animal Feeding Operations. <i>Scientific Reports</i> , 2020, 10, 8093.	1.6	8
20129	Discovery and Characterization of <i>Thermoproteus</i> Spherical Piliferous Virus 1: a Spherical Archaeal Virus Decorated with Unusual Filaments. <i>Journal of Virology</i> , 2020, 94, .	1.5	2
20130	Draft Genome Sequence of a <i>Streptococcus suis</i> Isolate from a Case of Cattle Meningitis. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	2

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20131	An integrated software for virus community sequencing data analysis. <i>BMC Genomics</i> , 2020, 21, 363.	1.2	5
20132	VAPYRIN-like is required for development of the moss <i>Physcomitrella patens</i> . <i>Development (Cambridge)</i> , 2020, 147, .	1.2	7
20133	Antimicrobial Resistance Profiles of Adherent Invasive <i>Escherichia coli</i> Show Increased Resistance to $\beta$ -Lactams. <i>Antibiotics</i> , 2020, 9, 251.	1.5	9
20134	Dynamic Expansion and Functional Evolutionary Profiles of Plant Conservative Gene Family SBP-Box in Twenty Two Flowering Plants and the Origin of miR156. <i>Biomolecules</i> , 2020, 10, 757.	1.8	7
20135	Phylogenetic tree building in the genomic age. <i>Nature Reviews Genetics</i> , 2020, 21, 428-444.	7.7	226
20136	A Highly Prevalent and Pervasive Densovirus Discovered among Sea Stars from the North American Atlantic Coast. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	20
20137	Complete genomic sequences of Venezuelan equine encephalitis virus subtype IIID isolates from mosquitoes. <i>Archives of Virology</i> , 2020, 165, 1715-1717.	0.9	1
20138	Paleoclimatic distribution and phylogeography of <i>Mussismilia braziliensis</i> (Anthozoa, Scleractinia), an endemic Brazilian reef coral. <i>Marine Biodiversity</i> , 2020, 50, 1.	0.3	3
20139	Is <i>Lasiodiplodia theobromae</i> the only species that causes leaf blight disease in Brazilian coconut palms?. <i>Tropical Plant Pathology</i> , 2020, 45, 434-442.	0.8	8
20140	Investigating the genomic landscape of novel coronavirus (2019-nCoV) to identify non-synonymous mutations for use in diagnosis and drug design. <i>Journal of Clinical Virology</i> , 2020, 128, 104441.	1.6	27
20141	A phylogenetically novel cyanobacterium most closely related to <i>Gloeobacter</i> . <i>ISME Journal</i> , 2020, 14, 2142-2152.	4.4	45
20142	Allele-aware chromosome-level genome assembly and efficient transgene-free genome editing for the autotetraploid cultivated alfalfa. <i>Nature Communications</i> , 2020, 11, 2494.	5.8	224
20143	Precise phylogenetic analysis of microbial isolates and genomes from metagenomes using PhyloPhlAn 3.0. <i>Nature Communications</i> , 2020, 11, 2500.	5.8	368
20144	Improved Genome Assembly and Annotation of the Soybean Aphid ( <i>Aphis glycines</i> Matsumura). <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 899-906.	0.8	22
20145	Functional Insights From the Evolutionary Diversification of Big Defensins. <i>Frontiers in Immunology</i> , 2020, 11, 758.	2.2	35
20146	Highly Conserved Homotrimer Cavity Formed by the SARS-CoV-2 Spike Glycoprotein: A Novel Binding Site. <i>Journal of Clinical Medicine</i> , 2020, 9, 1473.	1.0	73
20147	Clues of in vivo nuclear gene regulation by mitochondrial short non-coding RNAs. <i>Scientific Reports</i> , 2020, 10, 8219.	1.6	14
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20150	Prochlorococcus phage ferredoxin: structural characterization and electron transfer to cyanobacterial sulfite reductases. Journal of Biological Chemistry, 2020, 295, 10610-10623.	1.6	10
20151	Phylogenetic origin of <i>Magnolia pseudokobus</i> (Magnoliaceae), a rare <i>Magnolia</i> extinct in the wild, revealed by chloroplast genome sequencing, genome-wide SNP genotyping and microsatellite analysis. Journal of Forest Research, 2020, 25, 322-328.	0.7	2
20152	Multimiomics-based characterization of specialized metabolites biosynthesis in <i>Cornus Officinalis</i> . DNA Research, 2020, 27, .	1.5	8
20153	MtOrt: an empirical mitochondrial amino acid substitution model for evolutionary studies of Orthoptera insects. BMC Evolutionary Biology, 2020, 20, 57.	3.2	7
20154	Comparative (Within Species) Genomics of the <i>Vitis vinifera</i> L. Terpene Synthase Family to Explore the Impact of Genotypic Variation Using Phased Diploid Genomes. Frontiers in Genetics, 2020, 11, 421.	1.1	8
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20156	New Insights on Vitamin K Metabolism in Senegalese sole ( <i>Solea senegalensis</i> ) Based on Ontogenetic and Tissue-Specific Vitamin K Epoxide Reductase Molecular Data. International Journal of Molecular Sciences, 2020, 21, 3489.	1.8	4
20157	Genomic re-assessment of the transposable element landscape of the potato genome. Plant Cell Reports, 2020, 39, 1161-1174.	2.8	12
20158	Genetic analyses reveal female philopatric behavior and nest usage by multiple females of the solitary oil-collecting bee <i>Tetrapedia diversipes</i> (Hymenoptera: Apidae). Apidologie, 2020, 51, 815-825.	0.9	3
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20162	ProgSIO-MSA: Progressive-based single iterative optimization framework for multiple sequence alignment using an effective scoring system. Journal of Bioinformatics and Computational Biology, 2020, 18, 2050005.	0.3	1
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20164	The Genome of <i>Peronospora belbahrii</i> Reveals High Heterozygosity, a Low Number of Canonical Effectors, and TC-Rich Promoters. Molecular Plant-Microbe Interactions, 2020, 33, 742-753.	1.4	15
20165	The 18S ribosomal <i>scp&gt;RNA&lt;/scp&gt; m&lt;sup&gt;6&lt;/sup&gt; A methyltransferase Mettl5 is required for normal walking behavior in <i>Drosophila</i>. EMBO Reports, 2020, 21, e49443.</i>	2.0	52
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20170	Isolation of Gram-Positive, Antibiotic-Resistant Bacteria from Tactile Mobile Phones in a Northwestern Mexican City. <i>Journal of Community Health</i> , 2020, 45, 1050-1060.	1.9	4
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20173	Temporal flexibility of gene regulatory network underlies a novel wing pattern in flies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 11589-11596.	3.3	16
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20180	Analysis of microbiota in Hainan Yucha during fermentation by 16S rRNA gene high-throughput sequencing. <i>Journal of Food Processing and Preservation</i> , 2020, 44, e14523.	0.9	12
20181	Evaluating DCA-based method performances for RNA contact prediction by a well-curated data set. <i>Rna</i> , 2020, 26, 794-802.	1.6	13
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20183	Genomic Analyses of Human Sapoviruses Detected over a 40-Year Period Reveal Disparate Patterns of Evolution among Genotypes and Genome Regions. <i>Viruses</i> , 2020, 12, 516.	1.5	14
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20190	Evolution of <i>Fusarium tricinctum</i> and <i>Fusarium avenaceum</i> mitochondrial genomes is driven by mobility of introns and of a new type of palindromic microsatellite repeats. <i>BMC Genomics</i> , 2020, 21, 358.	1.2	8
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20197	Diversity and pathogenicity of <i>Botryosphaeriaceae</i> species associated with black root rot and stem cutting dry rot in <i>Manihot esculenta</i> in Brazil. <i>European Journal of Plant Pathology</i> , 2020, 157, 583-598.	0.8	19
20198	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
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20200	A multi-approach analysis highlights the relevance of RPA-1 as a telomere end-binding protein (TEBP) in <i>Leishmania amazonensis</i> . <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2020, 1864, 129607.	1.1	10
20201	Functional Divergence of the Arabidopsis Florigen-Interacting bZIP Transcription Factors FD and FDP. <i>Cell Reports</i> , 2020, 31, 107717.	2.9	49
20202	Functional and Genomic Variation between Human-Derived Isolates of <i>Lachnospiraceae</i> Reveals Inter- and Intra-Species Diversity. <i>Cell Host and Microbe</i> , 2020, 28, 134-146.e4.	5.1	210

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20209	Phylogenetic position of deep-sea opecoelid digenean <i>Tellervotrema beringi</i> (Mamaev, 1965) (Trematoda: Tj ETQq0,0 0 rgBT <sub>3</sub> /Overlock	0.5	0
20210	Rivers of Indochina as potential drivers of lineage diversification in the spotted flying lizard ( <i>Draco</i> ) Tj ETQq1 1 0.784314 rgBT <sub>5</sub> /Overlock	1.2	1
20211	<i>Ophiocordyceps desmidiospora</i> , a basal lineage within the "Zombie-Ant Fungi" clade. <i>Mycologia</i> , 2020, 112, 1171-1183.	0.8	6
20212	Population Genomic Analysis Reveals a Highly Conserved Mitochondrial Genome in <i>Fusarium asiaticum</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 839.	1.5	14
20213	Genetic and Clinical Heterogeneity in Thirteen New Cases with Aceruloplasminemia. Atypical Anemia as a Clue for an Early Diagnosis. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2374.	1.8	25
20214	Comparative Genomic and Proteomic Analyses of Three Widespread Phytophthora Species: <i>Phytophthora chlamydospora</i> , <i>Phytophthora gonapodyides</i> and <i>Phytophthora pseudosyringae</i> . <i>Microorganisms</i> , 2020, 8, 653.	1.6	36
20215	Description of a Novel Mycovirus in the Phytopathogen <i>Fusarium culmorum</i> and a Related EVE in the Yeast <i>Lipomyces starkeyi</i> . <i>Viruses</i> , 2020, 12, 523.	1.5	6
20216	<i>Calycomorphotria hydatis</i> gen. nov., sp. nov., a novel species in the family Planctomycetaceae with conspicuous subcellular structures. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 1877-1887.	0.7	17
20217	Biodegradation of artisanally refined diesel and the influence of organic wastes on oil-polluted soil remediation. <i>Scientific African</i> , 2020, 8, e00385.	0.7	9
20218	Complete Genome Sequence of an Alphabaculovirus from <i>Choristoneura diversana</i> . <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	0
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20220	RNA genome conservation and secondary structure in SARS-CoV-2 and SARS-related viruses: a first look. <i>Rna</i> , 2020, 26, 937-959.	1.6	211



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20223	Rediscovering an old foe: Optimised molecular methods for DNA extraction and sequencing applications for fungarium specimens of powdery mildew (Erysiphales). PLoS ONE, 2020, 15, e0232535.	1.1	11
20224	Are pangolins the intermediate host of the 2019 novel coronavirus (SARS-CoV-2)? PLoS Pathogens, 2020, 16, e1008421.	2.1	318
20225	<i>Toxoplasma gondii</i> requires its plant-like heme biosynthesis pathway for infection. PLoS Pathogens, 2020, 16, e1008499.	2.1	33
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20227	The Protector within: Comparative Genomics of APSE Phages across Aphids Reveals Rampant Recombination and Diverse Toxin Arsenals. Genome Biology and Evolution, 2020, 12, 878-889.	1.1	22
20228	An integrative approach to the systematics of the <i>Berthella californica</i> species complex (Heterobranchia: Pleurobranchidae). Journal of Molluscan Studies, 2020, 86, 186-200.	0.4	2
20229	Opportunistic sampling of wild native and invasive birds reveals a rich diversity of adenoviruses in Australia. Virus Evolution, 2020, 6, veaa024.	2.2	21
20230	Mitochondrial genome sequence of <i>Phytophthora sansomeana</i> and comparative analysis of <i>Phytophthora</i> mitochondrial genomes. PLoS ONE, 2020, 15, e0231296.	1.1	9
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20234	Green Tea and Pomegranate Extract Administered During Critical Moments of the Production Cycle Improves Blood Antiradical Activity and Alters Cecal Microbial Ecology of Broiler Chickens. Animals, 2020, 10, 785.	1.0	12
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20236	HDVdb: A Comprehensive Hepatitis D Virus Database. Viruses, 2020, 12, 538.	1.5	16
20237	Impact of an arbuscular mycorrhizal fungal inoculum and exogenous MeJA on fenugreek secondary metabolite production under water deficit. Environmental and Experimental Botany, 2020, 176, 104096.	2.0	23
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20240	Chromosome-Level Reference Genome and Population Genomic Analysis Provide Insights into the Evolution and Improvement of Domesticated Mulberry ( <i>Morus alba</i> ). <i>Molecular Plant</i> , 2020, 13, 1001-1012.	3.9	59
20241	Species delimitation analyses of NE Atlantic Chaetozone (Annelida, Cirratulidae) reveals hidden diversity among a common and abundant marine annelid. <i>Molecular Phylogenetics and Evolution</i> , 2020, 149, 106852.	1.2	14
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20243	Integrating DNA Sequences with Morphological Analysis Clarifies Phylogenetic Position of <i>Salvia grandifolia</i> (Lamiaceae): An Enigmatic Species Endemic to Southwestern China. <i>International Journal of Plant Sciences</i> , 2020, 181, 787-799.	0.6	11
20244	Molecular phylogeny and morphological diversity of the <i>Niviventer fulvescens</i> species complex with emphasis on species from China. <i>Zoological Journal of the Linnean Society</i> , 2021, 191, 528-547.	1.0	16
20245	<i>Tetranychus evansi</i> spider mite populations suppress tomato defenses to varying degrees. <i>Ecology and Evolution</i> , 2020, 10, 4375-4390.	0.8	11
20246	Complete plastomes of 17 species of maples (Sapindaceae: <i>Acer</i> ): comparative analyses and phylogenomic implications. <i>Plant Systematics and Evolution</i> , 2020, 306, 1.	0.3	4
20247	Prevalence of sterility mosaic disease (SMD) and variability in pigeonpea sterility mosaic virus (PPSMV) in southern-India. <i>Indian Phytopathology</i> , 2020, 73, 741-750.	0.7	3
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20250	Viral hijacking of the TENT4-ZCCHC14 complex protects viral RNAs via mixed tailing. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 581-588.	3.6	42
20251	dbPSP 2.0, an updated database of protein phosphorylation sites in prokaryotes. <i>Scientific Data</i> , 2020, 7, 164.	2.4	20
20252	STARCH SYNTHASE5, a Noncanonical Starch Synthase-Like Protein, Promotes Starch Granule Initiation in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2020, 32, 2543-2565.	3.1	49
20253	Genetic and phenotypic characterization of <i>Xanthomonas axonopodis</i> pv. <i>maculifoliogardeniae</i> causing bacterial leaf spot of <i>Ixora</i> in Taiwan. <i>Journal of Phytopathology</i> , 2020, 168, 478-489.	0.5	2
20254	Comparative Analysis of AbaR-Type Genomic Islands Reveals Distinct Patterns of Genetic Features in Elements with Different Backbones. <i>MSphere</i> , 2020, 5, .	1.3	10
20255	Genome-Wide Analysis, Characterization, and Expression Profile of the Basic Leucine Zipper Transcription Factor Family in Pineapple. <i>International Journal of Genomics</i> , 2020, 2020, 1-14.	0.8	10
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20258	Effects of Fermented Herbal Tea Residues on the Intestinal Microbiota Characteristics of Holstein Heifers Under Heat Stress. <i>Frontiers in Microbiology</i> , 2020, 11, 1014.	1.5	14
20259	Marine bacterial community analysis on 316L stainless steel coupons by Illumina MiSeq sequencing. <i>Biotechnology Letters</i> , 2020, 42, 1431-1448.	1.1	20
20260	Effects of <i>Vibrio harveyi</i> infection on serum biochemical parameters and expression profiles of interleukin-17 (IL-17) / interleukin-17 receptor (IL-17R) genes in spotted sea bass. <i>Developmental and Comparative Immunology</i> , 2020, 110, 103731.	1.0	15
20261	Epidemic of venereal treponematosi in wild monkeys: a paradigm for syphilis origin. <i>New Microbes and New Infections</i> , 2020, 35, 100670.	0.8	5
20262	Structure–function analysis of silkworm sucrose hydrolase uncovers the mechanism of substrate specificity in GH13 subfamily 17 $\alpha$ -glucosidases. <i>Journal of Biological Chemistry</i> , 2020, 295, 8784-8797.	1.6	7
20263	First Isolation of a Novel Aquatic Flavivirus from Chinook Salmon ( <i>Oncorhynchus tshawytscha</i> ) and Its <i>In Vivo</i> Replication in a Piscine Animal Model. <i>Journal of Virology</i> , 2020, 94, .	1.5	14
20264	Independent allopatric polyploidizations shaped the geographical structure and initial stage of reproductive isolation in an allotetraploid fern, <i>Lepisorus nigripes</i> (Polypodiaceae). <i>PLoS ONE</i> , 2020, 15, e0233095.	1.1	2
20265	Draft Genome Assembly of <i>Floccularia luteovirens</i> , an Edible and Symbiotic Mushroom on Qinghai-Tibet Plateau. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1167-1173.	0.8	5
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20268	Cattle as natural host for <i>Schistosoma haematobium</i> (Bilharz, 1852) Weinland, 1858 x <i>Schistosoma bovis</i> Sonsino, 1876 interactions, with new cercarial emergence and genetic patterns. <i>Parasitology Research</i> , 2020, 119, 2189-2205.	0.6	33
20269	The osmotic stress response operon betIBA is under the functional regulation of BetI and the quorum-sensing regulator AnoR in <i>Acinetobacter nosocomialis</i> . <i>Journal of Microbiology</i> , 2020, 58, 519-529.	1.3	6
20270	The reference genome of the selfing fish <i>Kryptolebias hermaphroditus</i> : Identification of phases I and II detoxification genes. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2020, 35, 100684.	0.4	2
20271	Spectral Diversification and Trans-Species Allelic Polymorphism during the Land-to-Sea Transition in Snakes. <i>Current Biology</i> , 2020, 30, 2608-2615.e4.	1.8	20
20272	Whole-genome sequence of <i>Phellinus gilvus</i> (mulberry Sanghuang) reveals its unique medicinal values. <i>Journal of Advanced Research</i> , 2020, 24, 325-335.	4.4	24
20273	Evolutionary conservation and functional impact of dopamine D2 receptor. <i>Neuroscience Letters</i> , 2020, 733, 135081.	1.0	0
20274	Exploring the prevalence and diversity of bovine ticks in five agro-ecological zones of Pakistan using phenetic and genetic tools. <i>Ticks and Tick-borne Diseases</i> , 2020, 11, 101472.	1.1	26

#	ARTICLE	IF	CITATIONS
20275	A D200N hemagglutinin substitution contributes to antigenic changes and increased replication of avian H9N2 influenza virus. <i>Veterinary Microbiology</i> , 2020, 245, 108669.	0.8	3
20276	Characterization of centromeric satellite DNAs (MALREP) in the Asian swamp eel ( <i>Monopterus albus</i> ) suggests the possible origin of repeats from transposable elements. <i>Genomics</i> , 2020, 112, 3097-3107.	1.3	11
20277	Revision of the West African species of <i>Scyllarus</i> Fabricius, 1775 (Decapoda: Achelata: Scyllaridae), with the description of three phyllosoma stages of <i>S. caparti</i> Holthuis, 1952 and an updated identification key. <i>Journal of Crustacean Biology</i> , 2020, 40, 412-424.	0.3	4
20278	Phylogeny and gene expression of the complete NITRATE TRANSPORTER 1/PEPTIDE TRANSPORTER FAMILY in <i>Triticum aestivum</i> . <i>Journal of Experimental Botany</i> , 2020, 71, 4531-4546.	2.4	37
20279	Taxonomic revision of the pampas cat <i>Leopardus colocola</i> complex (Carnivora: Felidae): an integrative approach. <i>Zoological Journal of the Linnean Society</i> , 2021, 191, 575-611.	1.0	22
20280	First come, first served: Possible role for priority effects in marine populations under different degrees of dispersal potential. <i>Journal of Biogeography</i> , 2020, 47, 1649-1662.	1.4	4
20281	Evidence for host-dependent RNA editing in the transcriptome of SARS-CoV-2. <i>Science Advances</i> , 2020, 6, eabb5813.	4.7	312
20282	The domesticated transposase ALP2 mediates formation of a novel Polycomb protein complex by direct interaction with MS11, a core subunit of Polycomb Repressive Complex 2 (PRC2). <i>PLoS Genetics</i> , 2020, 16, e1008681.	1.5	22
20283	Diversification rate vs. diversification density: Decoupled consequences of plant height for diversification of Alooideae in time and space. <i>PLoS ONE</i> , 2020, 15, e0233597.	1.1	10
20284	Large-Scale Hybridisation as an Extinction Threat to the Suweon Treefrog ( <i>Hylidae: Dryophytes</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.0	8
20285	Identification of Selective Novel Hits against <i>Plasmodium falciparum</i> Prolyl tRNA Synthetase Active Site and a Predicted Allosteric Site Using In Silico Approaches. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3803.	1.8	9
20286	Cryptic diversity and species boundaries within the <i>Paragalago zanzibaricus</i> species complex. <i>Molecular Phylogenetics and Evolution</i> , 2020, 150, 106887.	1.2	7
20287	Genome-enabled phylogenetic and functional reconstruction of an araphid pennate diatom <i>Plagiostrata</i> sp. CCMP470, previously assigned as a radial centric diatom, and its bacterial commensal. <i>Scientific Reports</i> , 2020, 10, 9449.	1.6	25
20288	Structural studies of geranylgeranylglyceryl phosphate synthase, a prenyltransferase found in thermophilic Euryarchaeota. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 542-557.	1.1	2
20289	Cyclic lipopeptide-producing <i>Pseudomonas koreensis</i> group strains dominate the cocoyam rhizosphere of a <i>Pythium</i> root rot suppressive soil contrasting with <i>P. putida</i> prominence in conducive soils. <i>Environmental Microbiology</i> , 2020, 22, 5137-5155.	1.8	15
20290	Genomic basis of environmental adaptation in the leathery sea squirt ( <i>Styela clava</i> ). <i>Molecular Ecology Resources</i> , 2020, 20, 1414-1431.	2.2	21
20291	Meta-Analysis and Evaluation by Insect-Mediated Baiting Reveal Different Patterns of Hypocrealean Entomopathogenic Fungi in the Soils From Two Regions of China. <i>Frontiers in Microbiology</i> , 2020, 11, 1133.	1.5	7
20292	How Many Tree Species of Birch Are in Alaska? Implications for Wetland Designations. <i>Frontiers in Plant Science</i> , 2020, 11, 750.	1.7	0

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20294	Morphological and functional development of the spiral intestine in cloudy catshark ( <i>Scyliorhinus torazame</i> ). <i>Journal of Experimental Biology</i> , 2020, 223, .	0.8	8
20295	Revisiting <i>Metarhizium</i> and the description of new species from Thailand. <i>Studies in Mycology</i> , 2020, 95, 171-251.	4.5	73
20296	Revealing the Venomous Secrets of the Spider's Web. <i>Journal of Proteome Research</i> , 2020, 19, 3044-3059.	1.8	5
20297	Chromosomal toxin-antitoxin systems in <i>Pseudomonas putida</i> are rather selfish than beneficial. <i>Scientific Reports</i> , 2020, 10, 9230.	1.6	20
20298	More Than One-to-Four via 2R: Evidence of an Independent <i>Amphioxus</i> Expansion and Two-Gene Ancestral Vertebrate State for MyoD-Related Myogenic Regulatory Factors (MRFs). <i>Molecular Biology and Evolution</i> , 2020, 37, 2966-2982.	3.5	15
20299	Nitrogen Fixation in Pozol, a Traditional Fermented Beverage. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	8
20300	Species diversity revealed in <i>Sigmella</i> Hebard, 1929 (Blattodea, ectobiidae) based on morphology and four molecular species delimitation methods. <i>PLoS ONE</i> , 2020, 15, e0232821.	1.1	5
20301	The Location of the Pseudoautosomal Boundary in <i>Silene latifolia</i> . <i>Genes</i> , 2020, 11, 610.	1.0	8
20302	BmApontic is involved in neurodevelopment in the silkworm <i>Bombyx mori</i> . <i>Journal of Integrative Agriculture</i> , 2020, 19, 1439-1446.	1.7	2
20303	Three highly acidic Equisetum XTHs differ from hetero-trans-1,2-glucanase in donor substrate specificity and are predominantly xyloglucan homo-transglucosylases. <i>Journal of Plant Physiology</i> , 2020, 251, 153210.	1.6	12
20304	Plant catalases as NO and H <sub>2</sub> S targets. <i>Redox Biology</i> , 2020, 34, 101525.	3.9	125
20305	A new species of <i>Creptotrematina</i> (Trematoda: Allocreadiidae) from characid fishes of Brazil: morphological and molecular data. <i>Journal of Helminthology</i> , 2020, 94, e163.	0.4	4
20306	Dual-Seq reveals genome and transcriptome of <i>Caedibacter taeniospiralis</i> , obligate endosymbiont of <i>Paramecium</i> . <i>Scientific Reports</i> , 2020, 10, 9727.	1.6	8
20307	The planctomycete <i>Stieleria maiorica</i> Mal15T employs stieleriocines to alter the species composition in marine biofilms. <i>Communications Biology</i> , 2020, 3, 303.	2.0	33
20308	Unexpected but unsurprising lineage diversity within the most widespread Neotropical crocodylian genus <i>Caiman</i> (Crocodylia, Alligatoridae). <i>Systematics and Biodiversity</i> , 2020, 18, 377-395.	0.5	36
20309	Genome-wide adaptive evolution to underground stresses in subterranean mammals: Hypoxia adaption, immunity promotion, and sensory specialization. <i>Ecology and Evolution</i> , 2020, 10, 7377-7388.	0.8	9
20310	Draft genomes of two outcrossing wild rice, <i>Oryza rufipogon</i> and <i>O. longistaminata</i> , reveal genomic features associated with mating system evolution. <i>Plant Direct</i> , 2020, 4, e00232.	0.8	9

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20311	Pattern recognition receptors in grass carp <i>Ctenopharyngodon idella</i> : II. Organization and expression analysis of NOD-like receptors. <i>Developmental and Comparative Immunology</i> , 2020, 110, 103734.	1.0	17
20312	Culture-Independent Analysis of Linuron-Mineralizing Microbiota and Functions in on-Farm Biopurification Systems via DNA-Stable Isotope Probing: Comparison with Enrichment Culture. <i>Environmental Science &amp; Technology</i> , 2020, 54, 9387-9397.	4.6	19
20313	Genome-wide associations of human gut microbiome variation and implications for causal inference analyses. <i>Nature Microbiology</i> , 2020, 5, 1079-1087.	5.9	144
20314	Diversifying selection detected in only a minority of xenobiotic-metabolizing <i>CYP1-3</i> genes among primate species. <i>Xenobiotica</i> , 2020, 50, 1406-1412.	0.5	1
20315	Mitochondrial genome of the Smoothnose wedgefish <i>Rhynchobatus laevis</i> from the Western Indian Ocean. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2083-2084.	0.2	5
20316	CRISPRcasIdentifier: Machine learning for accurate identification and classification of CRISPR-Cas systems. <i>GigaScience</i> , 2020, 9, .	3.3	31
20317	Expanding the Diversity of Bacterioplankton Isolates and Modeling Isolation Efficacy with Large-Scale Dilution-to-Extinction Cultivation. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	34
20318	Zooarchaeology, ancient mtDNA, and radiocarbon dating provide new evidence for the emergence of domestic cattle and caprines in the Tao River Valley of Gansu Province, northwest China. <i>Journal of Archaeological Science: Reports</i> , 2020, 31, 102262.	0.2	11
20319	TBtools: An Integrative Toolkit Developed for Interactive Analyses of Big Biological Data. <i>Molecular Plant</i> , 2020, 13, 1194-1202.	3.9	7,081
20320	Genetic diversity and population structure of <i>Camellia huana</i> (Theaceae), a limestone species with narrow geographic range, based on chloroplast DNA sequence and microsatellite markers. <i>Plant Diversity</i> , 2020, 42, 343-350.	1.8	26
20321	Light-harvesting complex II is an antenna of photosystem I in dark-adapted plants. <i>Nature Plants</i> , 2020, 6, 860-868.	4.7	32
20322	An integrative DNA barcoding framework of ladybird beetles (Coleoptera: Coccinellidae). <i>Scientific Reports</i> , 2020, 10, 10063.	1.6	19
20323	Tropical plants evolve faster than their temperate relatives: a case from the bamboos (Poaceae: <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 2</i> ). <i>2020</i> , 34, 482-493.	0.5	6
20324	The role of introgression and ecotypic parallelism in delineating intraspecific conservation units. <i>Molecular Ecology</i> , 2020, 29, 2793-2809.	2.0	31
20325	Whole genome characterization of autochthonous <i>Bos taurus brachyceros</i> and introduced <i>Bos indicus indicus</i> cattle breeds in Cameroon regarding their adaptive phenotypic traits and pathogen resistance. <i>BMC Genetics</i> , 2020, 21, 64.	2.7	7
20326	Configuration of active site segments in lytic polysaccharide monoxygenases steers oxidative xyloglucan degradation. <i>Biotechnology for Biofuels</i> , 2020, 13, 95.	6.2	22
20327	<i>Phaeotremella camelliae</i> sp. nov. (Phaeotremellaceae, Tremellales), A Novel Yeasts Isolated from Tea-Oil Fruits in Jiangxi Province, China. <i>Current Microbiology</i> , 2020, 77, 3168-3173.	1.0	3
20328	Isolation of <i>Clostridium</i> from Yunnan-Tibet hot springs and description of <i>Clostridium therrmarum</i> sp. nov. with lignocellulosic ethanol production. <i>Systematic and Applied Microbiology</i> , 2020, 43, 126104.	1.2	23

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20329	Cytochrome c nitrite reductase from the bacterium <i>Geobacter lovleyi</i> represents a new NrfA subclass. <i>Journal of Biological Chemistry</i> , 2020, 295, 11455-11465.	1.6	20
20330	Protein Level and Infantile Diarrhea in a Postweaning Piglet Model. <i>Mediators of Inflammation</i> , 2020, 2020, 1-15.	1.4	13
20331	Adapting a Phage to Combat Phage Resistance. <i>Antibiotics</i> , 2020, 9, 291.	1.5	33
20332	Transcriptome sequencing analysis of the MSDIN gene family encoding cyclic peptides in lethal <i>Amanita fuliginoides</i> . <i>Toxicon</i> , 2020, 183, 61-68.	0.8	3
20333	A new species of <i>Phrynobatrachus</i> (Amphibia: Anura: Phrynobatrachidae) from the Northern Mountains of Tanzania. <i>Journal of Natural History</i> , 2020, 54, 63-85.	0.2	3
20334	Increased diversity and concordant shifts in community structure of coral-associated Symbiodiniaceae and bacteria subjected to chronic human disturbance. <i>Molecular Ecology</i> , 2020, 29, 2477-2491.	2.0	26
20335	A new species rises from beneath Florida: molecular phylogenetic analyses reveal cryptic diversity among the metapopulation of <i>Crangonyx hobbsi</i> Shoemaker, 1941 (Amphipoda: Crangonyctidae). <i>Organisms Diversity and Evolution</i> , 2020, 20, 387-404.	0.7	5
20336	Canine papillomavirus type 16 associated to squamous cell carcinoma in a dog: virological and pathological findings. <i>Brazilian Journal of Microbiology</i> , 2020, 51, 2087-2094.	0.8	9
20337	A genoserotyping system for a fast and objective identification of <i>Salmonella</i> serotypes commonly isolated from poultry and pork food sectors in Belgium. <i>Food Microbiology</i> , 2020, 91, 103534.	2.1	12
20338	Genome sequence and comparative analysis of reindeer ( <i>Rangifer tarandus</i> ) in northern Eurasia. <i>Scientific Reports</i> , 2020, 10, 8980.	1.6	30
20339	Finding complexity in complexes: Assessing the causes of mitonuclear discordance in a problematic species complex of Mesoamerican toads. <i>Molecular Ecology</i> , 2020, 29, 3543-3559.	2.0	29
20340	An Africa-wide genomic evolution of insecticide resistance in the malaria vector <i>Anopheles funestus</i> involves selective sweeps, copy number variations, gene conversion and transposons. <i>PLoS Genetics</i> , 2020, 16, e1008822.	1.5	42
20341	Insight into the Lifestyle of <i>Amoeba Willaertia magna</i> during Bioreactor Growth Using Transcriptomics and Proteomics. <i>Microorganisms</i> , 2020, 8, 771.	1.6	5
20342	Nanopore sequencing from extraction-free direct PCR of dried serum spots for portable hepatitis B virus drug-resistance typing. <i>Journal of Clinical Virology</i> , 2020, 129, 104483.	1.6	9
20343	A five-gene molecular phylogeny reveals <i>Parapanteles Ashmead</i> (Hymenoptera: Braconidae) to be polyphyletic as currently composed. <i>Molecular Phylogenetics and Evolution</i> , 2020, 150, 106859.	1.2	4
20344	Epidemiology and Phylogenetic Analysis of Viral Respiratory Infections in Vietnam. <i>Frontiers in Microbiology</i> , 2020, 11, 833.	1.5	6
20345	Isolation and Complete Genome Sequence of a Novel Cyanophage S-B68. <i>Current Microbiology</i> , 2020, 77, 2385-2390.	1.0	3
20346	The full-length genome characterization and diversity of faba bean necrotic stunt virus in Iran. <i>European Journal of Plant Pathology</i> , 2020, 157, 239-250.	0.8	3

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20347	The first complete mitochondrial genome data of <i>Hippocampus kuda</i> originating from Malaysia. <i>Data in Brief</i> , 2020, 31, 105721.	0.5	8
20348	The first mitochondrial genomes of endosymbiotic rhabdocoels illustrate evolutionary relaxation of <i>atp8</i> and genome plasticity in flatworms. <i>International Journal of Biological Macromolecules</i> , 2020, 162, 454-469.	3.6	16
20349	<i>Metapochonia hahajimaensis</i> (Clavicipitaceae, Hypocreales), a new species from soil in Hahajima Island, Tokyo, Japan. <i>Mycoscience</i> , 2020, 61, 337-341.	0.3	0
20350	Protective Role of Bacterial Alkanesulfonate Monooxygenase under Oxidative Stress. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	16
20351	Rampant Nuclear Transfer and Substitutions of Plastid Genes in <i>Passiflora</i> . <i>Genome Biology and Evolution</i> , 2020, 12, 1313-1329.	1.1	15
20352	Revision of <i>Macroponema</i> Mawson, 1978 (Nematoda: Strongylida) from macropodid marsupials with the description of two new species. <i>Parasites and Vectors</i> , 2020, 13, 298.	1.0	1
20353	<i>Nonomuraea terrae</i> sp. nov., isolated from arid soil. <i>Archives of Microbiology</i> , 2020, 202, 2197-2205.	1.0	14
20354	Identification of a chitosanase from the marine metagenome and its molecular improvement based on evolution data. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 6647-6657.	1.7	7
20355	Interest of bacterial pangenome analyses in clinical microbiology. <i>Microbial Pathogenesis</i> , 2020, 149, 104275.	1.3	12
20356	Animal biosynthesis of complex polyketides in a photosynthetic partnership. <i>Nature Communications</i> , 2020, 11, 2882.	5.8	38
20357	A neurotransmitter produced by gut bacteria modulates host sensory behaviour. <i>Nature</i> , 2020, 583, 415-420.	13.7	155
20358	CobT and BzaC catalyze the regiospecific activation and methylation of the 5-hydroxybenzimidazole lower ligand in anaerobic cobamide biosynthesis. <i>Journal of Biological Chemistry</i> , 2020, 295, 10522-10534.	1.6	6
20359	A new section, <i>Lactifluus</i> section <i>Neotropicus</i> (Russulaceae), and two new <i>Lactifluus</i> species from the Atlantic Forest, Brazil. <i>Systematics and Biodiversity</i> , 2020, 18, 347-361.	0.5	6
20360	Identification of key bacterial populations affecting early embryonic development in cattle uterus. <i>Animal Science Journal</i> , 2020, 91, e13374.	0.6	0
20361	The Brittle Rachis Trait in Species Belonging to the Triticeae and Its Controlling Genes <i>Btr1</i> and <i>Btr2</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 1000.	1.7	12
20362	Debunking <i>Duosporium</i> . <i>Mycological Progress</i> , 2020, 19, 715-723.	0.5	1
20363	Hybrid Gene Origination Creates Human-Virus Chimeric Proteins during Infection. <i>Cell</i> , 2020, 181, 1502-1517.e23.	13.5	33
20364	Genome Assembly and Pathway Analysis of Edible Mushroom <i>Agrocybe cylindracea</i> . <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 341-351.	3.0	18



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20365	The systematic position of the enigmatic rare South African endemic <i>Carex acocksii</i> : Its relevance on the biogeography and evolution of <i>Carex</i> sect. <i>Schoenoxiphium</i> (Cyperaceae). <i>South African Journal of Botany</i> , 2020, 131, 475-483.	1.2	6
20366	Four mycangium types and four genera of ambrosia fungi suggest a complex history of fungus farming in the ambrosia beetle tribe Xyloterini. <i>Mycologia</i> , 2020, 112, 1104-1137.	0.8	19
20367	Biological identification of ascidians from Vizhinjam Bay, southwest Coast of India using CO1 gene sequences. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2020, 31, 209-217.	0.7	0
20368	Unprecedented Diversity of Unique CRISPR-Cas-Related Systems and Cas1 Homologs in Asgard Archaea. <i>CRISPR Journal</i> , 2020, 3, 156-163.	1.4	17
20369	Biochemical pedomorphosis and genetic assimilation in the hypoxia adaptation of Tibetan antelope. <i>Science Advances</i> , 2020, 6, eabb5447.	4.7	25
20370	Risk1, a Phosphatidylinositol 3-Kinase Effector, Promotes <i>Rickettsia typhi</i> Intracellular Survival. <i>MBio</i> , 2020, 11, .	1.8	28
20371	Detection of DNA of filariae closely related to <i>Mansonella perstans</i> in faecal samples from wild non-human primates from Cameroon and Gabon. <i>Parasites and Vectors</i> , 2020, 13, 313.	1.0	11
20372	Genomic and transcriptomic insights into methanogenesis potential of novel methanogens from mangrove sediments. <i>Microbiome</i> , 2020, 8, 94.	4.9	51
20373	Potassium Channel-Associated Bioelectricity of the Dermomyotome Determines Fin Patterning in Zebrafish. <i>Genetics</i> , 2020, 215, 1067-1084.	1.2	22
20374	Identification of putative lignin biosynthesis genes in <i>Betula pendula</i> . <i>Trees - Structure and Function</i> , 2020, 34, 1255-1265.	0.9	5
20375	New insight into the molecular phylogeny of the genus <i>Liparis</i> s.l. (Orchidaceae: Malaxideae) with a new generic segregate: <i>Blepharoglossum</i> . <i>Plant Systematics and Evolution</i> , 2020, 306, 1.	0.3	12
20376	MicroTom Metabolic Network: Rewiring Tomato Metabolic Regulatory Network throughout the Growth Cycle. <i>Molecular Plant</i> , 2020, 13, 1203-1218.	3.9	107
20377	The <i>Macroptilium gracile</i> species complex (Fabaceae, Papilionoideae): an integrative taxonomic study based on morphological, molecular and ecological data. <i>Botanical Journal of the Linnean Society</i> , 2020, 194, 118-139.	0.8	2
20378	Micro-Evolution Analysis Reveals Diverged Patterns of Polyol Transporters in Seven Gramineae Crops. <i>Frontiers in Genetics</i> , 2020, 11, 565.	1.1	13
20379	Amplicon-Based High-Throughput Sequencing Method Capable of Species-Level Identification of Coagulase-Negative Staphylococci in Diverse Communities. <i>Microorganisms</i> , 2020, 8, 897.	1.6	10
20380	An iron (II) dependent oxygenase performs the last missing step of plant lysine catabolism. <i>Nature Communications</i> , 2020, 11, 2931.	5.8	11
20381	An endophyte of <i>Macrochloa tenacissima</i> (esparto or needle grass) from Tunisia is a novel species in the <i>Fusarium redolens</i> species complex. <i>Mycologia</i> , 2020, 112, 792-807.	0.8	7
20382	Detection of heterogeneous vancomycin intermediate resistance in MRSA isolates from Latin America. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 2424-2431.	1.3	8

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20383	Comparative epidemiology, phylogenetics, and transmission patterns of severe influenza A/H3N2 in Australia from 2003 to 2017. <i>Influenza and Other Respiratory Viruses</i> , 2020, 14, 700-709.	1.5	3
20384	Initiator and executioner caspases in salivary gland apoptosis of <i>Rhipicephalus haemaphysaloides</i> . <i>Parasites and Vectors</i> , 2020, 13, 288.	1.0	27
20385	GAA gene mutation detection following clinical evaluation and enzyme activity analysis in Azeri Turkish patients with Pompe disease. <i>Metabolic Brain Disease</i> , 2020, 35, 1127-1134.	1.4	2
20386	Molecular analysis of several in-house rRT-PCR protocols for SARS-CoV-2 detection in the context of genetic variability of the virus in Colombia. <i>Infection, Genetics and Evolution</i> , 2020, 84, 104390.	1.0	39
20387	Phylogenetic position of <i>Aculamprotula polysticta</i> , comb. res. (Bivalvia : Unionidae) inferred from phylogenetic relationships in Unionida. <i>Invertebrate Systematics</i> , 2020, 34, 192.	0.5	3
20388	How "Gondwanan" is <i>Riethia</i> ? Molecular phylogenetics elucidates the mode and tempo of diversification in Austro-Pacific Chironominae (Diptera). <i>Invertebrate Systematics</i> , 2020, , .	0.5	1
20389	Molecular phylogeny and ultrastructure of two novel parasitic dinoflagellates, <i>Haplozoon gracile</i> sp. nov. and <i>H. pugnus</i> sp. nov. <i>Phycologia</i> , 2020, 59, 305-319.	0.6	3
20390	Detecting destabilizing species in the phylogenetic backbone of <i>Potentilla</i> (Rosaceae) using low-copy nuclear markers. <i>AoB PLANTS</i> , 2020, 12, plaa017.	1.2	14
20391	The origin and underlying driving forces of the SARS-CoV-2 outbreak. <i>Journal of Biomedical Science</i> , 2020, 27, 73.	2.6	82
20392	Diverse Bacteriocins Produced by Strains From the Human Milk Microbiota. <i>Frontiers in Microbiology</i> , 2020, 11, 788.	1.5	23
20393	A New IL6 Isoform in Chinese Soft-Shelled Turtle ( <i>Pelodiscus sinensis</i> ) Discovered: Its Regulation during Cold Stress and Infection. <i>Biology</i> , 2020, 9, 111.	1.3	4
20394	Detection of <i>Wolbachia</i> Infections in Natural and Laboratory Populations of the Moroccan Hessian Fly, <i>Mayetiola destructor</i> (Say). <i>Insects</i> , 2020, 11, 340.	1.0	4
20395	Evolutionary history of the Persian squirrel ( <i>Sciurus anomalus</i> ): It emerged on the Eurasian continent in the Miocene. <i>Zoologischer Anzeiger</i> , 2020, 287, 17-24.	0.4	6
20396	Tropical principal component analysis on the space of phylogenetic trees. <i>Bioinformatics</i> , 2020, 36, 4590-4598.	1.8	12
20397	Genetic and functional diversification of chemosensory pathway receptors in mosquito-borne filarial nematodes. <i>PLoS Biology</i> , 2020, 18, e3000723.	2.6	33
20398	Chromosome Level Genome Assembly of <i>Andrographis paniculata</i> . <i>Frontiers in Genetics</i> , 2020, 11, 701.	1.1	14
20399	Tracing the Origins of the Pituitary Adenylate-Cyclase Activating Polypeptide (PACAP). <i>Frontiers in Neuroscience</i> , 2020, 14, 366.	1.4	15
20400	Genome Sequence and Phylogeny of a <i>Bean Yellow Mosaic Virus</i> Isolate Obtained from a 14-Year-Old Australian Lentil Sample. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	2

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20402	Molecular Determinants Elucidate the Selectivity in Abscisic Acid Receptor and HAB1 Protein Interactions. <i>Frontiers in Chemistry</i> , 2020, 8, 425.	1.8	11
20403	Detection of Alpha, Beta, Gamma, and Unclassified Human Papillomaviruses in Cervical Cancer Samples From Mexican Women. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 234.	1.8	15
20404	Characterization of Two Satellite DNA Families in the Genome of the Oomycete Plant Pathogen <i>Phytophthora parasitica</i> . <i>Frontiers in Genetics</i> , 2020, 11, 557.	1.1	6
20405	Phenotypic and Genetic Characterization of the Cheese Ripening Yeast <i>Geotrichum candidum</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 737.	1.5	21
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20415	A multiplex qPCR TaqMan-assay to detect fungal antagonism between <i>Trichoderma atroviride</i> (Hypocreaceae) and <i>Botrytis cinerea</i> (Sclerotiniaceae) in blackberry fruits using a de novo <i>tef1-1</i> and an IGS-sequence based probes. <i>Biotechnology Reports (Amsterdam, Netherlands)</i> , 2020, 27, e00447.	2.1	2
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20420	Allosteric Influence of Extremophile Hairpin Motif Mutations on the Protein Splicing Activity of a Hyperthermophilic Intein. <i>Biochemistry</i> , 2020, 59, 2459-2467.	1.2	1
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20429	A Tetratricopeptide Repeat Protein Regulates Carotenoid Biosynthesis and Chromoplast Development in Monkeyflowers ( <i>Mimulus</i> ). <i>Plant Cell</i> , 2020, 32, 1536-1555.	3.1	39
20430	Genome-wide identification and expression analysis of WRKY transcription factors in pearl millet ( <i>Pennisetum glaucum</i> ) under dehydration and salinity stress. <i>BMC Genomics</i> , 2020, 21, 231.	1.2	56
20431	Genetic variation in <i>Austrostrongylus thyllogale</i> Johnston & Mawson, 1940 (Nematoda: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 272 Td (Tr) brachyurus (Quoy & Gaimard) (Marsupialia: Macropodidae) in Australia. <i>Parasites and Vectors</i> , 2020, 13, 135.	1.0	0
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20445	Whole genome phylogeny of <i>Gallus</i> : introgression and data-type effects. <i>Avian Research</i> , 2020, 11, .	0.5	17
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20456	Multiplex PCRs for the specific identification of marsupial and deer species from faecal samples as a basis for non-invasive epidemiological studies of parasites. <i>Parasites and Vectors</i> , 2020, 13, 144.	1.0	3
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20462	<i>Streptococcus halichoeri</i> : Comparative Genomics of an Emerging Pathogen. <i>International Journal of Genomics</i> , 2020, 2020, 1-9.	0.8	7
20463	Great Abundance of Satellite DNA in <i>Proceratophrys</i> (Anura). <i>Tj ETQqO O O rgBT /Overlock 10 Tf 50</i> 141-147.	0.6	16
20464	Estimating relative biomasses of organisms in microbiota using $\alpha$ -phylopeptidomics. <i>Microbiome</i> , 2020, 8, 30.	4.9	34
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20468	<i>Isaria macroscyticola</i> , a rare entomopathogenic species on <i>Cydnidae</i> (Hemiptera), is a synonym of <i>Purpureocillium lilacinum</i> ( <i>Ophiocordycipitaceae</i> ). <i>Mycoscience</i> , 2020, 61, 160-164.	0.3	3
20469	Functional exploration of the GH29 fucosidase family. <i>Glycobiology</i> , 2020, 30, 735-745.	1.3	22
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20487	Identification of salt tolerance-related genes of <i>Lactobacillus plantarum</i> D31 and T9 strains by genomic analysis. <i>Annals of Microbiology</i> , 2020, 70, .	1.1	17
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20490	Effects of Different Fertilizers on Rhizosphere Bacterial Communities of Winter Wheat in the North China Plain. <i>Agronomy</i> , 2020, 10, 93.	1.3	24

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20497	Resistance of South American opossums to vWF-binding venom C-type lectins. <i>Toxicon</i> , 2020, 178, 92-99.	0.8	8
20498	The CRISPR-Cas systems were selectively inactivated during evolution of <i>Bacillus cereus</i> group for adaptation to diverse environments. <i>ISME Journal</i> , 2020, 14, 1479-1493.	4.4	32
20499	Histone variant H3.3 residue S31 is essential for <i>Xenopus</i> gastrulation regardless of the deposition pathway. <i>Nature Communications</i> , 2020, 11, 1256.	5.8	38
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20504	High incidence of heteroplasmy in the mtDNA of a natural population of the spider crab <i>Maja brachydactyla</i> . <i>PLoS ONE</i> , 2020, 15, e0230243.	1.1	15
20505	The Hybrid Genome of a New Goldfish-Like Fish Lineage Provides Insights Into the Origin of the Goldfish. <i>Frontiers in Genetics</i> , 2020, 11, 122.	1.1	4
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20510	Chromosome-level analysis of the <i>Crassostrea hongkongensis</i> genome reveals extensive duplication of immune-related genes in bivalves. <i>Molecular Ecology Resources</i> , 2020, 20, 980-994.	2.2	45
20511	Cultivating the Macroalgal Holobiont: Effects of Integrated Multi-Trophic Aquaculture on the Microbiome of <i>Ulva rigida</i> (Chlorophyta). <i>Frontiers in Marine Science</i> , 2020, 7, .	1.2	61
20512	Animal Disease Surveillance in the 21st Century: Applications and Robustness of Phylodynamic Methods in Recent U.S. Human-Like H3 Swine Influenza Outbreaks. <i>Frontiers in Veterinary Science</i> , 2020, 7, 176.	0.9	1
20513	Novel phosphate-solubilizing bacteria enhance soil phosphorus cycling following ecological restoration of land degraded by mining. <i>ISME Journal</i> , 2020, 14, 1600-1613.	4.4	194
20514	Phylogeography of <i>Acartia tonsa</i> Dana, 1849 (Calanoida: Copepoda) and phylogenetic reconstruction of the genus <i>Acartia</i> Dana, 1846. <i>Marine Biodiversity</i> , 2020, 50, 1.	0.3	12
20515	Characterization of tick viromes collected from dogs in China. <i>Biosafety and Health</i> , 2020, 2, 79-88.	1.2	7
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20517	Protein Structure and Sequence Reanalysis of 2019-nCoV Genome Refutes Snakes as Its Intermediate Host and the Unique Similarity between Its Spike Protein Insertions and HIV-1. <i>Journal of Proteome Research</i> , 2020, 19, 1351-1360.	1.8	242
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20521	Assessment and comparison of putative amine receptor complement/diversity in the brain and eyestalk ganglia of the lobster, <i>Homarus americanus</i> . <i>Invertebrate Neuroscience</i> , 2020, 20, 7.	1.8	2
20522	Effects of dietary raw or <i>Enterococcus faecium</i> fermented soybean meal on growth, antioxidant status, intestinal microbiota, morphology, and inflammatory responses in turbot ( <i>Scophthalmus</i> ) Tj ETQq1 1 0.7843.14 rgBT 13 Overlock 1	1.4	13
20523	Consensus Mutagenesis and Ancestral Reconstruction Provide Insight into the Substrate Specificity and Evolution of the Front-End $\Delta^6$ -Desaturase Family. <i>Biochemistry</i> , 2020, 59, 1398-1409.	1.2	12
20524	The genome of <i>jojoba</i> ( <i>Simmondsia chinensis</i> ): A taxonomically isolated species that directs wax ester accumulation in its seeds. <i>Science Advances</i> , 2020, 6, eaay3240.	4.7	53
20525	Time-Course RNAseq Reveals <i>Exserohilum turcicum</i> Effectors and Pathogenicity Determinants. <i>Frontiers in Microbiology</i> , 2020, 11, 360.	1.5	23
20526	NLGenomeSweeper: A Tool for Genome-Wide NBS-LRR Resistance Gene Identification. <i>Genes</i> , 2020, 11, 333.	1.0	26

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20528	Hybridization and hybrid zone stability between two lizards explained by population genetics and niche quantification. <i>Zoological Journal of the Linnean Society</i> , 2020, 190, 757-769.	1.0	1
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20530	Gene duplications, divergence and recombination shape adaptive evolution of the fish ectoparasite <i>Gyrodactylus bullatarudis</i> . <i>Molecular Ecology</i> , 2020, 29, 1494-1507.	2.0	11
20531	Gut microbiota in neonates with congenital gastrointestinal surgical conditions: a prospective study. <i>Pediatric Research</i> , 2020, 88, 878-886.	1.1	11
20532	Phylogenetic relationships of Asian freshwater Mytiloidea (Bivalvia): a morphological and genetic comparison of <i>Sinomytilus harmandi</i> , <i>Limnoperna fortunei</i> and <i>Septifer bilocularis</i> . <i>Molluscan Research</i> , 2020, 40, 120-129.	0.2	5
20533	Dispersal Predicts Hybrid Zone Widths across Animal Diversity: Implications for Species Borders under Incomplete Reproductive Isolation. <i>American Naturalist</i> , 2020, 196, 9-28.	1.0	26
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20535	Systematics and Phylogenetic Relationships of New Zealand Benthic Octopuses (Cephalopoda: Tj ETQq0 0 0 rgBT /Qverlock 4 0 Tf 50 4	1.2	4
20536	Genomic and transcriptomic evidence of light-sensing, porphyrin biosynthesis, Calvin-Benson-Bassham cycle, and urea production in Bathyarchaeota. <i>Microbiome</i> , 2020, 8, 43.	4.9	31
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20672	Diversification of New World Cleomaceae with emphasis on <i>Tarenaya</i> and the description of <i>Itisiella</i> , a new genus. <i>Taxon</i> , 2020, 69, 321-336.	0.4	8
20673	Unexpected diversity in northern Europe: trematodes from salmonid fishes in Iceland with two new species of <i>Crepidostomum</i> Braun, 1900. <i>Parasitology Research</i> , 2020, 119, 2439-2462.	0.6	14
20674	<i>Maoricimonas rarisocia</i> gen. nov., sp. nov., a novel planctomycete isolated from marine sediments close to Mallorca Island. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 1901-1913.	0.7	17
20675	Epigenetic regulation of gonadal and brain aromatase expression in a cichlid fish with environmental sex determination. <i>General and Comparative Endocrinology</i> , 2020, 296, 113538.	0.8	7
20676	Molecular phylogenetic analysis of New Zealand mosquito species. <i>New Zealand Journal of Zoology</i> , 2020, 47, 324-349.	0.6	4
20677	NAD(P)H-dependent thioredoxin-disulfide reductase TrxR is essential for tellurite and selenite reduction and resistance in <i>Bacillus</i> sp. Y3. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	16
20678	ModelTeller: Model Selection for Optimal Phylogenetic Reconstruction Using Machine Learning. <i>Molecular Biology and Evolution</i> , 2020, 37, 3338-3352.	3.5	30
20679	Transposable element abundance correlates with mode of transmission in microsporidian parasites. <i>Mobile DNA</i> , 2020, 11, 19.	1.3	21
20680	<i>Drosophila</i> model to study Retinitis pigmentosa pathology associated with mutations in the core splicing factor Prp8. <i>DMM Disease Models and Mechanisms</i> , 2020, 13, .	1.2	8
20681	UPI $\phi$ phages, a new group of filamentous phages found in several members of Enterobacteriales. <i>Virus Evolution</i> , 2020, 6, veaa030.	2.2	9
20682	Genomic Analysis of Bovine <i>Staphylococcus aureus</i> Isolates from Milk To Elucidate Diversity and Determine the Distributions of Antimicrobial and Virulence Genes and Their Association with Mastitis. <i>MSystems</i> , 2020, 5, .	1.7	35
20683	Limited overall impacts of ectomycorrhizal inoculation on recruitment of boreal trees into Arctic tundra following wildfire belie species-specific responses. <i>PLoS ONE</i> , 2020, 15, e0235932.	1.1	4
20684	Complete Genome Sequencing and Transcriptome Analysis of Nitrogen Metabolism of <i>Succinivibrio dextrinosolvens</i> Strain Z6 Isolated From Dairy Cow Rumen. <i>Frontiers in Microbiology</i> , 2020, 11, 1826.	1.5	22
20685	Cyclotide Structures Revealed by NMR, with a Little Help from X-ray Crystallography. <i>ChemBioChem</i> , 2020, 21, 3463-3475.	1.3	11
20686	Cellular Importin $\beta$ Expression Dynamics in the Lung Regulate Antiviral Response Pathways against Influenza A Virus Infection. <i>Cell Reports</i> , 2020, 31, 107549.	2.9	11
20687	Identification of a superagonist variant of the immunodominant Yellow fever virus epitope NS4b 214-222 by combinatorial peptide library screening. <i>Molecular Immunology</i> , 2020, 125, 43-50.	1.0	0
20688	Clarifying the cryptogenic species <i>Polydora neocaeca</i> Williams & Radashevsky, 1999 (Annelida: Tj ETQq1 1 0.784314 rgBT /Overlo. <i>2020</i> , 50, .	0.3	9

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20690	Diversity, phylogeny, and historical biogeography of large-eye seabreams (Teleostei: Lethrinidae). <i>Molecular Phylogenetics and Evolution</i> , 2020, 151, 106902.	1.2	9
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20700	First report of porcine respirovirus 1 in South America. <i>Veterinary Microbiology</i> , 2020, 246, 108726.	0.8	19
20701	Discovery of Two Novel Negeviruses in a Dungfly Collected from the Arctic. <i>Viruses</i> , 2020, 12, 692.	1.5	18
20702	A Systematic Analysis of Mosquito-Microbiome Biosynthetic Gene Clusters Reveals Antimalarial Siderophores that Reduce Mosquito Reproduction Capacity. <i>Cell Chemical Biology</i> , 2020, 27, 817-826.e5.	2.5	17
20703	Sexual reproduction potential implied by functional analysis of SPO11 in <i>Phaeodactylum tricornutum</i> . <i>Gene</i> , 2020, 757, 144929.	1.0	5
20704	New insights into the evolution of host specificity of three <i>Penicillium</i> species and the pathogenicity of <i>P. italicum</i> involving the infection of Valencia orange ( <i>Citrus sinensis</i> ). <i>Virulence</i> , 2020, 11, 748-768.	1.8	8
20705	Activated L-Type Calcium Channels Inhibit Chemosensitized Nematocyst Discharge from Sea Anemone Tentacles. <i>Biological Bulletin</i> , 2020, 238, 180-192.	0.7	8
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20709	Landscape of Eukaryotic Transmembrane Beta Barrel Proteins. Journal of Proteome Research, 2020, 19, 1209-1221.	1.8	5
20710	Genome-scale data reveal the role of hybridization in lichen-forming fungi. Scientific Reports, 2020, 10, 1497.	1.6	26
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20715	Ecofriendly Degradation of Polyethylene Plastics Using Oil Degrading Microbes. Recent Innovations in Chemical Engineering, 2020, 13, 29-40.	0.2	2
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20726	Over 100 Million Years of Enzyme Evolution Underpinning the Production of Morphine in the Papaveraceae Family of Flowering Plants. <i>Plant Communications</i> , 2020, 1, 100029.	3.6	34
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20729	Broad diversity of simian immunodeficiency virus infecting <i>Chlorocebus</i> species (African green) Tj ETQq0 0 0 rgBT /Overlock 10 T of <i>Medical Primatology</i> , 2020, 49, 165-178.	0.3	4
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20732	Phylogenetic Systematics of the Water Toad ( <i>Bufo stejnegeri</i> ) Elucidates the Evolution of Semi-aquatic Toad Ecology and Pleistocene Glacial Refugia. <i>Frontiers in Ecology and Evolution</i> , 2020, 7, .	1.1	13
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20735	Key Transitions in the Evolution of Rapid and Slow Growing <i>Mycobacteria</i> Identified by Comparative Genomics. <i>Frontiers in Microbiology</i> , 2019, 10, 3019.	1.5	37
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20741	Phylogeographic and taxonomic considerations on <i>Goniolimon tataricum</i> (Plumbaginaceae) and its relatives from south-eastern Europe and the Apennine Peninsula. <i>Plant Systematics and Evolution</i> , 2020, 306, 1.	0.3	6
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20744	Expansion of known ssRNA phage genomes: From tens to over a thousand. <i>Science Advances</i> , 2020, 6, eaay5981.	4.7	112
20745	The genome evolution and low-phosphorus adaptation in white lupin. <i>Nature Communications</i> , 2020, 11, 1069.	5.8	50
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20748	Genetic Characterization of Piroplasmids in Donkeys and Horses from Nigeria. <i>Animals</i> , 2020, 10, 324.	1.0	12
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20750	Comprehensive Real-Time RT-PCR Assays for the Detection of Fifteen Viruses Infecting <i>Prunus</i> spp.. <i>Plants</i> , 2020, 9, 273.	1.6	14
20751	First Phylogeny of Bitterbush Family, Picramniaceae (Picramniales). <i>Plants</i> , 2020, 9, 284.	1.6	2
20752	Substantial Antigenic Drift in the Hemagglutinin Protein of Swine Influenza A Viruses. <i>Viruses</i> , 2020, 12, 248.	1.5	23
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20756	16S rRNA gene sequencing reveals an altered composition of the gut microbiota in chickens infected with a nephropathogenic infectious bronchitis virus. <i>Scientific Reports</i> , 2020, 10, 3556.	1.6	10
20757	Identification and molecular characterisation of fifteen tropical isolates of the entomopathogenic fungus <i>Metarhizium</i> . <i>Biocontrol Science and Technology</i> , 2020, 30, 490-498.	0.5	2
20758	Statistical Mitogenome Assembly with Repeats. <i>Journal of Computational Biology</i> , 2020, 27, 1407-1421.	0.8	8
20759	Whole genome sequencing and comparative genomic analysis of oleaginous red yeast <i>Sporobolomyces pararoseus</i> NGR identifies candidate genes for biotechnological potential and ballistospores-shooting. <i>BMC Genomics</i> , 2020, 21, 181.	1.2	9
20760	Shared Mutations in a Novel Glutaredoxin Repressor of Multicellular Trichome Fate Underlie Parallel Evolution of <i>Antirrhinum</i> Species. <i>Current Biology</i> , 2020, 30, 1357-1366.e4.	1.8	10

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20762	The double-mutation $\Delta M918I + L1014F$ allele is fixed in <i>Cimex hemipterus</i> populations in Guangxi, China. <i>Bulletin of Entomological Research</i> , 2020, 110, 506-511.	0.5	16
20763	Genome Detective Coronavirus Typing Tool for rapid identification and characterization of novel coronavirus genomes. <i>Bioinformatics</i> , 2020, 36, 3552-3555.	1.8	129
20764	Stress Reshapes the Physiological Response of Halophile Fungi to Salinity. <i>Cells</i> , 2020, 9, 525.	1.8	32
20765	Elucidating cryptic dynamics of <i>Theileria</i> communities in African buffalo using a high-throughput sequencing informatics approach. <i>Ecology and Evolution</i> , 2020, 10, 70-80.	0.8	19
20766	Hosts of asexual morph of <i>Erysiphe quercicola</i> from Thailand. <i>Tropical Plant Pathology</i> , 2020, 45, 122-135.	0.8	9
20767	Soybean aphid biotype 1 genome: Insights into the invasive biology and adaptive evolution of a major agricultural pest. <i>Insect Biochemistry and Molecular Biology</i> , 2020, 120, 103334.	1.2	15
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20770	Molecular characterization of ticks infesting livestock in Khyber Pakhtunkhwa Province, Pakistan. <i>International Journal of Acarology</i> , 2020, 46, 165-170.	0.3	7
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20772	Complete mitogenomes of the chlorophyte green algae <i>Scherffelia dubia</i> and <i>Tetraselmis</i> sp. CCMP 881 (Chlorodendrophyceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 138-139.	0.2	4
20773	Complete mitogenomes of the marine picoplanktonic green algae <i>Prasinoderma</i> sp. MBIC 10622 and <i>Prasinococcus capsulatus</i> CCMP 1194 (Palmophyllophyceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 166-168.	0.2	3
20774	Complete mitochondrial genome of <i>Cladosporium zixishanense</i> sp. nov. YFCC 8620 isolated from the spider in Yunnan, southwestern China. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 210-211.	0.2	0
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20777	The mitochondrial genome of the orange-striped green sea anemone <i>Diadumene lineata</i> (Actiniaria). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 591-592.	0.2	1
20778	The complete chloroplast genome of <i>Hevea camargoana</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 607-608.	0.2	4

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20781	Genetic Characterization of Full-Length HIV-2 Long Terminal Repeat Sequences: Identification of Rare Promoter Variants. AIDS Research and Human Retroviruses, 2020, 36, 533-538.	0.5	0
20782	Distinct mechanisms shape soil bacterial and fungal co-occurrence networks in a mountain ecosystem. FEMS Microbiology Ecology, 2020, 96, .	1.3	62
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20789	Assessment of a multiplex PCR and Nanopore-based method for dengue virus sequencing in Indonesia. Virology Journal, 2020, 17, 24.	1.4	26
20790	<i>Bradyrhizobium uaiense</i> sp. nov., a new highly efficient cowpea symbiont. Archives of Microbiology, 2020, 202, 1135-1141.	1.0	10
20791	Bioinformatics design and experimental validation of influenza A virus multi-epitopes that induce neutralizing antibodies. Archives of Virology, 2020, 165, 891-911.	0.9	13
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20794	The soil fungal community of native woodland in Andean Patagonian forest: A case study considering experimental forest management and seasonal effects. Forest Ecology and Management, 2020, 461, 117955.	1.4	16
20795	Phylogeographic analyses of a migratory freshwater fish ( <i>Megalobrama terminalis</i> ) reveal a shallow genetic structure and pronounced effects of sea-level changes. Gene, 2020, 737, 144478.	1.0	19
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20798	Extensive cryptic diversity of giant clams (Cardiidae: Tridacninae) revealed by DNA-sequence-based species delimitation approaches with new data from Hainan Island, South China Sea. <i>Journal of Molluscan Studies</i> , 2020, 86, 56-63.	0.4	9
20799	Reconstructing the evolutionary history of nitrogenases: Evidence for ancestral molybdenum cofactor utilization. <i>Geobiology</i> , 2020, 18, 394-411.	1.1	58
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20801	Species diversity in <i>Penicillium</i> and <i>Talaromyces</i> from herbivore dung, and the proposal of two new genera of penicillium-like fungi in <i>Aspergillaceae</i> . <i>Fungal Systematics and Evolution</i> , 2020, 5, 39-76.	0.9	20
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20803	Assembly mechanisms and environmental predictors of the phylogenetic diversity of cricetid rodents in southern Mexico. <i>Evolutionary Ecology</i> , 2020, 34, 175-191.	0.5	3
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20806	QTL-Seq and Sequence Assembly Rapidly Mapped the Gene <i>BrMYBL2.1</i> for the Purple Trait in <i>Brassica rapa</i> . <i>Scientific Reports</i> , 2020, 10, 2328.	1.6	31
20807	Similar genomic patterns of clinical infective endocarditis and oral isolates of <i>Streptococcus sanguinis</i> and <i>Streptococcus gordonii</i> . <i>Scientific Reports</i> , 2020, 10, 2728.	1.6	8
20808	First Draft Genome of the Sable, <i>Martes zibellina</i> . <i>Genome Biology and Evolution</i> , 2020, 12, 59-65.	1.1	5
20809	Inferring putative ancient whole-genome duplications in the 1000 Plants (1KP) initiative: access to gene family phylogenies and age distributions. <i>GigaScience</i> , 2020, 9, .	3.3	49
20810	Pervasive Suicidal Integrases in Deep-Sea Archaea. <i>Molecular Biology and Evolution</i> , 2020, 37, 1727-1743.	3.5	1
20811	Characterisation of evolutionarily conserved key players affecting eukaryotic flagellar motility and fertility using a moss model. <i>New Phytologist</i> , 2020, 227, 440-454.	3.5	26
20812	Simulation of Chordate Intron Evolution Using Randomly Generated and Mutated Base Sequences. <i>Evolutionary Bioinformatics</i> , 2020, 16, 117693432090310.	0.6	2
20813	Reappraising plastid markers of the red algae for phylogenetic community ecology in the genomic era. <i>Ecology and Evolution</i> , 2020, 10, 1299-1310.	0.8	6
20814	<i>Lysobacter prati</i> sp. nov., isolated from a plateau meadow sample. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 763-772.	0.7	17

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20816	Genomic monitoring to understand the emergence and spread of Usutu virus in the Netherlands, 2016–2018. <i>Scientific Reports</i> , 2020, 10, 2798.	1.6	43
20817	Expansion of the genus <i>Imleria</i> in North America to include <i>Imleria floridana</i> , sp. nov., and <i>Imleria pallida</i> , comb. nov.. <i>Mycologia</i> , 2020, 112, 423-437.	0.8	2
20818	Toward unified molecular surveillance of RSV: A proposal for genotype definition. <i>Influenza and Other Respiratory Viruses</i> , 2020, 14, 274-285.	1.5	52
20819	Unbiased Identification of Immunogenic <i>Staphylococcus aureus</i> Leukotoxin B-Cell Epitopes. <i>Infection and Immunity</i> , 2020, 88, .	1.0	5
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20821	Generalist <i>Eimeria</i> species in rodents: Multilocus analyses indicate inadequate resolution of established markers. <i>Ecology and Evolution</i> , 2020, 10, 1378-1389.	0.8	12
20822	<i>Euwallacea perbrevis</i> (Coleoptera: Curculionidae: Scolytinae), a confirmed pest on <i>Acacia crassicarpa</i> in Riau, Indonesia, and a new fungal symbiont; <i>Fusarium rekanum</i> sp. nov.. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 803-823.	0.7	21
20823	Population history of a social spider reveals connection between South American tropical forests. <i>Zoologischer Anzeiger</i> , 2020, 285, 139-146.	0.4	1
20824	<i>Simplicillium spumae</i> (Cordycipitaceae, Hypocreales), a new hyphomycetes from aquarium foam in Japan. <i>Mycoscience</i> , 2020, 61, 116-121.	0.3	3
20825	The genome of Shaw's sea snake ( <i>Hydrophis curtus</i> ) reveals secondary adaptation to its marine environment. <i>Molecular Biology and Evolution</i> , 2020, 37, 1744-1760.	3.5	28
20826	A molecular survey, whole genome sequencing and phylogenetic analysis of astroviruses from roe deer. <i>BMC Veterinary Research</i> , 2020, 16, 68.	0.7	4
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20828	Phylogenetic Characterization of <i>Botryosphaeria</i> Strains Associated with <i>Asphondylia</i> Galls on Species of <i>Lamiaceae</i> . <i>Diversity</i> , 2020, 12, 41.	0.7	15
20829	Hookworms Evade Host Immunity by Secreting a Deoxyribonuclease to Degrade Neutrophil Extracellular Traps. <i>Cell Host and Microbe</i> , 2020, 27, 277-289.e6.	5.1	53
20830	Evolution of the Small Family of Alternative Splicing Modulators Nuclear Speckle RNA-Binding Proteins in Plants. <i>Genes</i> , 2020, 11, 207.	1.0	10
20831	Phylogeography and demographic history of <i>Gyrodactylus konovalovi</i> (Monogenoidea: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 107 Td (Gyrodactylidae)). <i>Evolution</i> , 2020, 10, 1454-1468.	0.8	2
20832	Comparative Analysis and Molecular Evolution of Class I PI3K Regulatory Subunit p85± Reveal the Structural Similarity Between nSH2 and cSH2 Domains. <i>International Journal of Peptide Research and Therapeutics</i> , 2020, 26, 2555-2569.	0.9	0

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20834	Comparative genetic and physiological characterisation of <i>Pectinatus</i> species reveals shared tolerance to beer-associated stressors but halotolerance specific to pickle-associated strains. <i>Food Microbiology</i> , 2020, 90, 103462.	2.1	6
20835	Structural Effects and Functional Implications of Phalloidin and Jasplakinolide Binding to Actin Filaments. <i>Structure</i> , 2020, 28, 437-449.e5.	1.6	83
20836	Viable bacterial colonization is highly limited in the human intestine in utero. <i>Nature Medicine</i> , 2020, 26, 599-607.	15.2	180
20837	EasyPrimer: user-friendly tool for pan-PCR/HRM primers design. Development of an HRM protocol on <i>wzi</i> gene for fast <i>Klebsiella pneumoniae</i> typing. <i>Scientific Reports</i> , 2020, 10, 1307.	1.6	12
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20840	A comparative genomics methodology reveals a widespread family of membrane-disrupting T6SS effectors. <i>Nature Communications</i> , 2020, 11, 1085.	5.8	60
20841	Four high-quality draft genome assemblies of the marine heterotrophic nanoflagellate <i>Cafeteria roenbergensis</i> . <i>Scientific Data</i> , 2020, 7, 29.	2.4	22
20842	Variation among S-locus haplotypes and among stylar RNases in almond. <i>Scientific Reports</i> , 2020, 10, 583.	1.6	8
20843	Unorthodox features in two venerid bivalves with doubly uniparental inheritance of mitochondria. <i>Scientific Reports</i> , 2020, 10, 1087.	1.6	23
20844	Novel human reovirus isolated from children and its long-term circulation with reassortments. <i>Scientific Reports</i> , 2020, 10, 963.	1.6	16
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20846	Phylogenomic analysis of trichomycterid catfishes (Teleostei: Siluriformes) inferred from ultraconserved elements. <i>Scientific Reports</i> , 2020, 10, 2697.	1.6	45
20847	The Evolution History of Feâ€S Cluster A-Type Assembly Protein Reveals Multiple Gene Duplication Events and Essential Protein Motifs. <i>Genome Biology and Evolution</i> , 2020, 12, 160-173.	1.1	4
20848	The <i>Ligon lintless</i> Short Fiber Mutation Is Located within a Terminal Deletion of Chromosome 18 in Cotton. <i>Plant Physiology</i> , 2020, 183, 277-288.	2.3	17
20849	<i>Shewanella khirikhana</i> sp. nov. â€ a shrimp pathogen isolated from a cultivation pond exhibiting early mortality syndrome. <i>Microbial Biotechnology</i> , 2020, 13, 781-795.	2.0	25
20850	A method to generate multilocus barcodes of pinned insect specimens using MiSeq. <i>Molecular Ecology Resources</i> , 2020, 20, 692-705.	2.2	3

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20853	Cyanobacteria in an urban lake: hidden diversity revealed by metabarcoding. <i>Aquatic Ecology</i> , 2020, 54, 671-675.	0.7	3
20854	Population differentiation and historical demography of the threatened snowy plover <i>Charadrius nivosus</i> (Cassin, 1858). <i>Conservation Genetics</i> , 2020, 21, 387-404.	0.8	6
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20856	Insights into the Tricholomatineae (Agaricales, Agaricomycetes): a new arrangement of Biannulariaceae and <i>Callistosporium</i> , <i>Callistosporiaceae</i> fam. nov., <i>Xerophorus</i> stat. nov., and <i>Pleurocollybia</i> incorporated into <i>Callistosporium</i> . <i>Fungal Diversity</i> , 2020, 101, 211-259.	4.7	15
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20860	Recombinant expression, characterization and phylogenetic studies of novel cystatins-like proteins of sweet orange ( <i>Citrus sinensis</i> ) and clementine ( <i>Citrus clementina</i> ). <i>International Journal of Biological Macromolecules</i> , 2020, 152, 546-553.	3.6	6
20861	Dietary plasticity and the extinction of the passenger pigeon ( <i>Ectopistes migratorius</i> ). <i>Quaternary Science Reviews</i> , 2020, 233, 106225.	1.4	19
20862	Investigating the utility of traditional and genomic multi-locus datasets to resolve relationships in <i>Lipaigus</i> and <i>Tijuca</i> (Cotingidae). <i>Molecular Phylogenetics and Evolution</i> , 2020, 147, 106779.	1.2	2
20863	Complete Genome Sequence of <i>Paenibacillus</i> sp. JZ16, a Plant Growth Promoting Root Endophytic Bacterium of the Desert Halophyte <i>Zygophyllum Simplex</i> . <i>Current Microbiology</i> , 2020, 77, 1097-1103.	1.0	15
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20865	Study on a Novel Cold-Active and Halotolerant Monoacylglycerol Lipase Widespread in Marine Bacteria Reveals a New Group of Bacterial Monoacylglycerol Lipases Containing Unusual C(A/S)HSMG Catalytic Motifs. <i>Frontiers in Microbiology</i> , 2020, 11, 9.	1.5	14
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20867	A Novel Approach to Investigate the Effect of Tree Reconstruction Artifacts in Single-Gene Analysis Clarifies Opsin Evolution in Nonbilaterian Metazoans. <i>Genome Biology and Evolution</i> , 2020, 12, 3906-3916.	1.1	17
20868	Genetic Diversity and Phylogenetic Analysis of Human Bocavirus 2 in Pediatric Patients with Acute Gastroenteritis in Taiwan. <i>International Journal of Environmental Research and Public Health</i> , 2020, 17, 1086.	1.2	9

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20870	Characterization of plant growth-promoting rhizobacteria from perennial ryegrass and genome mining of novel antimicrobial gene clusters. <i>BMC Genomics</i> , 2020, 21, 157.	1.2	22
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20873	Exceptional subgenome stability and functional divergence in the allotetraploid Ethiopian cereal teff. <i>Nature Communications</i> , 2020, 11, 884.	5.8	101
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20875	Genomic diversity in flavobacterial pathogens of aquatic origin. <i>Microbial Pathogenesis</i> , 2020, 142, 104053.	1.3	14
20876	Bacterial community profiling highlights complex diversity and novel organisms in wildlife ticks. <i>Ticks and Tick-borne Diseases</i> , 2020, 11, 101407.	1.1	13
20877	The earliest farmers of northwest China exploited grain-fed pheasants not chickens. <i>Scientific Reports</i> , 2020, 10, 2556.	1.6	18
20878	Duplications and Functional Convergence of Intestinal Carbohydrate-Digesting Enzymes. <i>Molecular Biology and Evolution</i> , 2020, 37, 1657-1666.	3.5	11
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20880	Human surveillance and phylogeny of highly pathogenic avian influenza A(H5N8) during an outbreak in poultry in South Africa, 2017. <i>Influenza and Other Respiratory Viruses</i> , 2020, 14, 266-273.	1.5	9
20881	Novel Reassortant Avian Influenza A(H9N2) Virus Isolate in Migratory Waterfowl in Hubei Province, China. <i>Frontiers in Microbiology</i> , 2020, 11, 220.	1.5	16
20882	Ecogenomics of the Marine Benthic Filamentous Cyanobacterium <i>Adonisia</i> . <i>Microbial Ecology</i> , 2020, 80, 249-265.	1.4	4
20883	“Funny” channels in cardiac mitochondria modulate membrane potential and oxygen consumption. <i>Biochemical and Biophysical Research Communications</i> , 2020, 524, 1030-1036.	1.0	12
20884	Protein Interaction Energy Landscapes are Shaped by Functional and also Non-functional Partners. <i>Journal of Molecular Biology</i> , 2020, 432, 1183-1198.	2.0	10
20885	The genome sequence of celery ( <i>Apium graveolens</i> L.), an important leaf vegetable crop rich in apigenin in the Apiaceae family. <i>Horticulture Research</i> , 2020, 7, 9.	2.9	61
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20888	Total ammonia nitrogen (TAN) removal performance of a recirculating down-hanging sponge (DHS) reactor operated at 10 to 20°C with activated carbon. <i>Aquaculture</i> , 2020, 520, 734963.	1.7	13
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20892	Multiple lineages of hyperdiverse Zopheridae beetles survived the New Zealand Oligocene Drowning. <i>Journal of Biogeography</i> , 2020, 47, 927-940.	1.4	17
20893	Biogeographic study of human gut-associated crAssphage suggests impacts from industrialization and recent expansion. <i>PLoS ONE</i> , 2020, 15, e0226930.	1.1	38
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20898	A new lineage of segmented RNA viruses infecting animals. <i>Virus Evolution</i> , 2020, 6, vez061.	2.2	37
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20902	Candidatus <i>Neoehrlichia mikurensis</i> is widespread in questing <i>Ixodes ricinus</i> ticks in the Czech Republic. <i>Ticks and Tick-borne Diseases</i> , 2020, 11, 101371.	1.1	9
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20907	<i>Synnematotriadelphia</i> gen. nov. ( <i>S. stilboidea</i> comb. nov. and <i>S. synnematofera</i> comb. nov.) and <i>Triadelphia hexaformispora</i> sp. nov. in the family Triadelpiaceae. <i>Mycological Progress</i> , 2020, 19, 127-137.	0.5	5
20908	Genetic diversity and morphological variation in African boxthorn ( <i>Lycium ferocissimum</i> ) – Characterising the target weed for biological control. <i>Biological Control</i> , 2020, 143, 104206.	1.4	11
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20918	Phylogenetic relationships of a new genus and species of stevardiine fish (Characiformes: Characidae): <i>Tj ETQq1 1 0.784314 rgBT /Overl</i> <i>Research</i> , 2020, 58, 387-407.	0.6	4
20919	Plateau Grass and Greenhouse Flower? Distinct Genetic Basis of Closely Related Toad Tadpoles Respectively Adapted to High Altitude and Karst Caves. <i>Genes</i> , 2020, 11, 123.	1.0	4
20920	New EST-SSR Markers for Individual Genotyping of Opium Poppy Cultivars ( <i>Papaver somniferum</i> L.). <i>Plants</i> , 2020, 9, 10.	1.6	22
20921	Virus Discovery in Desert Tortoise Fecal Samples: Novel Circular Single-Stranded DNA Viruses. <i>Viruses</i> , 2020, 12, 143.	1.5	26
20922	Cellular localization, cloning and expression of <i>Leishmania braziliensis</i> Phospholipase A1. <i>Microbial Pathogenesis</i> , 2020, 141, 104010.	1.3	5

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20924	Increased replication of dissimilatory nitrate-reducing bacteria leads to decreased anammox bioreactor performance. <i>Microbiome</i> , 2020, 8, 7.	4.9	42
20925	Prevalence and genotyping of bovine <i>Cryptosporidium</i> species in the Mediterranean and Central Anatolia Region of Turkey. <i>Comparative Immunology, Microbiology and Infectious Diseases</i> , 2020, 69, 101425.	0.7	21
20926	Competitive oxidation and ubiquitylation on the evolutionarily conserved cysteine confer tissue-specific stabilization of Insig-2. <i>Nature Communications</i> , 2020, 11, 379.	5.8	12
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20928	Intragenic recombination influences rotavirus diversity and evolution. <i>Virus Evolution</i> , 2020, 6, vez059.	2.2	23
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20932	Taxonomic study of Endogonaceae in the Japanese islands: New species of <i>Endogone</i> , <i>Jimgerdemannia</i> , and <i>Vinositunica</i> , gen. nov.. <i>Mycologia</i> , 2020, 112, 309-328.	0.8	4
20933	Cleaner strategies on the effective elimination of toxic chromium from wastewater using coupled electrochemical/biological systems. <i>Environmental Progress and Sustainable Energy</i> , 2020, 39, e13399.	1.3	11
20934	Memory B Cell Activation, Broad Anti-influenza Antibodies, and Bystander Activation Revealed by Single-Cell Transcriptomics. <i>Cell Reports</i> , 2020, 30, 905-913.e6.	2.9	139
20935	<i>Casimicrobium huifangae</i> gen. nov., sp. nov., a Ubiquitous "Most-Wanted" Core Bacterial Taxon from Municipal Wastewater Treatment Plants. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	26
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20937	Mitochondrial genome to aid species delimitation and effective conservation of the Sharpnose Guitarfish ( <i>Glaucostegus granulatus</i> ). <i>Meta Gene</i> , 2020, 24, 100648.	0.3	13
20938	Snake Recombination Landscapes Are Concentrated in Functional Regions despite PRDM9. <i>Molecular Biology and Evolution</i> , 2020, 37, 1272-1294.	3.5	45
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20944	Comparative genomics of <i>Lactobacillus fermentum</i> suggests a free-living lifestyle of this lactic acid bacterial species. <i>Food Microbiology</i> , 2020, 89, 103448.	2.1	34
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20951	Cuticular Structure Proteomics in the Pea Aphid <i>Acyrtosiphon pisum</i> Reveals New Plant Virus Receptor Candidates at the Tip of Maxillary Stylets. <i>Journal of Proteome Research</i> , 2020, 19, 1319-1337.	1.8	25
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21152	A whole-plant monocot from the Lower Cretaceous. <i>Palaeoworld</i> , 2021, 30, 169-175.	0.5	6
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21160	The role of overseas genetic surveys to potentially accelerate biological control development for a new <i>Hydrilla verticillata</i> introduction in the USA. <i>BioControl</i> , 2021, 66, 271-280.	0.9	6
21161	Insight to the ancestral relations and varietal diversity of Indian tea [ <i>Camellia sinensis</i> (L.) Kuntze] through plastid and nuclear phylogenetic markers. <i>Genetic Resources and Crop Evolution</i> , 2021, 68, 773-783.	0.8	6
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21169	Characterizing Transcriptional Regulatory Sequences in Coronaviruses and Their Role in Recombination. <i>Molecular Biology and Evolution</i> , 2021, 38, 1241-1248.	3.5	46
21170	Molecular evolution and functional divergence of UDP-hexose 4-epimerases. <i>Current Opinion in Chemical Biology</i> , 2021, 61, 53-62.	2.8	14
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21178	Do Alignment and Trimming Methods Matter for Phylogenomic (UCE) Analyses?. <i>Systematic Biology</i> , 2021, 70, 440-462.	2.7	30
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21191	A new pleosporalean fungus isolated from superficial to deep human clinical specimens. <i>Medical Mycology</i> , 2021, 59, 278-288.	0.3	5
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21202	Antibiotic Resistance Patterns and <i>mcr-1</i> Detection in Avian Pathogenic <i>Escherichia coli</i> Isolates from Commercial Layer and Layer Breeder Flocks Demonstrating Colibacillosis in Greece. <i>Microbial Drug Resistance</i> , 2021, 27, 710-720.	0.9	7
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21204	The Cassandra retrotransposon landscape in sugar beet ( <i>Beta vulgaris</i> ) and related Amaranthaceae: recombination and re-shuffling lead to a high structural variability. <i>Annals of Botany</i> , 2021, 127, 91-109.	1.4	13
21205	The genome sequence of <i>Samia ricini</i> , a new model species of lepidopteran insect. <i>Molecular Ecology Resources</i> , 2021, 21, 327-339.	2.2	12
21206	Genomic and phenotypic analysis of siderophore-producing <i>Rhodococcus qingshengii</i> strain S10 isolated from an arid weathered serpentine rock environment. <i>Archives of Microbiology</i> , 2021, 203, 855-860.	1.0	6
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21208	De novo assembly of chloroplast genomes of <i>Corchorus capsularis</i> and <i>C. olitorius</i> yields species-specific InDel markers. <i>Crop Journal</i> , 2021, 9, 216-226.	2.3	4
21209	Molecular and morphological evidence for a new species of <i>Isodon</i> (Lamiaceae) from southern China. <i>Plant Diversity</i> , 2021, 43, 54-62.	1.8	3
21210	A phylogenetic approach to understand the evolution of reproduction in coleoid cephalopods. <i>Molecular Phylogenetics and Evolution</i> , 2021, 155, 106972.	1.2	5

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21212	Phylogenomics of the Mesoamerican alligator-lizard genera <i>Abronia</i> and <i>Mesaspis</i> (Anguillidae). <i>Trends in Ecology and Evolution</i> , 2021, 32, 1069-1077.	1.2	13
21213	Contrasting Gene Decay in Subterranean Vertebrates: Insights from Cavefishes and Fossorial Mammals. <i>Molecular Biology and Evolution</i> , 2021, 38, 589-605.	3.5	43
21214	Foliose <i>Ulva</i> Species Show Considerable Inter-specific Genetic Diversity, Low Intra-specific Genetic Variation, and the Rare Occurrence of Inter-specific Hybrids in the Wild. <i>Journal of Phycology</i> , 2021, 57, 219-233.	1.0	24
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21218	Giant African snail genomes provide insights into molluscan whole-genome duplication and aquatic-terrestrial transition. <i>Molecular Ecology Resources</i> , 2021, 21, 478-494.	2.2	33
21219	Chromosome-level genome assembly of <i>Paralithodes platypus</i> provides insights into evolution and adaptation of king crabs. <i>Molecular Ecology Resources</i> , 2021, 21, 511-525.	2.2	14
21220	Unravelling the taxonomy of an interstitial fish radiation: Three new species of <i>Gouania</i> (Teleostei: Gobiesocidae) from the Mediterranean Sea and redescription of <i>G. willdenowi</i> and <i>G. pigra</i> . <i>Journal of Fish Biology</i> , 2021, 98, 64-88.	0.7	7
21221	Population genomic transformations induced by isolation of wild bird avian influenza viruses (Orthomyxoviridae) in embryonated chicken eggs. <i>Infection, Genetics and Evolution</i> , 2021, 90, 104505.	1.0	3
21222	Expression and functional identification of two homologous nicotine dehydrogenases, NicA2 and Nox, from <i>Pseudomonas</i> sp. JY-Q. <i>Protein Expression and Purification</i> , 2021, 178, 105767.	0.6	6
21223	Acidobacteria are active and abundant members of diverse atmospheric H <sub>2</sub> -oxidizing communities detected in temperate soils. <i>ISME Journal</i> , 2021, 15, 363-376.	4.4	23
21224	Phylogenetic diversity and prevalence of mycoflora in ready-to-eat supermarket and roadside-vended peanuts. <i>Mycologia</i> , 2021, 113, 1-11.	0.8	7
21225	Ecogenomics and metabolic potential of the South Atlantic Ocean microbiome. <i>Science of the Total Environment</i> , 2021, 765, 142758.	3.9	16
21226	Metabolic resistance to organophosphate insecticides in natural populations of the whitefly <i>Bemisia tabaci</i> (Hemiptera: Aleyrodidae) in Egypt and molecular identification of mitotypes. <i>Phytoparasitica</i> , 2021, 49, 443-457.	0.6	5
21227	Genomic insights into waste valorized extracellular polymeric substances (EPS) produced by <i>Bacillus</i> sp. ISTL8. <i>Environmental Research</i> , 2021, 192, 110277.	3.7	20
21228	Functional characterization of the AGL1 aegerolysin in the mycoparasitic fungus <i>Trichoderma atroviride</i> reveals a role in conidiation and antagonism. <i>Molecular Genetics and Genomics</i> , 2021, 296, 131-140.	1.0	8



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21232	Experimentally-validated correlation analysis reveals new anaerobic methane oxidation partnerships with consortium-level heterogeneity in diazotrophy. <i>ISME Journal</i> , 2021, 15, 377-396.	4.4	31
21233	Analysis of RNA-protein networks with RNP-MaP defines functional hubs on RNA. <i>Nature Biotechnology</i> , 2021, 39, 347-356.	9.4	50
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21236	Assessing Changes and Associations in the <i>Xanthomonas perforans</i> Population Across Florida Commercial Tomato Fields Via a Statewide Survey. <i>Phytopathology</i> , 2021, 111, 1029-1041.	1.1	20
21237	Functional characterization of the HMP synthase of <i>Legionella pneumophila</i> (Lpg1565). <i>Molecular Microbiology</i> , 2021, 115, 539-553.	1.2	2
21238	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
21239	Genomic fingerprints of palaeogeographic history: The tempo and mode of rift tectonics across tropical Africa has shaped the diversification of the killifish genus <i>Nothobranchius</i> (Teleostei). <i>Journal of Biogeography</i> , 2021, 48, 1017-1033.	1.1	1
21240	Characterization of a New Nepovirus Infecting Grapevine. <i>Plant Disease</i> , 2021, 105, 1432-1439.	0.7	8
21241	Pinewood Nematode Alters the Endophytic and Rhizospheric Microbial Communities of <i>Pinus massoniana</i> . <i>Microbial Ecology</i> , 2021, 81, 807-817.	1.4	16
21242	Relatedness and the composition of communities over time: Evaluating phylogenetic community structure in the late Cenozoic record of bivalves. <i>Paleobiology</i> , 2021, 47, 301-313.	1.3	4
21243	Relationships between nitrogen cycling microbial community abundance and composition reveal the indirect effect of soil pH on oak decline. <i>ISME Journal</i> , 2021, 15, 623-635.	4.4	63
21244	Idiosyncratic responses to drivers of genetic differentiation in the complex landscapes of Isthmian Central America. <i>Heredity</i> , 2021, 126, 251-265.	1.2	5
21245	Evidence of introgression in endemic frogs from the <i>campo rupestre</i> contradicts the reduced hybridization hypothesis. <i>Biological Journal of the Linnean Society</i> , 2021, 133, 561-576.	0.7	6
21246	Chromosome-level genome assembly of <i>Lethenteron reissneri</i> provides insights into lamprey evolution. <i>Molecular Ecology Resources</i> , 2021, 21, 448-463.	2.2	25

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21248	Comparative analysis reveals the expansion of mitochondrial DNA control region containing unusually high G-C tandem repeat arrays in <i>Nasonia vitripennis</i> . International Journal of Biological Macromolecules, 2021, 166, 1246-1257.	3.6	9
21249	Broad distribution, high diversity and ancient origin of the ApeC-containing proteins. Molecular Phylogenetics and Evolution, 2021, 155, 107009.	1.2	7
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21255	Potential Mosquito Vectors of <i>Dirofilaria immitis</i> and <i>Dirofilaira repens</i> (Spirurida: Tj ETQq0 0 0 rgBT /Qverlock 10 Tf 50 4.	0.9	6
21256	Integrative taxonomy confirms the species status of the Himalayan langurs, <i>Semnopithecus schistaceus</i> Hodgson, 1840. Journal of Zoological Systematics and Evolutionary Research, 2021, 59, 543-556.	0.6	8
21257	Multiple origins of a single point mutation in the cotton bollworm tetraspanin gene confers dominant resistance to Bt cotton. Pest Management Science, 2021, 77, 1169-1177.	1.7	13
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21259	Genome-wide characterization and expression analyses of the auxin/indole-3-acetic acid (Aux/IAA) gene family in apple ( <i>Malus domestica</i> ). Gene, 2021, 768, 145302.	1.0	11
21260	Quantitative Proteomics Reveals UGA-Independent Misincorporation of Selenocysteine throughout the <i>Escherichia coli</i> Proteome. Journal of Proteome Research, 2021, 20, 212-221.	1.8	8
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21262	The effects of morphology, phylogeny and prey availability on trophic resource partitioning in an anuran community. Basic and Applied Ecology, 2021, 50, 181-191.	1.2	7
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21264	Comparative genomics of <i>Fusarium oxysporum</i> f. sp. <i>melonis</i> strains reveals nine lineages and a new sequence type of <i>AvrFom2</i> . Environmental Microbiology, 2021, 23, 2035-2053.	1.8	5

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21268	The Transporter Classification Database (TCDB): 2021 update. <i>Nucleic Acids Research</i> , 2021, 49, D461-D467.	6.5	192
21269	The evolutionary analysis of complement component C5 and the gene co-expression network and putative interaction between C5a and C5a anaphylatoxin receptor (C5AR/CD88) in human and two Cyprinid fish. <i>Developmental and Comparative Immunology</i> , 2021, 116, 103958.	1.0	3
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21272	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
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21275	<i>Streptococcus pseudopneumoniae</i> : Use of Whole-Genome Sequences To Validate Species Identification Methods. <i>Journal of Clinical Microbiology</i> , 2021, 59, .	1.8	4
21276	Characterization of marine microbial communities around an Arctic seabed hydrocarbon seep at Scott Inlet, Baffin Bay. <i>Science of the Total Environment</i> , 2021, 762, 143961.	3.9	12
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21279	<i>Dictyota cyanoloma</i> (Dictyotales, Phaeophyceae), a Newly Introduced Brown Algal Species in California. <i>Journal of Phycology</i> , 2021, 57, 370-378.	1.0	3
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21285	Streptozotocin induces brain glucose metabolic changes and alters glucose transporter expression in the Lobster cockroach; <i>Nauphoeta cinerea</i> (Blattodea: Blaberidae). <i>Molecular and Cellular Biochemistry</i> , 2021, 476, 1109-1121.	1.4	11
21286	A new assay for quantitative detection of hepatitis A virus. <i>Journal of Virological Methods</i> , 2021, 288, 114010.	1.0	12
21287	Prevalence and genome characterization of porcine rotavirus A in southern Mozambique. <i>Infection, Genetics and Evolution</i> , 2021, 87, 104637.	1.0	8
21288	Virome characterization of <i>Cryphonectria parasitica</i> isolates from Azerbaijan unveiled a new mymonavirus and a putative new RNA virus unrelated to described viral sequences. <i>Virology</i> , 2021, 553, 51-61.	1.1	24
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21291	Evidence for speciation underground in diving beetles (Dytiscidae) from a subterranean archipelago. <i>Evolution; International Journal of Organic Evolution</i> , 2021, 75, 166-175.	1.1	26
21292	Probing periodontal microbial dark matter using metataxonomics and metagenomics. <i>Periodontology 2000</i> , 2021, 85, 12-27.	6.3	16
21293	Diversity, community composition, and bioactivity of cultivable fungal endophytes in saline and dry soils in deserts. <i>Fungal Ecology</i> , 2021, 49, 101019.	0.7	6
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21296	K27-Linked Diubiquitin Inhibits UCHL3 via an Unusual Kinetic Trap. <i>Cell Chemical Biology</i> , 2021, 28, 191-201.e8.	2.5	11
21297	De Novo Genome Assembly of the Japanese Wheat Cultivar Norin 61 Highlights Functional Variation in Flowering Time and Fusarium-Resistant Genes in East Asian Genotypes. <i>Plant and Cell Physiology</i> , 2021, 62, 8-27.	1.5	16
21298	A new species of Wallinia Pearse, 1920 (Digenea: Allocreadiidae), in <i>Astyanax bimaculatus</i> (Linnaeus.) <i>Tj ETQq1 1 0.784314 rgBT /Overl</i> <i>Research</i> , 2021, 120, 37-44.	0.6	5
21299	Plant resistome profiling in evolutionary old bog vegetation provides new clues to understand emergence of multi-resistance. <i>ISME Journal</i> , 2021, 15, 921-937.	4.4	33
21300	Cervicovaginal microbiota dysbiosis correlates with HPV persistent infection. <i>Microbial Pathogenesis</i> , 2021, 152, 104617.	1.3	28

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21302	Untangling filamentous marine cyanobacterial diversity from the coast of South Florida with the description of <i>Vermifilaceae</i> fam. nov. and three new genera: <i>Leptochromothrix</i> gen. nov., <i>Ophiophycus</i> gen. nov., and <i>Vermifilum</i> gen. nov.. <i>Molecular Phylogenetics and Evolution</i> , 2021, 160, 107010.	1.2	13
21303	Use of the nucleotide diversity in COI mitochondrial gene as an early diagnostic of conservation status of animal species. <i>Conservation Letters</i> , 2021, 14, e12756.	2.8	25
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21306	Transcriptome sequencing reveals <i>Cnaphalocrocis medinalis</i> against baculovirus infection by oxidative stress. <i>Molecular Immunology</i> , 2021, 129, 63-69.	1.0	7
21307	Sigma Factor Modulation for Cyanobacterial Metabolic Engineering. <i>Trends in Microbiology</i> , 2021, 29, 266-277.	3.5	12
21308	Fâ€šox protein CFK1 interacts with and degrades <i>de novo</i> DNA methyltransferase in <i>Arabidopsis</i> . <i>New Phytologist</i> , 2021, 229, 3303-3317.	3.5	13
21309	The Early Evolution of Oral Poliovirus Vaccine Is Shaped by Strong Positive Selection and Tight Transmission Bottlenecks. <i>Cell Host and Microbe</i> , 2021, 29, 32-43.e4.	5.1	22
21310	Microanalysis of scale morphology in killifish, <i>Aphaniops hormuzensis</i> inhabiting ecologically diverse environments (Cyprinodontiformes; Aphaniidae). <i>Micron</i> , 2021, 140, 102949.	1.1	3
21311	Strong priming of soil organic matter induced by frequent input of labile carbon. <i>Soil Biology and Biochemistry</i> , 2021, 152, 108069.	4.2	70
21312	Historical biogeography of Heteroptera skippers via Beringian and postâ€šethyan corridors. <i>Zoologica Scripta</i> , 2021, 50, 100-111.	0.7	5
21313	Chemogenomics and bioinformatics approaches for prioritizing kinases as drug targets for neglected tropical diseases. <i>Advances in Protein Chemistry and Structural Biology</i> , 2021, 124, 187-223.	1.0	2
21314	Automated Prediction and Annotation of Small Open Reading Frames in Microbial Genomes. <i>Cell Host and Microbe</i> , 2021, 29, 121-131.e4.	5.1	22
21315	Mitochondrial DNA reveals genetically structured haplogroups of Bali sardinella ( <i>Sardinella lemuru</i> ) in Philippine waters. <i>Regional Studies in Marine Science</i> , 2021, 41, 101588.	0.4	4
21316	Genomic-based classification of <i>Catenulispora pinisilvae</i> sp. nov., novel actinobacteria isolated from a pine forest soil in Poland and emended description of <i>Catenulispora rubra</i> . <i>Systematic and Applied Microbiology</i> , 2021, 44, 126164.	1.2	14
21317	â€šHook, line, and sinkerâ€š™: Fluorescence in situ hybridisation (FISH) uncovers <i>Trypanosoma noyesi</i> in Australian questing ticks. <i>Ticks and Tick-borne Diseases</i> , 2021, 12, 101596.	1.1	5
21318	Discovery of two â€šchimericâ€š™ <i>Gastrotricha</i> and their systematic placement based on an integrative approach. <i>Zoological Journal of the Linnean Society</i> , 2021, 192, 710-735.	1.0	5

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21320	Reticulate Evolution, Ancient Chloroplast Haplotypes, and Rapid Radiation of the Australian Plant Genus <i>Adenanthos</i> (Proteaceae). <i>Frontiers in Ecology and Evolution</i> , 2021, 8, .	1.1	25
21321	Unraveling Reticulate Evolution in <i>Opuntia</i> (Cactaceae) From Southern Mexico. <i>Frontiers in Plant Science</i> , 2021, 11, 606809.	1.7	8
21322	New clinical and molecular evidence linking mutations in <i>ARSG</i> to Usher syndrome type IV. <i>Human Mutation</i> , 2021, 42, 261-271.	1.1	23
21323	Whole-genome sequence, functional annotation, and comparative genomics of the high biofilm-producing multidrug-resistant <i>Pseudomonas aeruginosa</i> MZ4A isolated from clinical waste. <i>Gene Reports</i> , 2021, 22, 100999.	0.4	2
21324	Ammonia oxidation at pH 2.5 by a new gammaproteobacterial ammonia-oxidizing bacterium. <i>ISME Journal</i> , 2021, 15, 1150-1164.	4.4	39
21325	Eusociality Shapes Convergent Patterns of Molecular Evolution across Mitochondrial Genomes of Snapping Shrimps. <i>Molecular Biology and Evolution</i> , 2021, 38, 1372-1383.	3.5	14
21326	A Conserved Oomycete CRN Effector Targets Tomato TCP14-2 to Enhance Virulence. <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 309-318.	1.4	17
21327	First report of voltage-gated sodium channel M918V and molecular diagnostics of nicotinic acetylcholine receptor R81T in the cotton aphid. <i>Journal of Applied Entomology</i> , 2021, 145, 261-269.	0.8	8
21328	Horizontal chromosome transfer and independent evolution drive diversification in <i>Fusarium oxysporum</i> f. sp. <i>fragariae</i> . <i>New Phytologist</i> , 2021, 230, 327-340.	3.5	26
21329	Molecular characterization of encephalomyocarditis virus strains isolated from an African elephant and rats in a French zoo. <i>Journal of Veterinary Diagnostic Investigation</i> , 2021, 33, 313-321.	0.5	4
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21331	Phylogenetic and geographical analysis of a retrovirus during the early stages of endogenous adaptation and exogenous spread in a new host. <i>Molecular Ecology</i> , 2021, 30, 2626-2640.	2.0	16
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21389	<i>CoreCruncher</i> : Fast and Robust Construction of Core Genomes in Large Prokaryotic Data Sets. <i>Molecular Biology and Evolution</i> , 2021, 38, 727-734.	3.5	17
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21403	Characterization of two complete mitochondrial genomes of <i>Pterocryptis anomala</i> (Siluridae) and its phylogeny and cryptic diversity. <i>Biologia (Poland)</i> , 2021, 76, 613-621.	0.8	0
21404	Proteome specialization of anaerobic fungi during ruminal degradation of recalcitrant plant fiber. <i>ISME Journal</i> , 2021, 15, 421-434.	4.4	46
21405	Spatiotemporal Changes in the Bacterial Community of the Meromictic Lake Uchum, Siberia. <i>Microbial Ecology</i> , 2021, 81, 357-369.	1.4	6
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21407	Genetic, morphological and acoustic differentiation of African trident bats (Rhinonycteridae: <i>Triaenops</i> ). <i>Zoological Journal of the Linnean Society</i> , 2021, 192, 236-257.	1.0	5
21408	Phylogeny, taxonomic reassessment and ecomorph™ relationship of the <i>Orientallactaga sibirica</i> complex (Rodentia: Dipodidae: Allactaginae). <i>Zoological Journal of the Linnean Society</i> , 2021, 192, 185-205.	1.0	5

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21410	Domestic dog origin of Carnivore Protovirus 1 infection in a rescued free-ranging guinea pig ( <i>Cavia porcellus</i> ). <i>Journal of Virology</i> , 2021, 95, e01410-14.	1.3	6
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21412	DELPHI: accurate deep ensemble model for protein interaction sites prediction. <i>Bioinformatics</i> , 2021, 37, 896-904.	1.8	63
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21416	Molecular data reshape our understanding of the life cycles of three digeneans (Monorchidae and) <i>Journal of Parasitology</i> , 2021, 111, 28-34.	0.8	6
21417	Microbial community structure in aquifers associated with arsenic: analysis of 16S rRNA and arsenite oxidase genes. <i>PeerJ</i> , 2021, 9, e10653.	0.9	12
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21421	Tight association of genome rearrangements with gene expression in conifer plastomes. <i>BMC Plant Biology</i> , 2021, 21, 33.	1.6	5
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21423	Identification and response of cytochrome P450 genes in the brackish water flea <i>Diaphanosoma celebensis</i> after exposure to benzo[a]pyrene and heavy metals. <i>Molecular Biology Reports</i> , 2021, 48, 657-664.	1.0	3
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21426	Analysis of proteolytic processing sites in potyvirus polyproteins revealed differential amino acid preferences of Nla-Pro protease in each of seven cleavage sites. <i>PLoS ONE</i> , 2021, 16, e0245853.	1.1	11
21428	Biopolymer production by halotolerant bacteria isolated from Caatinga biome. <i>Brazilian Journal of Microbiology</i> , 2021, 52, 547-559.	0.8	5
21429	<i>Colacogloea armeniaca</i> sp. nov., a novel pucciniomycetous yeast species isolated from apricots. <i>Mycoscience</i> , 2021, 62, 42-46.	0.3	2

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21432	Genome Sequences of Two GH Clade SARS-CoV-2 Strains Isolated from Patients with COVID-19 in South Korea. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	3
21433	Relicts from Glacial Times: The Ground Beetle <i>Pterostichus adstrictus</i> Eschscholtz, 1823 (Coleoptera: Tj ETQq1 1 0,784314 rgBT /Overlock 10 Tf 50 57	1.0	4
21434	Cytogenetic characterization and mapping of the repetitive DNAs in <i>Cycloramphus bolitoglossus</i> (Werner, 1897): More clues for the chromosome evolution in the genus <i>Cycloramphus</i> (Anura.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 57	1.0	4
21435	The Hunt for Ancient Prions: Archaeal Prion-Like Domains Form Amyloid-Based Epigenetic Elements. <i>Molecular Biology and Evolution</i> , 2021, 38, 2088-2103.	3.5	15
21436	Plastid genome evolution in Amazonian <i>Euterpe oleracea</i> Mart. palm and Atlantic forest <i>Euterpe edulis</i> Mart. palm. <i>Plant Molecular Biology</i> , 2021, 105, 559-574.	2.0	12
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21443	Comparison of Alginate Utilization Pathways in Culturable Bacteria Isolated From Arctic and Antarctic Marine Environments. <i>Frontiers in Microbiology</i> , 2021, 12, 609393.	1.5	11
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21445	Diversity of echinostomes (Digenea: Echinostomatidae) in their snail hosts at high latitudes. <i>Parasite</i> , 2021, 28, 59.	0.8	11
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21447	Genetic diversity in two threatened species of guitarfish (Elasmobranchii: Rhinobatidae) from the Brazilian and Argentinian coasts: an alert for conservation. <i>Neotropical Ichthyology</i> , 2021, 19, .	0.5	11
21448	Sex Chromosome Turnover in Bent-Toed Geckos ( <i>Cyrtodactylus</i> ). <i>Genes</i> , 2021, 12, 116.	1.0	21

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21451	Phanerozoic radiation of ammonia oxidizing bacteria. <i>Scientific Reports</i> , 2021, 11, 2070.	1.6	14
21452	A Model System for Feralizing Laboratory Mice in Large Farmyard-Like Pens. <i>Frontiers in Microbiology</i> , 2020, 11, 615661.	1.5	11
21453	Molecular and cellular characterization of European sea bass CD3 $\mu$ + T lymphocytes and their modulation by microalgal feed supplementation. <i>Cell and Tissue Research</i> , 2021, 384, 149-165.	1.5	10
21454	Leptospiral Immunoglobulin-Like Domain Proteins: Roles in Virulence and Immunity. <i>Frontiers in Immunology</i> , 2020, 11, 579907.	2.2	19
21455	Unification and extensive diversification of M/Orf3-related ion channel proteins in coronaviruses and other nidoviruses. <i>Virus Evolution</i> , 2021, 7, veab014.	2.2	17
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21470	Anaerococcus urinimassiliensis sp. nov., a new bacterium isolated from human urine. <i>Scientific Reports</i> , 2021, 11, 2684.	1.6	7

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21471	Arbuscular mycorrhizal fungal communities associated with switchgrass (&lt;i>Panicum) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 742 To	0.6	2
21472	Nitrogen cycling in coastal sediment microbial communities with seasonally variable benthic nutrient fluxes. <i>Aquatic Microbial Ecology</i> , 2021, 86, 1-19.	0.9	10
21473	Alternative pathways utilize or circumvent putrescine for biosynthesis of putrescine-containing rhizoferrin. <i>Journal of Biological Chemistry</i> , 2021, 296, 100146.	1.6	8
21474	Quantitative analysis of the splice variants expressed by the major hepatitis B virus genotypes. <i>Microbial Genomics</i> , 2021, 7, .	1.0	16
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21481	Structural Characterization of Act c 10.0101 and Pun g 1.0101â€™ Allergens from the Non-Specific Lipid Transfer Protein Family. <i>Molecules</i> , 2021, 26, 256.	1.7	4
21482	In silico comparative analysis of <i>Aeromonas</i> Type VI Secretion System. <i>Brazilian Journal of Microbiology</i> , 2021, 52, 229-243.	0.8	3
21483	Genome-wide signatures of mammalian skin covering evolution. <i>Science China Life Sciences</i> , 2021, 64, 1765-1780.	2.3	5
21484	Phylogeny of <i>Anisopappus</i> with species circumscriptions revisited (Asteraceae: Athroismeae). <i>Taxon</i> , 2021, 70, 351-364.	0.4	3
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21495	A new species of <i>Munida</i> Leach, 1820 (Crustacea: Decapoda: Anomura: Munididae) from seamounts of the Nazca-Desventuradas Marine Park. <i>PeerJ</i> , 2021, 9, e10531.	0.9	2
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21502	Systematics of tardigrada: A reanalysis of tardigrade taxonomy with specific reference to Guil et al. (2019). <i>Zoologica Scripta</i> , 2021, 50, 376-382.	0.7	11
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21507	Adding DNA barcoding to stream monitoring protocols - What's the additional value and congruence between morphological and molecular identification approaches?. <i>PLoS ONE</i> , 2021, 16, e0244598.	1.1	17
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21513	Association of Microbial Dysbiosis with Gallbladder Diseases Identified by Bile Microbiome Profiling. <i>Journal of Korean Medical Science</i> , 2021, 36, e189.	1.1	13
21514	Biological computation and computational biology: survey, challenges, and discussion. <i>Artificial Intelligence Review</i> , 2021, 54, 4169-4235.	9.7	7
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21520	Characterization of the Bubblegum acyl-CoA synthetase of <i>Microchloropsis gaditana</i> . <i>Plant Physiology</i> , 2021, 185, 815-835.	2.3	9
21521	Molecular Epidemiological Analysis of the Origin and Transmission Dynamics of the HIV-1 CRF01_AE Sub-Epidemic in Bulgaria. <i>Viruses</i> , 2021, 13, 116.	1.5	7
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21524	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
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21527	Genetic analyses reveal cryptic diversity in the widely distributed. <i>Invertebrate Systematics</i> , 2021, 35, 298-311.	0.5	6
21528	Bovine Collectins: Role in Health and Disease. , 2021, , 207-244.		0
21530	Morphological and molecular characterization of <i>Butlerius butleri</i> Goodey, 1929 (Nematoda: Tj ETQq1 1 0.784314 rgBT /Over 0.4		



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21532	Genome-wide Identification and Expression Pattern Analysis of the HD-Zip Transcription Factor Family in Pineapple ( <i>Ananas Comosus</i> ). <i>Tropical Plant Biology</i> , 2021, 14, 120-131.	1.0	4
21533	Hopeful monsters: unintended sequencing of famously malformed mite mitochondrial tRNAs reveals widespread expression and processing of sense-antisense pairs. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqaa111.	1.5	6
21534	Cold Adaptation Mechanisms of a Snow Alga <i>Chlamydomonas nivalis</i> During Temperature Fluctuations. <i>Frontiers in Microbiology</i> , 2020, 11, 611080.	1.5	8
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21542	DNA recombination and repair in <i>Wolbachia</i> : RecA and related proteins. <i>Molecular Genetics and Genomics</i> , 2021, 296, 437-456.	1.0	5
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21546	Genomic adaptation of <i>Pseudomonas</i> strains to acidity and antibiotics in hydrothermal vents at Kolumbo submarine volcano, Greece. <i>Scientific Reports</i> , 2021, 11, 1336.	1.6	9
21547	Characterization of Î³ fatty acid desaturases from oomycetes and their application toward eicosapentaenoic acid production in <i>Mortierella alpina</i> . <i>Bioscience, Biotechnology and Biochemistry</i> , 2021, 85, 1252-1265.	0.6	2
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21549	Convergent evolution of pain-inducing defensive venom components in spitting cobras. <i>Science</i> , 2021, 371, 386-390.	6.0	96

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21552	Structural-Genetic Characterization Of Novel Butaryl co-A Dehydrogenase and Proposition of Butanol Biosynthesis Pathway in Pusillimonas ginsengisoli SBSA. Journal of Molecular Evolution, 2021, 89, 81-94.	0.8	1

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21569	Diversification, Introgression, and Rampant Cytonuclear Discordance in Rocky Mountains Chipmunks ( <i>Sciuridae</i> : <i>Tamias</i> ). <i>Systematic Biology</i> , 2021, 70, 908-921.	2.7	20
21571	Functional Characterization of the $\hat{I}^3$ -Aminobutyric Acid Transporter from <i>Mycobacterium smegmatis</i> MC 2 155 Reveals Sodium-Driven GABA Transport. <i>Journal of Bacteriology</i> , 2021, 203, .	1.0	3
21572	Protist communities along freshwater–marine transition zones in Hudson Bay (Canada). <i>Elementa</i> , 2021, 9, .	1.1	9
21573	Human variant of scavenger receptor BI (R174C) exhibits impaired cholesterol transport functions. <i>Journal of Lipid Research</i> , 2021, 62, 100045.	2.0	8
21574	Live cell dynamics of production, explosive release and killing activity of phage tail-like weapons for <i>Pseudomonas</i> kin exclusion. <i>Communications Biology</i> , 2021, 4, 87.	2.0	34
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21580	The discovery, distribution, and diversity of DNA viruses associated with <i>Drosophila melanogaster</i> in Europe. <i>Virus Evolution</i> , 2021, 7, veab031.	2.2	25
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21585	TYGS and LPSN: A database tandem for fast and reliable genome-based classification and nomenclature of prokaryotes. <i>Nucleic Acids Research</i> , 2022, 50, D801-D807.	6.5	728
21586	A Comprehensive Guide to Potato Transcriptome. <i>Methods in Molecular Biology</i> , 2021, 2354, 155-192.	0.4	0
21588	Determination of the two-component systems regulatory network reveals core and accessory regulations across <i>Pseudomonas aeruginosa</i> lineages. <i>Nucleic Acids Research</i> , 2021, 49, 11476-11490.	6.5	28
21589	DNA barcoding of some taxa of genus <i>Acacia</i> and their phylogenetic relationship. <i>International Journal of Transgender Health</i> , 2021, 14, 588-598.	1.1	1
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21594	Genetic and evolutionary analyses of plastomes of the subfamily Cactoideae (Cactaceae) indicate relaxed protein biosynthesis and tRNA import from cytosol. Revista Brasileira De Botanica, 2021, 44, 97-116.	0.5	7
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21597	An integrated morphologicalâ€“molecular approach reveals new insights on the systematics of the octocoral. Invertebrate Systematics, 2021, 35, 261-281.	0.5	6
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21618	Massively parallel functional testing of MSH2 missense variants conferring Lynch syndrome risk. <i>American Journal of Human Genetics</i> , 2021, 108, 163-175.	2.6	66
21619	Plasma membrane phyloquinone biosynthesis in nonphotosynthetic parasitic plants. <i>Plant Physiology</i> , 2021, 185, 1443-1456.	2.3	8
21620	Middle East Respiratory Syndrome Coronavirus Gene 5 Modulates Pathogenesis in Mice. <i>Journal of Virology</i> , 2021, 95, .	1.5	10
21621	Genome-wide identification of citrus histone acetyltransferase and deacetylase families and their expression in response to arbuscular mycorrhizal fungi and drought. <i>Journal of Plant Interactions</i> , 2021, 16, 367-376.	1.0	8
21622	Reassessing species demarcation criteria in viroid taxonomy by pairwise identity matrices. <i>Virus Evolution</i> , 2021, 7, veab001.	2.2	13
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21627	<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
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21630	Chromosome-level genome assembly of the Chinese longsnout catfish <i>Leiocassis longirostris</i> . <i>Zoological Research</i> , 2021, 42, 417-422.	0.9	14
21632	<i>Pseudomonas cremoris</i> sp. nov., a novel proteolytic species isolated from cream. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	8
21633	Comprehensive analysis of genomic diversity of SARS-CoV-2 in different geographic regions of India: an endeavour to classify Indian SARS-CoV-2 strains on the basis of co-existing mutations. <i>Archives of Virology</i> , 2021, 166, 801-812.	0.9	55
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21636	Molecular detection of <i>Leishmania donovani</i> , <i>Leishmania major</i> , and <i>Trypanosoma</i> species in <i>Sergentomyia squamipleuris</i> sand flies from a visceral leishmaniasis focus in Merti sub-County, eastern Kenya. <i>Parasites and Vectors</i> , 2021, 14, 53.	1.0	3
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21638	Quorum Quenching Activity of the PGPR <i>Bacillus subtilis</i> UD1022 Alters Nodulation Efficiency of <i>Sinorhizobium meliloti</i> on <i>Medicago truncatula</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 596299.	1.5	18
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21642	Redescription of type species of the genus <i>Cytaea</i> Keyserling, 1882 (Araneae: Salticidae) – an integrative approach. , 2021, 88, 933-947.		0
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21672	Whole genome characterization of strains belonging to the Ralstonia solanacearum species complex and in silico analysis of TaqMan assays for detection in this heterogenous species complex. European Journal of Plant Pathology, 2021, 159, 593-613.	0.8	2

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21675	Assessing a generic synapomorphy of <i>Pseudodebis</i> Forster, 1964 (Lepidoptera : Nymphalidae : Satyrinae) and a recent speciation with a shift in elevation between two new species in the western Andes. <i>Invertebrate Systematics</i> , 2021, , .	0.5	1
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21687	Genomes of Diverse Isolates of <i>Prochlorococcus</i> High-Light-Adapted Clade II in the Western Pacific Ocean. <i>Frontiers in Marine Science</i> , 2021, 7, .	1.2	1
21689	The symbiosis between <i>Philidris</i> ants and the ant-plant <i>Dischidia major</i> includes fungal and algal associates. <i>Symbiosis</i> , 2021, 83, 305-315.	1.2	3
21690	<i>Alternaria</i> species associated with cladode brown spot in cactus prickly pear ( <i>Nopalea cochenillifera</i> ). <i>European Journal of Plant Pathology</i> , 2021, 160, 215-226.	0.8	1
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21707	Morphological and molecular identification and pathogenicity of <i>Alternaria</i> spp. associated with ginseng in Jilin province, China. <i>Canadian Journal of Plant Pathology</i> , 2021, 43, 537-550.	0.8	5
21708	Characterization of <i>Kazachstania slooffiae</i> , a Proposed Commensal in the Porcine Gut. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 146.	1.5	11
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21711	Impact of Pleistocene Eustatic Fluctuations on Evolutionary Dynamics in Southeast Asian Biodiversity Hotspots. <i>Systematic Biology</i> , 2021, 70, 940-960.	2.7	25
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21716	Genetic and endosymbiotic diversity of Greek populations of <i>Philaenus spumarius</i> , <i>Philaenus signatus</i> and <i>Neophilaenus campestris</i> , vectors of <i>Xylella fastidiosa</i> . <i>Scientific Reports</i> , 2021, 11, 3752.	1.6	12
21718	Hologenome analysis reveals dual symbiosis in the deep-sea hydrothermal vent snail <i>Gigantopelta aegis</i> . <i>Nature Communications</i> , 2021, 12, 1165.	5.8	38
21719	Genomic and Chemical Diversity of <i>Bacillus subtilis</i> Secondary Metabolites against Plant Pathogenic Fungi. <i>MSystems</i> , 2021, 6, .	1.7	55
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21728	Chromosomal Diversity in Two Allopatric Populations of <i>Farlowella hahni</i> (Teleostei: Siluriformes): Cytogenetics and Cytochrome Analyses. <i>Zebrafish</i> , 2021, 18, 66-72.	0.5	0
21729	Molecular characterization of a soybean FT homologue, GmFT7. <i>Scientific Reports</i> , 2021, 11, 3651.	1.6	7
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21732	A first look at the repeatome of <i>Benedenia humboldti</i> , a major pathogen in yellowtail aquaculture: Repetitive element characterization, nuclear rRNA operon assembly, and microsatellite discovery. <i>Marine Genomics</i> , 2021, 58, 100848.	0.4	1
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21736	Genome announcement of <i>Steinernema khuongi</i> and its associated symbiont from Florida. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	6
21737	The Barley ( <i>Hordeum vulgare</i> ssp. <i>vulgare</i> ) Respiratory Burst Oxidase Homolog (HvRBOH) Gene Family and Their Plausible Role on Malting Quality. <i>Frontiers in Plant Science</i> , 2021, 12, 608541.	1.7	10
21739	Predicting human RNA quadruplex helicases through comparative sequence approaches and helicase mRNA interactome analyses. <i>Biochemistry and Cell Biology</i> , 2021, 99, 1-18.	0.9	0
21740	Virulence tests of <i>Neofusicoccum parvum</i> , <i>Lasiodiplodia theobromae</i> , and <i>Phytophthora palmivora</i> on <i>Theobroma cacao</i> . <i>European Journal of Plant Pathology</i> , 2021, 159, 851-862.	0.8	7
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21742	Expansion and Accelerated Evolution of 9-Exon Odorant Receptors in <i>Polistes</i> Paper Wasps. <i>Molecular Biology and Evolution</i> , 2021, 38, 3832-3846.	3.5	22
21743	Molecular cloning and characterization of three ColDA genes in <i>Camellia oleifera</i> . <i>Revista Brasileira De Botanica</i> , 2021, 44, 391-400.	0.5	3
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21746	Genome of <i>Superficieibacter maynardsmithii</i> , a novel, antibiotic susceptible representative of Enterobacteriaceae. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	3
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21749	The complete mitochondrial genome sequence of the mountain crab <i>Indochinamon bhumibol</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 634-635.	0.2	1
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21751	NITD-688, a pan-serotype inhibitor of the dengue virus NS4B protein, shows favorable pharmacokinetics and efficacy in preclinical animal models. <i>Science Translational Medicine</i> , 2021, 13, .	5.8	43
21752	Antileishmanial macrolides from ant-associated <i>Streptomyces</i> sp. ISID311. <i>Bioorganic and Medicinal Chemistry</i> , 2021, 32, 116016.	1.4	14
21753	De novo assembly and characterisation of the transcriptome of the Beringian pseudoscorpion. <i>Canadian Entomologist</i> , 2021, 153, 301-313.	0.4	2
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21757	<i>Tethysphytum antarcticum</i> gen. et sp. nov. (Hapalidiales, Rhodophyta), a new non-geniculate coralline alga from Terra Nova Bay (Ross Sea, Antarctica): morpho-anatomical characterization and molecular phylogeny. European Journal of Phycology, 2021, 56, 416-427.	0.9	8
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21771	Morphometrical and Molecular Characterization of <i>Oesophagostomum columbianum</i> (Chabertiidae: Tj ETQq1 1 0.784314 rgBT /Ove) Goat ( <i>Capra hircus</i> ) in Sylhet, Bangladesh. Journal of Parasitology Research, 2021, 2021, 1-9.	0.5	2
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21774	Reduced proinsecticide activation by cytochrome P450 confers coumaphos resistance in the major bee parasite <i>Varroa destructor</i> . Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	42
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21778	Extremely low nucleotide diversity among thirty-six new chloroplast genome sequences from <i>Aldama</i> ( <i>Heliantheae</i> , <i>Asteraceae</i> ) and comparative chloroplast genomics analyses with closely related genera. <i>PeerJ</i> , 2021, 9, e10886.	0.9	15
21779	<i>Neottia wuyishanensis</i> ( <i>Orchidaceae</i> : <i>Neottieae</i> ), a new species from Fujian, China. <i>Plant Diversity</i> , 2021, 43, 426-431.	1.8	4
21780	Two new stygobiotic species of <i>Horatia</i> Bourguignat, 1887 ( <i>Hydrobiidae</i> ) from Croatia. <i>Subterranean Biology</i> , 0, 37, 89-104.	5.0	4
21781	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
21782	Identification of a bacteria-produced benzisoxazole with antibiotic activity against multi-drug resistant <i>Acinetobacter baumannii</i> . <i>Journal of Antibiotics</i> , 2021, 74, 370-380.	1.0	8
21783	Resprouting drives successional pathways and the resilience of Caatinga dry forest in human-modified landscapes. <i>Forest Ecology and Management</i> , 2021, 482, 118881.	1.4	36
21784	On the Evolutionary Origins of Land Plant Auxin Biology. <i>Cold Spring Harbor Perspectives in Biology</i> , 2021, 13, a040048.	2.3	8
21785	Genetic Analysis of the Role of the Conserved Inner Membrane Protein CvpA in Enterohemorrhagic <i>Escherichia coli</i> Resistance to Deoxycholate. <i>Journal of Bacteriology</i> , 2021, 203, .	1.0	7
21786	Host plant environmental filtering drives foliar fungal community assembly in symptomatic leaves. <i>Oecologia</i> , 2021, 195, 737-749.	0.9	4
21787	Comparative Analysis, Characterization and Evolutionary Study of Dirigent Gene Family in Cucurbitaceae and Expression of Novel Dirigent Peptide against Powdery Mildew Stress. <i>Genes</i> , 2021, 12, 326.	1.0	16
21788	Notes on <i>Trochila</i> ( <i>Ascomycota</i> , <i>Leotiomycetes</i> ), with new species and combinations. <i>MycKeys</i> , 0, 78, 21-47.	0.8	6
21789	VirSorter2: a multi-classifier, expert-guided approach to detect diverse DNA and RNA viruses. <i>Microbiome</i> , 2021, 9, 37.	4.9	441
21790	Comparative analysis of <i>Phytophthora</i> genomes reveals oomycete pathogenesis in crops. <i>Heliyon</i> , 2021, 7, e06317.	1.4	3
21792	Evolution of genome structure in the <i>Drosophila simulans</i> species complex. <i>Genome Research</i> , 2021, 31, 380-396.	2.4	55
21793	Simple sequence repeats drive genome plasticity and promote adaptive evolution in penaeid shrimp. <i>Communications Biology</i> , 2021, 4, 186.	2.0	37
21794	Single-cell analysis of human B cell maturation predicts how antibody class switching shapes selection dynamics. <i>Science Immunology</i> , 2021, 6, .	5.6	149
21795	A complex resistance locus in <i>Solanum americanum</i> recognizes a conserved <i>Phytophthora</i> effector. <i>Nature Plants</i> , 2021, 7, 198-208.	4.7	62

#	ARTICLE	IF	CITATIONS
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21797	Function of the HYDROXYCINNAMOYL-CoA:SHIKIMATE HYDROXYCINNAMOYL TRANSFERASE is evolutionarily conserved in embryophytes. <i>Plant Cell</i> , 2021, 33, 1472-1491.	3.1	45
21798	MLST-Based Analysis and Antimicrobial Resistance of <i>Staphylococcus epidermidis</i> from Cases of Sheep Mastitis in Greece. <i>Biology</i> , 2021, 10, 170.	1.3	9
21799	The use of statistical phylogenetics in virology. <i>Russian Journal of Infection and Immunity</i> , 2021, 11, 42-56.	0.2	0
21800	Evolutionary relationships, biogeography and morphological characters of <i>Glinus</i> (Molluginaceae), with special emphasis on the genus composition in Sub-Saharan Africa. <i>PhytoKeys</i> , 2021, 173, 1-92.	0.4	2
21801	Colonization of <i>Fusarium oxysporum</i> transformed with the red fluorescence protein gene (tdTomato) mediated by <i>Agrobacterium tumefaciens</i> in roots of two avocado cultivars. <i>Research, Society and Development</i> , 2021, 10, e22010212554.	0.0	0
21802	Two different begomovirus species are associated with yellow vein mosaic disease of okra in Sri Lanka. <i>Molecular Biology Reports</i> , 2021, 48, 1383-1391.	1.0	1
21803	The fungus <i>Leptosphaerulina</i> persists in <i>Anopheles gambiae</i> and induces melanization. <i>PLoS ONE</i> , 2021, 16, e0246452.	1.1	3
21804	The molecular targets of ivermectin and lotilaner in the human louse <i>Pediculus humanus humanus</i> : New prospects for the treatment of pediculosis. <i>PLoS Pathogens</i> , 2021, 17, e1008863.	2.1	20
21805	Genome-wide analysis of fluoride exporter genes in plants. <i>3 Biotech</i> , 2021, 11, 124.	1.1	2
21806	<i>Opsanus beta</i> (Goode & Bean, 1880) (Acanthopterygii: Batrachoididae), a non-indigenous toadfish in Sepetiba Bay, south-eastern Brazil. <i>Journal of the Marine Biological Association of the United Kingdom</i> , 2021, 101, 179-187.	0.4	5
21808	State-dependent protein-lipid interactions of a pentameric ligand-gated ion channel in a neuronal membrane. <i>PLoS Computational Biology</i> , 2021, 17, e1007856.	1.5	18
21809	Extrinsically reinforced hybrid speciation within Holarctic ermine ( <i>Mustela</i> spp.) produces an insular endemic. <i>Diversity and Distributions</i> , 2021, 27, 747-762.	1.9	8
21810	Four families of folate-independent methionine synthases. <i>PLoS Genetics</i> , 2021, 17, e1009342.	1.5	8
21811	Morphological description, DNA barcodes and phylogenetic placement of a new mite species: <i>Dinogamasus saengdaoae</i> sp. nov. (Mesostigmata: Laelapidae) found in the acarinarium of carpenter bees in Thailand. <i>Systematic and Applied Acarology</i> , 2021, 26, 474-495.	0.5	2
21812	The taxonomic status of <i>Myotis nesopolus larensis</i> (Chiroptera, Vespertilionidae) and new insights on the diversity of Caribbean <i>Myotis</i> . <i>ZooKeys</i> , 2021, 1015, 145-167.	0.5	8
21813	Chromosome-level genome assembly and structural variant analysis of two laboratory yeast strains from the Peterhof Genetic Collection lineage. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	7
21815	A phosphate starvation response gene ( <i>psr1</i> -like) is present and expressed in <i>Micromonas pusilla</i> and other marine algae. <i>Aquatic Microbial Ecology</i> , 2021, 86, 29-46.	0.9	5

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21817	Newly Discovered AqE Gene is Highly Conserved in Non-tetrapod Vertebrates. <i>Journal of Molecular Evolution</i> , 2021, 89, 214-224.	0.8	2
21819	The <i>Pharus latifolius</i> genome bridges the gap of early grass evolution. <i>Plant Cell</i> , 2021, 33, 846-864.	3.1	32
21820	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
21821	Shulin packages axonemal outer dynein arms for ciliary targeting. <i>Science</i> , 2021, 371, 910-916.	6.0	31
21822	<i>Myroides fluvii</i> sp. nov., isolated from the Han River, Republic of Korea. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	5
21823	Exploring the Chemical Space of Macro- and Micro-Algae Using Comparative Metabolomics. <i>Microorganisms</i> , 2021, 9, 311.	1.6	14
21824	Biosynthetic Interrogation of Soil Metagenomes Reveals Metamarin, an Uncommon Cyclomarin Congener with Activity against <i>Mycobacterium tuberculosis</i> . <i>Journal of Natural Products</i> , 2021, 84, 1056-1066.	1.5	18
21825	Diverse cressdnaviruses and an anellovirus identified in the fecal samples of yellow-bellied marmots. <i>Virology</i> , 2021, 554, 89-96.	1.1	11
21826	<i>Oceanomicrobium pacificus</i> gen. nov., sp. nov., a member of the family Rhodobacteraceae isolated from seawater of tropical western Pacific. <i>Antonie Van Leeuwenhoek</i> , 2021, 114, 303-311.	0.7	2
21828	North American Fireflies Host Low Bacterial Diversity. <i>Microbial Ecology</i> , 2021, 82, 793-804.	1.4	3
21829	Transethnic analysis of the human leukocyte antigen region for ulcerative colitis reveals not only shared but also ethnicity-specific disease associations. <i>Human Molecular Genetics</i> , 2021, 30, 356-369.	1.4	19
21830	A Combined Metagenomics and Metatranscriptomics Approach to Unravel Costa Rican Cocoa Box Fermentation Processes Reveals Yet Unreported Microbial Species and Functionalities. <i>Frontiers in Microbiology</i> , 2021, 12, 641185.	1.5	28
21831	Electric Blue: Molecular Evolution of Three-Finger Toxins in the Long-Glanded Coral Snake Species <i>Calliophis bivirgatus</i> . <i>Toxins</i> , 2021, 13, 124.	1.5	9
21832	Local dynamics of a white syndrome outbreak and changes in the microbial community associated with colonies of the scleractinian brain coral <i>Pseudodiploria strigosa</i> . <i>PeerJ</i> , 2021, 9, e10695.	0.9	17
21833	Complex microbial communities inhabiting natural <i>Cordyceps militaris</i> and the habitat soil and their predicted functions. <i>Antonie Van Leeuwenhoek</i> , 2021, 114, 465-477.	0.7	10
21834	Enrichment of novel <i>Verrucomicrobia</i> , <i>Bacteroidetes</i> , and <i>Krumholzibacteria</i> in an oxygen-limited methane and iron-fed bioreactor inoculated with Bothnian Sea sediments. <i>MicrobiologyOpen</i> , 2021, 10, e1175.	1.2	16
21835	Chloroplast genomes and phylogenetic analysis of two species of <i>Oedocladium</i> (Oedogoniales.) Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.9	5

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21836	The PSY Peptide Family's Expression, Modification and Physiological Implications. <i>Genes</i> , 2021, 12, 218.	1.0	18
21837	A <i>Sarcina</i> bacterium linked to lethal disease in sanctuary chimpanzees in Sierra Leone. <i>Nature Communications</i> , 2021, 12, 763.	5.8	17
21838	Mitochondrial genome of <i>Sabella spallanzanii</i> (Gmelin, 1791) (Sabellida: Sabellidae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 499-501.	0.2	7
21839	The complete chloroplast genome of <i>Keteleeria davidiana</i> var. <i>calcareo</i> (Pinaceae), an endangered species endemic to China. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 693-695.	0.2	2
21840	<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
21841	Comparative Mitogenomics in <i>Hyalella</i> (Amphipoda: Crustacea). <i>Genes</i> , 2021, 12, 292.	1.0	6
21842	DNA barcoding for identification of fishes in Xiangjiaba reservoir area in the downstream section of the Jinsha river. <i>Conservation Genetics Resources</i> , 2021, 13, 201-208.	0.4	3
21843	NGlyAlign: an automated library building tool to align highly divergent HIV envelope sequences. <i>BMC Bioinformatics</i> , 2021, 22, 54.	1.2	0
21844	Strain Characterization of <i>Streptococcus suis</i> Serotypes 28 and 31, Which Harbor the Resistance Genes <i>oprA</i> and <i>ant(6)-Ia</i> . <i>Pathogens</i> , 2021, 10, 213.	1.2	4
21845	First Occurrence of the Genus <i>Australatya</i> (Crustacea: Decapoda: Atyidae) in Melanesia and Polynesia with Description of a New Species. <i>Pacific Science</i> , 2021, 74, .	0.2	0
21846	Insight into One Health Approach: Endoparasite Infections in Captive Wildlife in Bangladesh. <i>Pathogens</i> , 2021, 10, 250.	1.2	7
21848	Re-Evaluation of the <i>Podosphaera tridactyla</i> Species Complex in Australia. <i>Journal of Fungi</i> (Basel), Tj ETQq1 1 0.784314 rgBT <sub>1</sub> /Overlo	1.5	1
21849	Tomato leaf curl Oman virus and associated Betasatellite causing leaf curl disease in tomato in Pakistan. <i>European Journal of Plant Pathology</i> , 2021, 160, 249-257.	0.8	6
21851	Ecological and spatial patterns associated with diversification of South American <i>Physaria</i> (Brassicaceae) through the general concept of species. <i>Organisms Diversity and Evolution</i> , 2021, 21, 161-188.	0.7	3
21852	Spatial phylogenetics of the native woody plant species in Hainan, China. <i>Ecology and Evolution</i> , 2021, 11, 2100-2109.	0.8	14
21853	The Genome of Banana Leaf Blight Pathogen <i>Fusarium sacchari</i> str. FS66 Harbors Widespread Gene Transfer From <i>Fusarium oxysporum</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 629859.	1.7	5
21854	<i>Novakomyces olei</i> sp. nov., the First Member of a Novel Taphrinomycotina Lineage. <i>Microorganisms</i> , 2021, 9, 301.	1.6	3
21855	Coevolution of group-living and aposematism in caterpillars: warning colouration may facilitate the evolution from group-living to solitary habits. <i>Bmc Ecology and Evolution</i> , 2021, 21, 25.	0.7	7



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21859	Characteristics of gut microbiota in pigs with different breeds, growth periods and genders. <i>Microbial Biotechnology</i> , 2022, 15, 793-804.	2.0	20
21860	<i>Lunatibacter salilacus</i> gen. nov., sp. nov., a member of the family Cyclobacteriaceae, isolated from a saline and alkaline lake sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	9
21861	Genetic variants of small airways and interstitial pulmonary disease in children. <i>Scientific Reports</i> , 2021, 11, 2715.	1.6	4
21863	APOBECs and Herpesviruses. <i>Viruses</i> , 2021, 13, 390.	1.5	44
21864	Conjugative plasmids interact with insertion sequences to shape the horizontal transfer of antimicrobial resistance genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	161
21865	Comparative Genomics Suggests a Taxonomic Revision of the <i>Staphylococcus cohnii</i> Species Complex. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	6
21866	Determinants of genome-wide distribution and evolution of uORFs in eukaryotes. <i>Nature Communications</i> , 2021, 12, 1076.	5.8	37
21867	Light environment drives evolution of color vision genes in butterflies and moths. <i>Communications Biology</i> , 2021, 4, 177.	2.0	34
21868	Chromosome-Level Genome Assembly of the American Cranberry ( <i>Vaccinium macrocarpon</i> Ait.) and Its Wild Relative <i>Vaccinium microcarpum</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 633310.	1.7	29
21869	Microbial production and consumption of hydrocarbons in the global ocean. <i>Nature Microbiology</i> , 2021, 6, 489-498.	5.9	56
21870	DNA Sequence Analyses Reveal Two New Species of <i>Caloglossa</i> (Delesseriaceae, Rhodophyta) from the Skin of West Indian Manatees. <i>Journal of Marine Science and Engineering</i> , 2021, 9, 163.	1.2	7
21871	Genome-wide analysis of Indian SARS-CoV-2 genomes to identify T-cell and B-cell epitopes from conserved regions based on immunogenicity and antigenicity. <i>International Immunopharmacology</i> , 2021, 91, 107276.	1.7	5
21872	The Distinctive Evolution of orfX <i>Clostridium parbotulinum</i> Strains and Their Botulinum Neurotoxin Type A and F Gene Clusters Is Influenced by Environmental Factors and Gene Interactions via Mobile Genetic Elements. <i>Frontiers in Microbiology</i> , 2021, 12, 566908.	1.5	11
21873	A new species of <i>Cynomops</i> (Chiroptera: Molossidae) from the northwestern slope of the Andes. <i>Mammalia</i> , 2021, 85, 273-286.	0.3	7
21875	Cytochrome P450 monooxygenase genes in the wild silkworm, <i>Bombyx mandarina</i> . <i>PeerJ</i> , 2021, 9, e10818.	0.9	6
21876	Ammonium Removal in Aquaponics Indicates Participation of <i>Comammox Nitrospira</i> . <i>Current Microbiology</i> , 2021, 78, 894-903.	1.0	12
21878	Characterization and complete genome sequence of <i>Privateer</i> , a highly prolate <i>Proteus mirabilis</i> podophage. <i>PeerJ</i> , 2021, 9, e10645.	0.9	6

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21880	Comparative Mitogenomic Analysis of Heptageniid Mayflies (Insecta: Ephemeroptera): Conserved Intergenic Spacer and tRNA Gene Duplication. <i>Insects</i> , 2021, 12, 170.	1.0	14
21881	Facilitation in the soil microbiome does not necessarily lead to niche expansion. <i>Environmental Microbiomes</i> , 2021, 16, 4.	2.2	5
21882	<i>Thermaurantiacus tibetensis</i> gen. nov., sp. nov., a novel moderately thermophilic bacterium isolated from hot spring microbial mat in Tibet. <i>Antonie Van Leeuwenhoek</i> , 2021, 114, 445-455.	0.7	10
21883	Molecular detection of cacao swollen shoot badnavirus species by amplification with four PCR primer pairs, and evidence that Cacao swollen shoot Togo B virus-like isolates are highly prevalent in CÔte d'Ivoire. <i>European Journal of Plant Pathology</i> , 2021, 159, 941-947.	0.8	4
21884	Protein dynamics analysis identifies candidate cancer driver genes and mutations in TCGA data. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 721-730.	1.5	6
21885	Aquila enables reference-assisted diploid personal genome assembly and comprehensive variant detection based on linked reads. <i>Nature Communications</i> , 2021, 12, 1077.	5.8	11
21886	Pineapple Mycobiome Related to Fruitlet Core Rot Occurrence and the Influence of Fungal Species Dispersion Patterns. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 175.	1.5	8
21887	Amplicon-Based Next Generation Sequencing for Rapid Identification of Rickettsia and Ectoparasite Species from Entomological Surveillance in Thailand. <i>Pathogens</i> , 2021, 10, 215.	1.2	9
21888	Fungal X-Intrinsic Protein Aquaporin from <i>Trichoderma atroviride</i> : Structural and Functional Considerations. <i>Biomolecules</i> , 2021, 11, 338.	1.8	3
21889	Organic nitrogen nutrition: LHT1.2 protein from hybrid aspen ( <i>Populus tremula</i> L. x <i>tremuloides</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 2021, 41, 1479-1496.	1.4	9
21890	Molecular identification of the potentially forensically relevant cluster flies <i>Pollenia rudis</i> (Fabricius) and <i>Pollenia vagabunda</i> (Meigen) (Diptera: Polleniidae) – non-recorded species in Algeria. <i>Forensic Sciences Research</i> , 2022, 7, 1-13.	0.9	4
21891	Evolutionary Conservation of Structural and Functional Coupling between the BRM AT-Hook and Bromodomain. <i>Journal of Molecular Biology</i> , 2021, 433, 166845.	2.0	4
21892	Pod pepper vein yellows virus, a new recombinant polerovirus infecting <i>Capsicum frutescens</i> in Yunnan province, China. <i>Virology Journal</i> , 2021, 18, 42.	1.4	10
21893	Insights into triterpene synthesis and unsaturated fatty-acid accumulation provided by chromosomal-level genome analysis of <i>Akebia trifoliata</i> subsp. <i>australis</i> . <i>Horticulture Research</i> , 2021, 8, 33.	2.9	23
21894	Implications of Historical and Contemporary Processes on Genetic Differentiation of a Declining Boreal Songbird: The Rusty Blackbird. <i>Diversity</i> , 2021, 13, 103.	0.7	3
21895	Insights into long-distance dispersal and ecological and morphological evolution in the fern genus <i>Microgramma</i> from phylogenetic inference. <i>Botanical Journal of the Linnean Society</i> , 2021, 196, 294-312.	0.8	10
21896	Systematic Detection of Large-Scale Multigene Horizontal Transfer in Prokaryotes. <i>Molecular Biology and Evolution</i> , 2021, 38, 2639-2659.	3.5	10

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21897	Gut Microbiomes of Freshwater Mussels (Unionidae) Are Taxonomically and Phylogenetically Variable across Years but Remain Functionally Stable. <i>Microorganisms</i> , 2021, 9, 411.	1.6	14
21898	Regional Comparison of Snow Leopard ( <i>Panthera uncia</i> ) Diet using DNA Metabarcoding. <i>Biodiversity and Conservation</i> , 2021, 30, 797-817.	1.2	21
21899	Protecting Intestinal Microenvironment Alleviates Acute Graft-Versus-Host Disease. <i>Frontiers in Physiology</i> , 2020, 11, 608279.	1.3	6
21900	Multiple genetic marker analysis challenges the introduction history of <i>Ulva australis</i> (Ulvales.) Tj ETQq1 1 0.784314 rgBT /Over	0.9	0
21901	Genome-wide characterization of PEBP family genes in nine Rosaceae tree species and their expression analysis in <i>P. mume</i> . <i>Bmc Ecology and Evolution</i> , 2021, 21, 32.	0.7	10
21902	Comparative Genomics Reveals Early Emergence and Biased Spatiotemporal Distribution of SARS-CoV-2. <i>Molecular Biology and Evolution</i> , 2021, 38, 2547-2565.	3.5	31
21903	Unraveling the Gut Microbiome of the Invasive Small Indian Mongoose ( <i>Urva auropunctata</i> ) in the Caribbean. <i>Microorganisms</i> , 2021, 9, 465.	1.6	7
21904	Dichloroacetate and Pyruvate Metabolism: Pyruvate Dehydrogenase Kinases as Targets Worth Investigating for Effective Therapy of Toxoplasmosis. <i>MSphere</i> , 2021, 6, .	1.3	6
21905	Spatial patterns in phage- <i>Rhizobium</i> coevolutionary interactions across regions of common bean domestication. <i>ISME Journal</i> , 2021, 15, 2092-2106.	4.4	20
21906	<i>Limosilactobacillus balticus</i> sp. nov., <i>Limosilactobacillus agrestis</i> sp. nov., <i>Limosilactobacillus albertensis</i> sp. nov., <i>Limosilactobacillus rudii</i> sp. nov. and <i>Limosilactobacillus fastidiosus</i> sp. nov., five novel <i>Limosilactobacillus</i> species isolated from the vertebrate gastrointestinal tract, and proposal of six subspecies of <i>Limosilactobacillus reuteri</i> adapted to the gastrointestinal tract of specific vertebrate hosts. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	60
21907	High dispersal capacity of <i>Culicoides obsoletus</i> (Diptera: Ceratopogonidae), vector of bluetongue and Schmallenberg viruses, revealed by landscape genetic analyses. <i>Parasites and Vectors</i> , 2021, 14, 93.	1.0	12
21908	Million-year-old DNA sheds light on the genomic history of mammoths. <i>Nature</i> , 2021, 591, 265-269.	13.7	179
21909	L1 retrotransposons exploit RNA m6A modification as an evolutionary driving force. <i>Nature Communications</i> , 2021, 12, 880.	5.8	32
21910	Genomic profiles of <i>Pseudomonas aeruginosa</i> gene clusters based on profile HMMs, reveal novel therapeutic targets for clinical intervention. <i>Journal of Bioinformatics and Sequence Analysis</i> , 2021, 11, 1-8.	0.5	0
21911	Complete Genome Sequences of Two Rat Pegivirus Strains in Indonesia. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	0
21912	Developmental and biophysical determinants of grass leaf size worldwide. <i>Nature</i> , 2021, 592, 242-247.	13.7	43
21913	Bioinformatic Analysis of Structure and Function of LIM Domains of Human Zyxin Family Proteins. <i>International Journal of Molecular Sciences</i> , 2021, 22, 2647.	1.8	12
21914	Transcriptional regulation of dosage compensation in <i>Carica papaya</i> . <i>Scientific Reports</i> , 2021, 11, 5854.	1.6	5

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21915	Transglycosylation abilities of $\beta$ -D-galactosidases from GH family 2. <i>3 Biotech</i> , 2021, 11, 168.	1.1	3
21916	A Morphological and Molecular Analysis of a Bloom of the Filamentous Green Alga <i>Pithophora</i> . <i>Water (Switzerland)</i> , 2021, 13, 760.	1.2	2
21918	Scaffolding proteins guide the evolution of algal light harvesting antennas. <i>Nature Communications</i> , 2021, 12, 1890.	5.8	11
21921	Resurrection of a Viral Internal Ribosome Entry Site from a 700 Year Old Ancient Northwest Territories Cripavirus. <i>Viruses</i> , 2021, 13, 493.	1.5	1
21922	Whole-genome analysis of probiotic product isolates reveals the presence of genes related to antimicrobial resistance, virulence factors, and toxic metabolites, posing potential health risks. <i>BMC Genomics</i> , 2021, 22, 210.	1.2	30
21923	Deciphering the transcriptomic regulation of heat stress responses in <i>Nothofagus pumilio</i> . <i>PLoS ONE</i> , 2021, 16, e0246615.	1.1	6
21924	Unveiling the unknown phylogenetic position of the scallop <i>Austrochlamys natans</i> and its implications for marine stewardship in the Magallanes Province. <i>Scientific Reports</i> , 2021, 11, 7241.	1.6	1
21925	Characterizing the culturable surface microbiomes of diverse marine animals. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	12
21926	Marine sediments harbor diverse archaea and bacteria with the potential for anaerobic hydrocarbon degradation via fumarate addition. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	13
21927	Genotypes and phylogenetic analysis of adenovirus in children with respiratory infection in Buenos Aires, Argentina (2000–2018). <i>PLoS ONE</i> , 2021, 16, e0248191.	1.1	7
21928	Analysis of protein determinants of host-specific infection properties of polyomaviruses using machine learning. <i>Genes and Genomics</i> , 2021, 43, 407-420.	0.5	0
21929	Mitochondrial DNA Analysis Clarifies Taxonomic Status of the Northernmost Snow Sheep ( <i>Ovis</i> ) Tj ETQq1 1 0.784314 rgBT /Qverlock 10	1.1	6
21930	The complete mitochondrial genome of <i>Sardinops sagax</i> (Jenyns, 1842) (Clupeiformes: Clupeidae) and phylogenetic analyses of sardines. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1080-1081.	0.2	0
21931	European eel ( <i>Anguilla anguilla</i> ) GI tract conserves a unique metagenomics profile in the recirculation aquaculture system (RAS). <i>Aquaculture International</i> , 2021, 29, 1529-1544.	1.1	5
21932	Molecular Epidemiology of <i>Xanthomonas euvesicatoria</i> Strains from the Balkan Peninsula Revealed by a New Multiple-Locus Variable-Number Tandem-Repeat Analysis Scheme. <i>Microorganisms</i> , 2021, 9, 536.	1.6	10
21933	A common bean truncated CRINKLY4 kinase controls gene-for-gene resistance to the fungus <i>Colletotrichum lindemuthianum</i> . <i>Journal of Experimental Botany</i> , 2021, 72, 3569-3581.	2.4	21
21934	New Insights into the Taxonomy of the Genus <i>Cantharellus</i> in China: Epityfication of <i>C. yunnanensis</i> W.F. Chiu and the First Record of <i>C. cibarius</i> Fr.. <i>Cryptogamie, Mycologie</i> , 2021, 42, .	0.2	12
21935	Morpho-molecular characterization of rock-inhabiting lichen <i>Dermatocarpon miniatum</i> (Verrucariaceae, Ascomycota) and its symbiont in Indian Himalayas. <i>Nucleus (India)</i> , 2021, 64, 193-202.	0.9	2

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21936	Discovery of Novel Herpes Simplexviruses in Wild Gorillas, Bonobos, and Chimpanzees Supports Zoonotic Origin of HSV-2. <i>Molecular Biology and Evolution</i> , 2021, 38, 2818-2830.	3.5	13
21937	A Test for the Rapid Detection of the Cefazolin Inoculum Effect in Methicillin-Susceptible <i>Staphylococcus aureus</i> . <i>Journal of Clinical Microbiology</i> , 2021, 59, .	1.8	6
21938	Effects of rumen-protected arginine supplementation on the plasma amino acids and gut microbiota of sika deer ( <i>Cervus nippon</i> ). <i>Animal Feed Science and Technology</i> , 2021, 273, 114828.	1.1	3
21939	Cocktail Therapy of Fosthiazate and Cupric-Ammonium Complex for Citrus Huanglongbing. <i>Frontiers in Plant Science</i> , 2021, 12, 643971.	1.7	11
21940	Effects of dietary hydrolyzable tannins on growth performance, antioxidant capacity, intestinal microflora and resistance against <i>Vibrio parahaemolyticus</i> of juvenile Pacific white shrimp, <i>Litopenaeus vannamei</i> (Boone, 1931). <i>Aquaculture Reports</i> , 2021, 19, 100601.	0.7	10
21941	Selective enrichment and metagenomic analysis of three novel comammox <i>Nitrospira</i> in a urine-fed membrane bioreactor. <i>ISME Communications</i> , 2021, 1, .	1.7	27
21942	ACE2 receptor usage reveals variation in susceptibility to SARS-CoV and SARS-CoV-2 infection among bat species. <i>Nature Ecology and Evolution</i> , 2021, 5, 600-608.	3.4	83
21943	A combined molecular and morphological phylogeny of the Loricariinae (Siluriformes: Loricariidae), with emphasis on the Harttiini and Farlowellini. <i>PLoS ONE</i> , 2021, 16, e0247747.	1.1	17
21944	Yeasts in the nests of the leaf-cutter ant <i>Acromyrmex balzani</i> in a Savanna biome: exploitation of community and metabolic diversity. <i>Antonie Van Leeuwenhoek</i> , 2021, 114, 751-764.	0.7	6
21945	Analysis of Fungal Genomes Reveals Commonalities of Intron Gain or Loss and Functions in Intron-Poor Species. <i>Molecular Biology and Evolution</i> , 2021, 38, 4166-4186.	3.5	19
21946	Methotrexate impacts conserved pathways in diverse human gut bacteria leading to decreased host immune activation. <i>Cell Host and Microbe</i> , 2021, 29, 362-377.e11.	5.1	70
21948	Marine macroalgal biodiversity of northern Madagascar: morpho-genetic systematics and implications of anthropic impacts for conservation. <i>Biodiversity and Conservation</i> , 2021, 30, 1501-1546.	1.2	22
21949	Molecular organization of the <i>E. coli</i> cellulose synthase macrocomplex. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 310-318.	3.6	28
21950	Distinct Functions of Ethylene and ACC in the Basal Land Plant <i>Marchantia polymorpha</i> . <i>Plant and Cell Physiology</i> , 2021, 62, 858-871.	1.5	14
21951	Genomic insights into the host specific adaptation of the <i>Pneumocystis</i> genus. <i>Communications Biology</i> , 2021, 4, 305.	2.0	23
21952	Integrated Application of Rapeseed Cake and Green Manure Enhances Soil Nutrients and Microbial Communities in Tea Garden Soil. <i>Sustainability</i> , 2021, 13, 2967.	1.6	21
21953	Environmental Temperatures Affect the Gastrointestinal Microbes of the Chinese Giant Salamander. <i>Frontiers in Microbiology</i> , 2021, 12, 543767.	1.5	23
21956	Genomic analysis of <i>Medicago ruthenica</i> provides insights into its tolerance to abiotic stress and demographic history. <i>Molecular Ecology Resources</i> , 2021, 21, 1641-1657.	2.2	17

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21958	Genomic characterization of 99 viruses from the bunyavirus families Nairoviridae, Peribunyaviridae, and Phenuiviridae, including 35 previously unsequenced viruses. <i>PLoS Pathogens</i> , 2021, 17, e1009315.	2.1	23
21959	DNA barcoding and cryptic diversity of deep-sea scavenging amphipods in the Clarion-Clipperton Zone (Eastern Equatorial Pacific). <i>Marine Biodiversity</i> , 2021, 51, 1.	0.3	15
21960	Genetic variability and phylogenetic analysis among strains of deformed wing virus infesting honey bees and other organisms. <i>Saudi Journal of Biological Sciences</i> , 2021, 28, 1548-1556.	1.8	0
21961	Thousands of previously unknown phages discovered in whole-community human gut metagenomes. <i>Microbiome</i> , 2021, 9, 78.	4.9	101
21962	The diversity and evolution of microbial dissimilatory phosphite oxidation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	17
21963	Molecular biogeography of the Mediterranean <i>Buthus</i> species complex (Scorpiones: Buthidae) at its southern Palearctic margin. <i>Biological Journal of the Linnean Society</i> , 2021, 133, 166-178.	0.7	9
21964	Genetic variation of <i>Ascosphaera apis</i> and colony attributes do not explain chalkbrood disease outbreaks in Australian honey bees. <i>Journal of Invertebrate Pathology</i> , 2021, 180, 107540.	1.5	5
21965	Cross-Species Metabolic Profiling of Floral Specialized Metabolism Facilitates Understanding of Evolutional Aspects of Metabolism Among Brassicaceae Species. <i>Frontiers in Plant Science</i> , 2021, 12, 640141.	1.7	1
21967	<i>Tritonibacter aquimaris</i> sp. nov. and <i>Tritonibacter litoralis</i> sp. nov., two novel members of the <i>Roseobacter</i> group isolated from coastal seawater. <i>Antonie Van Leeuwenhoek</i> , 2021, 114, 787-798.	0.7	10
21968	Importance of environmental factors over habitat connectivity in shaping bacterial communities in microbial mats and bacterioplankton in an Antarctic freshwater system. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	13
21972	<i>Marinobacter orientalis</i> sp. nov., a thiosulfate-oxidizing bacterium isolated from a marine solar saltern. <i>Antonie Van Leeuwenhoek</i> , 2021, 114, 765-775.	0.7	8
21973	Comparison of Current Methods for Signal Peptide Prediction in Phytoplasmata. <i>Frontiers in Microbiology</i> , 2021, 12, 661524.	1.5	15
21974	Transcriptional profiling of identified neurons in leech. <i>BMC Genomics</i> , 2021, 22, 215.	1.2	6
21976	Deep viral blood metagenomics reveals extensive anellovirus diversity in healthy humans. <i>Scientific Reports</i> , 2021, 11, 6921.	1.6	31
21977	Successful extraction of insect DNA from recent copal inclusions: limits and perspectives. <i>Scientific Reports</i> , 2021, 11, 6851.	1.6	6
21978	First report of the invasive snail <i>Pomacea canaliculata</i> in Kenya. <i>CABI Agriculture and Bioscience</i> , 2021, 2, .	1.1	12
21979	Transcriptional activity differentiates families of Marine Group II <i>Euryarchaeota</i> in the coastal ocean. <i>ISME Communications</i> , 2021, 1, .	1.7	2

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21980	Occurrence of lettuce chlorosis virus in <i>Passiflora</i> spp. in Brazil. <i>Journal of Plant Pathology</i> , 2021, 103, 443-447.	0.6	3
21981	Morphological and phylogenetic analyses of <i>Toniniopsis subincompta</i> s. lat. ( <i>Ramalinaceae</i> , <i>Lecanorales</i> ) in Eurasia. <i>Lichenologist</i> , 2021, 53, 171-183.	0.5	4
21982	ANTIFUNGAL ACTIVITY OF ACTINOBACTERIA WITH A POTENTIAL TO INHIBIT RICE BLAST FUNGUS <i>MAGNAPORTHE ORYZAE</i> (ANAMORPH <i>PYRICULARIA ORYZAE</i> ). <i>Asian Journal of Pharmaceutical and Clinical Research</i> , 0, , 121-125.	0.3	0
21984	Identification and phylogenetic analysis of RNA binding domain abundant in apicomplexans or RAP proteins. <i>Microbial Genomics</i> , 2021, 7, .	1.0	5
21986	Molecular phylogenetic analysis shows that causal agent of maize rough dwarf disease in Iran is closer to rice black-streaked dwarf virus. <i>European Journal of Plant Pathology</i> , 2021, 160, 411-425.	0.8	3
21987	Soil bacterial characteristics between surface and subsurface soils along a precipitation gradient in the Alxa Desert, China. <i>Journal of Arid Land</i> , 2021, 13, 257-273.	0.9	3
21988	Multimerization variants as potential drivers of neofunctionalization. <i>Science Advances</i> , 2021, 7, .	4.7	14
21990	Silk of the common clothes moth, <i>Tineola bisselliella</i> , a cosmopolitan pest belonging to the basal ditrysian moth line. <i>Insect Biochemistry and Molecular Biology</i> , 2021, 130, 103527.	1.2	7
21991	Ecological and Conservation Significance of Herpesvirus Infection in Neotropical Bats. <i>EcoHealth</i> , 2021, 18, 123-133.	0.9	9
21992	Gorgocephalidae (Digenea: Lepocreadioidea) in the Indo-West Pacific: new species, life-cycle data and perspectives on species delineation over geographic range. <i>Zoological Journal of the Linnean Society</i> , 2021, 193, 1416-1455.	1.0	18
21993	Complete mitochondrial genome of the distinct red-eared slider ( <i>Trachemys scripta</i> ssp., Testudines: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 26	0.2	0
21994	Complete mitochondrial genome of the Cumberland slider ( <i>Trachemys scripta troostii</i> , Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 26	0.2	1
21995	The complete mitochondrial genome of <i>Sarotherodon galilaeus</i> (Linnaeus, 1758) (Perciformes: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 26	0.2	3
21997	In Silico Prediction and Analysis of Unusual Lantibiotic Resistance Operons in the Genus <i>Corynebacterium</i> . <i>Microorganisms</i> , 2021, 9, 646.	1.6	6
22000	<i>Pigmentibacter ruber</i> gen. nov., sp. nov., a novel bacterium of the family <i>Silvanigrellaceae</i> isolated from human blood. <i>Antonie Van Leeuwenhoek</i> , 2021, 114, 731-739.	0.7	4
22001	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
22002	Structural-genetic insight and optimization of protease production from a novel strain of <i>Aeromonas veronii</i> CMF, a gut isolate of <i>Chrysomya megacephala</i> . <i>Archives of Microbiology</i> , 2021, 203, 2961-2977.	1.0	5
22003	Conservation of Archaeal C/D Box sRNA-Guided RNA Modifications. <i>Frontiers in Microbiology</i> , 2021, 12, 654029.	1.5	9

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22005	Phylogeny and taxonomy of <i>Erysiphe</i> species (powdery mildew): Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 707 Td <i>Mycoscience</i> , 2021, 62, 115-123.	0.3	8
22006	Mitochondria-rough-ER contacts in the liver regulate systemic lipid homeostasis. <i>Cell Reports</i> , 2021, 34, 108873.	2.9	76
22007	Dissecting the molecular diversity and commonality of bovine and human treponemes identifies key survival and adhesion mechanisms. <i>PLoS Pathogens</i> , 2021, 17, e1009464.	2.1	7
22008	Rational discovery of a cancer neoepitope harboring the KRAS G12D driver mutation. <i>Science China Life Sciences</i> , 2021, 64, 2144-2152.	2.3	6
22011	Dwarfs of the fortress: A new cryptic species of dwarf gecko of the genus <i>Cnemaspis</i> Strauch, 1887 (Squamata, Gekkonidae) from Rajgad fort in the northern Western Ghats of Maharashtra, India. <i>Evolutionary Systematics</i> , 2021, 5, 25-38.	0.2	6
22012	Comparison of Brassica Genomes reveals asymmetrical gene retention between functional groups of genes in recurrent polyploidizations. <i>Plant Molecular Biology</i> , 2021, 106, 193-206.	2.0	6
22013	Evolutionary analysis of rabies virus using the partial Nucleoprotein and Glycoprotein gene in Mumbai region of India. <i>Journal of General Virology</i> , 2021, 102, .	1.3	2
22014	Biogeography of ITS Variation in the <i>Helenium autumnale</i> (Asteraceae) Species Complex. <i>Systematic Botany</i> , 2021, 46, 235-247.	0.2	0
22015	Characterization of the novel mitochondrial genome segregation factor TAP110 in <i>Trypanosoma brucei</i> . <i>Journal of Cell Science</i> , 2021, 134, .	1.2	26
22016	Identification and characterization of adipokinetic hormone and its receptor in bumble bee queens, <i>Bombus lantschouensis</i> . <i>Journal of Apicultural Research</i> , 0, , 1-9.	0.7	0
22017	The Crown Pearl: a draft genome assembly of the European freshwater pearl mussel <i>Margaritifera margaritifera</i> (Linnaeus, 1758). <i>DNA Research</i> , 2021, 28, .	1.5	15
22018	DNA-SIP and repeated isolation corroborate <i>Variovorax</i> as a key organism in maintaining the genetic memory for linuron biodegradation in an agricultural soil. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	0
22019	Mitochondrial DNA analysis reveals gene drift and structuring in the declining European piddock <i>Pholas dactylus</i> (L., 1758) confirming high vulnerability. <i>Regional Studies in Marine Science</i> , 2021, 43, 101688.	0.4	0
22023	Revealing the high variability on nonconserved core and mobile elements of <i>Austropuccinia psidii</i> and other rust mitochondrial genomes. <i>PLoS ONE</i> , 2021, 16, e0248054.	1.1	5
22026	The evolution of hemocyanin genes in <i>Tectipleura</i> : a multitude of conserved introns in highly diverse gastropods. <i>Bmc Ecology and Evolution</i> , 2021, 21, 36.	0.7	3
22027	Ccdc113/Ccdc96 complex, a novel regulator of ciliary beating that connects radial spoke 3 to dynein g and the nexin link. <i>PLoS Genetics</i> , 2021, 17, e1009388.	1.5	31
22028	Draft Genome Sequence of <i>Dietzia</i> sp. Strain SYD-A1, Isolated from Coal Seam Formation Water. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	1



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22029	Extended phylogeography of the ancestral <i>Morchella anatolica</i> supports preglacial presence in Europe and Mediterranean origin of morels. <i>Mycologia</i> , 2021, 113, 559-573.	0.8	5
22031	High-Resolution Transcriptome Atlas and Improved Genome Assembly of Common Buckwheat, <i>Fagopyrum esculentum</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 612382.	1.7	17
22032	Tracing and exploring the evolutionary origin and systematic function of fish complement C9. <i>Molecular Genetics and Genomics</i> , 2021, 296, 665-676.	1.0	2
22033	The role of RNA-binding proteins in mediating adaptive responses in Gram-positive bacteria. <i>FEBS Journal</i> , 2022, 289, 1746-1764.	2.2	21
22034	Expanding the repertoire of electron acceptors for the anaerobic oxidation of methane in carbonates in the Atlantic and Pacific Ocean. <i>ISME Journal</i> , 2021, 15, 2523-2536.	4.4	6
22035	Bacterial cyclic diguanylate signaling networks sense temperature. <i>Nature Communications</i> , 2021, 12, 1986.	5.8	35
22036	Functional and genetic analysis of viral receptor ACE2 orthologs reveals a broad potential host range of SARS-CoV-2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	168
22037	Genomic diversity of <i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i> : pangenomic approach for highlighting unique genomic features with newly constructed complete genomes. <i>Veterinary Research</i> , 2021, 52, 46.	1.1	11
22038	Biology and genetic diversity of phasey bean mild yellows virus, a common virus in legumes in Australia. <i>Archives of Virology</i> , 2021, 166, 1575-1589.	0.9	9
22039	Retracing Storage Polysaccharide Evolution in Stramenopila. <i>Frontiers in Plant Science</i> , 2021, 12, 629045.	1.7	7
22040	Co-infections: Simultaneous detections of West Nile virus and Usutu virus in birds from Germany. <i>Transboundary and Emerging Diseases</i> , 2022, 69, 776-792.	1.3	26
22041	Evaluating the nitrogen-contaminated groundwater treatment by a denitrifying granular sludge bioreactor: effect of organic matter loading. <i>Environmental Science and Pollution Research</i> , 2021, 28, 41351-41364.	2.7	9
22042	Bet v 1 potential allergens are involved in anthracnose resistance of strawberry varieties. <i>Journal of Berry Research</i> , 2021, 11, 21-32.	0.7	5
22043	EZmito: a simple and fast tool for multiple mitogenome analyses. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1101-1109.	0.2	23
22044	Topological Analysis for Sequence Variability: Case Study on more than 2K SARS-CoV-2 sequences of COVID-19 infected 54 countries in comparison with SARS-CoV-1 and MERS-CoV. <i>Infection, Genetics and Evolution</i> , 2021, 88, 104708.	1.0	6
22045	Anaerobic endosymbiont generates energy for ciliate host by denitrification. <i>Nature</i> , 2021, 591, 445-450.	13.7	53
22047	Spatial and temporal patterns in bacterioplankton communities across a river-lake continuum. <i>Limnologia</i> , 2021, 87, 125863.	0.7	1
22048	Domestication Shapes the Community Structure and Functional Metagenomic Content of the Yak Fecal Microbiota. <i>Frontiers in Microbiology</i> , 2021, 12, 594075.	1.5	10

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22049	Stretch-activated ion channels identified in the touch-sensitive structures of carnivorous Droseraceae plants. <i>ELife</i> , 2021, 10, .	2.8	43
22050	A highly mutable GST is essential for bract colouration in <i>Euphorbia pulcherrima</i> Willd. Ex Klotzsch. <i>BMC Genomics</i> , 2021, 22, 208.	1.2	13
22051	Conservation and Innovation: Versatile Roles for LRP4 in Nervous System Development. <i>Journal of Developmental Biology</i> , 2021, 9, 9.	0.9	12
22052	A new species of <i>Cyrtodactylus</i> Gray, 1827 (Squamata: Gekkonidae) from Western Yunnan, China. <i>Journal of Natural History</i> , 2021, 55, 713-731.	0.2	3
22053	Four new species of sequestrate <i>Inocybe</i> from Chilean Nothofagaceae forests. <i>Mycologia</i> , 2021, 113, 629-642.	0.8	6
22054	Distribution and preservation of the components of the engulfment. What is beyond representative genomes?. <i>PLoS ONE</i> , 2021, 16, e0246651.	1.1	4
22055	Identification of conserved peptide upstream open reading frames (CPuORFs) in oil palm ( <i>Elaeis</i> ) Tj ETQq0 0 0 rgBT/Overlock_10 Tf 50 5	0.2	0
22056	An intriguing characteristic of enhancer-promoter interactions. <i>BMC Genomics</i> , 2021, 22, 163.	1.2	3
22057	Novel Chromosome-Borne Accessory Genetic Elements Carrying Multiple Antibiotic Resistance Genes in <i>Pseudomonas aeruginosa</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 638087.	1.8	15
22059	Crystal structure of timothy grass allergen Phl p 12.0101 reveals an unusual profilin dimer. <i>Acta Biochimica Polonica</i> , 2021, 68, 15-22.	0.3	3
22060	Soil Microbiome Structure and Function in Ecopiles Used to Remediate Petroleum-Contaminated Soil. <i>Frontiers in Environmental Science</i> , 2021, 9, .	1.5	11
22061	<i>Petalostelma</i> of Brazil and the initial evolution of <i>Metastelmatinae</i> (Apocynaceae). <i>Plant Systematics and Evolution</i> , 2021, 307, 1.	0.3	0
22063	Nucleoside Metabolism Is Induced in Common Bean During Early Seedling Development. <i>Frontiers in Plant Science</i> , 2021, 12, 651015.	1.7	2
22064	Root and crown rot pathogens found on dry beans grown in Mozambique. <i>Tropical Plant Pathology</i> , 2021, 46, 294-310.	0.8	1
22066	Comparative Genomics Reveals 13 Different Isoforms of Mytimycins (A-M) in <i>Mytilus galloprovincialis</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 3235.	1.8	7
22068	Seed Banks as Incidental Fungi Banks: Fungal Endophyte Diversity in Stored Seeds of Banana Wild Relatives. <i>Frontiers in Microbiology</i> , 2021, 12, 643731.	1.5	12
22069	Reconstructing the Evolutionary History of a Highly Conserved Operon Cluster in <i>Gammaproteobacteria</i> and <i>Bacilli</i> . <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	5
22070	<i>Altererythrobacter flava</i> sp. nov., a new member of the family <i>Erythrobacteraceae</i> , isolated from a surface seawater sample. <i>Antonie Van Leeuwenhoek</i> , 2021, 114, 497-506.	0.7	2

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22071	Crystal structure of the nonclassical cadherin-17 N-terminus and implications for its adhesive binding mechanism. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2021, 77, 85-94.	0.4	3
22073	mtDNAcombine: tools to combine sequences from multiple studies. <i>BMC Bioinformatics</i> , 2021, 22, 115.	1.2	1
22074	<i>Mastomys natalensis</i> (Smith, 1834) as a natural host for <i>Schistosoma haematobium</i> (Bilharz, 1852) Weinland, 1858 x <i>Schistosoma bovis</i> Sonsino, 1876 introgressive hybrids. <i>Parasitology Research</i> , 2021, 120, 1755-1770.	0.6	21
22075	The effects of weather variability on patterns of genetic diversity in Tasmanian bettongs. <i>Molecular Ecology</i> , 2021, 30, 1777-1790.	2.0	3
22076	Genome Mining and Evolutionary Analysis Reveal Diverse Type III Polyketide Synthase Pathways in Cyanobacteria. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	8
22077	Characterization of <i>Plasmodium falciparum</i> Pantothenate Kinase and Identification of Its Inhibitors From Natural Products. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 639065.	1.8	11
22078	Assembly and comparative analysis of the complete mitochondrial genome of <i>Suaeda glauca</i> . <i>BMC Genomics</i> , 2021, 22, 167.	1.2	67
22079	Muntingia yellow spot virus: a novel New World begomovirus infecting <i>Muntingia calabura</i> L.. <i>Archives of Virology</i> , 2021, 166, 1759-1762.	0.9	0
22080	DeepPPF: A deep learning framework for predicting protein family. <i>Neurocomputing</i> , 2021, 428, 19-29.	3.5	16
22081	<i>Plasmodium matutinum</i> Transmitted by <i>Culex pipiens</i> as a Cause of Avian Malaria in Captive African Penguins ( <i>Spheniscus demersus</i> ) in Italy. <i>Frontiers in Veterinary Science</i> , 2021, 8, 621974.	0.9	8
22082	Molecular species delimitation reveals high diversity in the mosquito <i>Anopheles tessellatus</i> Theobald, 1901 (Diptera, Culicidae) across its range. <i>Acta Tropica</i> , 2021, 215, 105799.	0.9	5
22083	Diversity of Culturable Bacteria Isolated From the Feces of Wild <i>Anopheles darlingi</i> (Diptera: Tj ETQq1 1 0.784314 rgBT /Overl	0.9	9
22084	Ancient Xinjiang mitogenomes reveal intense admixture with high genetic diversity. <i>Science Advances</i> , 2021, 7, .	4.7	16
22085	New <i>Cladosporium</i> Species from Normal and Galled Flowers of Lamiaceae. <i>Pathogens</i> , 2021, 10, 369.	1.2	11
22086	Diversity of the insect pathogenic fungi in the genus <i>Metarhizium</i> in New Zealand. <i>New Zealand Journal of Botany</i> , 2021, 59, 440-456.	0.8	7
22087	The discovery of a microbialite-associated freshwater fish in the world's largest saline soda lake, Lake Van (Turkey). <i>Zoosystematics and Evolution</i> , 2021, 97, 181-189.	0.4	11
22088	Reduced metagenome sequencing for strain-resolution taxonomic profiles. <i>Microbiome</i> , 2021, 9, 79.	4.9	14
22089	Bioactive Potential of Several Actinobacteria Isolated from Microbiologically Barely Explored Desert Habitat, Saudi Arabia. <i>Biology</i> , 2021, 10, 235.	1.3	16

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22090	Identification and Biotyping of <i>Pythium insidiosum</i> Isolated from Urban and Rural Areas of Thailand by Multiplex PCR, DNA Barcode, and Proteomic Analyses. <i>Journal of Fungi</i> (Basel, Switzerland), 2021, 7, 242.	1.5	9
22091	Physicochemical and Microbial Diversity Analyses of Indian Hot Springs. <i>Frontiers in Microbiology</i> , 2021, 12, 627200.	1.5	22
22093	Integrated analysis of the ringneck snake <i>Diadophis punctatus</i> complex (Colubridae: Dipsadidae) in a biodiversity hotspot provides the foundation for conservation reassessment. <i>Biological Journal of the Linnean Society</i> , 2021, 133, 105-119.	0.7	3
22094	<i>Pseudomonas allokribbensis</i> sp. nov. and <i>Pseudomonas gozinkensis</i> sp. nov., Two New Species Isolated from a Volcanic Island, Izu Oshima, Japan. <i>Current Microbiology</i> , 2021, 78, 1670-1677.	1.0	12
22095	A New Remarkable Dwarf Sedge ( <i>Carex phylloscirpoides</i> , Cyperaceae) from Northern Chile, with Insights on the Evolution of Austral <i>Carex</i> section <i>Racemosae</i> . <i>Systematic Botany</i> , 2021, 46, 34-47.	0.2	4
22096	Identification and Characterization of Perennial Ryegrass ( <i>Lolium perenne</i> ) Vernalization Genes. <i>Frontiers in Plant Science</i> , 2021, 12, 640324.	1.7	3
22097	Association of maternal gut microbiota and plasma metabolism with congenital heart disease in offspring: a multi-omic analysis. <i>Scientific Reports</i> , 2021, 11, 5339.	1.6	11
22099	Increased spatial resolution of sampling in the Carpathian basin helps to understand the phylogeny of central European stream-dwelling gudgeons. <i>BMC Zoology</i> , 2021, 6, .	0.3	5
22100	Evolved increases in hemoglobin-oxygen affinity and the Bohr effect coincided with the aquatic specialization of penguins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	8
22101	Dietary supplementation with <i>Bacillus subtilis</i> promotes growth performance of broilers by altering the dominant microbial community. <i>Poultry Science</i> , 2021, 100, 100935.	1.5	81
22102	Distinction between vaginal and cervical microbiota in high-risk human papilloma virus-infected women in China. <i>BMC Microbiology</i> , 2021, 21, 90.	1.3	19
22103	Non-target Site Herbicide Resistance Is Conferred by Two Distinct Mechanisms in Black-Grass ( <i>Alopecurus myosuroides</i> ). <i>Frontiers in Plant Science</i> , 2021, 12, 636652.	1.7	37
22104	The association of group IIB intron with integrons in hypersaline environments. <i>Mobile DNA</i> , 2021, 12, 8.	1.3	2
22106	Phylogenetic and developmental analyses indicate complex functions of $\text{Ca}^{2+}$ -activated potassium channels in zebrafish embryonic development. <i>Developmental Dynamics</i> , 2021, 250, 1477-1493.	0.8	5
22108	The iron-sulfur scaffold protein HCF101 unveils the complexity of organellar evolution in SAR, Haptista and Cryptista. <i>Bmc Ecology and Evolution</i> , 2021, 21, 46.	0.7	3
22109	Molecular phylogenetic study in Spirocercidae (Nematoda) with description of a new species <i>Spirobakerus sagittalis</i> sp. nov. in wild canid <i>Cerdocyon thous</i> from Brazil. <i>Parasitology Research</i> , 2021, 120, 1713-1725.	0.6	3
22110	Density Peak clustering of protein sequences associated to a Pfam clan reveals clear similarities and interesting differences with respect to manual family annotation. <i>BMC Bioinformatics</i> , 2021, 22, 121.	1.2	1
22111	Antibiotic Modulation of Capsular Exopolysaccharide in <i>Pelagicoccus enzymogenes</i> sp. nov. Isolated From Marine Sediment. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	11

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22113	Olea Europaea Geminivirus: A Novel Bipartite Geminivirid Infecting Olive Trees. <i>Viruses</i> , 2021, 13, 481.	1.5	16
22114	Detection and characterization of chicken astrovirus associated with hatchery disease in commercial day-old turkeys in southwestern Nigeria. <i>Archives of Virology</i> , 2021, 166, 1607-1614.	0.9	7
22115	Reinvestigation of THOUSAND-GRAIN WEIGHT 6 grain weight genes in wheat and rice indicates a role in pollen development rather than regulation of auxin content in grains. <i>Theoretical and Applied Genetics</i> , 2021, 134, 2051-2062.	1.8	9
22116	Highly Contaminated Marine Sediments Can Host Rare Bacterial Taxa Potentially Useful for Bioremediation. <i>Frontiers in Microbiology</i> , 2021, 12, 584850.	1.5	33
22117	Taxonomic identity and evolutionary relationships of South African taxa related to the <i>Spergularia media</i> group (Caryophyllaceae). <i>Plant Systematics and Evolution</i> , 2021, 307, 1.	0.3	5
22118	Genomes of the willow-galling sawflies <i>Euura lappo</i> and <i>Eupontania aestiva</i> (Hymenoptera: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tj 5 Genes, Genomes, Genetics, 2021, 11, .	0.8	3
22119	Molecular control of the floral transition in the mast seeding plant <i>Celmisia lyallii</i> (Asteraceae). <i>Molecular Ecology</i> , 2021, 30, 1846-1863.	2.0	9
22120	Crustacean diversity in the Puget Sound: reconciling species, phylogenetic, and functional diversity. <i>Marine Biodiversity</i> , 2021, 51, 1.	0.3	2
22121	Thermophilic aerobic organoheterotrophic soil bacteria from anthropogenically changed territories of Saint Petersburg and Leningrad region. <i>Ecological Genetics</i> , 2021, 19, 47-58.	0.1	0
22122	Dysbiosis of the shrimp ( <i>Penaeus monodon</i> ) gut microbiome with AHPND outbreaks revealed by 16S rRNA metagenomics analysis. <i>Aquaculture Research</i> , 2021, 52, 3336-3349.	0.9	19
22123	Chromosome-scale genome assembly of <i>Cucumis hystrix</i> a wild species interspecifically cross-compatible with cultivated cucumber. <i>Horticulture Research</i> , 2021, 8, 40.	2.9	18
22124	Ultrafast functional profiling of RNA-seq data for nonmodel organisms. <i>Genome Research</i> , 2021, 31, 713-720.	2.4	15
22125	Genomic investigation of the coronavirus disease-2019 outbreak in the Republic of Korea. <i>Scientific Reports</i> , 2021, 11, 6009.	1.6	10
22126	Filling in the gaps: A reevaluation of the <i>Lygus hesperus</i> peptidome using an expanded de novo assembled transcriptome and molecular cloning. <i>General and Comparative Endocrinology</i> , 2021, 303, 113708.	0.8	6
22127	Phloroglucinol Derivatives in Plant-Beneficial <i>Pseudomonas</i> spp.: Biosynthesis, Regulation, and Functions. <i>Metabolites</i> , 2021, 11, 182.	1.3	27
22128	Description of a new species of Southeast Asian reed snake from northern Laos (Squamata: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tj 5 1962. <i>Journal of Natural History</i> , 2021, 55, 531-560.	0.2	2
22129	Novel hydrocarbon-utilizing soil mycobacteria synthesize unique mycocerosic acids at a Sicilian everlasting fire. <i>Biogeosciences</i> , 2021, 18, 1463-1479.	1.3	2
22130	Identification of the SHINE clade of AP2/ERF domain transcription factors genes in <i>Carica papaya</i> ; Their gene expression and their possible role in wax accumulation and water deficit stress tolerance in a wild and a commercial papaya genotypes. <i>Environmental and Experimental Botany</i> , 2021, 183, 104341.	2.0	14

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22131	A survey of insecticide resistance-conferring mutations in multiple targets in <i>Anopheles sinensis</i> populations across Sichuan, China. <i>Parasites and Vectors</i> , 2021, 14, 169.	1.0	7
22132	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
22133	<i>Inocybe brijunica</i> sp. nov., a New Ectomycorrhizal Fungus from Mediterranean Croatia Revealed by Morphology and Multilocus Phylogenetic Analysis. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 199.	1.5	8
22134	Conservation of the glycogen metabolism pathway underlines a pivotal function of storage polysaccharides in <i>Chlamydiae</i> . <i>Communications Biology</i> , 2021, 4, 296.	2.0	10
22135	Phylogenomics of Plant-Associated Botryosphaeriaceae Species. <i>Frontiers in Microbiology</i> , 2021, 12, 652802.	1.5	28
22136	IMA genome - F14. <i>IMA Fungus</i> , 2021, 12, 5.	1.7	5
22138	The Mitochondrial Genome of a Plant Fungal Pathogen <i>Pseudocercospora fijiensis</i> (Mycosphaerellaceae), Comparative Analysis and Diversification Times of the Sigatoka Disease Complex Using Fossil Calibrated Phylogenies. <i>Life</i> , 2021, 11, 215.	1.1	8
22139	Screening of endophytic fungi from oil palm ( <i>Elaeis guineensis</i> ) in producing exopolysaccharides. <i>Biodiversitas</i> , 2021, 22, .	0.2	2
22141	A Vernalization Response in a Winter Safflower ( <i>Carthamus tinctorius</i> ) Involves the Upregulation of Homologs of FT, FUL, and MAF. <i>Frontiers in Plant Science</i> , 2021, 12, 639014.	1.7	5
22142	Diversity of short interspersed nuclear elements (SINEs) in lepidopteran insects and evidence of horizontal SINE transfer between baculovirus and lepidopteran hosts. <i>BMC Genomics</i> , 2021, 22, 226.	1.2	5
22143	Characterisation of a carotenoid producing extremely halophilic archaeon <i>Halorubrum sodomense</i> MS5.1 isolated from a solar saltern in Tamil Nadu, South India. <i>Indian Journal of Fisheries</i> , 2021, 68, .	0.3	5
22146	Gibberellin induced transcription factor bZIP53 regulates <i>CesA1</i> expression in maize kernels. <i>PLoS ONE</i> , 2021, 16, e0244591.	1.1	8
22148	Viral genomic, metagenomic and human transcriptomic characterization and prediction of the clinical forms of COVID-19. <i>PLoS Pathogens</i> , 2021, 17, e1009416.	2.1	30
22150	Long-Lived Species of Bivalves Exhibit Low MT-DNA Substitution Rates. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 626042.	1.6	7
22152	A valine residue deletion in <i>ZmSig2A</i> , a sigma factor, accounts for a revertible leaf-color mutation in maize. <i>Crop Journal</i> , 2021, 9, 1330-1343.	2.3	6
22153	Structure of the class XI myosin globular tail reveals evolutionary hallmarks for cargo recognition in plants. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 522-533.	1.1	0
22154	Characterisation of a G2P[4] Rotavirus Outbreak in Western Australia, Predominantly Impacting Aboriginal Children. <i>Pathogens</i> , 2021, 10, 350.	1.2	5
22155	Diversity of <i>Weissella confusa</i> in Pozol and Its Carbohydrate Metabolism. <i>Frontiers in Microbiology</i> , 2021, 12, 629449.	1.5	6

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22156	A conserved cell division protein directly regulates FtsZ dynamics in filamentous and unicellular actinobacteria. <i>ELife</i> , 2021, 10, .	2.8	12
22158	Comparison of the SARS-CoV-2 (2019-nCoV) M protein with its counterparts of SARS-CoV and MERS-CoV species. <i>Journal of King Saud University - Science</i> , 2021, 33, 101335.	1.6	18
22159	Predicted Input of Uncultured Fungal Symbionts to a Lichen Symbiosis from Metagenome-Assembled Genomes. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	19
22161	Genera specific distribution of DEAD-box RNA helicases in cyanobacteria. <i>Microbial Genomics</i> , 2021, 7, .	1.0	4
22162	Reducing noise and stutter in short tandem repeat loci with unique molecular identifiers. <i>Forensic Science International: Genetics</i> , 2021, 51, 102459.	1.6	9
22163	<i>Artabotrys angustipetalus</i> (Annonaceae), a new species from Thailand, including a plastid phylogeny and character evolutionary analyses of thorn occurrence in <i>Artabotrys</i> . <i>Willdenowia</i> , 2021, 51, .	0.5	4
22165	Volatile Organic Compound from <i>Trichoderma asperelloides</i> TSU1: Impact on Plant Pathogenic Fungi. <i>Journal of Fungi</i> (Basel, Switzerland), 2021, 7, 187.	1.5	38
22166	Amycolatomycins A and B, Cyclic Hexapeptides Isolated from an <i>Amycolatopsis</i> sp. 195334CR. <i>Antibiotics</i> , 2021, 10, 261.	1.5	7
22167	The chromosome-level genome of dragon fruit reveals whole-genome duplication and chromosomal co-localization of betacyanin biosynthetic genes. <i>Horticulture Research</i> , 2021, 8, 63.	2.9	25
22168	Keratin intermediate filament chains in tuatara ( <i>Sphenodon punctatus</i> ): A comparison of tuatara and human sequences. <i>Journal of Structural Biology</i> , 2021, 213, 107706.	1.3	5
22169	Genome-guided investigation of secondary metabolites produced by a potential new strain <i>Streptomyces</i> BA2 isolated from an endemic plant rhizosphere in Turkey. <i>Archives of Microbiology</i> , 2021, 203, 2431-2438.	1.0	12
22171	Evaluation of a Newly Identified Endophytic Fungus, <i>Trichoderma phayaoense</i> for Plant Growth Promotion and Biological Control of Gummy Stem Blight and Wilt of Muskmelon. <i>Frontiers in Microbiology</i> , 2021, 12, 634772.	1.5	34
22172	Detection of <i>Babesia odocoilei</i> in <i>Ixodes scapularis</i> Ticks Collected in Southern Ontario, Canada. <i>Pathogens</i> , 2021, 10, 327.	1.2	13
22173	Production of prebiotic xylooligosaccharides from arabino- and glucuronoxylan using a two-domain <i>Jonesia denitrificans</i> xylanase from GH10 family. <i>Enzyme and Microbial Technology</i> , 2021, 144, 109743.	1.6	6
22174	Microbial Community Field Surveys Reveal Abundant <i>Pseudomonas</i> Population in Sorghum Rhizosphere Composed of Many Closely Related Phylotypes. <i>Frontiers in Microbiology</i> , 2021, 12, 598180.	1.5	20
22176	Essential Oil Composition and DNA Barcode and Identification of <i>Aniba</i> species (Lauraceae) Growing in the Amazon Region. <i>Molecules</i> , 2021, 26, 1914.	1.7	5
22178	Taxogenomic and Comparative Genomic Analysis of the Genus <i>Saccharomonospora</i> Focused on the Identification of Biosynthetic Clusters PKS and NRPS. <i>Frontiers in Microbiology</i> , 2021, 12, 603791.	1.5	16
22179	Gene expression evolution in pattern-triggered immunity within <i>Arabidopsis thaliana</i> and across Brassicaceae species. <i>Plant Cell</i> , 2021, 33, 1863-1887.	3.1	27

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22180	<i>St</i>PIP1, a PAMP-induced peptide in potato, elicits plant defenses and is associated with disease symptom severity in a compatible interaction with <i>Potato virus Y</i>. <i>Journal of Experimental Botany</i> , 2021, 72, 4472-4488.	2.4	16
22181	Identification, subtyping, and tracking of dairy spoilage-associated <i>Pseudomonas</i> by sequencing the ileS gene. <i>Journal of Dairy Science</i> , 2021, 104, 2668-2683.	1.4	7
22183	Isolation and Characterization of <i>Klebsiella</i> Phages for Phage Therapy. <i>Phage</i> , 2021, 2, 26-42.	0.8	36
22184	Roles of three putative salmon louse ( <i>Lepeophtheirus salmonis</i> ) prostaglandin E2 synthases in physiology and host-parasite interactions. <i>Parasites and Vectors</i> , 2021, 14, 206.	1.0	10
22185	Morphological and genetic evidence supports the separation of two <i>Tapinoma</i> ants (Formicidae). <i>Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50 5</i>	0.5	6
22187	Biotechnological and Ecological Potential of <i>Micromonospora provocatoris</i> sp. nov., a Gifted Strain Isolated from the Challenger Deep of the Mariana Trench. <i>Marine Drugs</i> , 2021, 19, 243.	2.2	10
22189	Pan and Core Genome Analysis of 183 <i>Mycobacterium tuberculosis</i> Strains Revealed a High Inter-Species Diversity among the Human Adapted Strains. <i>Antibiotics</i> , 2021, 10, 500.	1.5	9
22190	Genome-Wide Identification and Characterization of TALE Superfamily Genes in Soybean ( <i>Glycine max</i> ). <i>Tj ETQq1 1 0.784314 rgBT/Overlock 12</i>	1.8	12
22191	Whole-genome sequence-based analysis of the <i>Paenibacillus aquistagni</i> strain DK1, a polyethylene-degrading bacterium isolated from landfill. <i>World Journal of Microbiology and Biotechnology</i> , 2021, 37, 80.	1.7	5
22192	Succession of endophytic fungi and arbuscular mycorrhizal fungi associated with the growth of plant and their correlation with secondary metabolites in the roots of plants. <i>BMC Plant Biology</i> , 2021, 21, 165.	1.6	26
22193	Dancing on the top: phylogeography and genetic diversity of high-altitude freshwater fairy shrimps (Branchiopoda, Anostraca) with a focus on the Tibetan Plateau. <i>Hydrobiologia</i> , 2021, 848, 2611-2626.	1.0	2
22194	Four single-basepair mutations in the ptx promoter of <i>Bordetella bronchiseptica</i> are sufficient to activate the expression of pertussis toxin. <i>Scientific Reports</i> , 2021, 11, 9373.	1.6	3
22197	Lizards of a different stripe: phylogenetics of the <i>Pedioplanis undata</i> species complex (Squamata). <i>Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50 5</i>	0.4	2
22199	Genetics of wild and mass-reared populations of a generalist aphid parasitoid and improvement of biological control. <i>PLoS ONE</i> , 2021, 16, e0249893.	1.1	8
22200	The chromosome-level <i>Hemerocallis citrina</i> Borani genome provides new insights into the rutin biosynthesis and the lack of colchicine. <i>Horticulture Research</i> , 2021, 8, 89.	2.9	25
22201	Expression Patterns in Reductive Iron Assimilation and Functional Consequences during Phagocytosis of <i>Lichtheimia corymbifera</i> , an Emerging Cause of Mucormycosis. <i>Journal of Fungi (Basel)</i> . <i>Tj ETQq1 1 0.784314 rgBT/Overlock 10 Tf 50 5</i>		
22202	Signatures of antagonistic pleiotropy in a bacterial flagellin epitope. <i>Cell Host and Microbe</i> , 2021, 29, 620-634.e9.	5.1	44
22203	Middle Pleistocene genome calibrates a revised evolutionary history of extinct cave bears. <i>Current Biology</i> , 2021, 31, 1771-1779.e7.	1.8	27



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22204	<i>Opium Poppy Mosaic Virus</i> Has an Xrn-Resistant, Translated Subgenomic RNA and a BTE 3â€² CITE. <i>Journal of Virology</i> , 2021, 95, .	1.5	17
22205	Updating specific PCR primer for detection of <i>Cryptocaryon irritans</i> from reared <i>Larimichthys polyactis</i> . <i>Experimental Parasitology</i> , 2021, 223, 108081.	0.5	11
22206	Phylogenetics of <i>Piresia</i> (Poaceae: Bambusoideae) reveals unexpected generic relationships within Olyreae with taxonomic and biogeographic implications. <i>Taxon</i> , 2021, 70, 492-514.	0.4	2
22207	Phylogenomics Reveals that <i>Asaia</i> Symbionts from Insects Underwent Convergent Genome Reduction, Preserving an Insecticide-Degrading Gene. <i>MBio</i> , 2021, 12, .	1.8	10
22209	A new species of crayfish of the genus <i>Cambarellus</i> (Decapoda: Cambaridae) from central Mexico. <i>Revista Mexicana De Biodiversidad</i> , 2021, 92, 923150.	0.4	0
22210	Two strains of a novel begomovirus encoding Rep proteins with identical 121 strands but different 125 strands are not compatible in replication. <i>Archives of Virology</i> , 2021, 166, 1691-1709.	0.9	4
22211	Taxonomy of the Apicomplexan Symbionts of Coral, including <i>Corallicolida</i> ord. nov., Reassignment of the Genus <i>Gemmocystis</i> , and Description of New Species <i>Corallicola aquarius</i> gen. nov. sp. nov. and <i>Anthozoaphila gnarlus</i> gen. nov. sp. nov.. <i>Journal of Eukaryotic Microbiology</i> , 2021, 68, e12852.	0.8	9
22212	Direct effects of selection on aboveground biomass contrast with indirect structure-mediated effects of complementarity in a subtropical forest. <i>Oecologia</i> , 2021, 196, 249-261.	0.9	10
22213	ProDroid â€” An Android malware detection framework based on profile hidden Markov model. <i>Pervasive and Mobile Computing</i> , 2021, 72, 101336.	2.1	35
22214	Fecal Microbiome Transplantation from Children with Autism Spectrum Disorder Modulates Tryptophan and Serotonergic Synapse Metabolism and Induces Altered Behaviors in Germ-Free Mice. <i>MSystems</i> , 2021, 6, .	1.7	49
22215	Molecular Evolution of CatSper in Mammals and Function of Sperm Hyperactivation in Gray Short-Tailed Opossum. <i>Cells</i> , 2021, 10, 1047.	1.8	14
22216	Complete nucleotide sequence of soybean leaf rugose mosaic virus, an atypical member of the genus <i>Bymovirus</i> . <i>Archives of Virology</i> , 2021, 166, 1885-1892.	0.9	1
22217	A Chromosome-Level Genome Assembly of the Spotted Scat ( <i>Scatophagus argus</i> ). <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	17
22218	<i>Affinibrenneria salicis</i> gen. nov. sp. nov. isolated from <i>Salix matsudana</i> bark canker. <i>Archives of Microbiology</i> , 2021, 203, 3473-3481.	1.0	2
22220	Phylogenomic Analyses of Nucleotide-Sugar Biosynthetic and Interconverting Enzymes Illuminate Cell Wall Composition in Fungi. <i>MBio</i> , 2021, 12, .	1.8	4
22221	The chromosome-scale reference genome of safflower ( <i>Carthamus tinctorius</i> ) provides insights into linoleic acid and flavonoid biosynthesis. <i>Plant Biotechnology Journal</i> , 2021, 19, 1725-1742.	4.1	60
22222	High-throughput sequencing clarifies the spatial structures of microbial communities in cadmium-polluted rice soils. <i>Environmental Science and Pollution Research</i> , 2021, 28, 47086-47098.	2.7	13
22223	SPDE: a multi-functional software for sequence processing and data extraction. <i>Bioinformatics</i> , 2021, 37, 3686-3687.	1.8	22

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22224	The Evolution of Calcification in Reef-Building Corals. <i>Molecular Biology and Evolution</i> , 2021, 38, 3543-3555.	3.5	19
22225	Novel Dicistroviruses in an Unexpected Wide Range of Invertebrates. <i>Food and Environmental Virology</i> , 2021, 13, 423-431.	1.5	7
22226	Complete genome sequences of three newly discovered cacao mild mosaic virus isolates from <i>Theobroma cacao</i> L. in Brazil and Puerto Rico and evidence for recombination. <i>Archives of Virology</i> , 2021, 166, 2027-2031.	0.9	7
22227	Plant flavones enrich rhizosphere Oxalobacteraceae to improve maize performance under nitrogen deprivation. <i>Nature Plants</i> , 2021, 7, 481-499.	4.7	247
22228	Modular basis for potent SARS-CoV-2 neutralization by a prevalent VH1-2-derived antibody class. <i>Cell Reports</i> , 2021, 35, 108950.	2.9	54
22229	Phylogenetic relationship of phototrophic heliobacteria and systematic reconsideration of species and genus assignments based on genome sequences of eight species. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	29
22230	Protein expression plasticity contributes to heat and drought tolerance of date palm. <i>Oecologia</i> , 2021, 197, 903-919.	0.9	17
22231	High CO <sub>2</sub> levels drive the TCA cycle backwards towards autotrophy. <i>Nature</i> , 2021, 592, 784-788.	13.7	75
22232	<i>Marinisubtilis pacificus</i> gen. nov., sp. nov., a Member of the Family Microbacteriaceae Isolated From a Deep-Sea Seamount. <i>Current Microbiology</i> , 2021, 78, 2136-2142.	1.0	10
22233	A Superfamily-wide Activity Atlas of Serine Hydrolases in <i>Drosophila melanogaster</i> . <i>Biochemistry</i> , 2021, 60, 1312-1324.	1.2	18
22234	<i>Pikeienuella piscinae</i> gen. nov., sp. nov., a novel genus in the family Rhodobacteraceae. <i>Journal of Microbiology</i> , 2021, 59, 546-551.	1.3	8
22235	An integrative approach to address species limits in the southernmost members of the <i>Liolaemus kingii</i> group (Squamata: Liolaemini). <i>Molecular Phylogenetics and Evolution</i> , 2021, 157, 107046.	1.2	5
22236	Phylogeny, divergence times, and diversification in Calophyllaceae: Linking key characters and habitat changes to the evolution of Neotropical Calophylleae. <i>Molecular Phylogenetics and Evolution</i> , 2021, 157, 107041.	1.2	7
22237	Two new species of Neofoleyellides (Nematoda: Onchocercidae) parasitising anuran amphibians in South Africa. <i>International Journal for Parasitology: Parasites and Wildlife</i> , 2021, 14, 298-307.	0.6	4
22238	Presence of complete murine viral genome sequences in patient-derived xenografts. <i>Nature Communications</i> , 2021, 12, 2031.	5.8	9
22241	An integrative approach reveals a new species of flightless leaf beetle (Chrysomelidae: Suinzona) from South Korea. <i>Scientific Reports</i> , 2021, 11, 8595.	1.6	3
22242	Influence of Non-canonical DNA Bases on the Genomic Diversity of Tevenvirinae. <i>Frontiers in Microbiology</i> , 2021, 12, 632686.	1.5	3
22243	Analysis of DnaK Expression from a Strain of <i>Mycoplasma fermentans</i> in Infected HCT116 Human Colon Carcinoma Cells. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3885.	1.8	6

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22244	Initiation of compatible wheat-Hessian fly interactions triggers the expression of a novel UDP-glycosyltransferase, MdesUGT1, in virulent Hessian fly larvae. <i>Arthropod-Plant Interactions</i> , 2021, 15, 363-374.	0.5	1
22245	Genome-Wide Analysis of Terpene Synthase Gene Family in <i>Mentha longifolia</i> and Catalytic Activity Analysis of a Single Terpene Synthase. <i>Genes</i> , 2021, 12, 518.	1.0	22
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22309	Cometabolic Vinyl Chloride Degradation at Acidic pH Catalyzed by Acidophilic Methanotrophs Isolated from Alpine Peat Bogs. <i>Environmental Science &amp; Technology</i> , 2021, 55, 5959-5969.	4.6	14
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22322	Suppression of root-knot nematode <i>Meloidogyne incognita</i> on tomato plants using the nematode trapping fungus <i>Arthrobotrys oligospora</i> Fresenius. <i>Journal of Applied Microbiology</i> , 2021, 131, 2402-2415.	1.4	29
22323	A tail of two pandas" whole genome k-mer signature analysis of the red panda ( <i>Ailurus fulgens</i> ) and the Giant panda ( <i>Ailuropoda melanoleuca</i> ). <i>BMC Genomics</i> , 2021, 22, 228.	1.2	0
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22330	Morphological and Molecular Characterization of the Plague Vector <i>Xenopsylla brasiliensis</i> . <i>Journal of Parasitology</i> , 2021, 107, 289-294.	0.3	1
22331	Phylogeographic structure and historical demography of tarakihi ( <i>Nemadactylus macropterus</i> ) and king tarakihi ( <i>Nemadactylus</i> n.sp.) in New Zealand. <i>New Zealand Journal of Marine and Freshwater Research</i> , 2022, 56, 247-271.	0.8	8
22333	Diversity of Batrachospermales (Rhodophyta) in the Iberian Peninsula. <i>Fottea</i> , 2021, 21, 73-81.	0.4	1
22336	Genomic-, phenotypic-, and toxicity-based safety assessment and probiotic potency of <i>Bacillus coagulans</i> IDCC 1201 isolated from green malt. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2021, 48, .	1.4	14
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22343	Revision of the genus <i>Mustelus</i> (Carcharhiniformes: Triakidae) in the northern Indian Ocean, with description of a new species and a discussion on the validity of <i>M. walkeri</i> and <i>M. ravidus</i> . <i>Marine Biodiversity</i> , 2021, 51, 1.	0.3	5
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22347	Genome-wide analyses of tandem repeats and transposable elements in patchouli. <i>Genes and Genetic Systems</i> , 2021, 96, 81-87.	0.2	1
22349	Mechanism and dynamics of fatty acid photodecarboxylase. <i>Science</i> , 2021, 372, .	6.0	93
22350	Hapo-G, haplotype-aware polishing of genome assemblies with accurate reads. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab034.	1.5	52
22351	The genome of <i>Geosiphon pyriformis</i> reveals ancestral traits linked to the emergence of the arbuscular mycorrhizal symbiosis. <i>Current Biology</i> , 2021, 31, 1570-1577.e4.	1.8	30

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22353	Evolution and insights into the structure and function of the DedA superfamily containing TMEM41B and VMP1. <i>Journal of Cell Science</i> , 2021, 134, .	1.2	28
22354	Phenotypic, molecular and pathogenic characterization of <i>Colletotrichum scovillei</i> infecting <i>Capsicum</i> species in Rio de Janeiro, Brazil. <i>PeerJ</i> , 2021, 9, e10782.	0.9	8
22355	Diversity of the genus <i>Brasilonema</i> (Nostocales, Cyanobacteria) in plant nurseries of central Florida (USA) with the description of three new species: <i>B. fioreae</i> sp. nov., <i>B. santannae</i> sp. nov. and <i>B. wernerae</i> sp. nov.. <i>Fottea</i> , 2021, 21, 82-99.	0.4	4
22356	Multiple Viral Infections Detected in <i>Phytophthora condilina</i> by Total and Small RNA Sequencing. <i>Viruses</i> , 2021, 13, 620.	1.5	23
22357	Effects of plant growth-promoting rhizobacteria strains producing ACC deaminase on photosynthesis, isoprene emission, ethylene formation and growth of <i>Mucuna pruriens</i> (L.) DC. in response to water deficit. <i>Journal of Biotechnology</i> , 2021, 331, 53-62.	1.9	26
22358	Gut microbiota profiles and characterization of cultivable fungal isolates in IBS patients. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 3277-3288.	1.7	31
22359	Methods for Identifying Microbial Natural Product Compounds that Target Kinetoplastid RNA Structural Motifs by Homology and De Novo Modeled 18S rRNA. <i>International Journal of Molecular Sciences</i> , 2021, 22, 4493.	1.8	1
22360	A review of the taxonomy of spiny-backed orb-weaving spiders of the subfamily Gasteracanthinae (Araneae, Araneidae) in Thailand. <i>ZooKeys</i> , 2021, 1032, 17-62.	0.5	2
22361	Methylotrophs and Hydrocarbon-Degrading Bacteria Are Key Players in the Microbial Community of an Abandoned Century-Old Oil Exploration Well. <i>Microbial Ecology</i> , 2022, 83, 83-99.	1.4	10
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22363	Sex-Biased Gene Expression and Evolution in the Cerebrum and Syrinx of Chinese Hwamei ( <i>Garrulax</i> ) Tj ETQq1 1 0.784314 rgBT /Overbo	1.0	1
22364	Identification and distribution of novel badnaviral sequences integrated in the genome of cacao ( <i>Theobroma cacao</i> ). <i>Scientific Reports</i> , 2021, 11, 8270.	1.6	12
22365	Three-Finger Toxins from Brazilian Coral Snakes: From Molecular Framework to Insights in Biological Function. <i>Toxins</i> , 2021, 13, 328.	1.5	3
22366	<i>Diphyllobothrium sprakeri</i> n. sp. (Cestoda: Diphyllobothriidae): a hidden broad tapeworm from sea lions off North and South America. <i>Parasites and Vectors</i> , 2021, 14, 219.	1.0	3
22367	Genetic Defects in DNAH2 Underlie Male Infertility With Multiple Morphological Abnormalities of the Sperm Flagella in Humans and Mice. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 662903.	1.8	22
22370	Draft genome of a biparental beetle species, <i>Lethrus apterus</i> . <i>BMC Genomics</i> , 2021, 22, 301.	1.2	0
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22376	The Chinese mitten crab genome provides insights into adaptive plasticity and developmental regulation. <i>Nature Communications</i> , 2021, 12, 2395.	5.8	38
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22378	Substitution Mapping of a Locus Responsible for Hybrid Breakdown in Populations Derived From Interspecific Introgression Line. <i>Frontiers in Plant Science</i> , 2021, 12, 633247.	1.7	2
22380	Molecular and morphological characterisation of the metacercariae of two species of <i>Cardiocephaloides</i> (Digenea: Strigeidae) infecting endemic South African klipfish (Perciformes: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 57		
22382	Molecular and morphological evidence of a new species of <i>Crassicutis</i> Manter 1936 (Digenea), a parasite of cichlids in South America. <i>Parasitology Research</i> , 2021, 120, 2429-2443.	0.6	3
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22386	Genome-wide identification, evolution, and transcriptome-based expression profiling analysis of suppressors of cytokine signaling (SOCS) in grass carp ( <i>Ctenopharyngodon idella</i> ). <i>Aquaculture</i> , 2021, 536, 736484.	1.7	3
22387	Molecular characterisation of <i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i> in Australia. <i>BMC Microbiology</i> , 2021, 21, 101.	1.3	6
22388	Are Feeding Modes Concealing Morphofunctional Diversity? The Case of the New World Parrotfishes. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	4
22389	Diversity of Kallymeniaceae (Gigartinales, Rhodophyta) associated with Hawaiian mesophotic reefs. <i>European Journal of Phycology</i> , 2022, 57, 68-78.	0.9	6
22391	Description of a metacercaria of a zoogonid trematode <i>Steganoderma</i> cf. <i>eamiqtrema</i> Blend and Racz, 2020 (Microphalloidea: Zoogonidae), with notes on the phylogenetic position of the genus <i>Steganoderma</i> Stafford, 1904, and resurrection of the subfamily <i>Lecithostaphylinae</i> Odhner, 1911. <i>Parasitology Research</i> , 2021, 120, 1669-1676.	0.6	4
22392	Genome-Wide Screening of AP2 Transcription Factors Involving in Fruit Color and Aroma Regulation of Cultivated Strawberry. <i>Genes</i> , 2021, 12, 530.	1.0	12
22393	A functional bacteria-derived restriction modification system in the mitochondrion of a heterotrophic protist. <i>PLoS Biology</i> , 2021, 19, e3001126.	2.6	6
22394	<i>In Vitro</i> Gut Modeling as a Tool for Adaptive Evolutionary Engineering of <i>Lactiplantibacillus plantarum</i> . <i>MSystems</i> , 2021, 6, .	1.7	9
22395	Molecular phylogeny and new light microscopic data of <i>Metchnikovella spiralis</i> (Microsporidia: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 100) <i>elegans</i> . <i>Parasitology</i> , 2021, 148, 779-786.	0.7	2
22397	<i>Sifarchaeota</i> , a Novel Asgard Phylum from Costa Rican Sediment Capable of Polysaccharide Degradation and Anaerobic Methylophony. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	24

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22399	Phylogenetic relationships and characterization of the complete chloroplast genome of <i>Rosa sterilis</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1544-1546.	0.2	3
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22401	Hidden by the name: A new fluorescent pumpkin toadlet from the <i>Brachycephalus ephippium</i> group (Anura: Brachycephalidae). <i>PLoS ONE</i> , 2021, 16, e0244812.	1.1	13
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22403	Isolation and Molecular Characterization of the Romaine Lettuce Phylloplane Mycobiome. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 277.	1.5	11
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22406	A multilocus phylogeny of the moss genus <i>Didymodon</i> and allied genera (Pottiaceae): Generic delimitations and their implications for systematics. <i>Journal of Systematics and Evolution</i> , 2022, 60, 281-304.	1.6	16
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22410	Phylogeny and taxonomy of the <i>Erysiphe adunca</i> complex (Erysiphaceae, Helotiales) on poplars and willows. <i>Mycological Progress</i> , 2021, 20, 517-537.	0.5	6
22411	Hypoxia exerts oxidative stress and changes in expression of antioxidant enzyme genes in gills of <i>Mytilus galloprovincialis</i> (Lamarck, 1819). <i>Marine Biology Research</i> , 2021, 17, 369-379.	0.3	6
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22416	The dystrophia myotonica WD repeat-containing protein DMWD and WDR20 differentially regulate USP12 deubiquitinase. <i>FEBS Journal</i> , 2021, 288, 5943-5963.	2.2	1

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22418	Bot Gummosis of Lemon ( <i>Citrus</i> – limon) Caused by <i>Neofusicoccum parvum</i> . <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 293.	1.5	2
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22427	Phylogenetic characterization and multidrug resistance of bacteria isolated from seafood cocktails. <i>Archives of Microbiology</i> , 2021, 203, 3317-3330.	1.0	2
22428	The Meishan pig genome reveals structural variation-mediated gene expression and phenotypic divergence underlying Asian pig domestication. <i>Molecular Ecology Resources</i> , 2021, 21, 2077-2092.	2.2	20
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22432	Pseudogenized Amelogenin Reveals Early Tooth Loss in True Toads ( <i>Anura: Bufonidae</i> ). <i>Integrative and Comparative Biology</i> , 2021, , .	0.9	2
22433	First molecular characterization of hypodermin genes of <i>Hypoderma bovis</i> and serodiagnosis of bovine hypodermosis with recombinant hypodermin C antigen and a synthetic peptide containing its linear B-cell epitope. <i>Veterinary Parasitology</i> , 2021, 292, 109394.	0.7	4
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22437	Universal Architectural Concepts Underlying Protein Folding Patterns. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 612920.	1.6	9
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22440	Roles of surface layer proteins in the regulation of <i>Pediococcus pentosaceus</i> on growth performance, intestinal microbiota, and resistance to <i>Aeromonas hydrophila</i> in the freshwater prawn <i>Macrobrachium rosenbergii</i> . <i>Aquaculture International</i> , 2021, 29, 1373-1391.	1.1	5
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22447	Population and comparative genetics of thermotolerance divergence between yeast species. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	6
22449	The molecular basis for sarcomere organization in vertebrate skeletal muscle. <i>Cell</i> , 2021, 184, 2135-2150.e13.	13.5	99
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22451	<i>Gorgorhynchoides pseudocarangis</i> n. sp. (Acanthocephala: Isthmosacanthidae) from <i>Pseudocaranx dentex</i> (Carangidae) in southeast Queensland, Australia, with comments on the Isthmosacanthidae. <i>Systematic Parasitology</i> , 2021, 98, 399-412.	0.5	2
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22458	Functional Analysis of Phenazine Biosynthesis Genes in <i>Burkholderia</i> spp.. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	10
22461	A chimeric HLA-A2:Î²2M:Î³ fusion protein for the study of virus-specific CD8+ T-cells. <i>Journal of Immunological Methods</i> , 2021, 492, 112997.	0.6	2
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22468	Exploration of glutathione reductase for abiotic stress response in bread wheat ( <i>Triticum aestivum</i> ) Tj ETQq1 1 0.784314 rgBT /Overl	2.8	44
22470	A high-quality carabid genome assembly provides insights into beetle genome evolution and cold adaptation. Molecular Ecology Resources, 2021, 21, 2145-2165.	2.2	13
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22473	Bacteriophage-Host Association in the Phytoplasma Insect Vector <i>Euscelidius variegatus</i> . Pathogens, 2021, 10, 612.	1.2	9
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22476	Invasive American mink ( <i>Neovison vison</i> ) as potential definitive host of <i>Sarcocystis elongata</i> , <i>S. entzerothi</i> , <i>S. japonica</i> , <i>S. truncata</i> and <i>S. silva</i> using different cervid species as intermediate hosts. Parasitology Research, 2021, 120, 2243-2250.	0.6	8
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22479	Genome-wide analysis of microRNA156 and its targets, the genes encoding SQUAMOSA promoter-binding protein-like (SPL) transcription factors, in the grass family Poaceae. Journal of Zhejiang University: Science B, 2021, 22, 366-382.	1.3	3
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22484	The identification of a transposon affecting the asexual reproduction of the wheat pathogen <i>Zymoseptoria tritici</i> . Molecular Plant Pathology, 2021, 22, 800-816.	2.0	17
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22488	Natural diversity provides a broad spectrum of cyanobacteriochrome-based diguanylate cyclases. <i>Plant Physiology</i> , 2021, 187, 632-645.	2.3	11
22489	<i>Alkalicella caledoniensis</i> gen. nov., sp. nov., a novel alkaliphilic anaerobic bacterium isolated from <sup>14</sup> C-Crouen <sup>TM</sup> alkaline thermal spring, New Caledonia. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	10
22490	Use of unbiased metagenomic and transcriptomic analyses to investigate the association between feline calicivirus and feline chronic gingivostomatitis in domestic cats. <i>American Journal of Veterinary Research</i> , 2021, 82, 381-394.	0.3	18
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22494	Perception and First Defense Responses Against <i>Pseudomonas syringae</i> pv. <i>phaseolicola</i> in <i>Phaseolus vulgaris</i> : Identification of Wall-Associated Kinase Receptors. <i>Phytopathology</i> , 2021, 111, 2332-2342.	1.1	4
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22499	A new species of <i>Sakuraeolis</i> from Mozambique, described using 3D reconstruction of anatomy and phylogenetic analysis. <i>Journal of Molluscan Studies</i> , 2021, 87, .	0.4	4
22501	A new genus and new species of macronyssid mite (Mesostigmata: Gamasina: Macronyssidae) from Brazilian caves including molecular data and key for genera occurring in Brazil. <i>Acarologia</i> , 2021, 61, 501-526.	0.2	4
22502	A Machine Learning Approach to Prioritizing Functionally Active F-box Members in <i>Arabidopsis thaliana</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 639253.	1.7	3
22503	Ecotoxicological effects of erythromycin on a multispecies biofilm model, revealed by metagenomic and metabolomic approaches. <i>Environmental Pollution</i> , 2021, 276, 116737.	3.7	16
22505	Genomic Resources for the North American Water Vole ( <i>Microtus richardsoni</i> ) and the Montane Vole ( <i>Microtus montanus</i> ). <i>GigaByte</i> , 0, 2021, 1-13.	0.0	1

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22509	Two new records of powdery mildews ( <i>Erysiphaceae</i> ) from Japan: <i>Erysiphe actinidiicola</i> sp. nov. and <i>Erysiphe</i> sp. on <i>Limonium tetragonum</i> . <i>Mycoscience</i> , 2021, 62, 198-204.	0.3	2
22510	Structures of a non-ribosomal peptide synthetase condensation domain suggest the basis of substrate selectivity. <i>Nature Communications</i> , 2021, 12, 2511.	5.8	53
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22512	Historical Biogeography and the Evolution of Hematophagy in Rhodniini (Heteroptera: Reduviidae: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.1	10
22513	Structure of the murine lysosomal multienzyme complex core. <i>Science Advances</i> , 2021, 7, .	4.7	7
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22518	<i>Massilia horti</i> sp. nov. and <i>Noviherbaspirillum arenae</i> sp. nov., two novel soil bacteria of the Oxalobacteraceae. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	12
22519	Describing the hidden species diversity of Chaetozoa (Annelida, Cirratulidae) in the Norwegian Sea using morphological and molecular diagnostics. <i>ZooKeys</i> , 2021, 1039, 139-176.	0.5	5
22520	A Pilot Study Investigating the Dynamics of Pigeon Circovirus Recombination in Domesticated Pigeons Housed in a Single Loft. <i>Viruses</i> , 2021, 13, 964.	1.5	7
22521	Super determinant1A, a RAWULdomain-containing protein, modulates axillary meristem formation and compound leaf development in tomato. <i>Plant Cell</i> , 2021, 33, 2412-2430.	3.1	8
22522	Oral Microbiome in Relation to Periodontitis Severity and Systemic Inflammation. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5876.	1.8	38
22523	Incidence, geographical distribution and genetic diversity of sugarcane striate virus in <i>Saccharum</i> species in China. <i>Plant Disease</i> , 2021, , PDIS10202307RE.	0.7	1
22524	Introgressing the <i>Aegilops tauschii</i> genome into wheat as a basis for cereal improvement. <i>Nature Plants</i> , 2021, 7, 774-786.	4.7	65
22525	Building a reference transcriptome for the hexaploid hard fescue turfgrass ( <i>Festuca brevipila</i> ) using a combination of PacBio Isoseq and Illumina sequencing. <i>Crop Science</i> , 2021, 61, 2798-2811.	0.8	3

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22526	<i>Listeria cossartiae</i> sp. nov., <i>Listeria immobilis</i> sp. nov., <i>Listeria portnoyi</i> sp. nov. and <i>Listeria rustica</i> sp. nov., isolated from agricultural water and natural environments. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	54
22527	Identification and characterization of andalusicin: N-terminally dimethylated class III lantibiotic from <i>Bacillus thuringiensis</i> sv. <i>andalousiensis</i> . <i>IScience</i> , 2021, 24, 102480.	1.9	18
22528	Functional trait relationships demonstrate life strategies in terrestrial prokaryotes. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	12
22529	Assembly of abundant and rare bacterial and fungal sub-communities in different soil aggregate sizes in an apple orchard treated with cover crop and fertilizer. <i>Soil Biology and Biochemistry</i> , 2021, 156, 108222.	4.2	76
22530	Elucidation of the Complicated Scenario of Primate APOBEC3 Gene Evolution. <i>Journal of Virology</i> , 2021, 95, .	1.5	11
22532	<i>Lagierella massiliensis</i> gen. nov., sp. nov., Isolated from a Stool Sample. <i>Current Microbiology</i> , 2021, 78, 2481-2487.	1.0	2
22533	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
22534	Characterization of single nucleotide polymorphism in IGF1 and IGF1R genes associated with growth traits in striped catfish ( <i>Pangasianodon hypophthalmus</i> Sauvage, 1878). <i>Aquaculture</i> , 2021, 538, 736542.	1.7	10
22535	Multiple lineages of <i>Streptomyces</i> produce antimicrobials within passalid beetle galleries across eastern North America. <i>ELife</i> , 2021, 10, .	2.8	11
22536	Endozoicomonadaceae symbiont in gills of <i>Acesta</i> clam encodes genes for essential nutrients and polysaccharide degradation. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	7
22537	Across the great divide: revision of the genus <i>Eupetaurus</i> (Sciuridae: Pteromyini), the woolly flying squirrels of the Himalayan region, with the description of two new species. <i>Zoological Journal of the Linnean Society</i> , 2022, 194, 502-526.	1.0	8
22538	Enhancing mitogenomic phylogeny and resolving the relationships of extinct megafaunal placental mammals. <i>Molecular Phylogenetics and Evolution</i> , 2021, 158, 107082.	1.2	7
22539	High Throughput Sequencing-Aided Survey Reveals Widespread Mixed Infections of Whitefly-Transmitted Viruses in Cucurbits in Georgia, USA. <i>Viruses</i> , 2021, 13, 988.	1.5	19
22542	Genetic Insights into Feline Parvovirus: Evaluation of Viral Evolutionary Patterns and Association between Phylogeny and Clinical Variables. <i>Viruses</i> , 2021, 13, 1033.	1.5	9
22543	CRISPR-mediated mutations in the ABC transporter gene ABCA2 confer pink bollworm resistance to Bt toxin Cry2Ab. <i>Scientific Reports</i> , 2021, 11, 10377.	1.6	23
22544	Gene expression and alternative splicing dynamics are perturbed in female head transcriptomes following heterospecific copulation. <i>BMC Genomics</i> , 2021, 22, 359.	1.2	6
22546	Four Species Linked by Three Hybrid Zones: Two Instances of Repeated Hybridization in One Species Group (Genus <i>Liolaemus</i> ). <i>Frontiers in Ecology and Evolution</i> , 2021, 9, .	1.1	6
22547	Decreased GLUT2 and glucose uptake contribute to insulin secretion defects in MODY3/HNF1A hiPSC-derived mutant $\beta^2$ cells. <i>Nature Communications</i> , 2021, 12, 3133.	5.8	36



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22550	Bacterial Evolutionary Precursors of Eukaryotic Copperâ€“Zinc Superoxide Dismutases. <i>Molecular Biology and Evolution</i> , 2021, 38, 3789-3803.	3.5	5
22551	Osmolyte Signatures for the Protection of <i>Aspergillus sydowii</i> Cells under Halophilic Conditions and Osmotic Shock. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 414.	1.5	9
22553	Epitope-targeting platform for broadly protective influenza vaccines. <i>PLoS ONE</i> , 2021, 16, e0252170.	1.1	7
22554	A tri-tuple coordinate system derived for fast and accurate analysis of the colored de Bruijn graph-based pangenomes. <i>BMC Bioinformatics</i> , 2021, 22, 282.	1.2	1
22555	Genomic features of humoral immunity support tolerance model in Egyptian rousette bats. <i>Cell Reports</i> , 2021, 35, 109140.	2.9	19
22557	Historical biogeography of Pomaderris (Rhamnaceae): Continental vicariance in Australia and repeated independent dispersals to New Zealand. <i>Molecular Phylogenetics and Evolution</i> , 2021, 158, 107085.	1.2	15
22558	Genome Sequencing Identified a SARS-CoV-2 Lineage B.1.1.7 Strain with a High Number of Mutations from Dhaka, Bangladesh. <i>Microbiology Resource Announcements</i> , 2021, 10, e0034521.	0.3	3
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22561	Complete Genome Sequence of Mirabilis Crinkle Mosaic Virus Isolated from Pokeweed in Japan. <i>Microbiology Resource Announcements</i> , 2021, 10, e0028321.	0.3	2
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22563	New distributional record of <i>Charybdis japonica</i> , <i>Coenobita violascens</i> , <i>Galene bispinosa</i> , and <i>Portunus reticulatus</i> (Crustacea: Decapoda) from Bangladesh waters of the Bay of Bengal. <i>Regional Studies in Marine Science</i> , 2021, 44, 101785.	0.4	4
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22566	Interâ€“domain horizontal gene transfer of nickelâ€“binding superoxide dismutase. <i>Geobiology</i> , 2021, 19, 450-459.	1.1	11
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22585	An Unsupervised Algorithm for Host Identification in Flaviviruses. <i>Life</i> , 2021, 11, 442.	1.1	2
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22608	On the evolution of chaperones and cochaperones and the expansion of proteomes across the Tree of Life. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	65
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22628	Antioxidant and antimicrobial activity displayed by a fungal endophyte <i>Alternaria alternata</i> isolated from <i>Picrorhiza kurroa</i> from Garhwal Himalayas, India. <i>Biocatalysis and Agricultural Biotechnology</i> , 2021, 33, 101955.	1.5	23
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22630	Genetic characterisation of <i>Campylobacter concisus</i> : Strategies for improved genomospecies discrimination. <i>Systematic and Applied Microbiology</i> , 2021, 44, 126187.	1.2	4
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22634	Antifungal Activity of Endophytic Bacteria Associated with Sweet Sorghum ( <i>Sorghum bicolor</i> ). <i>Journal of Mathematical and Fundamental Sciences</i> , 2021, 53, 16-30.	0.3	1
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22637	<i>Streptococcus vicugnae</i> sp. nov., isolated from faeces of alpacas ( <i>Vicugna pacos</i> ) and cattle ( <i>Bos Tj</i> ETQq1 1 0.784314 rgBT /Overlooked) respiratory tract of California sea lions ( <i>Zalophus californianus</i> ). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	16
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22645	Changes of gut microbiome composition and metabolites associated with hypertensive heart failure rats. <i>BMC Microbiology</i> , 2021, 21, 141.	1.3	27
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22648	Potential syntrophic relationship between coral-associated <i>Prosthecochloris</i> and its companion sulfate-reducing bacterium unveiled by genomic analysis. <i>Microbial Genomics</i> , 2021, 7, .	1.0	5
22649	How co-distribution of two related azaleas ( <i>Rhododendron</i> ) developed in the Japanese archipelago: insights from evolutionary and demographic analyses. <i>Tree Genetics and Genomes</i> , 2021, 17, 1.	0.6	0
22650	Disentangling taxonomy of <i>Biacetabulum</i> (Cestoda, Caryophyllidea), parasites of catostomid fishes in North America: proposal of <i>Megancestus</i> gen. n. to accommodate <i>B. carpodi</i> . <i>Parasitology Research</i> , 2021, 120, 1993-2001.	0.6	2
22651	Diversity and function of rhizosphere microorganisms between wild and cultivated medicinal plant <i>Glycyrrhiza uralensis</i> Fisch under different soil conditions. <i>Archives of Microbiology</i> , 2021, 203, 3657-3665.	1.0	12
22652	Detection of Flaviviral-Like DNA Sequences in <i>Aedes aegypti</i> (Diptera: Culicidae) Collected From Argentina. <i>Journal of Medical Entomology</i> , 2021, 58, 2406-2411.	0.9	2

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22658	Performance and microbial community structure of a full-scale ANITATMMox bioreactor for treating reject water located in Finland. <i>Chemosphere</i> , 2021, 271, 129526.	4.2	9
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22660	Diversification of the calponin family proteins by gene amplification and repeat expansion of calponin-like motifs. <i>Cytoskeleton</i> , 2021, 78, 199-205.	1.0	2
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22670	Multiple Mammarenaviruses Circulating in Angolan Rodents. <i>Viruses</i> , 2021, 13, 982.	1.5	10
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22673	&lt;i>Neoboletus infuscatus</i>, a new tropical bolete from Hainan, southern China. <i>Mycoscience</i> , 2021, 62, 205-211.	0.3	3
22674	A parsimonious approach for recognizing SARS-CoV-2 and host interactions. <i>Journal of Medical Virology</i> , 2021, 93, 4576-4584.	2.5	2
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22693	Extra-Heavy Crude Oil Degradation by <i>Alternaria</i> sp. Isolated from Deep-Sea Sediments of the Gulf of Mexico. Applied Sciences (Switzerland), 2021, 11, 6090.	1.3	10
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22697	Evidence of cryptic diversity in freshwater <i>Macrobrachium</i> prawns from Indochinese riverine systems revealed by DNA barcode, species delimitation and phylogenetic approaches. <i>PLoS ONE</i> , 2021, 16, e0252546.	1.1	7
22698	<i>Methylobrevia albus</i> sp. nov., isolated from freshwater lake sediment. <i>Archives of Microbiology</i> , 2021, 203, 4549-4556.	1.0	7
22699	The Chromosome-Level Genome of <i>Triplophysa dalaica</i> (Cypriniformes: Cobitidae) Provides Insights into Its Survival in Extremely Alkaline Environment. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	7
22700	An approach for estimating haplotype diversity from sequences with unequal lengths. <i>Methods in Ecology and Evolution</i> , 2021, 12, 1658-1667.	2.2	3
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22702	A qPCR assay for sensitive and rapid detection of African A-lineage honey bees ( <i>Apis mellifera</i> ). <i>Apidologie</i> , 2021, 52, 767-781.	0.9	2
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22708	Bacteria Isolated From the Antarctic Sponge <i>Iophon</i> sp. Reveals Mechanisms of Symbiosis in <i>Sporosarcina</i> , <i>Cellulophaga</i> , and <i>Nesterenkonia</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 660779.	1.5	5
22710	Low nitrogen availability inhibits the phosphorus starvation response in maize ( <i>Zea mays</i> ssp. <i>mays</i> L.). <i>BMC Plant Biology</i> , 2021, 21, 259.	1.6	16
22711	Species Delimitation of Scavenger Flies in the Valley of Mexico. <i>Journal of Medical Entomology</i> , 2021, 58, 2206-2215.	0.9	2
22712	Taxonomy and phylogeny of the basidiomycetous hyphomycete genus <i>Hormomyces</i> . <i>Fungal Systematics and Evolution</i> , 2021, 7, 177-196.	0.9	5
22713	The B Chromosomes of <i>Prochilodus lineatus</i> (Teleostei, Characiformes) Are Highly Enriched in Satellite DNAs. <i>Cells</i> , 2021, 10, 1527.	1.8	11
22714	The Functional Consequences of the Novel Ribosomal Pausing Site in SARS-CoV-2 Spike Glycoprotein RNA. <i>International Journal of Molecular Sciences</i> , 2021, 22, 6490.	1.8	12
22715	The first complete Zoroastrian-Parsi mitochondrial reference genome and genetic signatures of an endogamous non-smoking population. <i>Meta Gene</i> , 2021, 28, 100882.	0.3	1



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22718	Seasonal host and ecological drivers may promote restricted water as a viral vector. <i>Science of the Total Environment</i> , 2021, 773, 145446.	3.9	4
22719	Detection of "ancestral"™ western lineage of Citrus tristeza virus virulent genotype in declining Arunachal Wakro orange. <i>Tropical Plant Pathology</i> , 2021, 46, 493-505.	0.8	1
22720	18S rRNA variability maps reveal three highly divergent, conserved motifs within Rotifera. <i>Bmc Ecology and Evolution</i> , 2021, 21, 118.	0.7	6
22721	Ecophysiology of the Cosmopolitan OM252 Bacterioplankton ( <i>Gammaproteobacteria</i> ). <i>MSystems</i> , 2021, 6, e0027621.	1.7	5
22722	Cunninghamella saisamornae (Cunninghamellaceae, Mucorales), a new soil fungus from northern Thailand. <i>Phytotaxa</i> , 2021, 509, .	0.1	1
22723	Annotation of chitin biosynthesis genes in Diaphorina citri, the Asian citrus psyllid. <i>GigaByte</i> , 0, 2021, 1-12.	0.0	8
22724	Functional Characterization of the Cnidarian Antiviral Immune Response Reveals Ancestral Complexity. <i>Molecular Biology and Evolution</i> , 2021, 38, 4546-4561.	3.5	18
22725	Effect of co-application of Trichoderma spp. with organic composts on plant growth enhancement, soil enzymes and fungal community in soil. <i>Archives of Microbiology</i> , 2021, 203, 4281-4291.	1.0	21
22726	Endosymbiont Capture, a Repeated Process of Endosymbiont Transfer with Replacement in Trypanosomatids Angomonas spp.. <i>Pathogens</i> , 2021, 10, 702.	1.2	2
22727	Systematic analysis of the genus <i>Eriocaulon</i> L. in India based on molecular and morphological evidence. <i>Systematics and Biodiversity</i> , 2021, 19, 693-723.	0.5	5
22728	Description and phylogenetic position of three new species of Stauroneis Ehrenberg (Bacillariophyceae: Stauroneidaceae) from the Indian Subcontinent. <i>European Journal of Phycology</i> , 0, 1-20.	0.9	2
22729	Structural basis of omega-3 fatty acid transport across the blood-brain barrier. <i>Nature</i> , 2021, 595, 315-319.	18.7	61
22730	Gapless indica rice genome reveals synergistic contributions of active transposable elements and segmental duplications to rice genome evolution. <i>Molecular Plant</i> , 2021, 14, 1745-1756.	3.9	50
22731	Inferring trophic conditions in managed aquifer recharge systems from metagenomic data. <i>Science of the Total Environment</i> , 2021, 772, 145512.	3.9	2
22732	Roseobacters in a Sea of Poly- and Paraphyly: Whole Genome-Based Taxonomy of the Family Rhodobacteraceae and the Proposal for the Split of the "Roseobacter Clade" Into a Novel Family, Roseobacteraceae fam. nov.. <i>Frontiers in Microbiology</i> , 2021, 12, 683109.	1.5	263
22733	Genetic diversity and expanded host range of astroviruses detected in small mammals in Singapore. <i>One Health</i> , 2021, 12, 100218.	1.5	3
22734	Subtle environmental variation affects phenotypic differentiation of shallow divergent treefrog lineages in Amazonia. <i>Biological Journal of the Linnean Society</i> , 2021, 134, 177-197.	0.7	3

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22736	Integrating Genetics, Morphology, and Fungal Host Specificity in Conservation Studies of a Vulnerable, Selfing, Mycoheterotrophic Orchid ( <i>Corallorhiza bentleyi</i> Freudenst.). <i>Castanea</i> , 2021, 86, .	0.2	2
22737	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
22738	Transposon-mediated insertional mutagenesis unmasks recessive insecticide resistance in the aphid <i>Myzus persicae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	18
22739	Insight into the adaptive evolution of mitochondrial genomes in intertidal chitons. <i>Journal of Molluscan Studies</i> , 2021, 87, .	0.4	4
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22741	Interspecific Molecular Variation of <i>Lolium L.</i> Based on ISSR, SCoT and ITS. <i>Iranian Journal of Science and Technology, Transaction A: Science</i> , 2021, 45, 1263-1272.	0.7	5
22742	Two novel <i>Phytophthora</i> species from the southern tip of Africa. <i>Mycological Progress</i> , 2021, 20, 755-767.	0.5	11
22743	Coxsackievirus B4: an underestimated pathogen associated with a hand, foot, and mouth disease outbreak. <i>Archives of Virology</i> , 2021, 166, 2225-2234.	0.9	7
22744	A Single Nucleotide Polymorphism in <i>IptG</i> Increases Tolerance to Bile Salts, Acid, and Staining of Calcofluor-Binding Polysaccharides in <i>Salmonella enterica</i> Serovar Typhimurium E40. <i>Frontiers in Microbiology</i> , 2021, 12, 671453.	1.5	1
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22747	Streptozotocin activates inflammation-associated signalling and antioxidant response in the lobster cockroach; <i>Nauphoeta cinerea</i> (Blattodea: Blaberidae). <i>Chemico-Biological Interactions</i> , 2021, 345, 109563.	1.7	1
22748	Thermal Performance Curves of Multiple Isolates of <i>Batrachochytrium dendrobatidis</i> , a Lethal Pathogen of Amphibians. <i>Frontiers in Veterinary Science</i> , 2021, 8, 687084.	0.9	9
22749	Antifungal Peptides from a <i>Burkholderia</i> Strain Suppress Basal Stem Rot Disease of Oil Palm. <i>Phytopathology</i> , 2022, 112, 238-248.	1.1	2
22750	Genome-Wide Analysis of Codon Usage Patterns of SARS-CoV-2 Virus Reveals Global Heterogeneity of COVID-19. <i>Biomolecules</i> , 2021, 11, 912.	1.8	23
22751	<i>Gleditsia saxatilis</i> (Fabaceae), a new species from limestone areas of Guangxi, China based on morphological and molecular evidence. <i>Phytotaxa</i> , 2021, 508, .	0.1	0
22755	The diversification of termites: Inferences from a complete species-level phylogeny. <i>Zoologica Scripta</i> , 2021, 50, 769-779.	0.7	2
22756	<i>Baorangia duplicatopora</i> (Boletaceae, Boletales), a new bolete from tropical China. <i>Phytotaxa</i> , 2021, 508, .	0.1	2

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22757	Lack of $\Delta^5$ Desaturase Activity Impairs EPA and DHA Synthesis in Fish Cells from Red Sea Bream and Japanese Flounder. <i>Marine Biotechnology</i> , 2021, 23, 472-481.	1.1	5
22759	Crystal structure of an archaeal CorB magnesium transporter. <i>Nature Communications</i> , 2021, 12, 4028.	5.8	23
22760	Assessing Biosynthetic Gene Cluster Diversity of Specialized Metabolites in the Conserved Gut Symbionts of Herbivorous Turtle Ants. <i>Frontiers in Microbiology</i> , 2021, 12, 678100.	1.5	10
22761	Molecular characterization and aggressiveness of the <i>Ralstonia solanacearum</i> species complex from <i>Eucalyptus</i> spp. in Brazil. <i>Forest Pathology</i> , 2021, 51, e12704.	0.5	0
22762	A New Host Record for <i>Clinostomum</i> cf. <i>marginatum</i> (Trematoda: Digenea: Clinostomidae) from the Endemic Salado Salamander, <i>Eurycea chisholmensis</i> (Caudata: Plethodontidae), from the Edwards Plateau, Texas, U.S.A.. <i>Comparative Parasitology</i> , 2021, 88, .	0.0	0
22763	Molecular characterization of <i>Hedera</i> (Araliaceae) from Atlantic Iberian Peninsula. <i>Plant Biosystems</i> , 2022, 156, 769-775.	0.8	1
22764	Ethylene-regulated immature fruit abscission is associated with higher expression of <i>CoACO</i> genes in <i>Camellia oleifera</i> . <i>Royal Society Open Science</i> , 2021, 8, 202340.	1.1	6
22765	Recent Applications of Deep Learning Methods on Evolution- and Contact-Based Protein Structure Prediction. <i>International Journal of Molecular Sciences</i> , 2021, 22, 6032.	1.8	11
22766	Testing cophylogeny between coral reef invertebrates and their bacterial and archaeal symbionts. <i>Molecular Ecology</i> , 2021, 30, 3768-3782.	2.0	11
22767	N-(3-{4-[3-(trifluoromethyl)phenyl]piperazin-1-yl}propyl)-1H-indazole-3-carboxamide (D2AAK3) as a potential antipsychotic: In vitro, in silico and in vivo evaluation of a multi-target ligand. <i>Neurochemistry International</i> , 2021, 146, 105016.	1.9	10
22768	<i>Bacillus thuringiensis</i> chimeric proteins Cry1A.2 and Cry1B.2 to control soybean lepidopteran pests: New domain combinations enhance insecticidal spectrum of activity and novel receptor contributions. <i>PLoS ONE</i> , 2021, 16, e0249150.	1.1	12
22769	Comparative Genomics and Molecular Analysis of <i>Epidermophyton floccosum</i> . <i>Mycopathologia</i> , 2021, 186, 487-497.	1.3	5
22770	Patterns of transmission and horizontal gene transfer in the <i>Dioscorea sansibarensis</i> leaf symbiosis revealed by whole-genome sequencing. <i>Current Biology</i> , 2021, 31, 2666-2673.e4.	1.8	6
22771	Effects of Dispersants and Biosurfactants on Crude-Oil Biodegradation and Bacterial Community Succession. <i>Microorganisms</i> , 2021, 9, 1200.	1.6	15
22772	Identification of a Novel Class of Photolyases as Possible Ancestors of Their Family. <i>Molecular Biology and Evolution</i> , 2021, 38, 4505-4519.	3.5	8
22773	Sialic Acids as Receptors for Pathogens. <i>Biomolecules</i> , 2021, 11, 831.	1.8	27
22774	Phylogenomics illuminates the evolution of bobtail and bottletail squid (order Sepiolida). <i>Communications Biology</i> , 2021, 4, 819.	2.0	24
22775	Biochar and fertilizer improved the growth and quality of the ice plant ( <i>Mesembryanthemum</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Environment, 2021, 775, 144893.	3.9	40

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22776	Phylogenetic comparison and splice site conservation of eukaryotic U1 snRNP-specific U1-70K gene family. <i>Scientific Reports</i> , 2021, 11, 12760.	1.6	4
22777	Late Relapse and Reinfection in HCV Patients Treated with Direct-Acting Antiviral (DAA) Drugs. <i>Viruses</i> , 2021, 13, 1151.	1.5	7
22778	Discovery of Known and Novel Viruses in Wild and Cultivated Blueberry in Florida through Viral Metagenomic Approaches. <i>Viruses</i> , 2021, 13, 1165.	1.5	6
22779	Structural and Functional Impacts of Microbiota on <i>Pyropia yezoensis</i> and Surrounding Seawater in Cultivation Farms along Coastal Areas of the Yellow Sea. <i>Microorganisms</i> , 2021, 9, 1291.	1.6	9
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22781	Engineering yeast metabolism for the discovery and production of polyamines and polyamine analogues. <i>Nature Catalysis</i> , 2021, 4, 498-509.	16.1	26
22782	Systematics of the shrimp genus <i>Atya</i> (Decapoda, Atyidae) in the light of multigene-based phylogenetic and species delimitation inference. <i>Zoologica Scripta</i> , 2021, 50, 780-794.	0.7	2
22784	High-throughput sequencing yields a complete mitochondrial genome of the <i>Cryptotympana atrata</i> (Insecta: Hemiptera: Cicadidae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1883-1885.	0.2	0
22785	Functional and genomic characterization of <i>Komagataeibacter uvaceti</i> FXV3, a multiple stress resistant bacterium producing increased levels of cellulose. <i>Biotechnology Reports (Amsterdam)</i> , 2021, 10, 100000.	0.0	0
22786	Genome and Evolutionary Analysis of <i>Nosema ceranae</i> : A Microsporidian Parasite of Honey Bees. <i>Frontiers in Microbiology</i> , 2021, 12, 645353.	1.5	12
22787	Natural host range, incidence on overwintering cotton and diversity of cotton leafroll dwarf virus in Georgia USA. <i>Crop Protection</i> , 2021, 144, 105604.	1.0	13
22788	The response of tartary buckwheat and 19 bZIP genes to abscisic acid (ABA). <i>Molecular Biology Reports</i> , 2021, 48, 4341-4350.	1.0	5
22789	Genomic Analysis of <i>Pasteurella atlantica</i> Provides Insight on Its Virulence Factors and Phylogeny and Highlights the Potential of Reverse Vaccinology in Aquaculture. <i>Microorganisms</i> , 2021, 9, 1215.	1.6	4
22790	DNA barcoding for <i>Arecaceae</i> and <i>Fabaceae</i> species identification of two plant collections. <i>Acta Horticulturae</i> , 2021, , 218-226.	0.1	0
22791	Genome-wide identification and expression analysis of LBD transcription factor genes in Moso bamboo ( <i>Phyllostachys edulis</i> ). <i>BMC Plant Biology</i> , 2021, 21, 296.	1.6	24
22792	Identification and Functional Characterization of Genes Encoding Phenylacetaldehyde Reductases That Catalyze the Last Step in the Biosynthesis of Hydroxytyrosol in Olive. <i>Plants</i> , 2021, 10, 1268.	1.6	2
22793	Regulation of the Actin Cytoskeleton via Rho GTPase Signalling in <i>Dictyostelium</i> and Mammalian Cells: A Parallel Slalom. <i>Cells</i> , 2021, 10, 1592.	1.8	11
22794	Zoonotic vaccinia virus strains belonging to different genetic clades exhibit immunomodulation abilities that are proportional to their virulence. <i>Virology Journal</i> , 2021, 18, 124.	1.4	4

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22796	Tropane alkaloids and terpenes synthase genes of <i>Datura stramonium</i> (Solanaceae). <i>PeerJ</i> , 2021, 9, e11466.	0.9	2
22797	Intertypic reassortment of mammalian orthoreovirus identified in wastewater in Japan. <i>Scientific Reports</i> , 2021, 11, 12583.	1.6	5
22798	Five new species of <i>Moelleriella</i> infecting scale insects (Coccidae) in Thailand. <i>Mycological Progress</i> , 2021, 20, 847.	0.5	1
22799	Comparative Genomic Insights Into the Taxonomic Classification, Diversity, and Secondary Metabolic Potentials of <i>Kitasatospora</i> , a Genus Closely Related to <i>Streptomyces</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 683814.	1.5	11
22800	Two new species of the Balkan genus <i>Paladilhioopsis</i> Pavlovič, 1913 (Caenogastropoda, Moitessieriidae). <i>ZooKeys</i> , 2021, 1046, 157-176.	0.5	2
22801	Evolution of Interbacterial Antagonism in Bee Gut Microbiota Reflects Host and Symbiont Diversification. <i>MSystems</i> , 2021, 6, .	1.7	13
22802	Genome-Wide Identification, Diversification, and Expression Analysis of Lectin Receptor-Like Kinase (LecRLK) Gene Family in Cucumber under Biotic Stress. <i>International Journal of Molecular Sciences</i> , 2021, 22, 6585.	1.8	12
22803	Genome-Inferred Correspondence between Phylogeny and Metabolic Traits in the Wild <i>Drosophila</i> Gut Microbiome. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	5
22804	Taxonomic and Functional Variations Induced by an Overloading Event in Anaerobic Codigestion of Municipal Wastewater Sludge with Fats, Oils, and Grease. <i>ACS ES&amp;T Engineering</i> , 2021, 1, 1205-1216.	3.7	5
22805	Maternal genetic structure in ancient Shandong between 9500 and 1800 years ago. <i>Science Bulletin</i> , 2021, 66, 1129-1135.	4.3	10
22806	Balancing selection maintains ancient polymorphisms at conserved enhancers for the olfactory receptor genes of a Chinese marine fish. <i>Molecular Ecology</i> , 2021, 30, 4023-4038.	2.0	3
22807	Gastropod first intermediate hosts for two species of Monorchiidae Odhner, 1911 (Trematoda): I can't believe it's not bivalves!. <i>International Journal for Parasitology</i> , 2021, 51, 1035-1046.	1.3	9
22808	A new species of <i>Larinia</i> (Araneae: Araneidae) from Thailand. <i>Acta Arachnologica</i> , 2021, 70, 11-16.	0.0	0
22809	Molecular population genetics of <i>Sex-lethal</i> ( <i>Sxl</i> ) in the <i>Drosophila melanogaster</i> species group: a locus that genetically interacts with <i>Wolbachia pipientis</i> in <i>Drosophila melanogaster</i> . <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	2
22811	The riverine thruway hypothesis: rivers as a key mediator of gene flow for the aquatic paradoxical frog <i>Pseudis tocantins</i> (Anura, Hylidae). <i>Landscape Ecology</i> , 2021, 36, 3049-3060.	1.9	11
22812	Patterns of host tree use within a lineage of saproxylic snout-less weevils (Coleoptera: Curculionidae: <i>Tj ETQq0 0 0 rBT /Overlock 10 Tf</i>	1.2	6
22813	OCT1 is a yeast mitochondrial thiolase involved in the 3-oxoadipate pathway. <i>FEMS Yeast Research</i> , 2021, 21, .	1.1	2

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22815	Functional insights into two <i>Ocimum kilimandscharicum</i> 4-coumarate-CoA ligases involved in phenylpropanoid biosynthesis. <i>International Journal of Biological Macromolecules</i> , 2021, 181, 202-210.	3.6	8
22816	Concerted evolution reveals co-adapted amino acid substitutions in Na <sup>+</sup> K <sup>+</sup> -ATPase of frogs that prey on toxic toads. <i>Current Biology</i> , 2021, 31, 2530-2538.e10.	1.8	20
22817	Analysis of Methylation Dynamics Reveals a Tissue-Specific, Age-Dependent Decline in 5-Methylcytosine Within the Genome of the Vertebrate Aging Model <i>Nothobranchius furzeri</i> . <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 627143.	1.6	7
22818	Overcoming Culture Restriction for SARS-CoV-2 in Human Cells Facilitates the Screening of Compounds Inhibiting Viral Replication. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, e0009721.	1.4	58
22819	Selective enrichment of comammox from activated sludge using antibiotics. <i>Water Research</i> , 2021, 197, 117087.	5.3	31
22820	The epidemiology of Mayaro virus in the Americas: A systematic review and key parameter estimates for outbreak modelling. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009418.	1.3	27
22821	Genomic and Phenotypic Characterization of <i>Chloracidobacterium</i> Isolates Provides Evidence for Multiple Species. <i>Frontiers in Microbiology</i> , 2021, 12, 704168.	1.5	3
22822	Cryptic But Ubiquitous: <i>Claviradulomyceae</i> fam. nov. with Five Novel Species of the Lenticel Fungus <i>Claviradulomyces</i> from Brazil. <i>Cryptogamie, Mycologie</i> , 2021, 42, .	0.2	0
22823	The archaeal protein SepF is essential for cell division in <i>Haloferax volcanii</i> . <i>Nature Communications</i> , 2021, 12, 3469.	5.8	22
22824	Deadwood-Inhabiting Bacteria Show Adaptations to Changing Carbon and Nitrogen Availability During Decomposition. <i>Frontiers in Microbiology</i> , 2021, 12, 685303.	1.5	21
22825	Phylogenomic Analysis Reveals Dispersal-Driven Speciation and Divergence with Gene Flow in Lesser Sunda Flying Lizards (Genus <i>Draco</i> ). <i>Systematic Biology</i> , 2021, 71, 221-241.	2.7	11
22826	A recessive gene <i>pepy-1</i> encoding Pelota confers resistance to begomovirus isolates of PepYLCIV and PepYLCAV in <i>Capsicum annuum</i> . <i>Theoretical and Applied Genetics</i> , 2021, 134, 2947-2964.	1.8	27
22827	Two new species of Unikaryon (Microsporidia) hyperparasitic in microphallid metacercariae (Digenea) from Florida intertidal crabs. <i>Journal of Invertebrate Pathology</i> , 2021, 182, 107582.	1.5	6
22828	Unexpected Discovery of Hypermutator Phenotype Sounds the Alarm for Quality Control Strains. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	2
22829	A Chromosome-Level Genome Assembly of the Mandarin Fish ( <i>Siniperca chuatsi</i> ). <i>Frontiers in Genetics</i> , 2021, 12, 671650.	1.1	8
22830	CYP77B1 a fatty acid epoxygenase specific to flowering plants. <i>Plant Science</i> , 2021, 307, 110905.	1.7	5
22831	Gene-Gene Interactions Dictate Ciprofloxacin Resistance in <i>Pseudomonas aeruginosa</i> and Facilitate Prediction of Resistance Phenotype from Genome Sequence Data. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, e0269620.	1.4	16

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22833	Characterization of the complete chloroplast genome of an annual herb, <i>Chenopodium album</i> (Amaranthaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2107-2108.	0.2	0
22835	Genomic insights into the sessile life and biofouling of barnacles (Crustacea: Cirripedia). <i>Heliyon</i> , 2021, 7, e07291.	1.4	7
22837	Identification of diverse novel genomoviruses in gut of wild birds. <i>Biosafety and Health</i> , 2021, 3, 136-141.	1.2	2
22838	Characterization of the mitochondrial genome of the plain flowerpecker, <i>Dicaeum concolor</i> (Dicaeidae) from Yunnan Province, China. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2086-2087.	0.2	0
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22842	Protein-based condensation mechanisms drive the assembly of RNA-rich P granules. <i>ELife</i> , 2021, 10, .	2.8	16
22844	Bioinformatic Analysis of the <i>Campylobacter jejuni</i> Type VI Secretion System and Effector Prediction. <i>Frontiers in Microbiology</i> , 2021, 12, 694824.	1.5	10
22845	The Dispensable Roles of X-Linked Ubl4a and Its Autosomal Counterpart Ubl4b in Spermatogenesis Represent a New Evolutionary Type of X-Derived Retrogenes. <i>Frontiers in Genetics</i> , 2021, 12, 689902.	1.1	0
22846	Comparative Genomics of Prophages Sato and Sole Expands the Genetic Diversity Found in the Genus <i>Betatectivirus</i> . <i>Microorganisms</i> , 2021, 9, 1335.	1.6	1
22847	Zetaproteobacteria Pan-Genome Reveals Candidate Gene Cluster for Twisted Stalk Biosynthesis and Export. <i>Frontiers in Microbiology</i> , 2021, 12, 679409.	1.5	9
22848	ORFograph: search for novel insecticidal protein genes in genomic and metagenomic assembly graphs. <i>Microbiome</i> , 2021, 9, 149.	4.9	3
22849	Molecular characterization and phylogenetic analyses of <i>Lophodermella</i> needle pathogens (Rhytismataceae) on <i>Pinus</i> species in the USA and Europe. <i>PeerJ</i> , 2021, 9, e11435.	0.9	5
22850	Parasitic copepods <i>Caligus lacustris</i> (Copepoda: Caligidae) on the rainbow trout <i>Oncorhynchus mykiss</i> in cage aquaculture: morphology, population demography, and first insights into phylogenetic relationships. <i>Parasitology Research</i> , 2021, 120, 2455-2467.	0.6	2
22851	Cloning, characterization, and expression analysis of two MAPKKK genes in <i>Chrysanthemum</i> . <i>Pakistan Journal of Botany</i> , 2022, 54, .	0.2	1
22852	Chromosome-Scale Genome Assembly of the Resurrection Plant <i>Acanthochlamys bracteata</i> (Velloziaceae). <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	6
22853	Population matched (pm) germline allelic variants of immunoglobulin (IG) loci: Relevance in infectious diseases and vaccination studies in human populations. <i>Genes and Immunity</i> , 2021, 22, 172-186.	2.2	14
22854	Genome Assembly of the Cold-Tolerant Leaf Beetle <i>Gonioctena quinquepunctata</i> , an Important Resource for Studying Its Evolution and Reproductive Barriers between Species. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	2

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22855	Reclassification of <i>Facklamia ignava</i> , <i>Facklamia sourekkii</i> and <i>Facklamia tabacinasalis</i> as <i>Falseniella ignava</i> gen. nov., comb. nov., <i>Hutsoniella sourekkii</i> gen. nov., comb. nov., and <i>Ruoffia tabacinasalis</i> gen. nov., comb. nov., and description of <i>Ruoffia halotolerans</i> sp. nov., isolated from hypersaline Inland Sea of Qatar. <i>Antonie Van Leeuwenhoek</i> , 2021, 114, 1181-1193.	0.7	28
22856	<i>Brachybacterium subflavum</i> sp. nov., a novel actinobacterium isolated from the foregut of grass carp. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	7
22857	Structure of plant photosystem I-plastocyanin complex reveals strong hydrophobic interactions. <i>Biochemical Journal</i> , 2021, 478, 2371-2384.	1.7	15
22858	Ecomorphological divergence and lack of gene flow in two sympatric Balkan slow worms (Squamata: Tj ETQq1 1 0,784314 rgBT /Ove	0.7	4
22859	Global phylogeography of the smooth hammerhead shark: Glacial refugia and historical migration patterns. <i>Aquatic Conservation: Marine and Freshwater Ecosystems</i> , 2021, 31, 2348-2368.	0.9	6
22860	Microbiomes attached to fresh perennial ryegrass are temporally resilient and adapt to changing ecological niches. <i>Microbiome</i> , 2021, 9, 143.	4.9	9
22861	Twelve New Taxa of Xylaria Associated with Termite Nests and Soil from Northeast Thailand. <i>Biology</i> , 2021, 10, 575.	1.3	8
22862	Chemogenomic approach to identifying nematode chemoreceptor drug targets in the entomopathogenic nematode <i>Heterorhabditis bacteriophora</i> . <i>Computational Biology and Chemistry</i> , 2021, 92, 107464.	1.1	0
22863	The nearly complete genome of <i>Ginkgo biloba</i> illuminates gymnosperm evolution. <i>Nature Plants</i> , 2021, 7, 748-756.	4.7	98
22864	The Evolution of Interdependence in a Four-Way Mealybug Symbiosis. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	9
22866	The effect of recombination on the evolution of a population of <i>Neisseria meningitidis</i> . <i>Genome Research</i> , 2021, 31, 1258-1268.	2.4	4
22867	Crenobiont, stygophile and stygobiont molluscs in the hydrographic area of the Trebišnjica River Basin. <i>ZooKeys</i> , 2021, 1047, 61-89.	0.5	6
22868	Comparative Analyses of the Gut Microbiome of Two Fox Species, the Red Fox ( <i>Vulpes vulpes</i> ) and Corsac Fox ( <i>Vulpes corsac</i> ), that Occupy Different Ecological Niches. <i>Microbial Ecology</i> , 2022, 83, 753-765.	1.4	15
22869	Genome Analysis of a Verrucomicrobial Endosymbiont With a Tiny Genome Discovered in an Antarctic Lake. <i>Frontiers in Microbiology</i> , 2021, 12, 674758.	1.5	18
22870	Diverse Trajectories Drive the Expression of a Giant Virus in the Oomycete Plant Pathogen <i>Phytophthora parasitica</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 662762.	1.5	12
22871	Rhizobia and endophytic bacteria isolated from rainforest fragments within an iron ore mining site of the Eastern Brazilian Amazon. <i>Brazilian Journal of Microbiology</i> , 2021, 52, 1461-1474.	0.8	5
22872	A new species of tree hyrax (Procaviidae: <i>Dendrohyrax</i> ) from West Africa and the significance of the Niger-Volta interfluvium in mammalian biogeography. <i>Zoological Journal of the Linnean Society</i> , 2022, 194, 527-552.	1.0	11
22873	Genomic insights into the adaptation and evolution of the nautilus, an ancient but evolving living fossil. <i>Molecular Ecology Resources</i> , 2022, 22, 15-27.	2.2	15



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22874	Taxonomy and okadaic acid production of a strain of <i>Prorocentrum lima</i> (Dinophyceae) isolated from the Bay of Bengal, North Indian Ocean. <i>Toxicon</i> , 2021, 196, 32-43.	0.8	4
22876	Spatial abundance and distribution of picocyanobacterial communities in two contrasting lakes revealed using environmental DNA metabarcoding. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	7
22878	Integrative systematics of the tooth-tailed scorpions, <i>Odontobuthus</i> (Buthidae), with descriptions of three new species from the Iranian Plateau. <i>Zoological Journal of the Linnean Society</i> , 0, , .	1.0	0
22879	The DEAD-box RNA helicase RhIE2 is a global regulator of <i>Pseudomonas aeruginosa</i> lifestyle and pathogenesis. <i>Nucleic Acids Research</i> , 2021, 49, 6925-6940.	6.5	12
22880	TNFRSF13B polymorphisms counteract microbial adaptation to natural IgA. <i>JCI Insight</i> , 2021, 6, .	2.3	1
22881	Comparison of mitochondrial genome and development of specific PCR primers for identifying two scuticociliates, <i>Pseudocohnilembus persalinus</i> and <i>Uronema marinum</i> . <i>Parasites and Vectors</i> , 2021, 14, 318.	1.0	4
22882	Extremely Halophilic Biohydrogen Producing Microbial Communities from High-Salinity Soil and Salt Evaporation Pond. <i>Fuels</i> , 2021, 2, 241-252.	1.3	2
22883	A WIDESPREAD NOVEL GAMMAHERPESVIRUS IN APPARENTLY HEALTHY WILD QUOKKAS (SETONIX) Tj ETQq1 1 0.784314 rgBT /Over Wildlife Medicine, 2021, 52, 592-603.	0.3	1
22884	Novel clades of soil biphenyl degraders revealed by integrating isotope probing, multi-omics, and single-cell analyses. <i>ISME Journal</i> , 2021, 15, 3508-3521.	4.4	14
22885	Prognostic implications of troponin T variations in inherited cardiomyopathies using systems biology. <i>Npj Genomic Medicine</i> , 2021, 6, 47.	1.7	5
22886	Structural insights into an atypical secretory pathway kinase crucial for <i>Toxoplasma gondii</i> invasion. <i>Nature Communications</i> , 2021, 12, 3788.	5.8	12
22887	Triterpenoid saponin biosynthesis genes and their expression patterns during the development of sea cucumber <i>Apostichopus japonicus</i> . <i>Journal of Oceanology and Limnology</i> , 0, , 1.	0.6	2
22888	Curation Guidelines for <i>de novo</i> Generated Transposable Element Families. <i>Current Protocols</i> , 2021, 1, e154.	1.3	25
22889	Impact of specimen type on findings for bacterial composition within the intestinal tract of dogs and cats with and without chronic enteropathy. <i>American Journal of Veterinary Research</i> , 2021, 82, 494-501.	0.3	0
22890	Neurotropic Astroviruses in Animals. <i>Viruses</i> , 2021, 13, 1201.	1.5	11
22891	Intuitionistic fuzzy approach improve protein multiple sequence alignment. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2021, 10, 1.	1.2	0
22894	A Baseline Evaluation of Bioinformatics Capacity in Tanzania Reveals Areas for Training. <i>Frontiers in Education</i> , 2021, 6, .	1.2	1
22895	A chemosystematic investigation of selected <i>Stichococcus</i> -like organisms (Trebouxiophyta). <i>Algae</i> , 2021, 36, 123-135.	0.9	6

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22896	Strain diversity of plant-associated <i>Lactiplantibacillus plantarum</i> . <i>Microbial Biotechnology</i> , 2021, 14, 1990-2008.	2.0	20
22897	Proteome-wide prediction of bacterial carbohydrate-binding proteins as a tool for understanding commensal and pathogen colonisation of the vaginal microbiome. <i>Npj Biofilms and Microbiomes</i> , 2021, 7, 49.	2.9	11
22898	The complete chloroplast genome of <i>Euphorbia hirta</i> (Euphorbiaceae), a commonly used medicinal plant in China. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2166-2168.	0.2	0
22899	A catalog of the diversity and ubiquity of bacterial microcompartments. <i>Nature Communications</i> , 2021, 12, 3809.	5.8	55
22901	Hered and hunted goat genomes from the dawn of domestication in the Zagros Mountains. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	32
22902	Evolution of bacterial steroid biosynthesis and its impact on eukaryogenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	36
22903	The landscape of antibody binding in SARS-CoV-2 infection. <i>PLoS Biology</i> , 2021, 19, e3001265.	2.6	58
22904	Chromosome-scale genome assembly of areca palm ( <i>Areca catechu</i> ). <i>Molecular Ecology Resources</i> , 2021, 21, 2504-2519.	2.2	20
22906	Apple Ripening Is Controlled by a NAC Transcription Factor. <i>Frontiers in Genetics</i> , 2021, 12, 671300.	1.1	29
22907	Prokaryotic Diversity and Hydrogenotrophic Methanogenesis in an Alkaline Spring (La Crouen, New) Tj ETQq1 1 0.784314 rgBT /Overl	1.6	5
22908	Rapid radiation of angraecoids (Orchidaceae, Angraecinae) in tropical Africa characterised by multiple karyotypic shifts under major environmental instability. <i>Molecular Phylogenetics and Evolution</i> , 2021, 159, 107105.	1.2	7
22909	Complete genome sequence of <i>Arthrobacter</i> sp. PAMC25564 and its comparative genome analysis for elucidating the role of CAZymes in cold adaptation. <i>BMC Genomics</i> , 2021, 22, 403.	1.2	11
22910	Identification of a Sulfatase that Detoxifies Glucosinolates in the Phloem-Feeding Insect <i>Bemisia tabaci</i> and Prefers Indolic Glucosinolates. <i>Frontiers in Plant Science</i> , 2021, 12, 671286.	1.7	10
22913	Phylogenetic affinities of Forticulcitinae (Haploporidae) parasites of mullet from the Americas, with the description of three new species and notes on the genera and key species. <i>Systematic Parasitology</i> , 2021, 98, 455-476.	0.5	1
22914	Chromosomal Integration of Huge and Complex blaNDM-Carrying Genetic Elements in Enterobacteriaceae. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 690799.	1.8	12
22916	Microbial metagenome-assembled genomes of the Fram Strait from short and long read sequencing platforms. <i>PeerJ</i> , 2021, 9, e11721.	0.9	14
22917	Full-Genome Sequences of Alphacoronaviruses and Astroviruses from Myotis and Pipistrelle Bats in Denmark. <i>Viruses</i> , 2021, 13, 1073.	1.5	15
22918	Thermal Sensitivity of Heat Sensor TRPA1 Correlates With Temperatures Inducing Heat Avoidance Behavior in Terrestrial Ectotherms. <i>Frontiers in Ecology and Evolution</i> , 2021, 9, .	1.1	5

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22919	Integrative description of <i>Hypsibius repentinus</i> sp. nov. (Eutardigrada: Hypsibiidae) from Sweden. <i>Zoosystematica Rossica</i> , 2021, 30, 101-115.	0.2	2
22920	Potato Virus Y Biological Strain Group Y<sup>D</sup>: Hypersensitive Resistance Genes Elicited and Phylogenetic Placement. <i>Plant Disease</i> , 2021, 105, 3600-3609.	0.7	4
22921	The reduced genome of a heritable symbiont from an ectoparasitic feather feeding louse. <i>Bmc Ecology and Evolution</i> , 2021, 21, 108.	0.7	7
22922	Conversion of the Sensor Kinase DcuS to the Fumarate Sensitive State by Interaction of the Bifunctional Transporter DctA at the TM2/PASC-Linker Region. <i>Microorganisms</i> , 2021, 9, 1397.	1.6	4
22923	Is mRNA decapping by ApaH like phosphatases present in eukaryotes beyond the Kinetoplastida?. <i>Bmc Ecology and Evolution</i> , 2021, 21, 131.	0.7	2
22924	Comparative Genomics Identifies Putative Interspecies Mechanisms Underlying Crbn-Sall4-Linked Thalidomide Embryopathy. <i>Frontiers in Genetics</i> , 2021, 12, 680217.	1.1	2
22925	Genome analysis of <i>Pseudomonas</i> sp. OF001 and <i>Rubrivivax</i> sp. A210 suggests multicopper oxidases catalyze manganese oxidation required for cylindrospermopsin transformation. <i>BMC Genomics</i> , 2021, 22, 464.	1.2	1
22926	Genomic diversity, chromosomal rearrangements, and interspecies hybridization in the <i>Ogataea polymorpha</i> species complex. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	2
22927	<i>FGF</i> gene family characterization provides insights into its adaptive evolution in Carnivora. <i>Ecology and Evolution</i> , 2021, 11, 9837-9847.	0.8	3
22928	The ocular pyogranulomatous lesion in a Gentoo penguin ( <i>Pygoscelis papua</i> ) from the Antarctic Peninsula: evaluation of microbiological and histopathological analysis outcomes. <i>Veterinary Research Communications</i> , 2021, 45, 143-158.	0.6	9
22929	A near comprehensive phylogenetic framework gives new insights toward a natural classification of the African genus <i>Cyrtorchis</i> (Angraecinae, Orchidaceae). <i>Taxon</i> , 2021, 70, 720.	0.4	1
22930	Insights into the genomic evolution of insects from cricket genomes. <i>Communications Biology</i> , 2021, 4, 733.	2.0	41
22934	Helarchaeota and co-occurring sulfate-reducing bacteria in subseafloor sediments from the Costa Rica Margin. <i>ISME Communications</i> , 2021, 1, .	1.7	16
22935	Phylogeny and Evolutionary History of Respiratory Complex I Proteins in Melainabacteria. <i>Genes</i> , 2021, 12, 929.	1.0	1
22936	DNA barcodes and morphology reveal two new species of <i>Monodiamesa</i> Kieffer (Diptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 182 Td (	0.2	2
22937	OpiumPlex is a novel microsatellite system for profiling opium poppy ( <i>Papaver somniferum</i> L.). <i>Scientific Reports</i> , 2021, 11, 12799.	1.6	5
22939	A preliminary phylogenetic study of <i>Paraphlomis</i> (Lamiaceae) based on molecular and morphological evidence. <i>Plant Diversity</i> , 2021, 43, 206-215.	1.8	9
22942	A chromosome-level genome assembly of the blackspotted croaker ( <i>Protonibea diacanthus</i> ). <i>Aquaculture and Fisheries</i> , 2022, 7, 616-622.	1.2	1

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22943	Comparative Genomics of 42 <i>Arcanobacterium phocae</i> Strains. <i>Antibiotics</i> , 2021, 10, 740.	1.5	1
22944	efam: an expanded, metaproteome-supported HMM profile database of viral protein families. <i>Bioinformatics</i> , 2021, 37, 4202-4208.	1.8	15
22945	Extensive C→U transition biases in the genomes of a wide range of mammalian RNA viruses; potential associations with transcriptional mutations, damage- or host-mediated editing of viral RNA. <i>PLoS Pathogens</i> , 2021, 17, e1009596.	2.1	32
22946	Construction of DNA Tools for Hyperexpression in <i>Marchantia</i> Chloroplasts. <i>ACS Synthetic Biology</i> , 2021, 10, 1651-1666.	1.9	11
22947	Ancient mitochondrial genomes from the Argentinian Pampas inform the early peopling of the Southern Cone of South America. <i>IScience</i> , 2021, 24, 102553.	1.9	11
22948	Linking a Gene Cluster to Atranorin, a Major Cortical Substance of Lichens, through Genetic Dereplication and Heterologous Expression. <i>MBio</i> , 2021, 12, e0111121.	1.8	33
22949	Species diversity and mycotoxin production by members of the <i>Fusarium tricinctum</i> species complex associated with <i>Fusarium</i> head blight of wheat and barley in Italy. <i>International Journal of Food Microbiology</i> , 2021, 358, 109298.	2.1	29
22950	Diverse Viruses Carrying Genes for Microbial Extremotolerance in the Atacama Desert Hyperarid Soil. <i>MSystems</i> , 2021, 6, .	1.7	27
22951	Co-occurrence and patterns of phosphate solubilizing, salt and metal tolerant and antibiotic-resistant bacteria in diverse soils. <i>3 Biotech</i> , 2021, 11, 356.	1.1	4
22952	Divergence and introgression in small apes, the genus <i>Hylobates</i> , revealed by reduced representation sequencing. <i>Heredity</i> , 2021, 127, 312-322.	1.2	5
22953	<i>Gaeumannomyces nanograminis</i> , sp. nov., a hyphopodiate fungus identified from diseased roots of ultradwarf bermudagrass in the United States. <i>Mycologia</i> , 2021, 113, 1-11.	0.8	2
22954	A Comprehensive Phylogenetic and Bioinformatics Survey of Lectins in the Fungal Kingdom. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 453.	1.5	19
22955	A chromosome-level genome assembly of rugged rose ( <i>Rosa rugosa</i> ) provides insights into its evolution, ecology, and floral characteristics. <i>Horticulture Research</i> , 2021, 8, 141.	2.9	29
22956	Timer-based proteomic profiling of the ubiquitin-proteasome system reveals a substrate receptor of the GID ubiquitin ligase. <i>Molecular Cell</i> , 2021, 81, 2460-2476.e11.	4.5	39
22957	Metagenomic Exploration of Bacterial Community Structure of Earthworms' Gut. <i>Journal of Pure and Applied Microbiology</i> , 2021, 15, 1156-1172.	0.3	5
22958	Rapid genotyping of tilapia lake virus (TiLV) using Nanopore sequencing. <i>Journal of Fish Diseases</i> , 2021, 44, 1491-1502.	0.9	10
22959	Cryogenian Origin and Subsequent Diversification of the Plant Cell-Wall Enzyme XTH Family. <i>Plant and Cell Physiology</i> , 2021, 62, 1874-1889.	1.5	20
22960	A new cryptic species of the <i>Pristimantis lacrimosus</i> group ( <i>Anura</i> , <i>Strabomantidae</i> ) from the eastern slopes of the Ecuadorian Andes. <i>Evolutionary Systematics</i> , 0, 5, 151-175.	0.2	7

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22961	Variability of Mitochondrial DNA Control Region and Phylogeography of Russet Ground Squirrel ( <i>Spermophilus major</i> , Sciuridae, Rodentia). <i>Russian Journal of Genetics</i> , 2021, 57, 825-835.	0.2	3
22962	Two <i>Apriona</i> Species Sharing a Host Niche Have Different Gut Microbiome Diversity. <i>Microbial Ecology</i> , 2022, 83, 1059-1072.	1.4	10
22963	Functional Characterization of the Oxantel-Sensitive Acetylcholine Receptor from <i>Trichuris muris</i> . <i>Pharmaceuticals</i> , 2021, 14, 698.	1.7	6
22964	Pairwise learning for predicting pollination interactions based on traits and phylogeny. <i>Ecological Modelling</i> , 2021, 451, 109508.	1.2	7
22965	Plant PIEZO homologs modulate vacuole morphology during tip growth. <i>Science</i> , 2021, 373, 586-590.	6.0	58
22966	Coral symbionts evolved a functional polycistronic flavodiiron gene. <i>Photosynthesis Research</i> , 2022, 151, 113-124.	1.6	8
22967	A new species of the deep-sea shrimp genus <i>Spongicoloides</i> (Decapoda: Spongicolidae) from the South China Sea. <i>Zootaxa</i> , 2021, 5005, 276-290.	0.2	0
22968	Rapid ecosystem-scale consequences of acute deoxygenation on a Caribbean coral reef. <i>Nature Communications</i> , 2021, 12, 4522.	5.8	42
22969	PHYLOGEOGRAPHIC AND GENETIC DIVERSITY OF PORCELLIONIDES PRUINOSUS AND PORCELLIO LAEVIS BY USING THE MITOCHONDRIAL CYTOCHROME C OXIDASE SUBUNIT 1 SEQUENCE. <i>Egyptian Journal of Zoology</i> , 2021, .	0.0	0
22970	Dissecting the chromosome-level genome of the Asian Clam ( <i>Corbicula fluminea</i> ). <i>Scientific Reports</i> , 2021, 11, 15021.	1.6	5
22971	Mitochondrial Genomes from Two Specialized Subfamilies of Reduviidae (Insecta: Hemiptera) Reveal Novel Gene Rearrangements of True Bugs. <i>Genes</i> , 2021, 12, 1134.	1.0	8
22972	Genome-Wide Identification, Structure Characterization, and Expression Pattern Profiling of the Aquaporin Gene Family in <i>Betula pendula</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 7269.	1.8	4
22973	Comparison of Silks from <i>Pseudoips prasinana</i> and <i>Bombyx mori</i> Shows Molecular Convergence in Fibroin Heavy Chains but Large Differences in Other Silk Components. <i>International Journal of Molecular Sciences</i> , 2021, 22, 8246.	1.8	7
22975	A Mechanically Transmitted DNA Mycovirus Is Targeted by the Defence Machinery of Its Host, <i>Botrytis cinerea</i> . <i>Viruses</i> , 2021, 13, 1315.	1.5	27
22976	Nanopore metagenomic sequencing of influenza virus directly from respiratory samples: diagnosis, drug resistance and nosocomial transmission, United Kingdom, 2018/19 influenza season. <i>Eurosurveillance</i> , 2021, 26, .	3.9	17
22977	Putative mobilized colistin resistance genes in the human gut microbiome. <i>BMC Microbiology</i> , 2021, 21, 220.	1.3	6
22978	Effects of fermented <i>Broussonetia papyrifera</i> on growth, intestinal antioxidant, inflammation and microbiota of grass carp ( <i>Ctenopharyngodon idella</i> ). <i>Aquaculture Reports</i> , 2021, 20, 100673.	0.7	7
22980	Evolutionary history of <i>Hemerocallis</i> in Japan inferred from chloroplast and nuclear phylogenies and levels of interspecific gene flow. <i>Molecular Phylogenetics and Evolution</i> , 2021, 164, 107264.	1.2	14

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22982	Community structure and activity potentials of archaeal communities in hadal sediments of the Mariana and Mussau trenches. <i>Marine Life Science and Technology</i> , 2022, 4, 150-161.	1.8	6
22983	DNA transposons mediate duplications via transposition-independent and -dependent mechanisms in metazoans. <i>Nature Communications</i> , 2021, 12, 4280.	5.8	9
22985	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
22986	High-Quality Genome Assembly and Comprehensive Transcriptome of the Painted Lady Butterfly <i>Vanessa cardui</i> . <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	10
22987	The complete mitochondrial genome of the wood tiger moth ( <i>Arctia plantaginis</i> ) and phylogenetic analyses within Arctiinae. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2171-2173.	0.2	0
22988	Performance and scaling behavior of bioinformatic applications in virtualization environments to create awareness for the efficient use of compute resources. <i>PLoS Computational Biology</i> , 2021, 17, e1009244.	1.5	7
22989	A chromosome-level genome assembly of <i>Cairina moschata</i> and comparative genomic analyses. <i>BMC Genomics</i> , 2021, 22, 581.	1.2	4
22990	CAZyme prediction in ascomycetous yeast genomes guides discovery of novel xylanolytic species with diverse capacities for hemicellulose hydrolysis. <i>Biotechnology for Biofuels</i> , 2021, 14, 150.	6.2	10
22991	Analysis of the Taxonomy and Pathogenic Factors of <i>Pectobacterium aroidearum</i> L6 Using Whole-Genome Sequencing and Comparative Genomics. <i>Frontiers in Microbiology</i> , 2021, 12, 679102.	1.5	11
22992	Monitoring of Antimicrobial Resistance to Aminoglycosides and Macrolides in <i>Campylobacter coli</i> and <i>Campylobacter jejuni</i> From Healthy Livestock in Spain (2002–2018). <i>Frontiers in Microbiology</i> , 2021, 12, 689262.	1.5	9
22993	Molecular Systematics of the Native Seagrass, <i>Ruppia cf. Maritima</i> (Ruppiaceae, Alismatales), on Hawaii Island1. <i>Pacific Science</i> , 2021, 75, .	0.2	1
22994	Accurate large-scale phylogeny-aware alignment using BALi-Phy. <i>Bioinformatics</i> , 2021, 37, 4677-4683.	1.8	2
22995	Phormidepistatin from the Cyanobacterium UIC 10484: Assessing the Phylogenetic Distribution of the Statine Pharmacophore. <i>Journal of Natural Products</i> , 2021, 84, 2256-2264.	1.5	2
22996	Screening of Biological Effectiveness of Endophytic Fungi Associated with <i>Plectranthus amboinicus</i> : A focus on <i>Aspergillus terreus</i> . <i>International Journal of Pharmaceutical Sciences Review and Research</i> , 2021, 69, .	0.1	0
22997	Characterization and Molecular Identification of Poly Urethane Degrading Bacteria. <i>Journal of Pure and Applied Microbiology</i> , 2021, 15, 1291-1300.	0.3	0
22998	The Development of the Gut Microbiota and Short-Chain Fatty Acids of Layer Chickens in Different Growth Periods. <i>Frontiers in Veterinary Science</i> , 2021, 8, 666535.	0.9	28
22999	Bacteria associated with wood tissues of Esca-diseased grapevines: functional diversity and synergy with <i>Fomitiporia mediterranea</i> to degrade wood components. <i>Environmental Microbiology</i> , 2021, 23, 6104-6121.	1.8	19

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23000	Characterization of a novel strain of <i>Tribonema minus</i> demonstrating high biomass productivity in outdoor raceway ponds. <i>Bioresource Technology</i> , 2021, 331, 125007.	4.8	11
23001	Dynamic changes in microbial community structure in farming pond water and their effect on the intestinal microbial community profile in juvenile common carp ( <i>Cyprinus carpio</i> L.). <i>Genomics</i> , 2021, 113, 2547-2560.	1.3	9
23002	Improved genome assembly of Chinese shrimp ( <i>Fenneropenaeus chinensis</i> ) suggests adaptation to the environment during evolution and domestication. <i>Molecular Ecology Resources</i> , 2022, 22, 334-344.	2.2	14
23003	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
23004	Morphological and Molecular Characterisation of a New Species of <i>Parastrongyloides</i> (Rhabditida): <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50</i> <i>Acta Parasitologica</i> , 2021, , 1.	0.4	0
23005	An astonishing wealth of new proteasome homologs. <i>Bioinformatics</i> , 2021, 37, 4694-4703.	1.8	3
23006	A Novel Family of RNA-Binding Proteins Regulate Polysaccharide Metabolism in <i>Bacteroides thetaiotaomicron</i> . <i>Journal of Bacteriology</i> , 2021, 203, e0021721.	1.0	6
23007	Fish taxonomic, functional, and phylogenetic diversity and their vulnerabilities in the largest river in southeastern China. <i>Ecology and Evolution</i> , 2021, 11, 11533-11548.	0.8	10
23008	Molecular and morphological analyses reveal pseudocryptic diversity in <i>Micromeloides undatus</i> (Bruguière, 1792) (Gastropoda: Heterobranchia: Aplustridae). <i>Systematics and Biodiversity</i> , 2021, 19, 834-858.	0.5	5
23009	Integrating GWAS and transcriptomics to identify genes involved in seed dormancy in rice. <i>Theoretical and Applied Genetics</i> , 2021, 134, 3553-3562.	1.8	6
23010	Molecular Dynamics Simulations Reveal Interactions of an IgG1 Antibody With Selected Fc Receptors. <i>Frontiers in Chemistry</i> , 2021, 9, 705931.	1.8	4
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23013	Exceptional ancient DNA preservation and fibre remains of a Sasanian saltmine sheep mummy in Chehrābād, Iran. <i>Biology Letters</i> , 2021, 17, 20210222.	1.0	7
23014	Expression of several <i>Phytophthora cinnamomi</i> putative RxLRs provides evidence for virulence roles in avocado. <i>PLoS ONE</i> , 2021, 16, e0254645.	1.1	6
23015	The CCCH zinc finger family of soybean ( <i>Glycine max</i> L.): genome-wide identification, expression, domestication, GWAS and haplotype analysis. <i>BMC Genomics</i> , 2021, 22, 511.	1.2	9
23016	Localised expression of <i>OslAA29</i> suggests a key role for auxin in regulating development of the dorsal aleurone of early rice grains. <i>Planta</i> , 2021, 254, 40.	1.6	10
23019	Native range surveys for host-specific <i>Acacia auriculiformis</i> biocontrol agents – A role for DNA barcoding. <i>Biological Control</i> , 2021, 158, 104594.	1.4	10

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23021	Quantifying the effects of hydrogen on carbon assimilation in a seafloor microbial community associated with ultramafic rocks. <i>ISME Journal</i> , 2022, 16, 257-271.	4.4	12
23022	Identification and genetic characterization of an isolate of bovine adenovirus 7 from the United States, a putative member of a new species in the genus <i>Atadenovirus</i> . <i>Archives of Virology</i> , 2021, 166, 2835-2839.	0.9	3
23023	Exploring the Microdiversity Within Marine Bacterial Taxa: Toward an Integrated Biogeography in the Southern Ocean. <i>Frontiers in Microbiology</i> , 2021, 12, 703792.	1.5	9
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23025	Analysis of CRISPR systems of types II-A, I-E and I-C in strains of <i>Lactocaseibacillus</i> . <i>International Dairy Journal</i> , 2021, 118, 105027.	1.5	1
23026	A conserved role for arrow in posterior axis patterning across Arthropoda. <i>Developmental Biology</i> , 2021, 475, 91-105.	0.9	14
23027	The mitochondrial genome of a minute springtail species <i>Megalothorax incertus</i> (Collembola: Tj ETQq1 1 0.784314 rgBT /Overlo	0.2	2
23028	Analysis of Bacterial Communities on North Sea Macroalgae and Characterization of the Isolated <i>Planctomycetes Adhaeretor mobilis</i> gen. nov., sp. nov., <i>Roseimaritima multifibrata</i> sp. nov., <i>Rosistilla ulvae</i> sp. nov. and <i>Rubripirellula lacrimiformis</i> sp. nov.. <i>Microorganisms</i> , 2021, 9, 1494.	1.6	34
23029	<i>Ostreibacterium oceani</i> gen. nov., sp. nov., isolated from oyster, and description of <i>Ostreibacteriaceae</i> fam. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	8
23030	A newly developed PCR-based method revealed distinct <i>Fusobacterium nucleatum</i> subspecies infection patterns in colorectal cancer. <i>Microbial Biotechnology</i> , 2021, 14, 2176-2186.	2.0	15
23031	Transmission dynamics and forecasts of the COVID-19 pandemic in Mexico, March-December 2020. <i>PLoS ONE</i> , 2021, 16, e0254826.	1.1	11
23032	The methylome of the model arbuscular mycorrhizal fungus, <i>Rhizophagus irregularis</i> , shares characteristics with early diverging fungi and Dikarya. <i>Communications Biology</i> , 2021, 4, 901.	2.0	17
23033	Metagenomic and viromic data mining reveals viral threats in biologically treated domestic wastewater. <i>Environmental Science and Ecotechnology</i> , 2021, 7, 100105.	6.7	23
23034	Gene tree and species tree reconciliation with endosymbiotic gene transfer. <i>Bioinformatics</i> , 2021, 37, i120-i132.	1.8	5
23035	Three new species of Australian anthiadine fishes, with comments on the monophyly of <i>Pseudanthias</i> Bleeker (Teleostei: Serranidae). <i>Zootaxa</i> , 2021, 4996, 49-82.	0.2	2
23036	Genome-wide Identification and Expression Analysis of NAC Transcription Factor Family Genes during Fruit and Kernel Development in Siberian Apricot. <i>Journal of the American Society for Horticultural Science</i> , 2021, 146, 276-285.	0.5	2
23037	Responses of cucumber ( <i>Cucumis sativus</i> L.) rhizosphere microbial community to some agronomic management practices. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	4



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23039	Characterization of Nucleotide Binding Site-Encoding Genes in Sweetpotato, <i>Ipomoea batatas</i> (L.) Lam., and Their Response to Biotic and Abiotic Stresses. <i>Cytogenetic and Genome Research</i> , 2021, 161, 257-271.	0.6	7
23040	Root Endophytes and <i>Ginkgo biloba</i> Are Likely to Share and Compensate Secondary Metabolic Processes, and Potentially Exchange Genetic Information by LTR-RTs. <i>Frontiers in Plant Science</i> , 2021, 12, 704985.	1.7	12
23042	Direct Molecular Evidence for an Ancient, Conserved Developmental Toolkit Controlling Posttranscriptional Gene Regulation in Land Plants. <i>Molecular Biology and Evolution</i> , 2021, 38, 4765-4777.	3.5	1
23043	Oxygen-dependent changes in binding partners and post-translational modifications regulate the abundance and activity of HIF-1 $\alpha$ /2 $\alpha$ . <i>Science Signaling</i> , 2021, 14, .	1.6	26
23044	Analyses of Virulence Genes of <i>Clavibacter michiganensis</i> subsp. <i>michiganensis</i> Strains Reveal Heterogeneity and Deletions That Correlate with Pathogenicity. <i>Microorganisms</i> , 2021, 9, 1530.	1.6	4
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23046	<i>Sandaracinobacteroides hominis</i> gen. nov., sp. nov., isolated from human skin. <i>Archives of Microbiology</i> , 2021, 203, 5067-5074.	1.0	12
23047	Is mimicry a diversification-driver in ants? Biogeography, ecology, ethology, genetics and morphology define a second West-Palaeartic <i>Colobopsis</i> species (Hymenoptera: Formicidae). <i>Zoological Journal of the Linnean Society</i> , 2022, 194, 1424-1450.	1.0	9
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23049	The <i>Welwitschia</i> genome reveals a unique biology underpinning extreme longevity in deserts. <i>Nature Communications</i> , 2021, 12, 4247.	5.8	51
23050	Amelioration of metabolic disorders by a mushroom-derived polyphenols correlates with the reduction of Ruminococcaceae in gut of DIO mice. <i>Food Science and Human Wellness</i> , 2021, 10, 442-451.	2.2	17
23051	Pliocene origins, Pleistocene refugia, and postglacial range expansions in southern devil scorpions (Vaejovidae: <i>Vaejovis carolinianus</i> ). <i>Organisms Diversity and Evolution</i> , 2021, 21, 575-590.	0.7	0
23052	The clinical importance of tandem exon duplication-derived substitutions. <i>Nucleic Acids Research</i> , 2021, 49, 8232-8246.	6.5	11
23053	Improving the phylogenetic resolution of Malaysian and Javan mahseer (Cyprinidae), <i>Tor tambroides</i> and <i>Tor tambra</i> : Whole mitogenomes sequencing, phylogeny and potential mitogenome markers. <i>Gene</i> , 2021, 791, 145708.	1.0	16
23054	The complete mitochondrial genome of a non-biting midge <i>Polypedilum unifascium</i> (Tokunaga). <i>Tj ETQq1 1 0,784314,rgBT /Over</i>	0,2	19
23055	Update on Distribution and Conservation Status of Amphibians in the Democratic People's Republic of Korea: Conclusions Based on Field Surveys, Environmental Modelling, Molecular Analyses and Call Properties. <i>Animals</i> , 2021, 11, 2057.	1.0	18
23056	African lates perches (Teleostei, Latidae, Lates): Paraphyly of Nile perch and recent colonization of Lake Tanganyika. <i>Molecular Phylogenetics and Evolution</i> , 2021, 160, 107141.	1.2	9

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23058	Genomic analysis of field pennycress ( <i>Thlaspi arvense</i> ) provides insights into mechanisms of adaptation to high elevation. <i>BMC Biology</i> , 2021, 19, 143.	1.7	23
23059	Evolution of Subfamily I.1 Lipases in <i>Pseudomonas aeruginosa</i> . <i>Current Microbiology</i> , 2021, 78, 3494-3504.	1.0	6
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23061	Genome-Wide Characterization of B-Box Gene Family and Its Roles in Responses to Light Quality and Cold Stress in Tomato. <i>Frontiers in Plant Science</i> , 2021, 12, 698525.	1.7	31
23062	Description of three new <i>Alteromonas</i> species <i>Alteromonas antoniana</i> sp. nov., <i>Alteromonas lipotruae</i> sp. nov. and <i>Alteromonas lipotruae</i> sp. nov. isolated from marine environments, and proposal for reclassification of the genus <i>Salinimonas</i> as <i>Alteromonas</i> . <i>Systematic and Applied Microbiology</i> , 2021, 44, 126226.	1.2	39
23063	Microzooplankton diversity and potential role in carbon cycling of contrasting Southern Ocean productivity regimes. <i>Journal of Marine Systems</i> , 2021, 219, 103531.	0.9	9
23064	Safety assessment of <i>Streptococcus salivarius</i> DB-B5 as a probiotic candidate for oral health. <i>Food and Chemical Toxicology</i> , 2021, 153, 112277.	1.8	7
23065	Ancient saltern metagenomics: tracking changes in microbes and their viruses from the underground to the surface. <i>Environmental Microbiology</i> , 2021, 23, 3477-3498.	1.8	6
23066	Chromosomal-scale genome assembly of <i>Eleutherococcus senticosus</i> provides insights into chromosome evolution in Araliaceae. <i>Molecular Ecology Resources</i> , 2021, 21, 2204-2220.	2.2	10
23067	Excluding spatial sampling bias does not eliminate oversplitting in DNA-based species delimitation analyses. <i>Ecology and Evolution</i> , 2021, 11, 10327-10337.	0.8	8
23069	Phylogeny and taxonomy of <i>Phyllactinia</i> species (powdery mildew: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 307). <i>Mycoscience</i> , 2021, 62, 268-280.	0.3	4
23070	A chromosome-level genome assembly of the yellowfin seabream ( <i>Acanthopagrus latus</i> ; Hottuyn, 1782) provides insights into its osmoregulation and sex reversal. <i>Genomics</i> , 2021, 113, 1617-1627.	1.3	13
23071	Circular DNA viruses identified in short-finned pilot whale and orca tissue samples. <i>Virology</i> , 2021, 559, 156-164.	1.1	4
23072	Assessment of the global circulation and endemicity of dengue. <i>Transboundary and Emerging Diseases</i> , 2021, , .	1.3	0
23073	Discovery and Characterization of Epemicins A and B, New 30-Membered Macrolides from <i>Kutzneria</i> sp. CA-103260. <i>ACS Chemical Biology</i> , 2021, 16, 1456-1468.	1.6	8
23074	Genome sequence of <i>Apostasia ramifera</i> provides insights into the adaptive evolution in orchids. <i>BMC Genomics</i> , 2021, 22, 536.	1.2	9
23075	A chromosome-level genome assembly of the miiuy croaker ( <i>Miichthys miiuy</i> ) using nanopore sequencing and Hi-C. <i>Aquaculture and Fisheries</i> , 2024, 9, 218-225.	1.2	4

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23077	A sliver of the past: The decimation of the genetic diversity of the Mexican wolf. <i>Molecular Ecology</i> , 2021, 30, 6340-6354.	2.0	6
23078	Citizen science data opens multiple avenues for iridovirus research and prompts first detection of Invertebrate iridescent virus 31 in Australia. <i>Journal of Invertebrate Pathology</i> , 2021, 183, 107619.	1.5	0
23079	Phylogenomic systematics of the spotted skunks (Carnivora, Mephitidae, Spilogale): Additional species diversity and Pleistocene climate change as a major driver of diversification. <i>Molecular Phylogenetics and Evolution</i> , 2022, 167, 107266.	1.2	9
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23081	Evolution of a neuromuscular sexual dimorphism in the <i>Drosophila montium</i> species group. <i>Scientific Reports</i> , 2021, 11, 15272.	1.6	3
23082	Genetic Diversity and Population Structure of <i>Vibrio parahaemolyticus</i> Isolated From Clinical and Food Sources. <i>Frontiers in Microbiology</i> , 2021, 12, 708795.	1.5	6
23083	Sequence of the Mitochondrial Genome of <i>Lactuca virosa</i> Suggests an Unexpected Role in <i>Lactuca sativa</i> 's Evolution. <i>Frontiers in Plant Science</i> , 2021, 12, 697136.	1.7	4
23084	SNN-SB: Combining Partial Alignment Using Modified SNN Algorithm with Segment-Based for Multiple Sequence Alignments. <i>Journal of Physics: Conference Series</i> , 2021, 1962, 012048.	0.3	0
23085	Rotavirus A Genome Segments Show Distinct Segregation and Codon Usage Patterns. <i>Viruses</i> , 2021, 13, 1460.	1.5	8
23086	Microbial Profiles of Retail Pacific Oysters ( <i>Crassostrea gigas</i> ) From Guangdong Province, China. <i>Frontiers in Microbiology</i> , 2021, 12, 689520.	1.5	8
23087	De Novo Sequencing and High-Contiguity Genome Assembly of <i>Moniezia expansa</i> Reveals Its Specific Fatty Acid Metabolism and Reproductive Stem Cell Regulatory Network. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 693914.	1.8	3
23088	The Wild Sugarcane and Sorghum Kinomes: Insights Into Expansion, Diversification, and Expression Patterns. <i>Frontiers in Plant Science</i> , 2021, 12, 668623.	1.7	18
23089	Genomics and transcriptomics yields a system-level view of the biology of the pathogen <i>Naegleria fowleri</i> . <i>BMC Biology</i> , 2021, 19, 142.	1.7	18
23091	Evolution of hes gene family in vertebrates: the hes5 cluster genes have specifically increased in frogs. <i>Bmc Ecology and Evolution</i> , 2021, 21, 147.	0.7	3
23092	A New Method for Standardizing Inland Fish Community Surveys: Characterizing Habitat Associated with Small-Bodied Fish Species, Abundance, and Size Distributions in a Highly Modified Estuary. <i>Frontiers in Environmental Science</i> , 2021, 9, .	1.5	0
23094	The sequenced genomes of nonflowering land plants reveal the innovative evolutionary history of peptide signaling. <i>Plant Cell</i> , 2021, 33, 2915-2934.	3.1	30
23095	Nationwide genomic atlas of soil-dwelling <i>Listeria</i> reveals effects of selection and population ecology on pangenome evolution. <i>Nature Microbiology</i> , 2021, 6, 1021-1030.	5.9	54

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23097	Insulin signaling regulates longevity through protein phosphorylation in <i>Caenorhabditis elegans</i> . <i>Nature Communications</i> , 2021, 12, 4568.	5.8	38
23098	Genome analysis of cotton leafroll dwarf virus reveals variability in the silencing suppressor protein, genotypes and genomic recombinants in the USA. <i>PLoS ONE</i> , 2021, 16, e0252523.	1.1	10
23099	Maternal genetic origin of the late and final Neolithic human populations from present-day Poland. <i>American Journal of Physical Anthropology</i> , 2021, 176, 223-236.	2.1	3
23100	Ribosome heterogeneity in <i>Drosophila melanogaster</i> gonads through paralog-switching. <i>Nucleic Acids Research</i> , 2022, 50, 2240-2257.	6.5	28
23101	<i>Candidatus Chlorobium masyuteum</i> , a Novel Photoferrotrophic Green Sulfur Bacterium Enriched From a Ferruginous Meromictic Lake. <i>Frontiers in Microbiology</i> , 2021, 12, 695260.	1.5	8
23102	Evolutionary history and functional characterization of Lj-TICAM-a and Lj-TICAM-b formed via lineage-specific tandem duplication in lamprey ( <i>Lampetra japonica</i> ). <i>Genomics</i> , 2021, 113, 2756-2768.	1.3	3
23105	Phylogenetic relationships among subclades within the Trinity bristle snail species complex, riverine barriers, and re-classification. <i>California Fish and Wildlife Journal</i> , 2021, , 107-145.	0.2	4
23108	Identification and Characterization of DAMs Mutations Associated With Early Blooming in Sweet Cherry, and Validation of DNA-Based Markers for Selection. <i>Frontiers in Plant Science</i> , 2021, 12, 621491.	1.7	9
23109	Natural Selection Shapes Maintenance of Orthologous sRNAs in Divergent Host-Restricted Bacterial Genomes. <i>Molecular Biology and Evolution</i> , 2021, 38, 4778-4791.	3.5	2
23110	Genome-wide analysis of the B3 transcription factors reveals that RcABI3/VP1 subfamily plays important roles in seed development and oil storage in castor bean ( <i>Ricinus communis</i> ). <i>Plant Diversity</i> , 2022, 44, 201-212.	1.8	8
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23114	Characterization, Pathogenicity, Phylogeny, and Comparative Genomic Analysis of <i>Pseudomonas tolaasii</i> Strains Isolated from Various Mushrooms in China. <i>Phytopathology</i> , 2022, 112, 521-534.	1.1	2
23115	Full Genome Evolutionary Studies of Wheat Streak Mosaic-Associated Viruses Using High-Throughput Sequencing. <i>Frontiers in Microbiology</i> , 2021, 12, 699078.	1.5	13
23117	Draft Genome Sequences of the Three <i>Massilia</i> Strains AB1, ST3, and ZL223. <i>Microbiology Resource Announcements</i> , 2021, 10, e0045121.	0.3	1
23118	Phylogenomics of the bumblebee catfishes (Siluriformes: Pseudopimelodidae) using ultraconserved elements. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 0, , .	0.6	7
23121	Adaptation-Driven Evolution of Sirtuin 1 (SIRT1), a Key Regulator of Metabolism and Aging, in Marmot Species. <i>Frontiers in Ecology and Evolution</i> , 2021, 9, .	1.1	0
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23125	Relict groups of spiny frogs indicate Late Paleogene-Early Neogene trans-Tibet dispersal of thermophile faunal elements. <i>PeerJ</i> , 2021, 9, e11793.	0.9	7
23126	Chromosome-level genome assembly of <i>Scapharca kagoshimensis</i> reveals the expanded molecular basis of heme biosynthesis in ark shells. <i>Molecular Ecology Resources</i> , 2022, 22, 295-306.	2.2	5
23127	Revealing the full biosphere structure and versatile metabolic functions in the deepest ocean sediment of the Challenger Deep. <i>Genome Biology</i> , 2021, 22, 207.	3.8	27
23128	Analysis of geographic centrality and genetic diversity in the declining grasshopper species <i>Bryodemella tuberculata</i> (Orthoptera: Oedipodinae). <i>Biodiversity and Conservation</i> , 2021, 30, 2773-2796.	1.2	3
23129	Microplastics accumulate fungal pathogens in terrestrial ecosystems. <i>Scientific Reports</i> , 2021, 11, 13214.	1.6	95
23130	<i>Halobaculum halophilum</i> sp. nov. and <i>Halobaculum salinum</i> sp. nov., isolated from salt lake and saline soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	10
23131	Genomic evidence for the parallel regression of melatonin synthesis and signaling pathways in placental mammals. <i>Open Research Europe</i> , 0, 1, 75.	2.0	3
23132	Diverse Profile of Fermentation Byproducts From Thin Stillage. <i>Frontiers in Bioengineering and Biotechnology</i> , 2021, 9, 695306.	2.0	16
23135	A New Species of the Loricariid Catfish Genus <i>Loricariichthys</i> (Teleostei: Siluriformes) from Eastern Brazil. <i>Ichthyology and Herpetology</i> , 2021, 109, .	0.3	2
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23138	The Taxonomic Status of Florida Caiman: A Molecular Reappraisal. <i>Journal of Herpetology</i> , 2021, 55, .	0.2	1
23139	Diversity and biogeography of Mediterranean freshwater blennies (Blenniidae, Salaria ). <i>Diversity and Distributions</i> , 2021, 27, 1832-1847.	1.9	6
23140	Demographic Attritions, Elevational Refugia, and the Resilience of Insect Populations to Projected Global Warming. <i>American Naturalist</i> , 2021, 198, 113-127.	1.0	5
23141	Two NLR immune receptors acquired high-affinity binding to a fungal effector through convergent evolution of their integrated domain. <i>ELife</i> , 2021, 10, .	2.8	38
23142	Regulation of polyphosphate glucokinase gene expression through cotranscriptional processing in <i>Mycobacterium tuberculosis</i> H37Rv. <i>Journal of Biochemistry</i> , 2021, 170, 593-609.	0.9	0
23143	Increasing Frequency and Transmission of HIV-1 Non-B Subtypes Among Men Who Have Sex With Men in the Swiss HIV Cohort Study. <i>Journal of Infectious Diseases</i> , 2022, 225, 306-316.	1.9	5
23145	Antibiotic-Induced Dysbiosis of Microbiota Promotes Chicken Lipogenesis by Altering Metabolomics in the Cecum. <i>Metabolites</i> , 2021, 11, 487.	1.3	18

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23147	<i>Neanthes goodayi</i> sp. nov. (Annelida, Nereididae), a remarkable new annelid species living inside deep-sea polymetallic nodules. <i>European Journal of Taxonomy</i> , 0, 760, 160-185.	0.6	12
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23151	Evolution of the MLO gene families in octoploid strawberry ( <i>Fragaria</i> – <i>Ananassa</i> ) and progenitor diploid species identified potential genes for strawberry powdery mildew resistance. <i>Horticulture Research</i> , 2021, 8, 153.	2.9	11
23152	Robust and efficient software for reference-free genomic diversity analysis of genotyping-by-sequencing data on diploid and polyploid species. <i>Molecular Ecology Resources</i> , 2022, 22, 439-454.	2.2	6
23153	Co-circulation of multiple influenza A reassortants in swine harboring genes from seasonal human and swine influenza viruses. <i>ELife</i> , 2021, 10, .	2.8	16
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23178	Proposal of Carbonactinosporaceae fam. nov. within the class Actinomycetia. Reclassification of <i>Streptomyces thermoautotrophicus</i> as <i>Carbonactinospira thermoautotrophica</i> gen. nov., comb. nov. <i>Systematic and Applied Microbiology</i> , 2021, 44, 126223.	1.2	20
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23181	The CaCA superfamily genes in <i>Saccharum</i> : comparative analysis and their functional implications in response to biotic and abiotic stress. <i>BMC Genomics</i> , 2021, 22, 549.	1.2	11
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23248	A simple method for the cultivation of the "unculturable" asterinaceous fungi (Asterinales/Dothideomycetes). <i>Journal of Microbiological Methods</i> , 2021, 187, 106272.	0.7	2
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23279	<i>Shewanella cyperi</i> sp. nov., a facultative anaerobic bacterium isolated from mangrove sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	8
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23290	Addition of <i>Trichocladium canadense</i> to an anaerobic membrane bioreactor: evaluation of the microbial composition and reactor performance. <i>Biofouling</i> , 2021, 37, 711-723.	0.8	9
23291	An angiosperm NLR Atlas reveals that NLR gene reduction is associated with ecological specialization and signal transduction component deletion. <i>Molecular Plant</i> , 2021, 14, 2015-2031.	3.9	57
23292	A remarkable legion of guests: Diversity and host specificity of army ant symbionts. <i>Molecular Ecology</i> , 2021, 30, 5229-5246.	2.0	11
23293	Diversity and transmission of Aleutian mink disease virus in feral and farmed American mink and native mustelids. <i>Virus Evolution</i> , 2021, 7, veab075.	2.2	8
23294	Genetic variation of two weevil pests of sweet potato, <i>Cylas formicarius</i> (Coleoptera: Brentidae) and <i>Euscepes postfasciatus</i> (Coleoptera: Curculionidae), in Japan based on mitochondrial DNA. <i>Applied Entomology and Zoology</i> , 2021, 56, 483-496.	0.6	0
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23298	Targeting SARS-CoV-2 Nsp3 macrodomain structure with insights from human poly(ADP-ribose) glycohydrolase (PARG) structures with inhibitors. <i>Progress in Biophysics and Molecular Biology</i> , 2021, 163, 171-186.	1.4	39
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23301	Reassessing Banana Phylogeny and Organelle Inheritance Modes Using Genome Skimming Data. <i>Frontiers in Plant Science</i> , 2021, 12, 713216.	1.7	5
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23391	<i>Veronia nyctiphanis</i> gen. nov., sp. nov., Isolated from the Stomach of the Euphausiid <i>Nyctiphanes simplex</i> (Hansen, 1911) in the Gulf of California, and Reclassification of <i>Enterovibrio pacificus</i> as <i>Veronia pacifica</i> comb. nov.. <i>Current Microbiology</i> , 2021, 78, 3782-3790.	1.0	16
23392	Mitogenomes of Accipitriformes and Cathartiformes Were Subjected to Ancestral and Recent Duplications Followed by Gradual Degeneration. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	1
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23397	Delineating virulence of <i>Vibrio campbellii</i> : a predominant luminescent bacterial pathogen in Indian shrimp hatcheries. <i>Scientific Reports</i> , 2021, 11, 15831.	1.6	17
23398	Genome Analysis of <i>Phytophthora nicotianae</i> JM01 Provides Insights into Its Pathogenicity Mechanisms. <i>Plants</i> , 2021, 10, 1620.	1.6	4
23399	Distribution of Denitrification among Haloarchaea: A Comprehensive Study. <i>Microorganisms</i> , 2021, 9, 1669.	1.6	6
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23403	Reinstatement of Indian Ocean <i>Porolithon coarctatum</i> and <i>P. Agardineri</i> based on sequencing type specimens, and <i>P. Epiphyticum</i> <i>sp. nov.</i> (Corallinales, Rhodophyta), with comments on subfamilies Hydrolithoideae and Metagoniolithoideae. <i>Botanica Marina</i> , 2021, 64, 363-377.	0.6	3
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23406	Identification and Phenotypic Characterization of Hsp90 Phosphorylation Sites That Modulate Virulence Traits in the Major Human Fungal Pathogen <i>Candida albicans</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 637836.	1.8	9
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23408	Longitudinal Secretion of Paramyxovirus RNA in the Urine of Straw-Coloured Fruit Bats ( <i>Eidolon</i> ) Tj ETQq1 1 0.784314 rgBT /Qverlock	1.5	2
23409	Gene-Metabolite Network Analysis Revealed Tissue-Specific Accumulation of Therapeutic Metabolites in <i>Mallotus japonicus</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 8835.	1.8	3
23410	Genes underlying the evolution of tetrapod testes size. <i>BMC Biology</i> , 2021, 19, 162.	1.7	3
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23413	<i>Gemella massiliensis</i> sp. nov., a new bacterium isolated from the human sputum. <i>Archives of Microbiology</i> , 2021, 203, 5817-5823.	1.0	2
23414	Molecular diversity of rhizobia-nodulating native <i>Mimosa</i> of Brazilian protected areas. <i>Archives of Microbiology</i> , 2021, 203, 5533-5545.	1.0	2
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23418	Comparative Genomics of <i>Exiguobacterium</i> Reveals What Makes a Cosmopolitan Bacterium. <i>MSystems</i> , 2021, 6, e0038321.	1.7	13
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23422	Principles of Alternating Access in Multidrug and Toxin Extrusion (MATE) Transporters. <i>Journal of Molecular Biology</i> , 2021, 433, 166959.	2.0	14
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23427	Alpha Satellite Insertion Close to an Ancestral Centromeric Region. <i>Molecular Biology and Evolution</i> , 2021, 38, 5576-5587.	3.5	4
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23429	Biosynthetic Pathway of Proanthocyanidins in Major Cash Crops. <i>Plants</i> , 2021, 10, 1792.	1.6	7
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23432	DNA methylation atlas and machinery in the developing and regenerating annelid <i>Platynereis dumerilii</i> . <i>BMC Biology</i> , 2021, 19, 148.	1.7	18
23433	Multiple sequence alignment using enhanced bird swarm align algorithm. <i>Journal of Intelligent and Fuzzy Systems</i> , 2021, 41, 1097-1114.	0.8	0
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23437	Phylogenetics and infrafamilial classification of Commelinaceae (Commelinales). <i>Botanical Journal of the Linnean Society</i> , 2022, 198, 117-130.	0.8	2
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23446	Interspecies Recombination Has Driven the Macroevolution of Cassava Mosaic Begomoviruses. <i>Journal of Virology</i> , 2021, 95, e0054121.	1.5	23
23447	Crystal Structure of Inorganic Pyrophosphatase From <i>Schistosoma japonicum</i> Reveals the Mechanism of Chemicals and Substrate Inhibition. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 712328.	1.8	1
23448	Mixed Acid Fermentation of Carbohydrate-Rich Dairy Manure Hydrolysate. <i>Frontiers in Bioengineering and Biotechnology</i> , 2021, 9, 724304.	2.0	11
23449	Megabase-scale presence-absence variation with <i>Tripsacum</i> origin was under selection during maize domestication and adaptation. <i>Genome Biology</i> , 2021, 22, 237.	3.8	21
23450	A new species of <i>Solaropsis</i> Beck, 1837 (Gastropoda: Stylomatophora: Solaropsidae) from the Brazilian Amazon. <i>Folia Malacologica</i> , 2021, 29, 178-185.	0.1	1
23451	Closely related Lak megaphages replicate in the microbiomes of diverse animals. <i>IScience</i> , 2021, 24, 102875.	1.9	20
23452	Natural infection of Delta mutant of SARS-CoV-2 in Asiatic lions of India. <i>Transboundary and Emerging Diseases</i> , 2022, 69, 3047-3055.	1.3	38
23453	ANTAGONISTIC INTERACTIONS BETWEEN <i>Trichoderma</i> spp. AND <i>Phytophthora palmivora</i> (Butler) FROM OIL PALM IN COLOMBIA. <i>European Journal of Plant Pathology</i> , 2021, 161, 751.	0.8	6
23455	Testing the phylogenetic hypotheses of Stevardiinae Gill, 1858 in light of new phenotypic data (Teleostei: Characidae). <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2021, 59, 2060-2085.	0.6	7
23456	Metagenome-Assembled Genomes of Novel Taxa from an Acid Mine Drainage Environment. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0077221.	1.4	9
23457	Growth Enhancement of <i>Arabidopsis</i> ( <i>Arabidopsis thaliana</i> ) and Onion ( <i>Allium cepa</i> ) With Inoculation of Three Newly Identified Mineral-Solubilizing Fungi in the Genus <i>Aspergillus</i> Section <i>Nigri</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 705896.	1.5	10

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23459	Redondovirus Diversity and Evolution on Global, Individual, and Molecular Scales. <i>Journal of Virology</i> , 2021, 95, e0081721.	1.5	12
23460	Detection of bat-associated circoviruses in Korean bats. <i>Archives of Virology</i> , 2021, 166, 3013-3021.	0.9	1
23461	Testing the Genomic Shock Hypothesis Using Transposable Element Expression in Yeast Hybrids. <i>Frontiers in Fungal Biology</i> , 2021, 2, .	0.9	6
23462	Genetic diversity and population structure of <i>Rhipicephalus sanguineus sensu lato</i> across different regions of Colombia. <i>Parasites and Vectors</i> , 2021, 14, 424.	1.0	13
23463	Risk of transfusion-transmitted hepatitis E virus infection from pool-tested platelets and plasma. <i>Journal of Hepatology</i> , 2022, 76, 46-52.	1.8	17
23464	Ancient viral genomes reveal introduction of human pathogenic viruses into Mexico during the transatlantic slave trade. <i>ELife</i> , 2021, 10, .	2.8	23
23466	Dominant Bacterial Phyla from the Human Gut Show Widespread Ability To Transform and Conjugate Bile Acids. <i>MSystems</i> , 2021, 6, e0080521.	1.7	70
23467	<i>Xanthobacter oligotrophicus</i> sp.nov., isolated from paper mill sewage. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	5
23468	The Interspecific Fungal Hybrid <i>Verticillium longisporum</i> Displays Subgenome-Specific Gene Expression. <i>MBio</i> , 2021, 12, e0149621.	1.8	8
23469	Invasive snails, parasite spillback, and potential parasite spillover drive parasitic diseases of <i>Hippopotamus amphibius</i> in artificial lakes of Zimbabwe. <i>BMC Biology</i> , 2021, 19, 160.	1.7	19
23470	Ancient Gene Capture and Recent Gene Loss Shape the Evolution of Orthopoxvirus-Host Interaction Genes. <i>MBio</i> , 2021, 12, e0149521.	1.8	74
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23473	Single-Strand Conformation Polymorphism Fingerprint Method for Dictyostelids. <i>Frontiers in Microbiology</i> , 2021, 12, 708685.	1.5	2
23474	Positive selection as a key player for SARS-CoV-2 pathogenicity: Insights into ORF1ab, S and E genes. <i>Virus Research</i> , 2021, 302, 198472.	1.1	27
23475	Massive gene rearrangement in mitogenomes of phytoseiid mites. <i>International Journal of Biological Macromolecules</i> , 2021, 186, 33-39.	3.6	10
23476	Biochemical, structural and dynamical studies reveal strong differences in the thermal-dependent allosteric behavior of two extremophilic lactate dehydrogenases. <i>Journal of Structural Biology</i> , 2021, 213, 107769.	1.3	4
23478	Experimental and computational investigation of enzyme functional annotations uncovers misannotation in the EC 1.1.3.15 enzyme class. <i>PLoS Computational Biology</i> , 2021, 17, e1009446.	1.5	21

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23480	Novel structural annotation and functional expression analysis of GTP_EFTU conserved genes in pepper based on the PacBio sequencing data. <i>Horticultural Plant Journal</i> , 2021, 7, 443-456.	2.3	6
23482	Molecular characterization of the spectacled caiman ( <i>Caiman crocodilus</i> ) in the upper Magdalena River basin, Colombia: Demographic and phylogeographic insights. <i>Systematics and Biodiversity</i> , 2021, 19, 1040-1048.	0.5	5
23483	Microbiome degrading linear alkylbenzene sulfonate in activated sludge. <i>Journal of Hazardous Materials</i> , 2021, 418, 126365.	6.5	9
23484	Characterization and genomic analysis of the first <i>Oceanospirillum</i> phage, vB_OliS_GJ44, representing a novel siphoviral cluster. <i>BMC Genomics</i> , 2021, 22, 675.	1.2	7
23485	The widely distributed, edible seaweeds in Peru, <i>Chondracanthus chamissoi</i> and <i>Chondracanthus chamissoi</i> f. <i>glomeratus</i> (Gigartinaceae, Rhodophyta), are morphologically diverse but not phylogenetically distinct. <i>Journal of the World Aquaculture Society</i> , 2021, 52, 1290-1311.	1.2	3
23486	Viruses Without Borders: Global Analysis of the Population Structure, Haplotype Distribution, and Evolutionary Pattern of Iris Yellow Spot Orthotospovirus (Family Tospoviridae, Genus) Tj ETQq0 0 0 rgBT /Overlock 1.0 Tf 50 497 Td (Orthotospovirus)	1.0	497
23487	Genomic Diversity of Pigeon Pea ( <i>Cajanus cajan</i> L. Millsp.) Endosymbionts in India and Selection of Potential Strains for Use as Agricultural Inoculants. <i>Frontiers in Plant Science</i> , 2021, 12, 680981.	1.7	12
23489	Sequence diversity and evolution of infectious bursal disease virus in Iraq. <i>F1000Research</i> , 2021, 10, 293.	0.8	2
23490	<i>Methylomonas albis</i> sp. nov. and <i>Methylomonas fluvii</i> sp. nov.: Two cold-adapted methanotrophs from the river Elbe and emended description of the species <i>Methylovulum psychrotolerans</i> . <i>Systematic and Applied Microbiology</i> , 2021, 44, 126248.	1.2	18
23491	Biodiversity on sale: The shark meat market threatens elasmobranchs in Brazil. <i>Aquatic Conservation: Marine and Freshwater Ecosystems</i> , 2021, 31, 3437-3450.	0.9	12
23492	Tricycler: consensus long-read assemblies for bacterial genomes. <i>Genome Biology</i> , 2021, 22, 266.	3.8	175
23493	Neutral evolution test of the spike protein of SARS-CoV-2 and its implications in the binding to ACE2. <i>Scientific Reports</i> , 2021, 11, 18847.	1.6	13
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23496	Unraveling the bacterial diversity of Cangar Hot Spring, Indonesia by Next Generation Sequencing of 16S rRNA gene. <i>Biodiversitas</i> , 2021, 22, .	0.2	0
23497	Accurate consistency-based MSA reducing the memory footprint. <i>Computer Methods and Programs in Biomedicine</i> , 2021, 208, 106237.	2.6	2
23498	<i>Buchwaldoboletus xylophilus</i> and <i>Phlebopus portentosus</i> , two non-ectomycorrhizal boletes from tropical China. <i>Phytotaxa</i> , 2021, 520, 137-154.	0.1	7

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23499	The stem rust fungus <i>Puccinia graminis</i> f. sp. <i>tritici</i> induces centromeric small RNAs during late infection that are associated with genome-wide DNA methylation. <i>BMC Biology</i> , 2021, 19, 203.	1.7	15
23500	Detection of Cacao Mild Mosaic Virus (CaMMV) Using Nested PCR and Evidence of Uneven Distribution in Leaf Tissue. <i>Agronomy</i> , 2021, 11, 1842.	1.3	7
23501	Cloning and characterization of Thioredoxin 1 from the Cnidarian <i>Hydra</i> . <i>Journal of Biochemistry</i> , 2022, 171, 41-51.	0.9	4
23502	<i>Photorhabdus hindustanensis</i> sp. nov., <i>Photorhabdus akhurstii</i> subsp. <i>akhurstii</i> subsp. nov., and <i>Photorhabdus akhurstii</i> subsp. <i>bharatensis</i> subsp. nov., isolated from Heterorhabditis entomopathogenic nematodes. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	19
23503	Merging the cryptic genera <i>Radicilingua</i> and <i>Calonitophyllum</i> (Delesseriaceae, Rhodophyta): molecular phylogeny and taxonomic revision. <i>Algae</i> , 2021, 36, 165-174.	0.9	1
23504	Incipient diploidization of the medicinal plant <i>Perilla</i> within 10,000 years. <i>Nature Communications</i> , 2021, 12, 5508.	5.8	35
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23506	Evidence from the resurrected family Polyrrhabdinidae Kamm, 1922 (Apicomplexa: Gregarinomorpha) supports the epimerite, an attachment organelle, as a major eugregarine innovation. <i>PeerJ</i> , 2021, 9, e11912.	0.9	5
23507	A vaccine-induced public antibody protects against SARS-CoV-2 and emerging variants. <i>Immunity</i> , 2021, 54, 2159-2166.e6.	6.6	52
23509	New record of <i>Golovinomyces ambrosiae</i> on <i>Solanum azureum</i> (Solanaceae) in Mexico. <i>Botany</i> , 0, , .	0.5	1
23510	The genomic basis of army ant chemosensory adaptations. <i>Molecular Ecology</i> , 2021, 30, 6627-6641.	2.0	9
23511	Influence of Pleistocene climatic oscillations on the phylogeography and demographic history of endemic vulnerable trees (section <i>Magnolia</i> ) of the Tropical Montane Cloud Forest in Mexico. <i>PeerJ</i> , 2021, 9, e12181.	0.9	4
23512	Lineage-Specific Variation in IR Boundary Shift Events, Inversions, and Substitution Rates among <i>Caprifoliaceae</i> s.l. (Dipsacales) Plastomes. <i>International Journal of Molecular Sciences</i> , 2021, 22, 10485.	1.8	4
23513	A structural model for (GlcNAc) <sub>2</sub> translocation via a periplasmic chitooligosaccharide-binding protein from marine <i>Vibrio</i> bacteria. <i>Journal of Biological Chemistry</i> , 2021, 297, 101071.	1.6	3
23514	Evolution of protective symbiosis in palaemonid shrimps (Decapoda: Caridea) with emphases on host spectrum and morphological adaptations. <i>Molecular Phylogenetics and Evolution</i> , 2021, 162, 107201.	1.2	14
23515	Specific methylation of (11R)-carlactonoic acid by an <i>Arabidopsis</i> SABATH methyltransferase. <i>Planta</i> , 2021, 254, 88.	1.6	18
23516	The Archean origin of oxygenic photosynthesis and extant cyanobacterial lineages. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2021, 288, 20210675.	1.2	48
23517	Chloroplast genomes of five <i>Oedogonium</i> species: genome structure, phylogenetic analysis and adaptive evolution. <i>BMC Genomics</i> , 2021, 22, 707.	1.2	11

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23519	MOSGA 2: Comparative genomics and validation tools. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 5504-5509.	1.9	4
23521	Canker and wood rot pathogens present in young lemon orchards in southwest Arizona. <i>Plant Pathology</i> , 0, , .	1.2	3
23522	Deltaproteobacterium Strain KaireiS1, a Mesophilic, Hydrogen-Oxidizing and Sulfate-Reducing Bacterium From an Inactive Deep-Sea Hydrothermal Chimney. <i>Frontiers in Microbiology</i> , 2021, 12, 686276.	1.5	4
23523	The complete chloroplast genome of <i>Cycas bifida</i> , an extremely small population protected species. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2960-2961.	0.2	2
23524	Spontaneous changes in somatic compatibility in <i>Fusarium circinatum</i> . <i>Fungal Biology</i> , 2021, 125, 725-732.	1.1	1
23525	Haploid Genome Analysis Reveals a Tandem Cluster of Four HSP20 Genes Involved in the High-Temperature Adaptation of <i>Coriopsis trogii</i> . <i>Microbiology Spectrum</i> , 2021, 9, e0028721.	1.2	7
23526	Genomic Sequence Analysis of Methicillin- and Carbapenem-Resistant Bacteria Isolated from Raw Sewage. <i>Microbiology Spectrum</i> , 2021, 9, e0012821.	1.2	1
23527	Epidemiological and genetic characterization of measles virus circulating strains at Marseille, France during 2017-2019 measles outbreak. <i>Journal of Infection</i> , 2021, 83, 361-370.	1.7	6
23528	A genomic perspective on an old question: <i>Salmo trouts</i> or <i>Salmo trutta</i> (Teleostei: Salmonidae)?. <i>Molecular Phylogenetics and Evolution</i> , 2021, 162, 107204.	1.2	33
23529	Restricted Geographic Sampling Yields Low Parasitism Rates but Surprisingly Diverse Host Associations in Avian Lice (Insecta: Phthiraptera) from South Texas. <i>Diversity</i> , 2021, 13, 430.	0.7	1
23530	An inferred functional impact map of genetic variants in rice. <i>Molecular Plant</i> , 2021, 14, 1584-1599.	3.9	48
23531	First report of <i>Bursaphelenchus leoni</i> Baujard, 1980 (Nematoda: Parasitaphelenchidae) from Pine Forests of Turkey. <i>Kahramanmaraş S4t4S54m Aeniversitesi TarÄ±m Ve DoÄŸa Dergisi</i> , 0, , .	0.2	0
23532	Specification and DNA Barcoding of Thai Traditional Remedy for Chronic Kidney Disease: Pikad Tri-phol-sa-mut-than. <i>Plants</i> , 2021, 10, 2023.	1.6	2
23533	Novel Symbiotic Association Between <i>Euwallacea Ambrosia</i> Beetle and <i>Fusarium</i> Fungus on Fig Trees in Japan. <i>Frontiers in Microbiology</i> , 2021, 12, 725210.	1.5	9
23534	The Evolution of Alternative Buoyancy Mechanisms in Freshwater Fish Eggs. <i>Frontiers in Ecology and Evolution</i> , 2021, 9, .	1.1	6
23535	Relaxed selection on male mitochondrial genes in DUI bivalves eases the need for mitonuclear coevolution. <i>Journal of Evolutionary Biology</i> , 2021, 34, 1722-1736.	0.8	10
23536	Broad cross-reactivity across sarbecoviruses exhibited by a subset of COVID-19 donor-derived neutralizing antibodies. <i>Cell Reports</i> , 2021, 36, 109760.	2.9	80



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23539	Phenotypic and genotypic characterization of the new <i>Bacillus cereus</i> phage SWEP1. <i>Archives of Virology</i> , 2021, 166, 3183-3188.	0.9	8
23540	Exploration of Social Spreading Reveals That This Behavior Is Prevalent among <i>Pedobacter</i> and <i>Pseudomonas fluorescens</i> Isolates and That There Are Variations in the Induction of the Phenotype. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0134421.	1.4	0
23542	Four-Step Pathway from Phenylpyruvate to Benzylamine, an Intermediate to the High-Energy Propellant CL-20. <i>ACS Synthetic Biology</i> , 2021, 10, 2187-2196.	1.9	2
23543	Eight species of <i>Lintonium</i> Stunkard & Nigrelli, 1930 (Digenea: Fellodistomidae) in Australian tetraodontiform fishes. <i>Systematic Parasitology</i> , 2021, 98, 595-624.	0.5	4
23544	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
23545	Human respiratory syncytial virus diversity and epidemiology among patients hospitalized with severe respiratory illness in South Africa, 2012–2015. <i>Influenza and Other Respiratory Viruses</i> , 2022, 16, 222-235.	1.5	9
23546	Tracing Eukaryotic Ribosome Biogenesis Factors Into the Archaeal Domain Sheds Light on the Evolution of Functional Complexity. <i>Frontiers in Microbiology</i> , 2021, 12, 739000.	1.5	11
23547	Anaerobic 3-methylhopanoid production by an acidophilic photosynthetic purple bacterium. <i>Archives of Microbiology</i> , 2021, 203, 6041-6052.	1.0	5
23548	Comparative Genomics Provides Insight into the Function of Broad-Host Range Sponge Symbionts. <i>MBio</i> , 2021, 12, e0157721.	1.8	5
23550	Chromosome-Level Genome Assembly and Annotation of the Fiber Flax ( <i>Linum usitatissimum</i> ) Genome. <i>Frontiers in Genetics</i> , 2021, 12, 735690.	1.1	15
23551	Colonization and Development of the Fecal Microflora of South China Tiger Cubs (<i>Panthera tigris amoyensis</i>) by Sequencing of the 16S rRNA Gene. <i>Microbial Physiology</i> , 2022, 32, 18-29.	1.1	4
23552	Multiple sequence alignment quality comparison in T-Coffee, MUSCLE and M-Coffee based on different benchmarks. <i>Cumhuriyet Science Journal</i> , 2021, 42, 526-535.	0.1	0
23553	Genomic Stability and Genetic Defense Systems in <i>Dolosigranulum pigrum</i> , a Candidate Beneficial Bacterium from the Human Microbiome. <i>MSystems</i> , 2021, 6, e0042521.	1.7	11
23554	Global Analysis of the Specificities and Targets of Endoribonucleases from <i>Escherichia coli</i> Toxin-Antitoxin Systems. <i>MBio</i> , 2021, 12, e0201221.	1.8	15
23555	Analysis of major sperm proteins in two nematode species from two classes, <i>Enoplus brevis</i> (Enoplea,) Tj ETQq1 1 0.784314 rgBT /Over homology of protein sequences than expected for Nematoda phylum. <i>Organisms Diversity and Evolution</i> , 2022, 22, 117-130.	0.7	0
23556	A vast pool of lineage-specific microproteins encoded by long non-coding RNAs in plants. <i>Nucleic Acids Research</i> , 2021, 49, 10328-10346.	6.5	33
23557	Elm zigzag sawfly, <i>Aproceros leucopoda</i> (Hymenoptera: Argidae), recorded for the first time in North America through community science. <i>Canadian Entomologist</i> , 2022, 154, .	0.4	9

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23560	The complete chloroplast genome sequence of <i>Artocarpus gomezianus</i> (Moraceae) from Xishuangbanna, China. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2890-2892.	0.2	0
23561	Transcriptome analysis and genetic diversity of <i>Allium victorialis</i> germplasms from the Changbai Mountains. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2915-2923.	0.2	1
23562	Structural basis of P[II] rotavirus evolution and host ranges under selection of histo-blood group antigens. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	9
23563	G-quadruplexes in genomes of viruses infecting eukaryotes or prokaryotes are under different selection pressures from hosts. <i>Journal of Genetics and Genomics</i> , 2022, 49, 20-29.	1.7	6
23564	Dynamics of integron structures across a wastewater network – Implications to resistance gene transfer. <i>Water Research</i> , 2021, 206, 117720.	5.3	18
23565	The <i>Euscaphis japonica</i> genome and the evolution of malvids. <i>Plant Journal</i> , 2021, 108, 1382-1399.	2.8	6
23566	Haplotype divergence supports long-term asexuality in the oribatid mite <i>Oppiella nova</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	23
23567	Revision of the genus <i>Restingomyces</i> , including two new species from Mexico. <i>Mycologia</i> , 2021, 113, 1-11.	0.8	1
23568	Liste et identification pour les Anomaloniinae de la faune de France, avec la description d'une espèce nouvelle du genre Therion (Hymenoptera, Ichneumonidae). <i>Bulletin De La Société Entomologique De France</i> , 2021, 126, 253-328.	0.1	2
23569	Comparative Mitogenomic Analysis and the Evolution of <i>Rhizoctonia solani</i> Anastomosis Groups. <i>Frontiers in Microbiology</i> , 2021, 12, 707281.	1.5	5
23570	The GRAS gene family and its roles in seed development in litchi ( <i>Litchi chinensis</i> Sonn). <i>BMC Plant Biology</i> , 2021, 21, 423.	1.6	8
23571	Testing the potential contribution of <i>Wolbachia</i> to speciation when cytoplasmic incompatibility becomes associated with host-related reproductive isolation. <i>Molecular Ecology</i> , 2022, 31, 2935-2950.	2.0	8
23572	Capabilities of bioinformatics tools for optimizing physicochemical features of proteins used in Nano biosensors: A short overview of the tools related to bioinformatics. <i>Biochemistry and Biophysics Reports</i> , 2021, 27, 101094.	0.7	1
23573	Molecular phylogenetics of Malesian <i>Diospyros</i> (Ebenaceae) based trnL-F spacer sequences. <i>Biodiversitas</i> , 2021, 22, .	0.2	0
23574	Evolutionary history of the roan antelope across its African range. <i>Journal of Biogeography</i> , 2021, 48, 2812-2827.	1.4	4
23575	Observations on the population genetic structure of the leaf galling nematode, <i>Ditylenchus gallaeformans</i> . <i>Phytopathology</i> , 2021, .	1.1	0
23577	Integrated Assessment of Ocean Acidification Risks to Pteropods in the Northern High Latitudes: Regional Comparison of Exposure, Sensitivity and Adaptive Capacity. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	23

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23579	The taxonomic distribution of histamine-secreting bacteria in the human gut microbiome. <i>BMC Genomics</i> , 2021, 22, 695.	1.2	22
23580	Complete Genome Sequence of <i>Weissella confusa</i> LM1 and Comparative Genomic Analysis. <i>Frontiers in Microbiology</i> , 2021, 12, 749218.	1.5	6
23581	Chromosome-level genome assembly of <i>Gynostemma pentaphyllum</i> provides insights into gypenoside biosynthesis. <i>DNA Research</i> , 2021, 28, .	1.5	14
23582	Haemoprotozoan surveillance in peri-urban native and introduced wildlife from Australia. <i>Current Research in Parasitology and Vector-borne Diseases</i> , 2021, 1, 100052.	0.7	8
23583	Protein-coding repeat polymorphisms strongly shape diverse human phenotypes. <i>Science</i> , 2021, 373, 1499-1505.	6.0	96
23584	Chromosome-scale assembly reveals asymmetric paleo-subgenome evolution and targets for the acceleration of fungal resistance breeding in the nut crop, pecan. <i>Plant Communications</i> , 2021, 2, 100247.	3.6	10
23585	High-Quality de novo Chromosome-Level Genome Assembly of a Single <i>Bombyx mori</i> With BmNPV Resistance by a Combination of PacBio Long-Read Sequencing, Illumina Short-Read Sequencing, and Hi-C Sequencing. <i>Frontiers in Genetics</i> , 2021, 12, 718266.	1.1	5
23586	Isolation and endemism in subterranean aquatic snails: unexpected case of <i>Montenegrospeum bogici</i> (Pezomachus) et al. (2021) (Gastropoda: Truncatelloidea: Hydrobiidae). <i>Hydrobiologia</i> , 2021, 848, 4967-4990.	1.0	7
23587	A high-quality chromosome-level genome of wild <i>Rosa rugosa</i> . <i>DNA Research</i> , 2021, 28, .	1.5	10
23588	Mitochondrial loci enable specific qPCR detection of the pathogen causing contemporary impatiens downy mildew epidemics. <i>Plant Disease</i> , 2021, , .	0.7	3
23589	<i>Flavobacterium ercyesense</i> sp. nov., a putative non-pathogenic fish symbiont. <i>Archives of Microbiology</i> , 2021, 203, 5783-5792.	1.0	10
23590	Transient effect of bisphenol A (BPA) and di-(2-ethylhexyl) phthalate (DEHP) on the cosmopolitan marine diatom <i>Chaetoceros decipiens-lorenzianus</i> . <i>Environmental Pollution</i> , 2021, 285, 117362.	3.7	5
23591	Baseline Hepatitis C Virus NS5A Resistance-Associated Polymorphisms in Patients With and Without Human Immunodeficiency Virus Coinfection in Mexico. <i>Microbial Drug Resistance</i> , 2021, 27, 1195-1202.	0.9	1
23592	Investigation of the Food-Transmitted Parasites <i>Trichinella</i> spp. and <i>Alaria</i> spp. in Wild Boars in Greece by Classical and Molecular Methods and Development of a Novel Real-Time PCR for <i>Alaria</i> spp. Detection. <i>Animals</i> , 2021, 11, 2803.	1.0	1
23593	Characterization of the $\beta$ -tubulin gene family in <i>Ascaris lumbricoides</i> and <i>Ascaris suum</i> and its implication for the molecular detection of benzimidazole resistance. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009777.	1.3	13
23594	Comparative transcriptome analysis at the onset of speciation in a mimetic butterfly "The Ithomiini <i>Melinaea marsaeus</i> ". <i>Journal of Evolutionary Biology</i> , 2021, 34, 1704-1721.	0.8	2
23595	<i>Candida albicans</i> <i>ENT2</i> contributes to efficient endocytosis, cell wall integrity, filamentation, and virulence. <i>MSphere</i> , 2021, 6, e0070721.	1.3	6

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23598	Growth Promotion of Rapeseed ( <i>Brassica napus</i> L.) and Blackleg Disease ( <i>Leptosphaeria maculans</i> ) Suppression Mediated by Endophytic Bacteria. <i>Agronomy</i> , 2021, 11, 1966.	1.3	10
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23607	Spread of Mink SARS-CoV-2 Variants in Humans: A Model of Sarbecovirus Interspecies Evolution. <i>Frontiers in Microbiology</i> , 2021, 12, 675528.	1.5	35
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23621	<i>Phallus chiangmaiensis</i> sp. nov. and a Record of <i>P. merulinus</i> in Thailand. <i>Mycobiology</i> , 2021, 49, 1-15.	0.6	0
23622	Hidden service publishing flow homology comparison using profile hidden markov model. <i>International Journal of Intelligent Systems</i> , 0, , .	3.3	1
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23630	Novel putative polyethylene terephthalate (PET) plastic degrading enzymes from the environmental metagenome. <i>Proteins: Structure, Function and Bioinformatics</i> , 2022, 90, 504-511.	1.5	17
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23636	Comparative Phylogenomic Analysis Reveals Evolutionary Genomic Changes and Novel Toxin Families in Endophytic <i>Liberibacter</i> Pathogens. <i>Microbiology Spectrum</i> , 2021, 9, e0050921.	1.2	6

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23640	Genomic Insights into the Ecological Role and Evolution of a Novel <i>Thermoplasmata</i> Order, <i>Candidatus</i> <i>Sysuiplasmatales</i> . <i>Applied and Environmental Microbiology</i> , 2021, 87, e0106521.	1.4	3
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23642	Methyl jasmonate elicits distinctive hydrolyzable tannin, flavonoid, and phyto-oxylipin responses in pomegranate ( <i>Punica granatum</i> L.) leaves. <i>Planta</i> , 2021, 254, 89.	1.6	6
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23651	MtNPF6.5 mediates chloride uptake and nitrate preference in <i>Medicago</i> roots. <i>EMBO Journal</i> , 2021, 40, e106847.	3.5	14
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23654	Phylogenetic Comparison and Splicing Analysis of the U1 snRNP-specific Protein U1C in Eukaryotes. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 696319.	1.6	1
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23671	Genomic Investigation of Methicillin-Resistant <i>Staphylococcus aureus</i> ST113 Strains Isolated from Tertiary Care Hospitals in Pakistan. <i>Antibiotics</i> , 2021, 10, 1121.	1.5	4
23672	<i>Oceaniferula marina</i> gen.nov., sp.nov., an anti-fluoroquinolone bacterium isolated from marine sediment. <i>Antonie Van Leeuwenhoek</i> , 2021, 114, 1855-1865.	0.7	8
23673	Whole-Genome Sequencing Evaluation of MALDI-TOF MS as a Species Identification Tool for <i>Streptococcus suis</i> . <i>Journal of Clinical Microbiology</i> , 2021, 59, e0129721.	1.8	8
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23683	Transitions to asexuality and evolution of gene expression in <i>Artemia</i> brine shrimp. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2021, 288, 20211720.	1.2	6
23684	The genome of the naturally evolved obesity-prone Ossabaw miniature pig. <i>IScience</i> , 2021, 24, 103081.	1.9	9
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23724	Virome analysis for identification of viruses associated with asymptomatic infection of purple passion fruit ( <i>Passiflora edulis</i> f. <i>edulis</i> ) in Colombia. Journal of Horticultural Science and Biotechnology, 2022, 97, 187-200.	0.9	3
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23837	<i>Alkalicaulis</i> <i>satelles</i> gen. nov., sp. nov., a novel haloalkaliphile isolated from a laboratory culture cyanobacterium <i>Geitlerinema</i> species and proposals of <i>Maricaulaceae</i> fam. nov., <i>Robiginitomaculaceae</i> fam. nov., <i>Maricaulales</i> ord. nov. and <i>Hyphomonadales</i> ord. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	37
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23846	Metabolic Phenotypes as Potential Biomarkers for Linking Gut Microbiome With Inflammatory Bowel Diseases. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 603740.	1.6	8
23847	Immunoinformatics aided design of peptide-based vaccines against ebolaviruses. <i>Vitamins and Hormones</i> , 2021, 117, 157-187.	0.7	1
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23866	Local Alignment of DNA Sequence Based on Deep Reinforcement Learning. <i>IEEE Open Journal of Engineering in Medicine and Biology</i> , 2021, 2, 170-178.	1.7	4
23867	Nucleotide Signature and SNP Double Peak Methods Detect Adulterants and Substitution in Panax Products. <i>Compendium of Plant Genomes</i> , 2021, , 31-44.	0.3	0
23868	Methicillin-resistant <i>Staphylococcus pseudintermedius</i> synthesizes deoxyadenosine to cause persistent infection. <i>Virulence</i> , 2021, 12, 989-1002.	1.8	8
23869	An Optimization Approach for Multiple Sequence Alignment using Divide-Conquer and Genetic Algorithm. <i>International Journal of Advanced Computer Science and Applications</i> , 2021, 12, .	0.5	0
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23877	Genome-wide analysis of general phenylpropanoid and monolignol-specific metabolism genes in sugarcane. <i>Functional and Integrative Genomics</i> , 2021, 21, 73-99.	1.4	10
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24060	Conserved biophysical features of the CaV2 presynaptic Ca <sup>2+</sup> channel homologue from the early-diverging animal <i>Trichoplax adhaerens</i> . <i>Journal of Biological Chemistry</i> , 2020, 295, 18553-18578.	1.6	4

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24074	Molecular data reveal hidden diversity in the central Andean species <i>Weberbaueria spathulifolia</i> (Thelypodieae: Brassicaceae). Botanical Journal of the Linnean Society, 2020, 193, 523-545.	0.8	1
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24076	viruSITEâ€™”integrated database for viral genomics. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw162.	1.4	62
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24097	OUP accepted manuscript. <i>Virus Evolution</i> , 2020, 6, veaa007.	2.2	34

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24099	Phylogenetic revision of the shrimp genera <i>Ephyrina</i> , <i>Meningodora</i> and <i>Notostomus</i> (Acanthephyridae: Caridea). <i>Zoological Journal of the Linnean Society</i> , 2021, 193, 1002-1019.	1.0	7
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24101	Species Identification in Plant-Associated Prokaryotes and Fungi Using DNA. <i>Phytobiomes Journal</i> , 2020, 4, 103-114.	1.4	7
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24103	First Report of <i>Orobanche laxissima</i> Parasitizing Pallas Ash ( <i>Fraxinus pallisae</i> ) in Georgia. <i>Plant Disease</i> , 2020, 104, 1878-1878.	0.7	4
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24105	Phylogenomics insights into order and families of Lysobacterales. <i>Access Microbiology</i> , 2019, 1, e000015.	0.2	22
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24107	<i>Moniliella carnis</i> sp. nov. and <i>Moniliella dehoogii</i> sp. nov., two novel species of black yeasts isolated from meat processing environments. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2012, 62, 3088-3094.	0.8	10
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24111	<i>Fusibacter fontis</i> sp. nov., a sulfur-reducing, anaerobic bacterium isolated from a mesothermic Tunisian spring. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 3501-3506.	0.8	38
24112	<i>Bradyrhizobium tropiciagri</i> sp. nov. and <i>Bradyrhizobium emrapense</i> sp. nov., nitrogen-fixing symbionts of tropical forage legumes. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 4424-4433.	0.8	72
24113	<i>Hymenobacter terrenus</i> sp. nov., isolated from biological soil crusts. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 4557-4562.	0.8	16
24114	<i>Bacillus endolithicus</i> sp. nov., isolated from pebbles. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 4568-4573.	0.8	13
24115	<i>Alistipes inops</i> sp. nov. and <i>Coprobacter secundus</i> sp. nov., isolated from human faeces. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 4580-4588.	0.8	60

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24117	Evolutionary relationships of completely sequenced Clostridia species and close relatives. International Journal of Systematic and Evolutionary Microbiology, 2015, 65, 4276-4283.	0.8	19
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24122	<i>Athalassotoga saccharophila</i> gen. nov., sp. nov., isolated from an acidic terrestrial hot spring, and proposal of Mesoaciditogales ord. nov. and Mesoaciditogaceae fam. nov. in the phylum Thermotogae. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 1045-1051.	0.8	40
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24124	<i>Trichosporon heliocopridis</i> sp. nov., a urease-negative basidiomycetous yeast associated with dung beetles ( <i>Heliocopris bucephalus</i> Fabricius). International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 1180-1186.	0.8	4
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24130	<i>Mycoavidus cysteinexigens</i> gen. nov., sp. nov., an endohyphal bacterium isolated from a soil isolate of the fungus <i>Mortierella elongata</i> . International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 2052-2057.	0.8	76
24131	<i>Brucella vulpis</i> sp. nov., isolated from mandibular lymph nodes of red foxes ( <i>Vulpes vulpes</i> ). International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 2090-2098.	0.8	155
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24133	<i>Racemicystis crocea</i> gen. nov., sp. nov., a soil myxobacterium in the family Polyangiaceae. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 2389-2395.	0.8	21

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24136	<i>Bradyrhizobium stylosanthis</i> sp. nov., comprising nitrogen-fixing symbionts isolated from nodules of the tropical forage legume <i>Stylosanthes</i> spp.. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 3078-3087.	0.8	38
24137	<i>Flavisolibacter tropicus</i> sp. nov., isolated from tropical soil. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 3413-3419.	0.8	22
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24139	<i>Lactococcus garvieae</i> subsp. bovis subsp. nov., lactic acid bacteria isolated from wild gaur ( <i>Bos</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 3805-3809.	0.8	29
24140	<i>Gordonia hongkongensis</i> sp. nov., isolated from blood culture and peritoneal dialysis effluent of patients in Hong Kong. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 3942-3950.	0.8	22
24141	<i>Acinetobacter dijkschoorniae</i> sp. nov., a member of the <i>Acinetobacter calcoaceticus</i> " <i>Acinetobacter baumannii</i> complex mainly recovered from clinical samples in different countries. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 4105-4111.	0.8	96
24142	Phylogenetic characterisation of two novel Anaplasmataceae from Australian <i>Ixodes holocyclus</i> ticks: "Candidatus <i>Neoehrlichia australis</i> " and "Candidatus <i>Neoehrlichia arcana</i> ". International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 4256-4261.	0.8	43
24143	The natural history of cutaneous propionibacteria, and reclassification of selected species within the genus <i>Propionibacterium</i> to the proposed novel genera <i>Acidipropionibacterium</i> gen. nov., <i>Cutibacterium</i> gen. nov. and <i>Pseudopropionibacterium</i> gen. nov.. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 4422-4432.	0.8	410
24144	<i>Serpentinicella alkaliphila</i> gen. nov., sp. nov., a novel alkaliphilic anaerobic bacterium isolated from the serpentinite-hosted Prony hydrothermal field, New Caledonia. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 4464-4470.	0.8	27
24145	<i>Balneicella halophila</i> gen. nov., sp. nov., an anaerobic bacterium, isolated from a thermal spring and description of <i>Balneicellaceae</i> fam. nov.. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 4692-4696.	0.8	16
24146	Re-evaluation of the taxonomy of the <i>Mitis</i> group of the genus <i>Streptococcus</i> based on whole genome phylogenetic analyses, and proposed reclassification of <i>Streptococcus dentisani</i> as <i>Streptococcus oralis</i> subsp. <i>dentisani</i> comb. nov., <i>Streptococcus tigurinus</i> as <i>Streptococcus oralis</i> subsp. <i>tigurinus</i> comb. nov., and <i>Streptococcus oligofermentans</i> as a later synonym of <i>Streptococcus cristatus</i> . International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 4803-4820.	0.8	176
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24148	<i>Peptococcus simiae</i> sp. nov., isolated from rhesus macaque faeces and emended description of the genus <i>Peptococcus</i> . International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 5187-5191.	0.8	14
24149	Proposal of a type strain for <i>Frankia alni</i> (Woronin 1866) Von Tubeuf 1895, emended description of <i>Frankia alni</i> , and recognition of <i>Frankia casuarinae</i> sp. nov. and <i>Frankia elaeagni</i> sp. nov.. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 5201-5210.	0.8	68
24150	Proposal to reclassify <i>Propionibacterium acnes</i> type I as <i>Propionibacterium acnes</i> subsp. <i>acnes</i> subsp. nov. and <i>Propionibacterium acnes</i> type II as <i>Propionibacterium acnes</i> subsp. <i>defendens</i> subsp. nov.. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 5358-5365.	0.8	50
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24153	<i>Spirosoma soli</i> sp. nov., isolated from biological soil crusts. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 5568-5574.	0.8	18
24154	<i>Deinococcus ruber</i> sp. nov., a radiation-resistant bacterium isolated from soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 72-76.	0.8	10
24155	<i>Spirosoma swuense</i> sp. nov., isolated from wet soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 532-536.	0.8	27
24156	<i>Acidicapsa acidisoli</i> sp. nov., from the acidic soil of a deciduous forest. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 862-867.	0.8	11
24157	<i>Planococcus versutus</i> sp. nov., isolated from soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 944-950.	0.8	24
24158	<i>Desulfuribacillus stibiiarsenatis</i> sp. nov., an obligately anaerobic, dissimilatory antimonate- and arsenate-reducing bacterium isolated from anoxic sediments, and emended description of the genus <i>Desulfuribacillus</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 1011-1017.	0.8	37
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24160	<i>Frankia coriariae</i> sp. nov., an infective and effective microsymbiont isolated from <i>Coriaria japonica</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 1266-1270.	0.8	37
24161	<i>Fournierella massiliensis</i> gen. nov., sp. nov., a new human-associated member of the family Ruminococcaceae. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 1393-1399.	0.8	33
24162	<i>Vitiosangium cumulatum</i> gen. nov., sp. nov. and <i>Vitiosangium subalbum</i> sp. nov., soil myxobacteria, and emended descriptions of the genera <i>Archangium</i> and <i>Angiococcus</i> , and of the family Cystobacteraceae. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 1422-1430.	0.8	27
24163	<i>Streptomyces jeddahensis</i> sp. nov., an oleaginous bacterium isolated from desert soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 1676-1682.	0.8	25
24164	An evaluation of <i>Thiomicrospira</i> , <i>Hydrogenovibrio</i> and <i>Thioalkalimicrobium</i> : reclassification of four species of <i>Thiomicrospira</i> to each <i>Thiomicrospira</i> gen. nov. and <i>Hydrogenovibrio</i> , and reclassification of all four species of <i>Thioalkalimicrobium</i> to <i>Thiomicrospira</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 1140-1151.	0.8	118
24165	<i>Bradyrhizobium mercantei</i> sp. nov., a nitrogen-fixing symbiont isolated from nodules of <i>Deguelia costata</i> (syn. <i>Lonchocarpus costatus</i> ). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 1827-1834.	0.8	32
24166	ContEst16S: an algorithm that identifies contaminated prokaryotic genomes using 16S RNA gene sequences. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 2053-2057.	0.8	377
24167	Reclassification of <i>Thiobacillus aquaesulis</i> (Wood & Kelly, 1995) as <i>Annwoodia aquaesulis</i> gen. nov., comb. nov., transfer of <i>Thiobacillus</i> (Beijerinck, 1904) from the Hydrogenophilales to the Nitrosomonadales, proposal of Hydrogenophilalia class. nov. within the â€ˆProteobacteriaâ€™™, and four new families within the orders Nitrosomonadales and Rhodocyclales. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 1191-1205.	0.8	124
24168	Molecular characterization of â€ˆCandidatus Borrelia tachyglossiâ€™™ (family Spirochaetaceae) in echidna ticks, <i>Bothriocroton concolor</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 1075-1080.	0.8	39
24169	A proposal of <i>Leuconostoc mesenteroides</i> subsp. <i>jonggajibkimchii</i> subsp. nov. and reclassification of <i>Leuconostoc mesenteroides</i> subsp. <i>suionicum</i> (Gu et al., 2012) as <i>Leuconostoc suionicum</i> sp. nov. based on complete genome sequences. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 2225-2230.	0.8	40

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24170	Silvanigrella aquatica gen. nov., sp. nov., isolated from a freshwater lake, description of Silvanigrellaceae fam. nov. and Silvanigrellales ord. nov., reclassification of the order Bdellovibrionales in the class Oligoflexia, reclassification of the families Bacteriovoracaceae and Halobacteriovoraceae in the new order Bacteriovoracales ord. nov., and reclassification of the family Pseudobacteriovoracaceae in the order Oligoflexales. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 2555-2571.	0.8	76
24171	Proposal for the reclassification of obligately putrine-fermenting bacteria <i>Clostridium acidurici</i> (Barker 1938) and <i>Clostridium purinilyticum</i> (D'Aurte et al. 1981) as <i>Gottschalkia acidurici</i> gen. nov. comb. nov. and <i>Gottschalkia purinilytica</i> comb. nov. and of <i>Eubacterium angustum</i> (Beuscher and Tj ETQq1 1 0.784314 rgBT6 Overlo International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 2711-2719.	0.8	13
24172	<i>Mycobacterium eburneum</i> sp. nov., a non-chromogenic, fast-growing strain isolated from sputum. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 3174-3181.	0.8	13
24173	<i>Bradyrhizobium namibiense</i> sp. nov., a symbiotic nitrogen-fixing bacterium from root nodules of <i>Lablab purpureus</i> , hyacinth bean, in Namibia. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 4884-4891.	0.8	31
24174	<i>Streptomyces phaeopurpureus</i> Shinobu 1957 (Approved Lists 1980) and <i>Streptomyces griseorubiginosus</i> (Ryabova and Preobrazhenskaya 1957) Pridham et al. 1958 (Approved Lists 1980) are heterotypic subjective synonyms. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 3111-3116.	0.8	5
24175	<i>Frankia asymbiotica</i> sp. nov., a non-infective actinobacterium isolated from <i>Morella californica</i> root nodule. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 4897-4901.	0.8	34
24176	Draft genome and description of <i>Consotaella salsifontis</i> gen. nov. sp. nov., a halophilic, free-living, nitrogen-fixing alphaproteobacterium isolated from an ancient terrestrial saline spring. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 3744-3751.	0.8	10
24177	<i>Spathaspora boniae</i> sp. nov., a D-xylose-fermenting species in the <i>Candida albicans</i> /Lodderomyces clade. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 3798-3805.	0.8	20
24178	Reclassification of <i>Halothiobacillus hydrothermalis</i> and <i>Halothiobacillus halophilus</i> to <i>Guyparkeria</i> gen. nov. in the Thioalkalibacteraceae fam. nov., with emended descriptions of the genus <i>Halothiobacillus</i> and family Halothiobacillaceae. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 3919-3928.	0.8	52
24179	<i>Rhizobium esperanzae</i> sp. nov., a N <sub>2</sub> -fixing root symbiont of <i>Phaseolus vulgaris</i> from Mexican soils. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 3937-3945.	0.8	41
24180	<i>Microbulbifer aggregans</i> sp. nov., isolated from estuarine sediment from a mangrove forest. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 4089-4094.	0.8	13
24181	Reclassification of <i>Thiomicrospira hydrogeniphila</i> (Watsuji et al. 2016) to <i>Thiomicrothabodus hydrogeniphila</i> comb. nov., with emended description of <i>Thiomicrothabodus</i> (Boden et al., 2017). International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 4205-4209.	0.8	18
24182	<i>Corynebacterium gottingense</i> sp. nov., isolated from a clinical patient. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 4494-4499.	0.8	11
24183	<i>Phaeobacter piscinae</i> sp. nov., a species of the <i>Roseobacter</i> group and potential aquaculture probiont. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 4559-4564.	0.8	20
24184	<i>Caecibacterium sporiformans</i> gen. nov., sp. nov., an anaerobic, butyrate-producing, spore-forming bacterium isolated from chicken caecum. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 4589-4594.	0.8	10
24185	<i>Ramlibacter alkalitolerans</i> sp. nov., alkali-tolerant bacterium isolated from soil of ginseng. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 4619-4623.	0.8	14
24186	Two novel species of rapidly growing mycobacteria: <i>Mycobacterium lehmannii</i> sp. nov. and <i>Mycobacterium neumannii</i> sp. nov. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 4948-4955.	0.8	12
24188	<i>Cyberlindnera xishuangbannaensis</i> f.a., sp. nov., a yeast isolated from rotting wood. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 5051-5055.	0.8	8

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24189	Larkinella soli sp. nov., isolated from biological soil crusts. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 5134-5138.	0.8	8
24190	Pseudomonas floridensis sp. nov., a bacterial pathogen isolated from tomato. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 64-70.	0.8	22
24191	Taxonomic analyses of members of the Streptomyces cinnabarinus cluster, description of Streptomyces cinnabarigriseus sp. nov. and Streptomyces davaonensis sp. nov.. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 382-393.	0.8	26
24192	Pseudomonas fluvialis sp. nov., a novel member of the genus Pseudomonas isolated from the river Ganges, India. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 402-408.	0.8	15
24193	Leptospira venezuelensis sp. nov., a new member of the intermediate group isolated from rodents, cattle and humans. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 513-517.	0.8	45
24194	Mixta gen. nov., a new genus in the Erwiniaceae. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 1396-1407.	0.8	53
24195	Tritonibacter horizontis gen. nov., sp. nov., a member of the Rhodobacteraceae, isolated from the Deepwater Horizon oil spill. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 736-744.	0.8	25
24196	Listeria costaricensis sp. nov.. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 844-850.	0.8	39
24197	Paenibacillus translucens sp. nov., isolated from tidal flat sediment. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 936-941.	0.8	8
24198	Frankia saprophytica sp. nov., an atypical, non-infective (Nod <sup>-</sup> ) and non-nitrogen fixing (Fix <sup>-</sup> ) actinobacterium isolated from Coriaria nepalensis root nodules. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 1090-1095.	0.8	20
24199	Lysobacter silvestris sp. nov., isolated from alpine forest soil, and reclassification of Luteimonas tolerans as Lysobacter tolerans comb. nov.. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 1571-1577.	0.8	20
24200	Streptomyces boninensis sp. nov., isolated from soil from a limestone cave in the Ogasawara Islands. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 1795-1799.	0.8	15
24201	Lactobacillus micheneri sp. nov., Lactobacillus timberlakei sp. nov. and Lactobacillus quenuiae sp. nov., lactic acid bacteria isolated from wild bees and flowers. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 1879-1884.	0.8	57
24202	Virgibacillus indicus sp. nov. and Virgibacillus profundi sp. nov, two moderately halophilic bacteria isolated from marine sediment by using microfluidic streak plates. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 2015-2023.	0.8	17
24203	Metschnikowia maroccana f.a., sp. nov., a new yeast species associated with floral nectar from Morocco. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 2028-2035.	0.8	7
24204	Evaluation of the genus Thiothrix Winogradsky 1888 (Approved Lists 1980) emend. Aruga et al. 2002: reclassification of Thiothrix disciformis to Thiolinea disciformis gen. nov., comb. nov., and of Thiothrix flexilis to Thiofilum flexile gen. nov., comb. nov., with emended description of Thiothrix. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 2226-2239.	0.8	36
24205	Whole-genome-based revisit of Photorhabdus phylogeny: proposal for the elevation of most Photorhabdus subspecies to the species level and description of one novel species Photorhabdus bodei sp. nov., and one novel subspecies Photorhabdus laumondii subsp. clarkei subsp. nov.. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 2664-2681.	0.8	132
24206	Blastococcus atacamensis sp. nov., a novel strain adapted to life in the Yungay core region of the Atacama Desert. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 2712-2721.	0.8	33

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24207	Phylogenomic analyses of a clade within the roseobacter group suggest taxonomic reassignments of species of the genera <i>Aestuariivita</i> , <i>Citreicella</i> , <i>Loktanella</i> , <i>Nautella</i> , <i>Pelagibaca</i> , <i>Ruegeria</i> , <i>Thalassobius</i> , <i>Thiobacimonas</i> and <i>Tropicibacter</i> , and the proposal of six novel genera. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 2393-2411.	0.8	293
24208	<i>Scheffersomyces stambukii</i> f.a., sp. nov., a d-xylose-fermenting species isolated from rotting wood. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 2306-2312.	0.8	8
24209	<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
24210	<i>Solimicrobium silvestre</i> gen. nov., sp. nov., isolated from alpine forest soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 2491-2498.	0.8	11
24211	<i>Nocardioides allogilvus</i> sp. nov., a novel actinobacterium isolated from a karst cave. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 2485-2490.	0.8	17
24212	<i>Mangrovicella endophytica</i> gen. nov., sp. nov., a new member of the family <i>Aurantimonadaceae</i> isolated from <i>Aegiceras corniculatum</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 2838-2845.	0.8	10
24213	<i>Frankia irregularis</i> sp. nov., an actinobacterium unable to nodulate its original host, <i>Casuarina equisetifolia</i> , but effectively nodulates members of the actinorhizal <i>Rhamnales</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 2883-2914.	0.8	28
24214	<i>Bradyrhizobium ripae</i> sp. nov., a nitrogen-fixing symbiont isolated from nodules of wild legumes in Namibia. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 3688-3695.	0.8	22
24215	<i>Mycobacterium syngnathidarum</i> sp. nov., a rapidly growing mycobacterium identified in syngnathid fish. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 3696-3700.	0.8	14
24216	<i>Megasphaera stantonii</i> sp. nov., a butyrate-producing bacterium isolated from the cecum of a healthy chicken. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 3409-3415.	0.8	21
24217	<i>Streptomyces venetus</i> sp. nov., an actinomycete with a blue aerial mycelium. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 3333-3339.	0.8	8
24218	<i>Catenibacillus scindens</i> gen. nov., sp. nov., a C-deglycosylating human intestinal representative of the <i>Lachnospiraceae</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 3356-3361.	0.8	12
24219	<i>Kyrpidia spormannii</i> sp. nov., a thermophilic, hydrogen-oxidizing, facultative autotroph, isolated from hydrothermal systems at S�o Miguel Island, and emended description of the genus <i>Kyrpidia</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 3735-3740.	0.8	28
24220	<i>Desertimonas flava</i> gen. nov., sp. nov. isolated from a desert soil, and proposal of <i>Ilumatobacteraceae</i> fam. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 3593-3599.	0.8	22
24221	Description of a novel species of fast growing mycobacterium: <i>Mycobacterium kyogaense</i> sp. nov., a scotochromogenic strain received as <i>Mycobacterium vaccae</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 3726-3734.	0.8	10
24222	<i>Ignatzschineria cameli</i> sp. nov., isolated from necrotic foot tissue of dromedaries ( <i>Camelus</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 TFS <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 3627-3634.	0.8	21
24223	<i>Prevotella rara</i> sp. nov., isolated from human faeces. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 3818-3825.	0.8	14
24224	<i>Aestuariivirga litoralis</i> gen. nov., sp. nov., a proteobacterium isolated from a water sample, and proposal of <i>Aestuariivirgaceae</i> fam. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 299-306.	0.8	13

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24225	<i>Sphingopyxis lindanitolerans</i> sp. nov. strain WS5A3pT enriched from a pesticide disposal site. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 3935-3941.	0.8	13
24226	<i>Listeria thailandensis</i> sp. nov.. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 74-81.	0.8	55
24227	Reclassification of <i>Xanthomonas gardneri</i> (ex ÅutiÄ•1957) Jones et al. 2006 as a later heterotypic synonym of <i>Xanthomonas cynarae</i> TrÄ©baol et al. 2000 and description of <i>X. cynarae</i> pv. <i>cynarae</i> and <i>X. cynarae</i> pv. <i>gardneri</i> based on whole genome analyses. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 343-349.	0.8	35
24228	<i>Capsulimonas corticalis</i> gen. nov., sp. nov., an aerobic capsulated bacterium, of a novel bacterial order, <i>Capsulimonadales</i> ord. nov., of the class <i>Armatimonadia</i> of the phylum <i>Armatimonadetes</i> . International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 220-226.	0.8	22
24229	<i>Pandoraea fibrosis</i> sp. nov., a novel <i>Pandoraea</i> species isolated from clinical respiratory samples. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 645-651.	0.8	23
24230	<i>Photorhabdus khanii</i> subsp. <i>guanajuatensis</i> subsp. nov., isolated from <i>Heterorhabditis atacamensis</i> , and <i>Photorhabdus luminescens</i> subsp. <i>mexicana</i> subsp. nov., isolated from <i>Heterorhabditis mexicana</i> entomopathogenic nematodes. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 652-661.	0.8	41
24231	<i>Calidifontimicrobium sediminis</i> gen. nov., sp. nov., a new member of the family <i>Comamonadaceae</i> . International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 434-440.	0.8	13
24232	<i>Hymenobacter crusticola</i> sp. nov., isolated from biological soil crust. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 547-551.	0.8	13
24233	Polyphasic classification of the gifted natural product producer <i>Streptomyces rosefaciens</i> sp. nov.. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 899-908.	0.8	16
24234	<i>Collinsella vaginalis</i> sp. nov. strain Marseille-P2666T, a new member of the <i>Collinsella</i> genus isolated from the genital tract of a patient suffering from bacterial vaginosis. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 949-956.	0.8	12
24235	<i>Botryobacter ruber</i> gen. nov., sp. nov., a novel member of the family <i>Hymenobacteraceae</i> . International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 821-827.	0.8	9
24236	<i>Butyricimonas faecalis</i> sp. nov., isolated from human faeces and emended description of the genus <i>Butyricimonas</i> . International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 833-838.	0.8	17
24237	<i>Nocardioides ferulae</i> sp. nov., isolated from root of an endangered medicinal plant <i>Ferula songorica</i> Pall. ex Spreng. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 1253-1258.	0.8	14
24238	<i>Streptacidiphilus bronchialis</i> sp. nov., a ciprofloxacin-resistant bacterium from a human clinical specimen; reclassification of <i>Streptomyces griseoplanus</i> as <i>Streptacidiphilus griseoplanus</i> comb. nov. and emended description of the genus <i>Streptacidiphilus</i> . International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 1060-1069.	0.8	20
24239	Transfer of <i>Meiothermus chliarophilus</i> (Terreiro et al. 1995) Nobre et al. 1996, <i>Meiothermus roseus</i> Ming et al. 2016, <i>Meiothermus terrae</i> Yu et al. 2014 and <i>Meiothermus timidus</i> Pires et al. 2005, to <i>Calidithermus</i> gen. nov., as <i>Calidithermus chliarophilus</i> comb. nov., <i>Calidithermus roseus</i> comb. nov., <i>Calidithermus terrae</i> comb. nov. and <i>Calidithermus timidus</i> comb. nov., respectively, and emended description of the genus <i>Meiothermus</i> . International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 1060-1069.	0.8	28
24240	<i>Methanofervidicoccus abyssi</i> gen. nov., sp. nov., a hydrogenotrophic methanogen, isolated from a hydrothermal vent chimney in the Mid-Cayman Spreading Center, the Caribbean Sea. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 1225-1230.	0.8	17
24241	<i>Lactobacillus suantsaii</i> sp. nov., isolated from suan-tsai, a traditional Taiwanese fermented mustard green. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 1484-1489.	0.8	10
24242	<i>Novosphingobium meiothermophilum</i> sp. nov., isolated from a hot spring. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 1737-1743.	0.8	15

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24243	<i>Thalassorhabdomicrobium marinisediminis</i> gen. nov., sp. nov., a member of the family Hyphomonadaceae isolated from the Bohai Sea. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 1794-1799.	0.8	8
24244	<i>Tengunoibacter tsumagoiensis</i> gen. nov., sp. nov., <i>Dictyobacter robayashii</i> sp. nov., <i>Dictyobacter alpinus</i> sp. nov., and description of Dictyobacteraceae fam. nov. within the order Ktedonobacterales isolated from Tengu-no-mugimeshi, a soil-like granular mass of micro-organisms, and emended descriptions of the genera Ktedonobacter and Dictyobacter. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 1910-1918.	0.8	39
24245	<i>Mesorhizobium atlanticum</i> sp. nov., a new nitrogen-fixing species from soils of the Brazilian Atlantic Forest biome. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 1800-1806.	0.8	17
24246	<i>Staphylococcus debuckii</i> sp. nov., a coagulase-negative species from bovine milk. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 2239-2249.	0.8	10
24247	<i>Vagococcus bubulae</i> sp. nov., isolated from ground beef, and <i>Vagococcus vulneris</i> sp. nov., isolated from a human foot wound. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 2268-2276.	0.8	26
24248	<i>Vibrio echinoideorum</i> sp. nov., isolated from an epidermal lesion on the test of a green sea urchin ( <i>Strongylocentrotus droebachiensis</i> ). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 2277-2282.	0.8	10
24249	Reclassification of <i>Ochrobactrum lupini</i> as a later heterotypic synonym of <i>Ochrobactrum anthropi</i> based on whole-genome sequence analysis. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 2312-2314.	0.8	25
24250	<i>Streptomyces huasconensis</i> sp. nov., an haloalkalitolerant actinobacterium isolated from a high altitude saline wetland at the Chilean Altiplano. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 2315-2322.	0.8	18
24251	<i>Leptospira yasudae</i> sp. nov. and <i>Leptospira stimsonii</i> sp. nov., two new species of the pathogenic group isolated from environmental sources. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 1450-1456.	0.8	43
24252	<i>Pseudomonas nitrititolerans</i> sp. nov., a nitrite-tolerant denitrifying bacterium isolated from a nitrification/denitrification bioreactor. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 2471-2476.	0.8	9
24253	<i>Poseidonibacter antarcticus</i> sp. nov., isolated from Antarctic intertidal sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 2717-2722.	0.8	10
24254	<i>Croceibacterium</i> gen. nov., with description of <i>Croceibacterium ferulae</i> sp. nov., an endophytic bacterium isolated from <i>Ferula sinkiangensis</i> K. M. Shen and reclassification of <i>Porphyrobacter mercurialis</i> as <i>Croceibacterium mercuriale</i> comb. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 2547-2554.	0.8	18
24255	<i>Dysosmobacter welbionis</i> gen. nov., sp. nov., isolated from human faeces and emended description of the genus <i>Oscillibacter</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 4851-4858.	0.8	29
24256	Genome analysis-based union of the genus <i>Mesoplasma</i> with the genus <i>Entomoplasma</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 2735-2738.	0.8	44
24257	Reclassification of 'Polyangium brachysporum' DSM 7029 as <i>Schlegelella brevitalea</i> sp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 2877-2883.	0.8	30
24258	<i>Bradyrhizobium niftali</i> sp. nov., an effective nitrogen-fixing symbiont of partridge pea [ <i>Chamaecrista fasciculata</i> (Michx.) Greene], a native caesalpinoid legume broadly distributed in the USA. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 3448-3459.	0.8	21
24259	<i>Mycolicibacterium stelleriae</i> sp. nov., a rapidly growing scotochromogenic strain isolated from <i>Stellera chamaejasme</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 3465-3471.	0.8	14
24260	Reclassification of <i>Micrococcus aloeverae</i> and <i>Micrococcus yunnanensis</i> as later heterotypic synonyms of <i>Micrococcus luteus</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 3512-3518.	0.8	17

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24261	Genome-based reclassification of <i>Bacillus okuhidensis</i> as a later heterotypic synonym of <i>Bacillus halodurans</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 3599-3602.	0.8	13
24262	<i>Apibacter muscae</i> sp. nov., a novel bacterial species isolated from house flies. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 3586-3592.	0.8	7
24263	<i>Facilibium subflavum</i> gen. nov., sp. nov. and <i>Cysteiniphilum halobium</i> sp. nov., new members of the family <i>Fastidiosibacteraceae</i> isolated from coastal seawater. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 3757-3764.	0.8	14
24264	<i>Antribacter gilvus</i> gen. nov., sp. nov., a new member of the family <i>Promicromonosporaceae</i> from a karstic cavern. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 3792-3799.	0.8	8
24265	<i>Leucothrix sargassi</i> sp. nov., isolated from a marine alga [ <i>Sargassum natans</i> (L.) Gaillon]. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 3857-3862.	0.8	7
24266	<i>Bradyrhizobium frederickii</i> sp. nov., a nitrogen-fixing lineage isolated from nodules of the caesalpinioid species <i>Chamaecrista fasciculata</i> and characterized by tolerance to high temperature in vitro. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 3863-3877.	0.8	17
24267	<i>Prevotella brunnea</i> sp. nov., isolated from a wound of a patient. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 3933-3938.	0.8	7
24268	<i>Fluviibacterium aquatile</i> gen. nov., sp. nov., isolated from estuary sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 105-111.	0.8	8
24269	Phylogenomic analysis of <i>Haemophilus parasuis</i> and proposed reclassification to <i>Glaesserella parasuis</i> , gen. nov., comb. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 180-186.	0.8	51
24270	<i>Natronospirillum operosum</i> gen. nov., sp. nov., a haloalkaliphilic satellite isolated from decaying biomass of a laboratory culture of cyanobacterium <i>Geitlerinema</i> sp. and proposal of <i>Natronospirillaceae</i> fam. nov., <i>Saccharospirillaceae</i> fam. nov. and <i>Gynuellaceae</i> fam. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 511-521.	0.8	19
24271	<i>Azospirillum thermophilum</i> sp. nov., isolated from a hot spring. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 550-554.	0.8	13
24272	<i>Phytobacter palmae</i> sp. nov., a novel endophytic, N <sub>2</sub> fixing, plant growth promoting Gammaproteobacterium isolated from oil palm ( <i>Elaeis guineensis</i> Jacq.). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 841-848.	0.8	19
24273	Description of <i>Erysipelothrix piscisicarius</i> sp. nov., an emergent fish pathogen, and assessment of virulence using a tiger barb ( <i>Puntigrus tetrazona</i> ) infection model. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 857-867.	0.8	28
24274	<i>Pseudomonas saxonica</i> sp. nov., isolated from raw milk and skimmed milk concentrate. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 935-943.	0.8	10
24275	<i>Ktedonosporobacter rubrisoli</i> gen. nov., sp. nov., a novel representative of the class <i>Ktedonobacteria</i> , isolated from red soil, and proposal of <i>Ktedonosporobacteraceae</i> fam. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 1015-1025.	0.8	18
24276	<i>Pseudorivibacter rhizosphaerae</i> gen. nov., sp. nov., isolated from rhizosphere soil of <i>Camellia sinensis</i> (L.) O. Ktze and emended description of the genus <i>Rivibacter</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 1071-1078.	0.8	12
24277	<i>Frankia soli</i> sp. nov., an actinobacterium isolated from soil beneath <i>Ceanothus jepsonii</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 1203-1209.	0.8	18
24278	<i>Tepidiforma bonchosmolovskayae</i> gen. nov., sp. nov., a moderately thermophilic Chloroflexi bacterium from a Chukotka hot spring (Arctic, Russia), representing a novel class, <i>Tepidiformia</i> , which includes the previously uncultivated lineage OLB14. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 1192-1202.	0.8	44

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24280	Comparative genome sequence analysis of several species in the genus <i>Tepidimonas</i> and the description of a novel species <i>Tepidimonas charontis</i> sp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 1596-1604.	0.8	8
24281	Genome-based analyses reveal a synonymy among <i>Halorubrum distributum</i> Zvyagintseva and Tarasov 1989; Oren and Ventosa 1996, <i>Halorubrum terrestre</i> Ventosa et al. 2004, <i>Halorubrum arcis</i> Xu et al. 2007 and <i>Halorubrum litoreum</i> Cui et al. 2007. Emended description of <i>Halorubrum distributum</i> Zvyagintseva and Tarasov 1989; Oren and Ventosa 1996. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 1698-1705.	0.8	14
24282	<i>Chitinophaga vietnamensis</i> sp. nov., a multi-drug resistant bacterium infecting humans. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 1758-1768.	0.8	16
24283	<i>Dictyobacter vulcani</i> sp. nov., belonging to the class Ktedonobacteria, isolated from soil of the Mt Zao volcano. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 1805-1813.	0.8	10
24284	<i>Acetobacter oryzoeni</i> sp. nov., isolated from Korean rice wine vinegar. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 2026-2033.	0.8	17
24285	Genome-based classification of three novel actinobacteria from the Karakum Desert: <i>Jiangella asiatica</i> sp. nov., <i>Jiangella aurantiaca</i> sp. nov. and <i>Jiangella ureilytica</i> sp. nov. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 1993-2002.	0.8	15
24286	<i>Methylobacterium crusticola</i> sp. nov., isolated from biological soil crusts. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 2089-2095.	0.8	18
24287	<i>Pseudomonas haemolytica</i> sp. nov., isolated from raw milk and skimmed milk concentrate. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 2339-2347.	0.8	15
24288	Reclassification of <i>Sphingomonas aerea</i> as a later heterotypic synonym of <i>Sphingomonas carotini</i> based on whole-genome sequence analysis. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 2355-2358.	0.8	7
24289	Reclassification of <i>Clostridium diolis</i> Biebl and SprÅner 2003 as a later heterotypic synonym of <i>Clostridium beijerinckii</i> Donker 1926 (Approved Lists 1980) emend. Keis et al. 2001. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 2463-2466.	0.8	12
24290	Phylogenomic revision of the family Streptosporangiaceae, reclassification of <i>Desertactinospora gelatinilytica</i> as <i>Spongiactinospora gelatinilytica</i> comb. nov. and a taxonomic home for the genus <i>Sinosporangium</i> in the family Streptosporangiaceae. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 2569-2579.	0.8	17
24291	<i>Haemophilus seminalis</i> sp. nov., isolated from human semen. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 2588-2595.	0.8	10
24292	Genomic and genetic sequence information of strains assigned to the genus <i>Rhodopseudomonas</i> reveal the great heterogeneity of the group and identify strain <i>Rhodopseudomonas palustris</i> DSM 123T as the authentic type strain of this species. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 3932-3938.	0.8	17
24293	<i>Vitreimonas flagellata</i> gen. nov., sp. nov., a novel member of the family Hyphomonadaceae isolated from an activated sludge sample. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 2632-2639.	0.8	10
24294	<i>Antarcticimicrobium sediminis</i> gen. nov., sp. nov., isolated from Antarctic intertidal sediment, transfer of <i>Ruegeria lutea</i> to <i>Antarcticimicrobium</i> gen. nov. as <i>Antarcticimicrobium luteum</i> comb. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 2624-2631.	0.8	12
24295	<i>Streptobacillus canis</i> sp. nov. isolated from a dog. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 2648-2656.	0.8	14
24296	A taxonomic note on the genus <i>Lactobacillus</i> : Description of 23 novel genera, emended description of the genus <i>Lactobacillus</i> Beijerinck 1901, and union of <i>Lactobacillaceae</i> and <i>Leuconostocaceae</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 2782-2858.	0.8	2,775



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24298	<i>Algibacter pacificus</i> sp. nov., isolated from a deep-sea seamount. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 2907-2911.	0.8	9
24299	<i>Arthrobacter bussei</i> sp. nov., a pink-coloured organism isolated from cheese made of cow's milk. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 3027-3036.	0.8	18
24300	<i>Oceanivirga miroungae</i> sp. nov., isolated from oral cavity of northern elephant seal ( <i>Mirounga</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 103037-3048.	0.8	9
24301	<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
24302	<i>Nocardiopsis deserti</i> sp. nov., isolated from a high altitude Atacama Desert soil. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 3210-3218.	0.8	15
24303	<i>Francisella salimarina</i> sp. nov., isolated from coastal seawater. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 3264-3272.	0.8	12
24304	<i>Amycolatopsis anabasis</i> sp. nov., a novel endophytic actinobacterium isolated from roots of <i>Anabasis elatior</i> . International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 3391-3398.	0.8	10
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24306	<i>Flavobacterium profundum</i> sp. nov., isolated from a deep-sea seamount. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 3633-3638.	0.8	5
24307	<i>Halomonas lactosivorans</i> sp. nov., isolated from salt-lake sediment. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 3504-3512.	0.8	17
24308	<i>Halocatena pleomorpha</i> gen. nov. sp. nov., an extremely halophilic archaeon of family Halobacteriaceae isolated from saltpan soil. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 3693-3700.	0.8	15
24309	<i>Bacillus pasinlerensis</i> sp. nov., a thermophilic bacterium isolated from a hot spring in Turkey. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 3865-3871.	0.8	17
24310	<i>Massilia arenosa</i> sp. nov., isolated from the soil of a cultivated maize field. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 3912-3920.	0.8	16
24311	<i>Pseudomonas izuensis</i> sp. nov., a novel species isolated from Izu Oshima, Japan. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 4212-4216.	0.8	5
24312	Genetic diversity of <i>Agrobacterium</i> species isolated from nodules of common bean and soybean in Brazil, Mexico, Ecuador and Mozambique, and description of the new species <i>Agrobacterium fabacearum</i> sp. nov.. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 4233-4244.	0.8	29
24313	<i>Gluconobacter aidae</i> sp. nov., an acetic acid bacteria isolated from tropical fruits in Thailand. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 4351-4357.	0.8	10
24314	<i>Pelagihabitans pacificus</i> gen. nov., sp. nov., a member of the family Flavobacteriaceae isolated from a deep-sea seamount. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 4569-4575.	0.8	14

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24316	<i>Bradyrhizobium archetypum</i> sp. nov., <i>Bradyrhizobium australiense</i> sp. nov. and <i>Bradyrhizobium murdochi</i> sp. nov., isolated from nodules of legumes indigenous to Western Australia. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 4623-4636.	0.8	28
24317	<i>Isoptericola halalbus</i> sp. nov., a halotolerant actinobacterium isolated from saline lake sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 4661-4667.	0.8	6
24318	<i>Sphaerochaeta halotolerans</i> sp. nov., a novel spherical halotolerant spirochete from a Russian heavy oil reservoir, emended description of the genus <i>Sphaerochaeta</i> , reclassification of <i>Sphaerochaeta coccoides</i> to a new genus <i>Parasphaerochaeta</i> gen. nov. as <i>Parasphaerochaeta coccoides</i> comb. nov. and proposal of <i>Sphaerochaetaceae</i> fam. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 4748-4759.	0.8	30
24319	<i>Streptomyces harenosi</i> sp. nov., a home for a gifted strain isolated from Indonesian sand dune soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 4874-4882.	0.8	11
24320	Strains of <i>Bradyrhizobium cosmicum</i> sp. nov., isolated from contrasting habitats in Japan and Canada possess photosynthesis gene clusters with the hallmark of genomic islands. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 5063-5074.	0.8	15
24321	<i>Rubrobacter tropicus</i> sp. nov. and <i>Rubrobacter marinus</i> sp. nov., isolated from deep-sea sediment of the South China Sea. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 5576-5585.	0.8	13
24322	<i>Oceanipulchritudo coccoides</i> gen. nov., sp. nov., isolated from marine sediment within the family <i>Puniceococcaceae</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 5654-5664.	0.8	11
24323	<i>Seramator thermalis</i> gen. nov., sp. nov., a novel cellulose- and xylan-degrading member of the family <i>Dysgonamonadaceae</i> isolated from a hot spring. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 5717-5724.	0.8	8
24324	<i>Listeria valentina</i> sp. nov., isolated from a water trough and the faeces of healthy sheep. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 5868-5879.	0.8	47
24325	Phylogenomic analyses of the <i>Staphylococcaceae</i> family suggest the reclassification of five species within the genus <i>Staphylococcus</i> as heterotypic synonyms, the promotion of five subspecies to novel species, the taxonomic reassignment of five <i>Staphylococcus</i> species to <i>Mammaliicoccus</i> gen. nov., and the formal assignment of <i>Nosocomiicoccus</i> to the family <i>Staphylococcaceae</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 5926-5936.	0.8	198
24326	<i>Staphylococcus borealis</i> sp. nov., isolated from human skin and blood. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 6067-6078.	0.8	23
24327	<i>Bifidobacteria</i> in two-toed sloths ( <i>Choloepus didactylus</i> ): phylogenetic characterization of the novel taxon <i>Bifidobacterium choloepi</i> sp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 6115-6125.	0.8	13
24328	<i>Pelagovum pacificum</i> gen. nov., sp. nov., a novel member of the family <i>Rhodobacteraceae</i> isolated from surface seawater of the Mariana Trench. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 6155-6162.	0.8	9
24329	<i>Sneathia vaginalis</i> sp. nov. (Fusobacteriales, Leptotrichiaceae) as a replacement of the species "Sneathia amnii"™ Harwich et al. 2012 and "Leptotrichia amnionii"™ Shukla et al. 2002, and emended description of <i>Sneathia</i> Collins et al. 2001. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 71, .	0.8	17
24330	<i>Pseudomonas kielensis</i> sp. nov. and <i>Pseudomonas baltica</i> sp. nov., isolated from raw milk in Germany. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 71, .	0.8	11
24331	<i>Hanseniaspora terricola</i> sp. nov., an ascomycetous yeast isolated from Tibet. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 71, .	0.8	1
24332	<i>Rhabdotherrmincola sediminis</i> gen. nov., sp. nov., a new actinobacterium isolated from hot spring sediment, and emended description of the family <i>Iamiaceae</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 71, .	0.8	13

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24334	Direct whole-genome deep-sequencing of human respiratory syncytial virus A and B from Vietnamese children identifies distinct patterns of inter- and intra-host evolution. <i>Journal of General Virology</i> , 2015, 96, 3470-3483.	1.3	30
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24336	Transcription of densovirus endogenous sequences in the <i>Myzus persicae</i> genome. <i>Journal of General Virology</i> , 2016, 97, 1000-1009.	1.3	15
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24338	Conservation of the E8 CDS of the E8 <sup>E2</sup> protein among mammalian papillomaviruses. <i>Journal of General Virology</i> , 2016, 97, 2333-2345.	1.3	11
24339	A highly pathogenic avian-derived influenza virus H5N1 with 2009 pandemic H1N1 internal genes demonstrates increased replication and transmission in pigs. <i>Journal of General Virology</i> , 2017, 98, 18-30.	1.3	13
24340	Genetic diversity of currently circulating rubella viruses: a need to define more precise viral groups. <i>Journal of General Virology</i> , 2017, 98, 396-404.	1.3	28
24341	Revisiting the genotyping scheme for varicella-zoster viruses based on whole-genome comparisons. <i>Journal of General Virology</i> , 2017, 98, 1434-1438.	1.3	28
24342	A porcine enterovirus G associated with enteric disease contains a novel papain-like cysteine protease. <i>Journal of General Virology</i> , 2017, 98, 1305-1310.	1.3	43
24343	Proposed revision to the taxonomy of the genus Pestivirus, family Flaviviridae. <i>Journal of General Virology</i> , 2017, 98, 2106-2112.	1.3	264
24344	The genomic evolution of H1 influenza A viruses from swine detected in the United States between 2009 and 2016. <i>Journal of General Virology</i> , 2017, 98, 2001-2010.	1.3	54
24345	Characterization of five unclassified orthobunyaviruses (Bunyaviridae) from Africa and the Americas. <i>Journal of General Virology</i> , 2017, 98, 2258-2266.	1.3	13
24346	Polycipiviridae: a proposed new family of polycistronic picorna-like RNA viruses. <i>Journal of General Virology</i> , 2017, 98, 2368-2378.	1.3	32
24347	Genomic characterization of a novel iridovirus from redclaw crayfish <i>Cherax quadricarinatus</i> : evidence for a new genus within the family Iridoviridae. <i>Journal of General Virology</i> , 2017, 98, 2589-2595.	1.3	38
24348	The emergence and evolution of influenza A (H1N1) viruses in swine in Canada and the United States. <i>Journal of General Virology</i> , 2017, 98, 2663-2675.	1.3	23
24349	Comprehensive evolutionary and phylogenetic analysis of Hepacivirus N (HNV). <i>Journal of General Virology</i> , 2018, 99, 890-896.	1.3	10
24350	Complete genome sequence and construction of an infectious full-length cDNA clone of celery latent virus "an unusual member of a putative new genus within the Potyviridae. <i>Journal of General Virology</i> , 2019, 100, 308-320.	1.3	12

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24352	Evolving by deleting: patterns of molecular evolution of Apple stem pitting virus isolates from Poland. <i>Journal of General Virology</i> , 2019, 100, 1442-1456.	1.3	9
24353	Prevalence of a vertically transmitted single-stranded DNA virus in spinybacked orbweavers ( <i>Gasteracantha cancriformis</i> ) from Florida, USA. <i>Journal of General Virology</i> , 2019, 100, 1253-1265.	1.3	5
24354	A highly divergent hepacivirus-like flavivirus in domestic ducks. <i>Journal of General Virology</i> , 2019, 100, 1234-1240.	1.3	19
24355	Genetic diversity and evolution of the emerging picornavirus Senecavirus A. <i>Journal of General Virology</i> , 2020, 101, 175-187.	1.3	13
24356	Effect of <i>Wolbachia</i> wAlbB on a positive-sense RNA negev-like virus: a novel virus persistently infecting <i>Aedes albopictus</i> mosquitoes and cells. <i>Journal of General Virology</i> , 2020, 101, 216-225.	1.3	16
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24360	Isolation and molecular characterization of group B <i>Streptococcus</i> from laboratory Long-Evans rats ( <i>Rattus norvegicus</i> ) with and without invasive group B streptococcal disease. <i>Journal of Medical Microbiology</i> , 2018, 67, 97-109.	0.7	3
24361	The nursing home elder microbiome stability and associations with age, frailty, nutrition and physical location. <i>Journal of Medical Microbiology</i> , 2018, 67, 40-51.	0.7	69
24362	Effects of <i>Eclipta prostrata</i> on gut microbiota of SAMP6 mice with osteoporosis. <i>Journal of Medical Microbiology</i> , 2019, 68, 402-416.	0.7	17
24363	Genomic profile of Brazilian methicillin-resistant <i>Staphylococcus aureus</i> resembles clones dispersed worldwide. <i>Journal of Medical Microbiology</i> , 2019, 68, 693-702.	0.7	6
24364	Potential RNA-dependent RNA polymerase inhibitors as prospective therapeutics against SARS-CoV-2. <i>Journal of Medical Microbiology</i> , 2020, 69, 864-873.	0.7	49
24365	K-Pax2: Bayesian identification of cluster-defining amino acid positions in large sequence datasets. <i>Microbial Genomics</i> , 2015, 1, e000025.	1.0	12
24366	Directional gene flow and ecological separation in <i>Yersinia enterocolitica</i> . <i>Microbial Genomics</i> , 2015, 1, e000030.	1.0	16
24367	CLIMB (the Cloud Infrastructure for Microbial Bioinformatics): an online resource for the medical microbiology community. <i>Microbial Genomics</i> , 2016, 2, e000086.	1.0	176
24368	Monomorphic genotypes within a generalist lineage of <i>Campylobacter jejuni</i> show signs of global dispersion. <i>Microbial Genomics</i> , 2016, 2, e000088.	1.0	31
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24371	Comparative scaffolding and gap filling of ancient bacterial genomes applied to two ancient <i>Yersinia pestis</i> genomes. <i>Microbial Genomics</i> , 2017, 3, e000123.	1.0	3
24372	The complete replicons of 16 <i>Ensifer meliloti</i> strains offer insights into intra- and inter-replicon gene transfer, transposon-associated loci, and repeat elements. <i>Microbial Genomics</i> , 2018, 4, .	1.0	21
24373	The comparative genomics of <i>Bifidobacterium callitrichos</i> reflects dietary carbohydrate utilization within the common marmoset gut. <i>Microbial Genomics</i> , 2018, 4, .	1.0	16
24374	Using glycolysis enzyme sequences to inform <i>Lactobacillus</i> phylogeny. <i>Microbial Genomics</i> , 2018, 4, .	1.0	9
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24380	Comparative genomics of the fish pathogens <i>Edwardsiella ictaluri</i> 93-146 and <i>Edwardsiella piscicida</i> C07-087. <i>Microbial Genomics</i> , 2020, 6, .	1.0	14
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24382	Comparative genomic analysis of three intestinal species reveals reductions in secreted pathogenesis determinants in bovine-specific and non-pathogenic <i>Cryptosporidium</i> species. <i>Microbial Genomics</i> , 2020, 6, .	1.0	13
24383	Genomic sequence analysis of <i>Dissulfurirhabdus thermomarina</i> SH388 and proposed reassignment to <i>Dissulfurirhabdaceae</i> fam. nov.. <i>Microbial Genomics</i> , 2020, 6, .	1.0	2
24384	Analysis of complete <i>Campylobacter concisus</i> genomes identifies genomospecies features, secretion systems and novel plasmids and their association with severe ulcerative colitis. <i>Microbial Genomics</i> , 2020, 6, .	1.0	13
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24392	Effective identification of <i>Lactobacillus casei</i> group species: genome-based selection of the gene mutL as the target of a novel multiplex PCR assay. <i>Microbiology (United Kingdom)</i> , 2017, 163, 950-960.	0.7	27
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24394	Dissimilar pigment regulation in <i>Serpula lacrymans</i> and <i>Paxillus involutus</i> during inter-kingdom interactions. <i>Microbiology (United Kingdom)</i> , 2018, 164, 65-77.	0.7	23
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24396	The enigmatic role of fungal annexins: the case of <i>Cryptococcus neoformans</i> . <i>Microbiology (United Kingdom)</i> , 2018, 164, 1146-1155.	0.7	10
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24399	Arterivirus nsp12 versus the coronavirus nsp16 2â€²-O-methyltransferase: comparison of the C-terminal cleavage products of two nidovirus pp1ab polyproteins. <i>Journal of General Virology</i> , 2015, 96, 2643-2655.	1.3	14
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24989	Crystal structures of lymphocytic choriomeningitis virus endonuclease domain complexed with diketo-acid ligands. <i>IUCr</i> , 2018, 5, 223-235.	1.0	12
24990	Structure of mammalian plasma fetuin-B and its mechanism of selective metallopeptidase inhibition. <i>IUCr</i> , 2019, 6, 317-330.	1.0	28

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25003	Phylogenetic position of <i>Neofinetia</i> and <i>Sedirea</i> (Orchidaceae) and their species identification using the chloroplast matK and the nuclear ITS sequences. <i>Korean Journal of Plant Taxonomy</i> , 2014, 44, 39-50.	0.3	4
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25005	DNA barcoding of Schisandraceae in Korea. <i>Korean Journal of Plant Taxonomy</i> , 2016, 46, 273-282.	0.3	4
25006	Molecular phylogeny and divergence of photosynthetic pathways of Korean <i>Cypereae</i> (Cyperaceae). <i>Korean Journal of Plant Taxonomy</i> , 2016, 46, 314-325.	0.3	2
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25011	Taxonomy of the Family <i>Campylobacteraceae</i> ., 0, , 1-25.		66
25012	Anaerobic Respiratory Iron(II) Oxidation. , 0, , 157-171.		1
25013	Phylogeny and Comparative Genomics: the Shifting Landscape in the Genomics Era. , 0, , 84-141.		23
25014	Horizontal Gene Transfer to a Defensive Symbiont with a Reduced Genome in a Multipartite Beetle Microbiome. MBio, 2020, 11, .	1.8	52
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25031	<i>Sphaerotheca pashchima</i> , a new species of burrowing frog (Anura: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 34)	0.1	4
25032	Molecular characterization of stinkhorn fungus <i>Asero</i> coccinea Imazeki et Yoshimi ex Kasuya 2007 (Basidiomycota: Agaricomycetes: Phallales) from India. <i>Journal of Threatened Taxa</i> , 2020, 12, 15530-15534.	0.1	1
25033	The identity and distribution of <i>Bhavana annandalei</i> Hora, 1920 (Cypriniformes: Balitoridae), a hillstream loach endemic to the Western Ghats of India. <i>Journal of Threatened Taxa</i> , 2020, 12, 16262-16271.	0.1	1
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25035	<i>Indirana chiravasi</i> , a new species of Leaping Frog (Anura: Ranixalidae) from Western Ghats of India. <i>Journal of Threatened Taxa</i> , 2014, 6, 6293-6312.	0.1	16
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25038	<i>Indirana salelkari</i> , a new species of leaping frog (Anura: Ranixalidae) from Western Ghats of Goa, India. <i>Journal of Threatened Taxa</i> , 2015, 7, 7493-7509.	0.1	7
25039	Scaling new heights: first record of Boulenger's Lazy Toad <i>Scutigiger boulengeri</i> (Amphibia: Anura: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 34) 7655-7663.	0.1	4
25040	Re-evaluation of species allied to <i>Mithrax hispidus</i> (Decapoda: Brachyura: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 34)	0.2	9
25041	A new <i>Leptobrachium</i> (Anura: Megophryidae) from the highlands of southeastern Laos. <i>Zootaxa</i> , 2012, 3155, .	0.2	9
25042	New species of cynipid inquilines of the genus <i>Ufo</i> Melika & Pujade-Villar, 2005 (Hymenoptera: Cynipidae: Synergini). <i>Zootaxa</i> , 2012, 3478, 143-163.	0.2	7
25043	A molecular phylogeny recovers <i>Strabomantis aramunha</i> Cassimiro, Verdade and Rodrigues, 2008 and <i>Haddadus binotatus</i> (Spix, 1824) (Anura: Terrarana) as sister taxa. <i>Zootaxa</i> , 2013, 3741, 569.	0.2	6
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25045	Intact HIV-1 proviruses accumulate at distinct chromosomal positions during prolonged antiretroviral therapy. <i>Journal of Clinical Investigation</i> , 2019, 129, 988-998.	3.9	209
25046	Anti-influenza H7 human antibody targets antigenic site in hemagglutinin head domain interface. <i>Journal of Clinical Investigation</i> , 2020, 130, 4734-4739.	3.9	13
25047	H7N9 influenza virus neutralizing antibodies that possess few somatic mutations. <i>Journal of Clinical Investigation</i> , 2016, 126, 1482-1494.	3.9	62

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25051	Genomic mechanisms for cold tolerance and production of exopolysaccharides in the Arctic cyanobacterium <i>Phormidesmis priestleyi</i> BC1401. <i>BMC Genomics</i> , 2016, 17, 533.	1.2	81
25052	Role of diversity-generating retroelements for regulatory pathway tuning in cyanobacteria. <i>BMC Genomics</i> , 2020, 21, 664.	1.2	13
25053	Analysis of heterogeneous genomic samples using image normalization and machine learning. <i>BMC Genomics</i> , 2020, 21, 405.	1.2	4
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25055	Genomic and phenotypic characterisation of invasive neonatal and colonising group B <i>Streptococcus</i> isolates from Slovenia, 2001â€“2018. <i>BMC Infectious Diseases</i> , 2020, 20, 958.	1.3	9
25057	New ST623 of <i>Cryptococcus neoformans</i> isolated from a patient with non-Hodgkinâ€™s lymphoma in the Brazilian Amazon. <i>Annals of Clinical Microbiology and Antimicrobials</i> , 2020, 19, 20.	1.7	5
25058	The tree that hides the forest: cryptic diversity and phylogenetic relationships in the Palaearctic vector <i>Obsoletus/Scoticus</i> Complex (Diptera: Ceratopogonidae) at the European level. <i>Parasites and Vectors</i> , 2020, 13, 265.	1.0	15
25059	Interactions between <i>Schistosoma haematobium</i> group species and their <i>Bulinus</i> spp. intermediate hosts along the Niger River Valley. <i>Parasites and Vectors</i> , 2020, 13, 268.	1.0	23
25060	Proteins involved in the biosynthesis of lipophosphoglycan in <i>Leishmania</i> : a comparative genomic and evolutionary analysis. <i>Parasites and Vectors</i> , 2020, 13, 44.	1.0	9
25061	Reclassification of <i>Chromobacterium violaceum</i> ATCC 31532 and its quorum biosensor mutant CV026 to <i>Chromobacterium subtsugae</i> . <i>AMB Express</i> , 2020, 10, 202.	1.4	29
25062	Sequence analysis and protein interactions of Arabidopsis CIA2 and CIL proteins. , 2020, 61, 20.		4
25063	ycf1-ndhF genes, the most promising plastid genomic barcode, sheds light on phylogeny at low taxonomic levels in <i>Prunus persica</i> . <i>Journal of Genetic Engineering and Biotechnology</i> , 2020, 18, 42.	1.5	24
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25068	Mammalian Diversity and Matses Ethnomammalogy in Amazonian Peru Part 3: Marsupials ( <i>Didelphimorphia</i> ). <i>Bulletin of the American Museum of Natural History</i> , 2019, 2019, 1.	1.2	43
25069	A Revision of the Didelphid Marsupial Genus <i>Marmosa</i> Part 2. Species of the <i>Rapposa</i> Group (Subgenus) <i>Tj ETQq0 0.0 rgBT /Overlock 10</i>	1.2	37
25070	Optimization of high endoglucanase yields production from polypore fungus, <i>Microporus xanthopus</i> strain KA038 under solid-state fermentation using green tea waste. <i>Biology Open</i> , 2019, 8, .	0.6	10

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25072	<i>Tanousia zrmanjae</i> (Brusina, 1866) (Caenogastropoda: Truncatelloidea: Hydrobiidae): a living fossil. <i>Folia Malacologica</i> , 2015, 23, 263-271.	0.1	17
25073	<i>Agrafia Szarowska et Falniowski</i> , 2011 (Caenogastropoda: Hydrobiidae) in the Caucasus. <i>Folia Malacologica</i> , 2017, 25, 237-247.	0.1	17
25074	A new <i>Montenegrospeum</i> species from south Croatia (Mollusca: Gastropoda: Hydrobiidae). <i>Folia Malacologica</i> , 2018, 26, 25-34.	0.1	13
25075	<i>Viviparus mamillatus</i> (KÅ¼ster, 1852), and partial congruence between the morphology-, allozyme- and DNA-based phylogeny in European <i>Viviparidae</i> (Caenogastropoda: Architaenioglossa). <i>Folia Malacologica</i> , 2019, 27, 43-51.	0.1	6
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25077	Species distinctness of <i>Bithynia cettinensis</i> Clessin, 1887 and <i>B. zeta</i> GlÅ¼ter et PeÅ¼iÅ¼Ź, 2007 (Caenogastropoda: Truncatelloidea). <i>Folia Malacologica</i> , 2019, 27, 111-118.	0.1	4
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25079	First record of the <i>Ligia baudiniana</i> species complex in the American Gulf of Mexico Coastline, as confirmed by morphological and molecular approaches. <i>F1000Research</i> , 2017, 6, 1602.	0.8	3
25080	Purine-rich low complexity regions are potential RNA binding hubs in the human genome. <i>F1000Research</i> , 2018, 7, 76.	0.8	5
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25082	Interaction of N-3-oxododecanoyl homoserine lactone with transcriptional regulator LasR of <i>Pseudomonas aeruginosa</i> : Insights from molecular docking and dynamics simulations. <i>F1000Research</i> , 0, 8, 324.	0.8	7
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25084	Profile Comparer Extended: phylogeny of lytic polysaccharide monooxygenase families using profile hidden Markov model alignments. <i>F1000Research</i> , 2019, 8, 1834.	0.8	5
25085	Genomic evidence of multiple SARS-CoV-2 introductions into Morocco. <i>F1000Research</i> , 0, 9, 679.	0.8	2
25086	Mursamacin: a novel class of antibiotics from soil-dwelling roundworms of Central Kenya that inhibits methicillin-resistant <i>Staphylococcus aureus</i> . <i>F1000Research</i> , 0, 5, 2431.	0.8	2
25087	Insights into population structure of East African sweetpotato cultivars from hybrid assembly of chloroplast genomes. <i>Gates Open Research</i> , 2018, 2, 41.	2.0	1
25088	The first genome sequences of human bocaviruses from Vietnam. <i>Wellcome Open Research</i> , 2016, 1, 16.	0.9	2

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25090	Comparative genomics identifies male accessory gland proteins in five <i>Glossina</i> species. Wellcome Open Research, 2017, 2, 73.	0.9	8
25091	Identification of <i>Spiroplasma insolitum</i> symbionts in <i>Anopheles gambiae</i> . Wellcome Open Research, 2017, 2, 90.	0.9	8
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25093	Complete assembly of a dengue virus type 3 genome from a recent genotype III clade by metagenomic sequencing of serum. Wellcome Open Research, 2018, 3, 44.	0.9	6
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25399	Multiple Co-Evolutionary Networks Are Supported by the Common Tertiary Scaffold of the LacI/GalR Proteins. PLoS ONE, 2013, 8, e84398.	1.1	26
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25419	HIV-2 Integrase Polymorphisms and Longitudinal Genotypic Analysis of HIV-2 Infected Patients Failing a Raltegravir-Containing Regimen. PLoS ONE, 2014, 9, e92747.	1.1	19
25420	A Reference Pan-Genome Approach to Comparative Bacterial Genomics: Identification of Novel Epidemiological Markers in Pathogenic <i>Campylobacter</i> . PLoS ONE, 2014, 9, e92798.	1.1	122
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25447	Evidence for Loss of a Partial Flagellar Glycolytic Pathway during Trypanosomatid Evolution. <i>PLoS ONE</i> , 2014, 9, e103026.	1.1	5
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25450	Evolution of Oleosin in Land Plants. <i>PLoS ONE</i> , 2014, 9, e103806.	1.1	16
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25467	Determining the Phylogenetic and Phylogeographic Origin of Highly Pathogenic Avian Influenza (H7N3) in Mexico. PLoS ONE, 2014, 9, e107330.	1.1	25
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25492	Mitochondrial Genome Sequencing and Development of Genetic Markers for the Detection of DNA of Invasive Bighead and Silver Carp ( <i>Hypophthalmichthys nobilis</i> and <i>H. molitrix</i> ) in Environmental Water Samples from the United States. PLoS ONE, 2015, 10, e0117803.	1.1	44
25493	New Insights into Flavivirus Evolution, Taxonomy and Biogeographic History, Extended by Analysis of Canonical and Alternative Coding Sequences. PLoS ONE, 2015, 10, e0117849.	1.1	139
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25505	Transcriptome Markers of Viral Persistence in Naturally-Infected Andes Virus (Bunyaviridae) Seropositive Long-Tailed Pygmy Rice Rats. PLoS ONE, 2015, 10, e0122935.	1.1	6

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25507	Molecular Phylogeny Reveals High Diversity, Geographic Structure and Limited Ranges in Neotenic Net-Winged Beetles <i>Platerodrilus</i> (Coleoptera: Lycidae). PLoS ONE, 2015, 10, e0123855.	1.1	25
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25519	Candidatus <i>Frankia Datiscae</i> Dg1, the Actinobacterial Microsymbiont of <i>Datisca glomerata</i> , Expresses the Canonical nod Genes nodABC in Symbiosis with Its Host Plant. PLoS ONE, 2015, 10, e0127630.	1.1	131
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25523	<i>Saccharomyces cerevisiae</i> Eukaryotic Elongation Factor 1A (eEF1A) Is Methylated at Lys-390 by a METTL21-Like Methyltransferase. PLoS ONE, 2015, 10, e0131426.	1.1	47

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25533	A Survey of the ATP-Binding Cassette (ABC) Gene Superfamily in the Salmon Louse (Lepeophtheirus) Tj ETQq1 1 0.784314 rgBT / Overbo	1.1	19
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25667	Patterns and rates of viral evolution in HIV-1 subtype B infected females and males. PLoS ONE, 2017, 12, e0182443.	1.1	16
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25706	Expression of the RNA-binding protein RBP10 promotes the bloodstream-form differentiation state in <i>Trypanosoma brucei</i> . <i>PLoS Pathogens</i> , 2017, 13, e1006560.	2.1	83
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25708	Association of papillomavirus E6 proteins with either MAML1 or E6AP clusters E6 proteins by structure, function, and evolutionary relatedness. <i>PLoS Pathogens</i> , 2017, 13, e1006781.	2.1	36
25709	Effect of analytical treatment interruption and reinitiation of antiretroviral therapy on HIV reservoirs and immunologic parameters in infected individuals. <i>PLoS Pathogens</i> , 2018, 14, e1006792.	2.1	74
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25714	Genomic organization and evolution of ruminant lysozyme c genes. <i>Zoological Research</i> , 2015, 36, 1-17.	0.6	11
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25718	Contribution of a DNA barcode to an assessment of the specificity of ant taxa (Hymenoptera:) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 10	1.2	8
25719	<i>Hemipristicola gunterae</i> gen. n., sp. n. (Cestoda: Tetracystidae: Phyllobothriidae) from the snaggletooth shark, <i>Hemipristis elongata</i> (Carcharhiniformes: Hemigaleidae), from Moreton Bay, Australia. <i>Folia Parasitologica</i> , 2011, 58, 187-196.	0.7	8
25720	Description of <i>Sarcocystis lari</i> sp. n. (Apicomplexa: Sarcocystidae) from the great black-backed gull, <i>Larus marinus</i> (Charadriiformes: Laridae), on the basis of cyst morphology and molecular data. <i>Folia Parasitologica</i> , 2014, 61, 11-17.	0.7	24
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25722	Neotropical Monogonoidea. 58. Three new species of <i>Gyrodactylus</i> (Gyrodactylidae) from <i>Scleromystax</i> spp. (Callichthyidae) and the proposal of COII gene as an additional fragment for barcoding gyrodactylids. <i>Folia Parasitologica</i> , 2014, 61, 213-222.	0.7	25
25723	A review of the currently recognised zoogonid cercariae, including the identification and emergence ecology of <i>Cercaria capricornia</i> XI (Digenea: Zoogonidae) from <i>Nassarius olivaceus</i> (Gastropoda:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 10	0.7	10
25724	Genetic and morphological evidence reveals the existence of a new family, genus and species of Echinorhynchida (Acanthocephala). <i>Folia Parasitologica</i> , 2014, 61, 377-384.	0.7	22

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25726	Two new species of Hepatozoon (Apicomplexa: Hepatozoidae) parasitising species of <i>Philothamnus</i> (Ophidia: Colubridae) from South Africa. <i>Folia Parasitologica</i> , 2018, 65, .	0.7	16
25727	A novel endosymbiont-containing trypanosomatid <i>Phytomonas borealis</i> sp. n. from the predatory bug <i>Picromerus bidens</i> (Heteroptera: Pentatomidae). <i>Folia Parasitologica</i> , 2020, 67, .	0.7	10
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25729	Allelic Variation of the <i>Athyrium christensenianum</i> Complex (Athyriaceae). <i>Cytologia</i> , 2020, 85, 9-14.	0.2	1
25730	Combining morphology, scanning electron microscopy, and molecular phylogeny to evaluate the taxonomic power of scales in genus <i>Aphanius</i> Nardo, 1827 (Teleostei: Cyprinodontidae). <i>Archives of Polish Fisheries</i> , 2017, 25, 77-87.	0.6	12
25731	Functional divergence and adaptive selection of KNOX gene family in plants. <i>Open Life Sciences</i> , 2020, 15, 346-363.	0.6	19
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25733	Proteasomal degradation induced by DPP9-mediated processing competes with mitochondrial protein import. <i>EMBO Journal</i> , 2020, 39, e103889.	3.5	24
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25736	<i>Erysiphe salmonii</i> (Erysiphales, Ascomycota), another East Asian powdery mildew fungus introduced to Ukraine. <i>Ukrainian Botanical Journal</i> , 2017, 74, 212-219.	0.1	11
25737	SOIL AMENDED WITH ORGANIC FERTILIZERS AS A SOURCE OF ACTINOMYCETES WITH HIGH POTENTIAL AS BIOCONTROL AGENTS. <i>Journal of Microbiology, Biotechnology and Food Sciences</i> , 2019, 8, 1352-1359.	0.4	6
25738	Genome characterization of a Potato virus S (PVS) variant from tuber sprouts of <i>Solanum phureja</i> Juz. et Buk. <i>Agronomia Colombiana</i> , 2016, 34, 51-60.	0.1	23
25739	Molecular characterization of Potato virus Y (PVY) and Potato virus V (PVV) isolates naturally infecting cape gooseberry ( <i>Physalis peruviana</i> ) in Antioquia, Colombia. <i>Agronomia Colombiana</i> , 2018, 36, 13-23.	0.1	11
25740	Finding of a novel fungal immunomodulatory protein coding sequence in <i>Ganoderma australe</i> . <i>Revista Colombiana De Biotecnología</i> , 2014, 16, 90-95.	0.5	6
25741	Inter and Intra Variation of Potato Yellow Vein Virus in Three Potato Species From Colombia. <i>Revista Facultad Nacional De Agronomía Medellín</i> , 2015, 68, 7387-7398.	0.2	5
25742	Complete genome sequence of a Passion fruit yellow mosaic virus (PFYMV) isolate infecting purple passionfruit ( <i>Passiflora edulis</i> f. <i>edulis</i> ). <i>Revista Facultad Nacional De Agronomía Medellín</i> , 2019, 72, 8643-8654.	0.2	5

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25746	Identification of soybean trans-factors associated with plastid RNA editing sites. <i>Genetics and Molecular Biology</i> , 2020, 43, e20190067.	0.6	2
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25750	Species delimitation reveals an underestimated diversity of Andean catfishes of the family Astroblepidae (Teleostei: Siluriformes). <i>Neotropical Ichthyology</i> , 2020, 18, .	0.5	6
25751	A new Northeast Asian Lynceus (Crustacea: Branchiopoda: Laevicaudata) with uniquely modified thoracopods and an evaluation of DNA barcoding for clam shrimp species identification. <i>Nauplius</i> , 0, 28, .	0.3	2
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25755	Mitochondrial DNA Sequence Phylogeny of <i>Daucus</i> . <i>Systematic Botany</i> , 2020, 45, 403-408.	0.2	3
25756	Polyploidy in <i>Paullinia</i> (Paullinieae, Sapindaceae) and its Systematic Implications. <i>Systematic Botany</i> , 2020, 45, 873-878.	0.2	2
25757	<i>Lecanora markjohnstonii</i> (Lecanoraceae, lichenized Ascomycetes), a new sorediate crustose lichen from the southeastern United States. <i>Bryologist</i> , 2018, 121, 498-512.	0.1	10
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25759	Genome Size Diversification in Central American Bolitoglossine Salamanders (Caudata;) Tj ETQq1 1 0.784314 rgBT/Overlock_10 Tf 50	1.4	7
25760	A New Species of Fairy Wrasse (Teleostei: Labridae: Cirrhilabrus) from Mesophotic Coral Ecosystems of the Verde Island Passage, Philippines. <i>Copeia</i> , 2020, 108, 91.	1.4	5
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25763	Distribution of <i>Bemisia tabaci</i> (Gennadius) (Hemiptera: Aleyrodidae) Mitotypes in Commercial Cotton Fields in the Punjab Province of Pakistan. <i>Florida Entomologist</i> , 2020, 103, 41.	0.2	5
25764	A New Cryptic Species of the <i>Adenomera andreae</i> Clade from Southwestern Amazonia (Anura, Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 66)	0.2	10
25765	Multilocus Phylogeography of Eastern Red-Backed Salamanders ( <i>Plethodon cinereus</i> ): Cryptic Appalachian Diversity and Postglacial Range Expansion. <i>Herpetologica</i> , 2020, 76, 61.	0.2	13
25766	Laboulbeniales (Ascomycota) of the Boston Harbor Islands II (and Other Localities): Species Parasitizing Carabidae, and the <i>Laboulbenia flagellata</i> Species Complex. <i>Northeastern Naturalist</i> , 2019, 25, 110.	0.1	14
25767	A New Species of <i>Pseudopaludicola</i> Miranda-Ribeiro, 1926 (Anura: Leptodactylidae: Leiuperinae) from an Amazonia-Cerrado Transitional Zone, State of Tocantins, Brazil. <i>Journal of Herpetology</i> , 2019, 53, 68.	0.2	7
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25771	Evaluaci3n de la posici3n filogen3tica de la familia monot3pica Halophytaceae (Portulacinae,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 66)	0.3	8
25772	Homologs of RNA Ligase 2 of the Bacteriophage T4 in Metagenomes of Ocean Microbiota. <i>Mathematical Biology and Bioinformatics</i> , 2019, 14, 683-704.	0.1	1
25773	Comparative Mitogenomic and Phylogenetic Analyses of a Schizothoracine Fish, <i>Gymnodiptychus dybowskii</i> from Two Water Systems in Xinjiang. <i>Pakistan Journal of Zoology</i> , 2018, 50, .	0.1	3
25774	Relation between Gene Content and Taxonomy in Chloroplasts. <i>International Journal of Bioscience, Biochemistry, Bioinformatics (IJBBB)</i> , 2017, 7, 41-50.	0.2	1
25775	Insights to the genetic structure of <i>Calanus helgolandicus</i> (Calanoida: Copepoda) from deep-sea specimens in the Balearic Sea. <i>Crustacean Research</i> , 2019, 48, 119-132.	0.2	2
25776	StructAnalyzer - a tool for sequence vs. structure similarity analysis. <i>Acta Biochimica Polonica</i> , 2017, 63, 753-757.	0.3	5
25777	DNA barcoding indicates hidden diversity of <i>Euscorpius</i> (Scorpiones: Euscorpiidae) in Turkey. <i>Euscorpius</i> , 2016, 2016, 1-12.	0.4	8
25778	Adaptive sequence convergence of the tumor suppressor ADAMTS9 between small-bodied mammals displaying exceptional longevity. <i>Aging</i> , 2017, 9, 573-582.	1.4	9
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25781	Staurosporine, an inhibitor of hormonally up-regulated neu-associated kinase. <i>Oncotarget</i> , 2018, 9, 35962-35973.	0.8	13
25782	Parasites of the genus <i>Nosema</i> , <i>Crithidia</i> and <i>Lotmaria</i> in the honeybee and bumblebee populations: a case study in India. <i>Vavilovskii Zhurnal Genetiki I Seleksii</i> , 2017, 21, 943-951.	0.4	9
25783	Microbiomes of Inflammatory Thoracic Aortic Aneurysms Due to Giant Cell Arteritis and Clinically Isolated Aortitis Differ From Those of Non-Inflammatory Aneurysms. <i>Pathogens and Immunity</i> , 2019, 4, 105.	1.4	22
25784	Feral pig ( <i>Sus scrofa</i> ) predation of a green and golden bell frog ( <i>Litoria aurea</i> )., 2016, 40, 191-195.		3
25785	Usage of Banana Pseudostem Waste for the Production of Potassic Biofertilizer using Cellulolytic Bacteria. <i>International Journal of Current Microbiology and Applied Sciences</i> , 2016, 5, 336-349.	0.0	6
25788	Population Structure of Two Flightless Weevils of Genus <i>Scepticus</i> Roelofs (Coleoptera,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 502 Td (	0.3	2
25789	Systematics of <i>Calliophis intestinalis</i> with the Resurrection of <i>Calliophis nigrotaeniatus</i> (Elapidae,) Tj ETQq1 1 0.784314 rgBT, /Overlock 10 Tf 50 502 Td (	0.3	2
25790	Isolation and Molecular Identification of Entomopathogenic Nematodes ( <i>Steinernema</i> and) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 422 Td (	0.1	4
25792	<i>Discopersicus</i> n. gen., a New Member of the Family Tylenchidae Orley, 1880 with Detailed SEM Study on Two Known Species of the Genus <i>Discotylenchus</i> Siddiqi, 1980 (Nematoda; Tylenchidae) from Iran. <i>Journal of Nematology</i> , 2016, 48, 214-221.	0.4	14
25793	Data on Some Species of the Genus <i>Coslenchus</i> Siddiqi, 1978 (Rhabditida, Tylenchidae) from Iran. <i>Journal of Nematology</i> , 2016, 48, 28-33.	0.4	4
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25795	Taxonomy and Systematics of the Genus <i>Makatinus</i> Heyns, 1965 (Nematoda: Dorylaimida:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 262 Td (	0.4	3
25796	A New Species of the Rare Genus <i>Anguillonema</i> Fuchs, 1938 (Nematoda: Hexatylinea, Sphaerularioidea) with Its Molecular Phylogenetic Study. <i>Journal of Nematology</i> , 2017, 49, 286-294.	0.4	5
25797	Morphological and Molecular Characterization of <i>Labrys filiformis</i> n. sp. (Rhabditida:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 182 Td (	0.4	10
25798	Samplings of Millipedes in Japan and Scarab Beetles in Hong Kong result in five new Species of <i>Pristionchus</i> (Nematoda: Diplogastridae). <i>Journal of Nematology</i> , 2018, 50, 587-610.	0.4	8
25799	Two new Species of <i>Pristionchus</i> (Nematoda: Diplogastridae) include the Gonochoristic Sister Species of <i>P. fissidentatus</i>. <i>Journal of Nematology</i> , 2019, 51, 1-14.	0.4	7
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25804	The In Silico Drug Discovery Toolbox: Applications in Lead Discovery and Optimization. Current Medicinal Chemistry, 2019, 26, 3838-3873.	1.2	47
25805	Advances in the Understanding of the Cannabinoid Receptor 1 " Focusing on the Inverse Agonists Interactions. Current Medicinal Chemistry, 2019, 26, 1908-1919.	1.2	18
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25807	Leptomonas pyrrocoris: Genomic insight into Parasite's Physiology. Current Genomics, 2018, 19, 150-156.	0.7	9
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25809	Understanding the Structural Basis for Inhibition of Cyclin-Dependent Kinases. New Pieces in the Molecular Puzzle. Current Drug Targets, 2017, 18, 1104-1111.	1.0	48
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25811	Computational RNA Structure Prediction. Current Bioinformatics, 2008, 3, 32-45.	0.7	37
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25823	Tube-nosed variationsâ€œa new species of the genus &lt;i&gt;Murina&lt;/i&gt; (Chiroptera:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.9	4
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25930	DNA metabarcoding of Neotropical ichthyoplankton: Enabling high accuracy with lower cost. Metabarcoding and Metagenomics, 0, 3, .	0.0	21
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25934	<i>Architrypethelium murisporum</i> (Ascomycota, Trypetheliaceae), a remarkable new lichen species from Thailand challenging ascospore septation as an indicator of phylogenetic relationships. <i>MycoKeys</i> , 2018, 34, 25-34.	0.8	5
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25945	Phylogenetic and morphological classification of <i>Ophiocordyceps</i> species on termites from Thailand. <i>MycoKeys</i> , 2019, 56, 101-129.	0.8	24
25946	<i>Clitopilus lampangensis</i> (Agaricales, Entolomataceae), a new species from northern Thailand. <i>MycoKeys</i> , 2019, 58, 69-82.	0.8	4
25947	The <i>Ganoderma weberianum-resinaceum</i> lineage: multilocus phylogenetic analysis and morphology confirm <i>G. mexicanum</i> and <i>G. parvulum</i> in the Neotropics. <i>MycoKeys</i> , 2019, 59, 95-131.	0.8	22
25948	Two new species of <i>Lactifluus</i> (Fungi, Russulales) from tropical <i>Quercus</i> forest in eastern Mexico. <i>MycoKeys</i> , 2019, 59, 27-45.	0.8	7
25949	Morphology and secondary chemistry in species recognition of <i>Parmelia omphalodes</i> group “evidence from molecular data with notes on the ecological niche modelling and genetic variability of photobionts. <i>MycoKeys</i> , 2019, 61, 39-74.	0.8	6

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25950	Descriptions of five new species in <i>Entoloma</i> subgenus <i>Claudopus</i> from China, with molecular phylogeny of <i>Entoloma</i> s.l.. <i>MycoKeys</i> , 2019, 61, 1-26.	0.8	6
25951	Additions to the genus <i>Chroogomphus</i> (Boletales, Gomphidiaceae) from Pakistan. <i>MycoKeys</i> , 2020, 66, 23-38.	0.8	4
25952	A taxonomic revision of the genus <i>Conidiobolus</i> (Ancylistaceae, Entomophthorales): four clades including three new genera. <i>MycoKeys</i> , 2020, 66, 55-81.	0.8	32
25953	Studies of Neotropical tree pathogens in <i>Moniliophthora</i> : a new species, <i>M. mayarum</i> , and new combinations for <i>Crinipellis ticoi</i> and <i>C. brasiliensis</i> . <i>MycoKeys</i> , 2020, 66, 39-54.	0.8	7
25954	New species of <i>Retiboletus</i> (Boletales, Boletaceae) from China based on morphological and molecular data. <i>MycoKeys</i> , 2020, 67, 33-44.	0.8	5
25955	Three new <i>Curvularia</i> species from clinical and environmental sources. <i>MycoKeys</i> , 2020, 68, 1-21.	0.8	4
25956	New species of <i>Pseudosperma</i> (Agaricales, Inocybaceae) from Pakistan revealed by morphology and multi-locus phylogenetic reconstruction. <i>MycoKeys</i> , 2020, 69, 1-31.	0.8	11
25957	Checklist of thallus-forming <i>Laboulbeniomycetes</i> from Belgium and the Netherlands, including <i>Hesperomyces halyziae</i> and <i>Laboulbenia quarantena</i> spp. nov.. <i>MycoKeys</i> , 2020, 71, 23-86.	0.8	14
25958	Diversity of <i>Akanthomyces</i> on moths (Lepidoptera) in Thailand. <i>MycoKeys</i> , 2020, 71, 1-22.	0.8	12
25959	Evidence for geographic substructuring of mtDNA variation in the East European Hermit beetle ( <i>Osmoderma barnabita</i> ). <i>Nature Conservation</i> , 0, 19, 171-189.	0.0	12
25960	Unravelling the origin and introduction pattern of the tropical species <i>Paracaprella pusilla</i> Mayer, 1890 (Crustacea, Amphipoda, Caprellidae) in temperate European waters: first molecular insights from a spatial and temporal perspective. <i>NeoBiota</i> , 0, 47, 43-80.	1.0	7
25961	Origin of the <i>Diplazium hachijoense</i> complex (Athuriaceae). <i>PhytoKeys</i> , 2019, 124, 57-76.	0.4	10
25962	The <i>Callerya</i> Group redefined and Tribe <i>Wisterieae</i> (Fabaceae) emended based on morphology and data from nuclear and chloroplast DNA sequences. <i>PhytoKeys</i> , 2019, 125, 1-112.	0.4	26
25963	<i>Lysimachia fanii</i> , a new species of Primulaceae from limestone area of Guangxi, China. <i>PhytoKeys</i> , 2019, 130, 75-84.	0.4	9
25964	New taxa of <i>Rhododendron tschonoskii</i> alliance (Ericaceae) from East Asia. <i>PhytoKeys</i> , 2019, 134, 97-114.	0.4	6
25965	New distribution records of two bamboo species in Yunnan, China with description of the inflorescence for <i>Melocalamus yunnanensis</i> (Poaceae, Bambusoideae). <i>PhytoKeys</i> , 2016, 62, 41-56.	0.4	4
25966	A molecular phylogeny of <i>Caraganeae</i> (Leguminosae, Papilionoideae) reveals insights into new generic and infrageneric delimitations. <i>PhytoKeys</i> , 2016, 70, 111-137.	0.4	17
25967	Reproductive biology and variation of nuclear ribosomal ITS and ETS sequences in the <i>Calligonum mongolicum</i> complex (Polygonaceae). <i>PhytoKeys</i> , 2017, 76, 71-88.	0.4	5

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25969	Mitochondrial sequence data indicate vicariance by Erosion as a mechanism of species diversification in North American Ptomaphagus (Coleoptera, Leiodidae, Cholevinae) cave beetles. <i>Subterranean Biology</i> , 0, 29, 35-57.	5.0	9
25970	Species limits and phylogeography of Newportia (Scolopendromorpha) and implications for widespread morphospecies. <i>ZooKeys</i> , 2015, 510, 65-77.	0.5	5
25971	A new species of Liolaemus related to <i>L. nigroviridis</i> from the Andean highlands of Central Chile (Iguania, Liolaemidae). <i>ZooKeys</i> , 2016, 555, 91-114.	0.5	8
25972	Tsukiyamaia, a new genus of the tribe Baorini (Lepidoptera, Hesperiiidae, Hesperiiinae). <i>ZooKeys</i> , 2016, 555, 37-55.	0.5	5
25973	The Knight and the King: two new species of giant bent-toed gecko ( <i>Cyrtodactylus</i> , Gekkonidae). <i>ZooKeys</i> , 2016, 562, 105-130.	0.5	14
25974	Species delimitation in northern European water scavenger beetles of the genus <i>Hydrobius</i> (Coleoptera, Hydrophilidae). <i>ZooKeys</i> , 2016, 564, 71-120.	0.5	24
25975	A new blue-tailed Monitor lizard (Reptilia, Squamata, Varanus) of the <i>Varanus indicus</i> group from Mussau Island, Papua New Guinea. <i>ZooKeys</i> , 2016, 568, 129-154.	0.5	12
25976	New species in the <i>Sitalcina sura</i> species group (Opiliones, Laniatores, Phalangodidae), with evidence for a biogeographic link between California desert canyons and Arizona sky islands. <i>ZooKeys</i> , 2016, 586, 1-36.	0.5	14
25977	Eleven nominal species of <i>Burmoniscus</i> are junior synonyms of <i>B. kathmandius</i> (Schmalfuss, 1983) (Crustacea, Isopoda, Oniscidea). <i>ZooKeys</i> , 2016, 607, 1-24.	0.5	9
25978	How reliably can northeast Atlantic sand lances of the genera <i>Ammodytes</i> and <i>Hyperoplus</i> be distinguished? A comparative application of morphological and molecular methods. <i>ZooKeys</i> , 2016, 617, 139-164.	0.5	12
25979	Two complete mitochondrial genomes from <i>Praticolella mexicana</i> Perez, 2011 (Polygyridae) and gene order evolution in Helicoidea (Mollusca, Gastropoda). <i>ZooKeys</i> , 2016, 626, 137-154.	0.5	7
25980	Two new species and a remarkable record of the genus <i>Dendronotus</i> from the North Pacific and Arctic oceans (Nudibranchia). <i>ZooKeys</i> , 2016, 630, 19-42.	0.5	16
25981	Morphological and molecular evidence indicate <i>Dendronotus primorjensis</i> is a valid species that has priority over <i>D. dudkai</i> (Nudibranchia). <i>ZooKeys</i> , 2016, 634, 15-28.	0.5	13
25982	<i>Iranocichla persa</i> , a new cichlid species from southern Iran (Teleostei, Cichlidae). <i>ZooKeys</i> , 2016, 636, 141-161.	0.5	12
25983	Phylogenetic analysis of the genus <i>Laparocerus</i> , with comments on colonisation and diversification in Macaronesia (Coleoptera, Curculionidae, Entiminae). <i>ZooKeys</i> , 2017, 651, 1-77.	0.5	22
25984	Taxonomic reassessment of two subspecies of Chinese skink in Taiwan based on morphological and molecular investigations (Squamata, Scincidae). <i>ZooKeys</i> , 2017, 687, 131-148.	0.5	7
25985	Abyssal fauna of the UK-1 polymetallic nodule exploration area, Clarion-Clipperton Zone, central Pacific Ocean: Mollusca. <i>ZooKeys</i> , 2017, 707, 1-46.	0.5	23

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25987	Genome-wide SNP data and morphology support the distinction of two new species of Kovarikia Soleglad, Fet & Graham, 2014 endemic to California (Scorpionida, Vaejovidae). ZooKeys, 2018, 739, 79-106.	0.5	3
25988	Re-evaluation of the discriminatory power of DNA barcoding on some specimens of African Cyprinidae (subfamilies Cyprininae and Danioninae). ZooKeys, 2018, 746, 105-121.	0.5	7
25989	A molecular and conchological dissection of the <i>Georissa</i> of Malaysian Borneo (Gastropoda). Tj ETQq1 1 0.784314 rgBT / Overlock 10 Tf 50	0.5	7
25990	First report of <i>Trichogramma danausicida</i> and <i>Trichogramma cacaeciae</i> reared from <i>Thaumatotibia leucotreta</i> eggs in Israel. ZooKeys, 0, 779, 19-25.	0.5	2
25991	<i>Araneus bonali</i> sp. n., a novel lichen-patterned species found on oak trunks (Araneae, Araneidae). ZooKeys, 2018, 779, 119-145.	0.5	2
25992	Establishment of a new genus, <i>Brephallus</i> Wang et al., gen. nov. (Blattodea, Blaberidae, Epilamprinae) based on two species from <i>Pseudophoraspis</i> , with details of polymorphism in species of <i>Pseudophoraspis</i> . ZooKeys, 2018, 785, 117-131.	0.5	5
25993	Analysis of mitochondrial genomes resolves the phylogenetic position of Chinese freshwater mussels ( <i>Bivalvia</i> , Unionidae). ZooKeys, 2019, 812, 23-46.	0.5	21
25994	Conchological and molecular analysis of the <i>Georissa</i> of Borneo with descriptions of three new species (Gastropoda, Neritimorpha, Hydrocenidae). ZooKeys, 2019, 840, 35-86.	0.5	6
25995	Phylogeography and species distribution modelling of <i>Cryptocephalus barii</i> (Coleoptera). Tj ETQq1 1 0.784314 rgBT / Overlock 10 Tf 50	0.5	23
25996	Three new species of <i>Herpetogramma</i> Lederer (Lepidoptera, Crambidae) from China. ZooKeys, 2019, 865, 67-85.	0.5	3
25997	Abyssal fauna of polymetallic nodule exploration areas, eastern Clarion-Clipperton Zone, central Pacific Ocean: Annelida: Capitellidae, Opheliidae, Scalibregmatidae, and Travisidae. ZooKeys, 2019, 883, 1-82.	0.5	29
25998	A new species of stygobitic snail in the genus <i>Antrorbis</i> Hershler & Thompson, 1990 (Gastropoda, Cochliopidae) from the Appalachian Valley and Ridge of eastern Tennessee, USA. ZooKeys, 2019, 898, 103-120.	0.5	3
25999	<i>Phestilla subodiosus</i> sp. nov. (Nudibranchia, Trinchetiidae), a corallivorous pest species in the aquarium trade. ZooKeys, 2020, 909, 1-24.	0.5	10
26000	A new species of <i>Leptobranchella</i> (Anura, Megophryidae) from Guizhou Province, China. ZooKeys, 2020, 923, 115-140.	0.5	15
26001	Evolutionary relationships and population genetics of the Afrotropical leaf-nosed bats (Chiroptera). Tj ETQq1 1 0.784314 rgBT / Overlock 18	0.5	18
26002	A partial molecular phylogeny of <i>Rhadinaea</i> and related genera (Squamata, Dipsadidae) with comments on the generic assignment of <i>Rhadinaea eduardoi</i> . ZooKeys, 2020, 943, 145-155.	0.5	6
26003	An annotated checklist and integrative biodiversity discovery of barnacles (Crustacea, Cirripedia) from the Moluccas, East Indonesia. ZooKeys, 2020, 945, 17-83.	0.5	6

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26005	Revealing the stygobiotic and crenobiotic molluscan biodiversity hotspot in Caucasus: Part I. The phylogeny of stygobiotic Sadlerianinae Szarowska, 2006 (Mollusca, Gastropoda, Hydrobiidae) from Georgia with descriptions of five new genera and twenty-one new species. ZooKeys, 2020, 955, 1-77.	0.5	12
26006	Uncovering the shell game with barcodes: diversity of meiofaunal Caecidae snails (Truncatelloidea). Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.5	2
26007	A new species of Kerkia Radoman, 1978 (Caenogastropoda, Hydrobiidae) from Bosnia and Herzegovina. ZooKeys, 2020, 973, 17-33.	0.5	5
26008	Three new species of frogs of the genus Pristimantis (Anura, Strabomantidae) with a redefinition of the P. lacrimosus species group. ZooKeys, 2020, 993, 121-155.	0.5	11
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26014	Diamond frogs forever: a new species of Rhombophryne Boettger, 1880 (Microhylidae, Cophylinae) from Montagne d'Ambré National Park, northern Madagascar. Zoosystematics and Evolution, 2020, 96, 313-323.	0.4	6
26015	Molecular phylogenetic analysis of Punctoidea (Gastropoda, Stylommatophora). Zoosystematics and Evolution, 2020, 96, 397-410.	0.4	11
26016	Upsurge in Curvularia Infections and Global Emerging Antifungal Drug Resistance. Asian Journal of Scientific Research, 2017, 10, 299-307.	0.3	10
26017	Molecular Characteristics of Anopheles maculipennis Meigen in Zanjan, North West of Iran, Inferred from ITS2 Sequence Analysis. Pakistan Journal of Biological Sciences, 2008, 11, 539-545.	0.2	4
26018	A Pathogenic Isolate of Monopartite PepYLCV DNA A-like Genome Differs Significantly in C1 Gene and CR Sequence, but not in their other Genes. Plant Pathology Journal, 2016, 15, 124-134.	0.7	4
26019	Dissemination of Carbapenem-Resistance among Multidrug Resistant Pseudomonas aeruginosa carrying Metallo-Beta-Lactamase Genes, including the Novel bla IMP - 65 Gene in Thailand. Infection and Chemotherapy, 2019, 51, 107.	1.0	18
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26024	Integrative taxonomy supports the presence of two species of &#x26;#x26;#x26;Kyphosus&#x26;#x26;#x26; (Perciformes: Kyphosidae) in Atlantic European waters. <i>Scientia Marina</i> , 2017, 81, 467.	0.3	5
26025	Following the Phoenician example: western Mediterranean colonization by <em>Spirobranchus</em> cf. <em>tetraceros</em> (Annelida: Serpulidae). <i>Scientia Marina</i> , 2020, 84, 83.	0.3	6
26026	Comparative Analyses of the Complete Mitochondrial Genomes of Three Lamprotula (Bivalvia): Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 58; Species Delimitation. <i>Malacologia</i> , 2020, 63, 51.	0.2	9
26027	A <i>Sporolactobacillus</i>, <i>Clostridium</i>, and <i>Paenibacillus</i>- Dominant Microbial Consortium Improved Anaerobic RDX Detoxification by Starch Addition. <i>Journal of Microbiology and Biotechnology</i> , 2020, 30, 839-847.	0.9	3
26028	Acinetobacter pullorum sp. nov., Isolated from Chicken Meat. <i>Journal of Microbiology and Biotechnology</i> , 2020, 30, 526-532.	0.9	9
26029	Use of SciDBMaker as Tool for the Design of Specialized Biological Databases. , 0, , 251-265.		1
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26033	Identification and analysis of biomarkers for mismatch repair proteins: A bioinformatic approach. <i>Journal of Natural Science, Biology and Medicine</i> , 2012, 3, 139.	1.0	7
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26039	Detection of &#x26;#x26;#x26;bla&#x26;#x26;#x26;NDM-1 and Genetic Relatedness in Clinical Isolates of &#x26;#x26;#x26;Escherichia coli&#x26;#x26;#x26; Producing Extended Spectrum &#x26;#x26;#x26;l2&#x26;#x26;#x26;-Lactamase from Tertiary Care Centres in South India. <i>Advances in Microbiology</i> , 2016, 06, 125-132.	0.3	1

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26159	A new genus of horse from Pleistocene North America. <i>ELife</i> , 2017, 6, .	2.8	61
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26176	ASPEN, a methodology for reconstructing protein evolution with improved accuracy using ensemble models. <i>ELife</i> , 2019, 8, .	2.8	4
26177	A single clonal lineage of transmissible cancer identified in two marine mussel species in South America and Europe. <i>ELife</i> , 2019, 8, .	2.8	60
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26180	Phage integration alters the respiratory strategy of its host. <i>ELife</i> , 2019, 8, .	2.8	24
26181	Compensatory sequence variation between trans-species small RNAs and their target sites. <i>ELife</i> , 2019, 8, .	2.8	27
26182	A novel lineage of candidate pheromone receptors for sex communication in moths. <i>ELife</i> , 2019, 8, .	2.8	51
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26188	Altered expression of a quality control protease in <i>E. coli</i> reshapes the in vivo mutational landscape of a model enzyme. <i>ELife</i> , 2020, 9, .	2.8	37
26189	Local frustration determines loop opening during the catalytic cycle of an oxidoreductase. <i>ELife</i> , 2020, 9, .	2.8	13
26190	Conformational distributions of isolated myosin motor domains encode their mechanochemical properties. <i>ELife</i> , 2020, 9, .	2.8	28
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26194	Evolution of a plant gene cluster in Solanaceae and emergence of metabolic diversity. <i>ELife</i> , 2020, 9, .	2.8	47
26195	A large effective population size for established within-host influenza virus infection. <i>ELife</i> , 2020, 9, .	2.8	15
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26202	Mitochondrial genomes of twelve species of hyperdiverse Trigonopterus weevils. <i>PeerJ</i> , 2020, 8, e10017.	0.9	10
26203	Description of a new member of the family <i>Erysipelotrichaceae</i> : <i>Dakotella fusiforme</i> gen. nov., sp. nov., isolated from healthy human feces. <i>PeerJ</i> , 2020, 8, e10071.	0.9	6
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26205	DNA barcoding for identification of anuran species in the central region of South America. <i>PeerJ</i> , 2020, 8, e10189.	0.9	6
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26207	Phospho-islands and the evolution of phosphorylated amino acids in mammals. <i>PeerJ</i> , 2020, 8, e10436.	0.9	5
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26209	Let's be pals again: major systematic changes in Palaemonidae (Crustacea: Decapoda). <i>PeerJ</i> , 2015, 3, e1167.	0.9	34



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26211	Expression of temperature-sensitive ion channel TRPM8 in sperm cells correlates with vertebrate evolution. PeerJ, 2015, 3, e1310.	0.9	26
26212	Variation in the flowering time orthologs <i>BrFLC</i> and <i>BrSOC1</i> in a natural population of <i>Brassica rapa</i> . PeerJ, 2015, 3, e1339.	0.9	19
26213	Multiphasic strain differentiation of atypical mycobacteria from elephant trunk wash. PeerJ, 2015, 3, e1367.	0.9	3
26214	Genetic models reveal historical patterns of sea lamprey population fluctuations within Lake Champlain. PeerJ, 2015, 3, e1369.	0.9	4
26215	Comparative genomics of <i>Synechococcus</i> and proposal of the new genus <i>Parasynechococcus</i> . PeerJ, 2016, 4, e1522.	0.9	46
26216	The identification of immune genes in the milk transcriptome of the Tasmanian devil ( <i>Sarcophilus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	0.9	16
26217	Phylogenetic and morphologic evidence confirm the presence of a new montane cloud forest associated bird species in Mexico, the Mountain Elaenia ( <i>Elaenia frantzii</i> ; Aves: Passeriformes) Tj ETQq1 1 0.784314 rgBT /Overlo	0.9	14
26218	Analysis of five complete genome sequences for members of the class Peribacteria in the recently recognized Peregrinibacteria bacterial phylum. PeerJ, 2016, 4, e1607.	0.9	57
26219	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. PeerJ, 2016, 4, e1616.	0.9	56
26220	First insights into the diversity of gill monogeneans of <i>Gnathochromis</i> ™ and <i>Limnochromis</i> (Teleostei, Cichlidae) in Burundi: do the parasites mirror host ecology and phylogenetic history?. PeerJ, 2016, 4, e1629.	0.9	19
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26222	From commensalism to parasitism in Carapidae (Ophidiiformes): heterochronic modes of development?. PeerJ, 2016, 4, e1786.	0.9	9
26223	Molecular phylogeny of porcelain crabs (Porcellanidae: <i>Petrolisthes</i> and allies) from the south eastern Pacific: the genera <i>Allopetrolisthes</i> and <i>Liopetrolisthes</i> are not natural entities. PeerJ, 2016, 4, e1805.	0.9	6
26224	Epidemiological dynamics of an urban Dengue 4 outbreak in São Paulo, Brazil. PeerJ, 2016, 4, e1892.	0.9	13
26225	Advertisement call and genetic structure conservatism: good news for an endangered Neotropical frog. PeerJ, 2016, 4, e2014.	0.9	15
26226	Sparc: a sparsity-based consensus algorithm for long erroneous sequencing reads. PeerJ, 2016, 4, e2016.	0.9	36
26227	Effects of 16S rDNA sampling on estimates of the number of endosymbiont lineages in sucking lice. PeerJ, 2016, 4, e2187.	0.9	14

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26229	Genome-wide identification and characterization of TIFY family genes in Moso Bamboo ( <i>Phyllostachys edulis</i> ) and expression profiling analysis under dehydration and cold stresses. PeerJ, 2016, 4, e2620.	0.9	37
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26236	Three new karst-dwelling <i>Cnemaspis</i> Strauch, 1887 (Squamata; Gekkoniade) from Peninsular Thailand and the phylogenetic placement of <i>C. punctatouchalis</i> and <i>C. vandeventeri</i> . PeerJ, 2017, 5, e2884.	0.9	15
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26262	Comparative genomic analysis of a new tellurite-resistant <i>Psychrobacter</i> strain isolated from the Antarctic Peninsula. PeerJ, 2018, 6, e4402.	0.9	30
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26266	Genetic diversity and molecular evolution of <i>Ornithogalum mosaic virus</i> based on the coat protein gene sequence. PeerJ, 2018, 6, e4550.	0.9	11
26267	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
26268	Biochemical and genetic analyses of the oomycete <i>Pythium insidiosum</i> provide new insights into clinical identification and urease-based evolution of metabolism-related traits. PeerJ, 2018, 6, e4821.	0.9	6
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26274	Variable retention harvesting influences belowground plant-fungal interactions of <i>Nothofagus pumilio</i> seedlings in forests of southern Patagonia. PeerJ, 2018, 6, e5008.	0.9	9
26275	Comprehensive analysis of mitogen-activated protein kinase cascades in chrysanthemum. PeerJ, 2018, 6, e5037.	0.9	11
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26279	Recent genome reduction of <i>Wolbachia</i> in <i>Drosophila recens</i> targets phage WO and narrows candidates for reproductive parasitism. PeerJ, 2014, 2, e529.	0.9	51
26280	Imputing missing distances in molecular phylogenetics. PeerJ, 2018, 6, e5321.	0.9	5
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26283	Phylogeography of <i>Swertia perennis</i> in Europe based on cpDNA markers. PeerJ, 2018, 6, e5512.	0.9	6
26284	<i>Lysmata arvorendensis</i> nov. sp. a new species of shrimp from the south coast of Brazil with a key to species of <i>Lysmata</i> (Caridea: Lysmatidae) recorded in the southwestern Atlantic. PeerJ, 2018, 6, e5561.	0.9	6
26285	Metabolic marker gene mining provides insight in global <i>mcrA</i> diversity and, coupled with targeted genome reconstruction, sheds further light on metabolic potential of the <i>Methanomassiliicoccales</i> . PeerJ, 2018, 6, e5614.	0.9	34
26286	A new species of <i>Brachycephalus</i> (Anura: Brachycephalidae) from southern Brazil. PeerJ, 2018, 6, e5683.	0.9	10
26287	Effects of wine-cap <i>Stropharia</i> cultivation on soil nutrients and bacterial communities in forestlands of northern China. PeerJ, 2018, 6, e5741.	0.9	20
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26289	Virus discovery in all three major lineages of terrestrial arthropods highlights the diversity of single-stranded DNA viruses associated with invertebrates. PeerJ, 2018, 6, e5761.	0.9	51
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26294	Combining ultraconserved elements and mtDNA data to uncover lineage diversity in a Mexican highland frog ( <i>Sarcohyala</i> ; Hylidae). PeerJ, 2018, 6, e6045.	0.9	31
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26296	The origin of exotic pet sugar gliders ( <i>Petaurus breviceps</i> ) kept in the United States of America. PeerJ, 2019, 7, e6180.	0.9	9
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26301	Relative abundance and molecular evolution of Lake Sinai Virus (Sinaivirus) clades. PeerJ, 2019, 7, e6305.	0.9	18
26302	Genome-wide identification and comparative evolutionary analysis of the Dof transcription factor family in physic nut and castor bean. PeerJ, 2019, 7, e6354.	0.9	16
26303	Integrative taxonomic reassessment of <i>Odontophrynus</i> populations in Argentina and phylogenetic relationships within Odontophrynidae (Anura). PeerJ, 2019, 7, e6480.	0.9	6
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26310	Artifactual pyrosequencing reads in multiple-displacement-amplified sediment metagenomes from the Red Sea. PeerJ, 2013, 1, e69.	0.9	4
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26313	The comparative population genetics of <i>Neisseria meningitidis</i> and <i>Neisseria gonorrhoeae</i> . PeerJ, 2019, 7, e7216.	0.9	20
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26315	A holistic evolutionary and structural study of <i>flaviviridae</i> provides insights into the function and inhibition of HCV helicase. PeerJ, 2013, 1, e74.	0.9	28
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26320	A draft genome and transcriptome of common milkweed ( <i>Asclepias syriaca</i> ) as resources for evolutionary, ecological, and molecular studies in milkweeds and Apocynaceae. PeerJ, 2019, 7, e7649.	0.9	19
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26324	Development of molecular markers for invasive alien plants in Korea: a case study of a toxic weed, <i>Cenchrus longispinus</i> L., based on next generation sequencing data. PeerJ, 2019, 7, e7965.	0.9	2
26325	Genomic diversity of prevalent <i>Staphylococcus epidermidis</i> multidrug-resistant strains isolated from a Children's Hospital in Mexico City in an eight-years survey. PeerJ, 2019, 7, e8068.	0.9	9
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26350	Bioinformatics Analysis on DNA Barcode Sequences for Species Identification: A Review. Annual Research & Review in Biology, 0, , 1-12.	0.4	3
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26373	Taxonomic identity of <i>Crepidiastrum</i> <i>nakaii</i> recorded on Hongdo Island. <i>Korean Journal of Plant Taxonomy</i> , 2021, 51, 198-204.	0.3	0
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27534	Characterization of <i>Peptacetobacter hominis</i> gen. nov., sp. nov., isolated from human faeces, and proposal for the reclassification of <i>Clostridium hiranonis</i> within the genus <i>Peptacetobacter</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 2988-2997.	0.8	18
27536	Micromorphological, anatomical and molecular study of <i>Hedera</i> species (Araliaceae) in Iran. <i>Acta Biologica Szegediensis</i> , 2020, 63, 91-101.	0.7	3
27537	<i>Aequorivita sinensis</i> sp. nov., isolated from sediment of the East China Sea, and reclassification of <i>Vitellibacter todarodis</i> as <i>Aequorivita todarodis</i> comb. nov. and <i>Vitellibacter aquimaris</i> as <i>Aequorivita aquimaris</i> comb. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 3323-3327.	0.8	13

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27545	Evolutionary History and Diversity of Unionoid Mussels (Mollusca: Bivalvia) in the Japanese Archipelago. <i>Plankton and Benthos Research</i> , 2020, 15, 97-111.	0.2	7
27546	<i>Lutibacter citreus</i> sp. nov., isolated from Arctic surface sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 3154-3161.	0.8	6
27553	Genetic barcoding of Ecuadorian epilithic diatom species suitable as water quality bioindicators. , 2020, 343, 41-52.		2
27554	A new species of the genus <i>Agorius</i> (Araneae: Salticidae) from Sarawak, Borneo. <i>Acta Arachnologica</i> , 2020, 69, 37-41.	0.0	0
27561	Bingde yeti tirilen sÄ±rÄ±rÄ±lerinde Bovine Viral DiyarÄ± enfeksiyonunun varliÄ±nÄ±n ve yaygÄ±nlÄ±Ä± belirlenmesi. <i>Etlik Veteriner Mikrobiyoloji Dergisi</i> , 2020, 31, 34-38.	0.2	2
27565	A new species of <i>Araneus</i> (Araneae: Araneidae) from Japan. <i>Acta Arachnologica</i> , 2020, 69, 11-15.	0.0	0
27566	Biodegradation of Pesticide Chlorpyrifos by Bacteria <i>Staphylococcus aureus</i> (Accession no.) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T 20, 21-26.	0.1	3
27567	<i>Cyclobacterium salsum</i> sp. nov. and <i>Cyclobacterium roseum</i> sp. nov., isolated from a saline lake. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 3785-3793.	0.8	9
27570	Population Genetic Structure and Natural Establishment of Hybrids Between <i>Sarracenia flava</i> and <i>Sarracenia minor</i> in Francis Marion National Forest. <i>Castanea</i> , 2020, 85, 108.	0.2	1
27575	<i>Stemmatostoma cribbi</i> n. sp. (Digenea: Cryptogonimidae) from Freshwater Fishes in the Wet Tropics Bioregion of Queensland, Australia. <i>Journal of Parasitology</i> , 2020, 106, 411.	0.3	3
27582	Effects of supplementary feeding on the rumen morphology and bacterial diversity in lambs. <i>PeerJ</i> , 2020, 8, e9353.	0.9	16
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27588	<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
27591	A new species of <i>Notomastus</i> (Annelida, Capitellidae) from southern China, with remarks on its morphology and distribution. <i>ZooKeys</i> , 2020, 946, 1-16.	0.5	1
27594	Exploring utility of genomic epidemiology to trace origins of highly pathogenic influenza A/H7N9 in Guangdong. <i>Virus Evolution</i> , 2020, 6, veaa097.	2.2	6
27596	Genomic evidence of multiple SARS-CoV-2 introductions into Morocco. <i>F1000Research</i> , 0, 9, 679.	0.8	1
27598	Application of bioinformatics and molecular dynamics simulation approaches for identification of fibroblast growth factor 10 analogues with potentially improved thermostability. <i>Growth Factors</i> , 2020, 38, 197-209.	0.5	1

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27601	<i>Prevotella vespertina</i> sp. nov., isolated from an abscess of a hospital patient. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 4576-4582.	0.8	9
27602	Genome-based reclassification of <i>Paenibacillus panacisoli</i> DSM 21345T as <i>Paenibacillus massiliensis</i> subsp. <i>panacisoli</i> subsp. nov. and description of <i>Paenibacillus massiliensis</i> subsp. <i>massiliensis</i> subsp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 4838-4842.	0.8	10
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27605	The species of the <i>varius</i> group of <i>Coccophagus</i> (Hymenoptera: Aphelinidae) from China, with description of a new species, DNA sequence data, and a new country record. <i>Journal of Natural History</i> , 2020, 54, 1879-1896.	0.2	1
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27622	<i>Colletotrichum fusiforme</i> JAYAWARDENA, BHAT, N.TANGTHIR, K.D.HYDE, A NEW FUNGAL RECORD FROM THE INDIAN SUBCONTINENT. <i>Journal of Experimental Biology and Agricultural Sciences</i> , 2020, 8, 500-507.	0.1	0
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27625	Temperate Eurasian Origins of Hawaiian <i>Chenopodium</i> (Amaranthaceae), Plus Description of a New Subspecies Endemic to Molokaï. <i>Systematic Botany</i> , 2020, 45, 554-566.	0.2	2
27626	Multiple Sequence Alignment Algorithm Using Adaptive Evolutionary Clustering. <i>Lecture Notes in Networks and Systems</i> , 2021, , 349-364.	0.5	0
27630	Morphological, Molecular, and Biogeographic Evidence for Specific Recognition of <i>Euthamia hirtipes</i> and <i>Euthamia scabra</i> (Asteraceae, Astereae). <i>Systematic Botany</i> , 2020, 45, 658-667.	0.2	1
27633	<i>Hepatica transsilvanica</i> Fuss (Ranunculaceae) is an Allotetraploid Relict of the Tertiary Flora in Europe – Molecular Phylogenetic Evidence. <i>Acta Societatis Botanicorum Poloniae</i> , 2020, 89, .	0.8	4
27637	Cryptic genetic variation enhances primate L1 retrotransposon survival by enlarging the functional coiled coil sequence space of ORF1p. <i>PLoS Genetics</i> , 2020, 16, e1008991.	1.5	6
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27645	Crossing the borders: First record of Bleeding Wrasse, <i>Polylepion cruentum</i> Gomon, 1977 (Labriformes, Labridae), in the Northern Peru. <i>Papeis Avulsos De Zoologia</i> , 0, 61, e20216185.	0.4	2
27646	TBEV analyzer platform for evolutionary analysis and monitoring tick-borne encephalitis virus: 2020 update. <i>Biostatistics and Epidemiology</i> , 0, , 1-17.	0.4	2
27647	A Rapid Evolving microRNA Cluster Rewires Its Target Regulatory Networks in <i>Drosophila</i> . <i>Frontiers in Genetics</i> , 2021, 12, 760530.	1.1	1
27648	Taxonomic and identification review of adventive <i>Fiorinia Targioni Tozzetti</i> (Hemiptera, Coccothraupidae). <i>Tj ETQq0 0 0 rgBT /Overlock 10 T</i>	0.5	2
27649	Metabolomics Analyses Reveal Metabolites Affected by Plant Growth-Promoting Endophytic Bacteria in Roots of the Halophyte <i>Mesembryanthemum crystallinum</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 11813.	1.8	13
27650	Genome-Wide Identification and Functional Exploration of SBP-Box Gene Family in Black Pepper ( <i>Piper</i> ). <i>Tj ETQq0 0 0 rgBT /Overlock 10 T</i>	1.0	3
27651	Contrasting Patterns of Sensory Adaptation in Living and Extinct Flightless Birds. <i>Diversity</i> , 2021, 13, 538.	0.7	1
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27654	The complete genome sequence of a bile-isolated <i>Stenotrophomonas maltophilia</i> ZT1. <i>Gut Pathogens</i> , 2021, 13, 64.	1.6	0
27655	Infection Process and Genome Assembly Provide Insights into the Pathogenic Mechanism of Destructive Mycoparasite <i>Calcarisporium cordycipiticol</i> a with Host Specificity. <i>Journal of Fungi</i> (Basel, Switzerland), 2021, 7, 918.	1.5	8
27657	A Study on the Genetics of Primary Ciliary Dyskinesia. <i>Journal of Clinical Medicine</i> , 2021, 10, 5102.	1.0	5
27658	A new species of free-living marine nematode, <i>Diplolaimella ariakensis</i> n. sp. (Nematoda). <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50</i>	0.2	1
27659	Morphology and molecular phylogeny of <i>Bindiferia</i> gen. nov. (Dinophyceae), a new marine, sand-dwelling dinoflagellate genus formerly classified within <i>Amphidinium</i> . <i>Phycologia</i> , 0, , 1-13.	0.6	6
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27663	<i>Hedysarum sunhangii</i> (Fabaceae, Hedysareae), a new species from Pamir-Alay (Babatag Ridge -) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 66	0.1	2
27664	A New Shrimp Genus (Crustacea: Decapoda) from the Deep Atlantic and an Unusual Cleaning Mechanism of Pelagic Decapods. <i>Diversity</i> , 2021, 13, 536.	0.7	4
27665	Observation of the Gut Microbiota Profile in C57BL/6 Mice Induced by <i>Plasmodium berghei</i> ANKA Infection. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 680383.	1.8	10
27666	Performance of 16S Metagenomic Profiling in Formalin-Fixed Paraffin-Embedded versus Fresh-Frozen Colorectal Cancer Tissues. <i>Cancers</i> , 2021, 13, 5421.	1.7	11
27667	The <i>Melastoma dodecandrum</i> genome and the evolution of Myrtales. <i>Journal of Genetics and Genomics</i> , 2022, 49, 120-131.	1.7	14
27668	Plastid phylogenomic insights into relationships of all flowering plant families. <i>BMC Biology</i> , 2021, 19, 232.	1.7	109
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27670	Genome Survey Sequencing of an Iconic "Trophy"™ Sportfish, the Roosterfish <i>Nematistius pectoralis</i> : Genome Size, Repetitive Elements, Nuclear RNA Gene Operon, and Microsatellite Discovery. <i>Genes</i> , 2021, 12, 1710.	1.0	6
27671	A new species of <i>Galerina</i> (Hymenogastraceae, Agaricales) from northeast China. <i>Phytotaxa</i> , 2021, 524, 27-36.	0.1	1
27672	The Population Genetics, Virulence, and Public Health Concerns of <i>Escherichia coli</i> Collected From Rats Within an Urban Environment. <i>Frontiers in Microbiology</i> , 2021, 12, 631761.	1.5	2
27673	Systematic Characterization of TCP Gene Family in Four Cotton Species Revealed That GhTCP62 Regulates Branching in <i>Arabidopsis</i> . <i>Biology</i> , 2021, 10, 1104.	1.3	11
27674	Gut Microbiota in Canine Idiopathic Epilepsy: Effects of Disease and Treatment. <i>Animals</i> , 2021, 11, 3121.	1.0	11
27675	Diversity and Host Relationships of the Mycoparasite <i>Sepedonium</i> (Hypocreales, Ascomycota) in Temperate Central Chile. <i>Microorganisms</i> , 2021, 9, 2261.	1.6	1
27676	Bioexploration and Phylogenetic Placement of Entomopathogenic Fungi of the Genus <i>Beauveria</i> in Soils of Lebanon Cedar Forests. <i>Journal of Fungi</i> (Basel, Switzerland), 2021, 7, 924.	1.5	2
27677	Bioactive Properties and Metabolite Profiles of Endolichenic Fungi in Mangrove Ecosystem of Negombo Lagoon, Sri Lanka. <i>Natural Product Communications</i> , 2021, 16, 1934578X2110486.	0.2	0
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27681	The Evolutionary History of Vertebrate Adhesion GPCRs and Its Implication on Their Classification. <i>International Journal of Molecular Sciences</i> , 2021, 22, 11803.	1.8	7
27683	Genome and systems biology of <i>Melilotus albus</i> provides insights into coumarins biosynthesis. <i>Plant Biotechnology Journal</i> , 2022, 20, 592-609.	4.1	24
27684	Phylogenetic relationships, population demography, and species delimitation of the <i>Alouatta belzebul</i> species complex (Atelidae: Alouattinae). <i>Primates</i> , 2022, 63, 65-78.	0.7	2
27687	Comprehensive analyses of bioinformatics applications in the fight against COVID-19 pandemic. <i>Computational Biology and Chemistry</i> , 2021, 95, 107599.	1.1	21
27688	A vertebrate-specific qPCR assay as an endogenous internal control for robust species identification. <i>Forensic Science International: Genetics</i> , 2022, 56, 102628.	1.6	4
27689	Characterization of germline development and identification of genes associated with germline specification in pineapple. <i>Horticulture Research</i> , 2021, 8, 239.	2.9	5
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27700	Tracing species replacement in Iberian marbled newts. <i>Ecology and Evolution</i> , 2021, 11, 402-414.	0.8	6
27702	The Bark Beetle <i>Dendroctonus rhizophagus</i> (Curculionidae: Scolytinae) Has Digestive Capacity to Degrade Complex Substrates: Functional Characterization and Heterologous Expression of an $\alpha$ -Amylase. <i>International Journal of Molecular Sciences</i> , 2021, 22, 36.	1.8	3
27703	A Proline-Rich Element in the Type III Secretion Protein FlhB Contributes to Flagellar Biogenesis in the Beta- and Gamma-Proteobacteria. <i>Frontiers in Microbiology</i> , 2020, 11, 564161.	1.5	3
27704	Reconstructed evolutionary history of the yeast septins Cdc11 and Shs1. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, 1-19.	0.8	1
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27707	Phylogenetic analysis of <i>Neottia japonica</i> (Orchidaceae) based on ITS and matK regions. <i>Korean Journal of Plant Taxonomy</i> , 2020, 50, 385-394.	0.3	2
27709	TpportHMM: Predicting the substrate class of transmembrane transport proteins using profile Hidden Markov Models. , 2020, , .		2
27710	Retrospective Survey of <i>Borrelia</i> spp. From Rodents and Ticks in Thailand. <i>Journal of Medical Entomology</i> , 2021, 58, 1331-1344.	0.9	6
27711	Discovery of a New Species of Enigmatic Odd-Scaled Snake (Serpentes: Xenodermidae: Achalinus) from Ha Giang Province, Vietnam. <i>Copeia</i> , 2020, 108, .	1.4	13
27712	Phylogeny-Aware Alignment with PRANK and PAGAN. <i>Methods in Molecular Biology</i> , 2021, 2231, 17-37.	0.4	15
27713	Crossroads of highly pathogenic H5N1: overlap between wild and domestic birds in the Black Sea-Mediterranean impacts global transmission. <i>Virus Evolution</i> , 2021, 7, .	2.2	11
27714	<i>Pseuduvaria khaosokensis</i> (Annonaceae), a New Species from Southern Thailand as Evidenced by Plastid Phylogeny and Morphology. <i>Annales Botanici Fennici</i> , 2020, 58, .	0.0	0
27715	Integrative taxonomy of enigmatic deep-sea true whelks in the sister-genera <i>Enigmaticolus</i> and <i>Thermosiphon</i> (Gastropoda: Buccinidae). <i>Zoological Journal of the Linnean Society</i> , 2021, 193, 230-240.	1.0	3
27716	Prevalencia de cinco virus de ARN en tubérculos-semilla de papa cultivados en Antioquia (Colombia). <i>Biocología En El Sector Agropecuario Y Agroindustrial</i> , 2020, 19, 66-78.	0.2	1
27717	The First Draft Genome of a Cold-Water Coral <i>Trachythela</i> sp. (Alcyonacea: Stolonifera: Tj ETQq0 0 0 rgBT /Qyerlock 10 Tf 50 342	1.1	5
27718	Genome-wide characterization and expression and co-expression analysis suggested diverse functions of WOX genes in bread wheat. <i>Heliyon</i> , 2020, 6, e05762.	1.4	18
27719	Metagenomic Analysis of Rhizosphere Bacteria in Desert Plant <i>Calotropis procera</i> . <i>Geomicrobiology Journal</i> , 2021, 38, 375-383.	1.0	7
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27729	A new species of the genus <i>Leptobranchella</i> Smith, 1925 (Anura, Megophryidae) from Guizhou, China. <i>ZooKeys</i> , 2020, 1008, 139-157.	0.5	8



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27730	Genome-based classification of <i>Calidifontibacillus erzurumensis</i> gen. nov., sp. nov., isolated from a hot spring in Turkey, with reclassification of <i>Bacillus azotoformans</i> as <i>Calidifontibacillus azotoformans</i> comb. nov. and <i>Bacillus oryztterrae</i> as <i>Calidifontibacillus oryztterrae</i> comb. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 6418-6427.	0.8	19
27731	The genera <i>Helvella</i> and <i>Dissingia</i> ( <i>Ascomycota</i> : <i>Pezizomycetes</i> ) in Europe – Notes on species from Spain. <i>Fungal Systematics and Evolution</i> , 2020, 6, 65-93.	0.9	4
27733	Tissue-selective alternate promoters guide NLRP6 expression. <i>Life Science Alliance</i> , 2021, 4, e202000897.	1.3	1
27734	A New Forest-Dwelling Frog Species of the Genus <i>Adenomera</i> (Leptodactylidae) from Northwestern Brazilian Amazonia. <i>Copeia</i> , 2020, 108, .	1.4	2
27735	A New, Miniaturized Genus and Species of Snake (Cyclocoridae) from the Philippines. <i>Copeia</i> , 2020, 108, .	1.4	5
27736	Phenotypic variation and polymorphism confirmed among white-bellied swiftlets of the <i>Collocalia esculenta</i> group (Apodidae, Collocaliini) by mitochondrial and nuclear DNA evidence. <i>Bulletin of the British Ornithologists' Club</i> , 2020, 140, .	0.1	0
27737	Genome-wide identification and evolution of HECT genes in wheat. <i>PeerJ</i> , 2020, 8, e10457.	0.9	8
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27740	Genetic and toxinological divergence among populations of <i>Tityus trivittatus</i> Kraepelin, 1898 (Scorpiones: Buthidae) inhabiting Paraguay and Argentina. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008899.	1.3	4
27741	Expression and phylogeny of multidrug resistance protein 2 and 4 in African white backed vulture ( <i>Gyps africanus</i> ). <i>PeerJ</i> , 2020, 8, e10422.	0.9	1
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27746	Globins in the marine annelid <i>Platynereis dumerilii</i> shed new light on hemoglobin evolution in bilaterians. <i>BMC Evolutionary Biology</i> , 2020, 20, 165.	3.2	9
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27769	Molecular Evolution of [NiFe] Hydrogenase-related Energy Conservation Systems. <i>Journal of Geography (Chigaku Zasshi)</i> , 2020, 129, 825-835.	0.1	2
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27777	Effect of different salinity on the growth performance and proximate composition of isolated indigenous microalgae species. <i>Aquaculture Reports</i> , 2022, 22, 100925.	0.7	19
27778	<i>Aphelenchus yinyuensis</i> n. sp. (Tylenchina: Aphelenchoididae) found in <i>Terminalia</i> sp. in China. <i>Journal of Nematology</i> , 2020, 52, 1-12.	0.4	1
27779	Laccase Engineering by Directed and Computational Evolution. <i>Microbiology Monographs</i> , 2020, , 191-212.	0.3	2
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27783	Phylogenetic and population genetic analyses reveal three distinct lineages of the invasive brown root-rot pathogen, <i>Phellinus noxius</i> , and bioclimatic modeling predicts differences in associated climate niches. <i>European Journal of Plant Pathology</i> , 2020, 156, 751-766.	0.8	9

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27801	Morphological and molecular characterization of <i>Pratylenchus</i> species from Yam ( <i>Dioscorea</i> spp.) in West Africa. <i>Journal of Nematology</i> , 2020, 52, 1-25.	0.4	7
27802	A Categorization of Relevant Sequence Alignment Algorithms with Respect to Data Structures. <i>International Journal of Advanced Computer Science and Applications</i> , 2020, 11, .	0.5	0
27804	An Easy Protocol for Evolutionary Analysis of Intrinsically Disordered Proteins. <i>Methods in Molecular Biology</i> , 2020, 2141, 147-177.	0.4	4
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27806	RECONSTRUCTION OF NITROGENASE PREDECESSORS SUGGESTS ORIGIN FROM MATURASE-LIKE ENZYMES. , 2020, , .		0
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27817	First report of root-knot nematodes ( <i>Meloidogyne</i> species) infecting Chinese Elm ( <i>Ulmus parvifolia</i> ) in Florida, USA. <i>Journal of Nematology</i> , 2020, 52, 1-4.	0.4	5
27818	Taxonomic characterizations of soil <i>Streptomyces cavourensis</i> DW102 and its activity against fungal pathogens. <i>Journal of Pharmacy and Bioallied Sciences</i> , 2020, 12, 462.	0.2	1
27819	Occurrence and molecular characterization of <i>Meloidogyne graminicola</i> on rice in Central Punjab, Pakistan. <i>Journal of Nematology</i> , 2020, 52, 1-17.	0.4	2
27820	Bioinf-PHP: Bioinformatics Pipeline for Protein Homology and Phylogeny. <i>Lecture Notes in Computer Science</i> , 2020, , 261-269.	1.0	0
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27827	In silico detection tools to identify fungal secondary metabolites and their biosynthetic gene clusters. , 2020, , 23-35.		0
27830	<i>Candidatus Anthektikosiphon siderophilum</i> OHK22, a New Member of the Chloroflexi Family Herpetosiphonaceae from Oku-okuhachikurou Onsen. <i>Microbes and Environments</i> , 2020, 35, n/a.	0.7	12
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27832	Isolation, identification, and pathogenicity of <i>Steinernema carpocapsae</i> and its bacterial symbiont in Cauca-Colombia. <i>Journal of Nematology</i> , 2020, 52, 1-16.	0.4	3
27833	Persimmon anthracnose: a comparative study of aggressiveness on shoot and fruit among <i>Colletotrichum horii</i> isolates in southern Brazil. <i>Ciencia Rural</i> , 2020, 50, .	0.3	2
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27842	DNA Sequence Data from the Holotype of <i>Marmosa elegans coquimbensis</i> Tate, 1931 (Mammalia:) Tj ETQq1 1 0.784314 rgBT /Overlock 0,2	0,2	5
27853	New record of <i>Tulostoma squamosum</i> (Agaricales: Basidiomycota) from India based on morphological features and phylogenetic analysis. <i>Journal of Threatened Taxa</i> , 2020, 12, 15375-15381.	0.1	1
27856	Morphology lies: a case-in-point with a new non-biting midge species from Oriental China (Diptera,) Tj ETQq1 1 0.784314 rgBT /Overlock 0,5	0,5	2

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27866	Banat donkey, a neglected donkey breed from the central Balkans (Serbia). PeerJ, 2020, 8, e8598.	0.9	3
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27903	Incidence and detection of negative-stranded RNA viruses infecting apple and pear trees in California. Journal of Phytopathology, 2022, 170, 15-20.	0.5	6
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27907	Microbial Diversity in Cultivated and Feral Vanilla <i>Vanilla planifolia</i> Orchids Affected by Stem and Rot Disease. <i>Microbial Ecology</i> , 2022, 84, 821-833.	1.4	8
27908	Cotton Leafroll Dwarf Virus US Genomes Comprise Divergent Subpopulations and Harbor Extensive Variability. <i>Viruses</i> , 2021, 13, 2230.	1.5	14
27909	Two C1-oxidizing AA9 lytic polysaccharide monooxygenases from <i>Sordaria brevicollis</i> differ in thermostability, activity, and synergy with cellulase. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 8739-8759.	1.7	7
27910	MtDNA species-level phylogeny and delimitation support significantly underestimated diversity and endemism in the largest Neotropical cichlid genus ( <i>Cichlidae</i> : <i>Crenicichla</i> ). <i>PeerJ</i> , 2021, 9, e12283.	0.9	6
27911	A complete sequence of mitochondrial genome of <i>Neolamarckia cadamba</i> and its use for systematic analysis. <i>Scientific Reports</i> , 2021, 11, 21452.	1.6	6
27913	Identification and pathogenicity of <i>Fusarium</i> spp. associated with the sheath rot disease of rice ( <i>Oryza</i> ) Tj ETQq0 0 0 rgBT /Overlock 10	0.6	11
27915	BioProv - A provenance library for bioinformatics workflows. <i>Journal of Open Source Software</i> , 2021, 6, 3622.	2.0	1
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27921	Interspecific Gene Flow and Mitochondrial Genome Capture during the Radiation of Jamaican Anolis Lizards ( <i>Squamata</i> ; <i>Iguanidae</i> ). <i>Systematic Biology</i> , 2022, 71, 501-511.	2.7	9
27922	Genomic characterization of an African G4P[6] human rotavirus strain identified in a diarrheic child in Kenya: Evidence for porcine-to-human interspecies transmission and reassortment. <i>Infection, Genetics and Evolution</i> , 2021, 96, 105133.	1.0	10
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27925	High-quality reference genome sequences of two coconut cultivars provide insights into evolution of monocot chromosomes and differentiation of fiber content and plant height. <i>Genome Biology</i> , 2021, 22, 304.	3.8	32
27926	<i>Phlebotomus papatasi</i> Antimicrobial Peptides in Larvae and Females and a Gut-Specific Defensin Upregulated by <i>Leishmania major</i> Infection. <i>Microorganisms</i> , 2021, 9, 2307.	1.6	10
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27928	The chromosome-level genome assembly of <i>Astragalus sinicus</i> and comparative genomic analyses provide new resources and insights for understanding legume-rhizobial interactions. <i>Plant Communications</i> , 2022, 3, 100263.	3.6	11

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27931	Snow mold fungus <i>Racodium therryanum</i> is phylogenetically <i>Herpotrichia juniperi</i>. <i>Mycoscience</i> , 2021, 62, 406-409.	0.3	0
27932	Geographic Variation in the Green Rat Snake <i>Senticolis triaspis</i> (Squamata: Colubridae): Evidence from Mitochondrial DNA, Morphology, and Niche Modeling. <i>Ichthyology and Herpetology</i> , 2021, 109, .	0.3	0
27933	Independent evolutionary transitions to pueriparity across multiple timescales in the viviparous genus <i>Salamandra</i> . <i>Molecular Phylogenetics and Evolution</i> , 2022, 167, 107347.	1.2	3
27934	Circulation patterns of human seasonal Influenza A viruses in Chile before H1N1pdm09 pandemic. <i>Scientific Reports</i> , 2021, 11, 21469.	1.6	0
27935	An 82 bp tandem repeat family typical of 3' non-coding end of Gypsy/TAT LTR retrotransposons is conserved in <i>Coffea</i> spp. pericentromeres. <i>Genome</i> , 2022, 65, 137-151.	0.9	4
27936	Maize Zmcy710a8 Mutant as a Tool to Decipher the Function of Stigmasterol in Plant Metabolism. <i>Frontiers in Plant Science</i> , 2021, 12, 732216.	1.7	0
27937	Stochastic processes regulate belowground community assembly in alpine grasslands on the Tibetan Plateau. <i>Environmental Microbiology</i> , 2022, 24, 179-194.	1.8	28
27938	Variimorphobacter saccharofermentans gen. nov., sp. nov., a new member of the family Lachnospiraceae, isolated from a maize-fed biogas fermenter. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	12
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27948	First Ecological Characterization of Whip Black Coral Assemblages (Hexacorallia: Antipatharia) in the Easter Island Ecoregion, Southeastern Pacific. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	3
27949	The transcriptome of <i>Balamuthia mandrillaris</i> trophozoites for structure-guided drug design. <i>Scientific Reports</i> , 2021, 11, 21664.	1.6	7
27950	Use of Slaughterhouses as Sentinel Points for Genomic Surveillance of Foot-and-Mouth Disease Virus in Southern Vietnam. <i>Viruses</i> , 2021, 13, 2203.	1.5	4
27951	Citrullination Was Introduced into Animals by Horizontal Gene Transfer from Cyanobacteria. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	16
27952	<i>Coniochaeta elegans</i> sp. nov., <i>Coniochaeta montana</i> sp. nov. and <i>Coniochaeta nivea</i> sp. nov., three new species of endophytes with distinctive morphology and functional traits. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	3

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27955	In-Depth Annotation of the <i>Drosophila</i> Bithorax-Complex Reveals the Presence of Several Alternative ORFs That Could Encode for Motif-Rich Peptides. <i>Cells</i> , 2021, 10, 2983.	1.8	0
27956	Identification and Characterization of Citrus Concave Gum-Associated Virus Infecting Citrus and Apple Trees by Serological, Molecular and High-Throughput Sequencing Approaches. <i>Plants</i> , 2021, 10, 2390.	1.6	10
27957	<i>Clostridium zeae</i> sp. nov., isolated from corn silage. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	6
27959	An Evolutionary Study of <i>Carex</i> Subg. <i>Psyllophorae</i> (Cyperaceae) Sheds Light on a Strikingly Disjunct Distribution in the Southern Hemisphere, With Emphasis on Its Patagonian Diversification. <i>Frontiers in Plant Science</i> , 2021, 12, 735302.	1.7	3
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27962	Genomic diversity and molecular dynamics interaction on mutational variances among RB domains of SARS-CoV-2 interplay drug inactivation. <i>Infection, Genetics and Evolution</i> , 2021, , 105128.	1.0	2
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27964	Vermetid gastropods as key intermediate hosts for a lineage of marine turtle blood flukes (Digenea): Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 5 <i>Parasitology</i> , 2022, 52, 225-241.	1.3	7
27966	Positive interactions are common among culturable bacteria. <i>Science Advances</i> , 2021, 7, eabi7159.	4.7	107
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28275	Molecular Diversity of <i>Bacillus thuringiensis</i> and Bioinformatics Analysis of Local Isolate of Auky Island, Padaido District in Biak Numfor Papua as a Control of <i>Anopheles</i> Mosquito Larvae. <i>Journal of Pure and Applied Microbiology</i> , 2021, 15, 2295-2301.	0.3	0
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28277	<i>Hoyosella suaedae</i> sp. nov., a novel bacterium isolated from rhizosphere soil of <i>Suaeda aralocaspica</i> (Bunge) Freitag & SchÄtze. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	9

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28283	Chloranthus genome provides insights into the early diversification of angiosperms. <i>Nature Communications</i> , 2021, 12, 6930.	5.8	44
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28289	A systematic drug repurposing approach to identify promising inhibitors from FDA-approved drugs against Nsp4 protein of SARS-CoV-2. <i>Journal of Biomolecular Structure and Dynamics</i> , 2023, 41, 550-559.	2.0	5
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28302	Chromosome-Scale Reference Genome of <i>Amphicarpaea edgeworthii</i> : A New Resource for Amphicarpic Plants Research and Complex Flowering Pattern. <i>Frontiers in Plant Science</i> , 2021, 12, 770660.	1.7	3
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28322	Morphological observations and molecular confirmation of larvae of <i>Levisquilla inermis</i> (Crustacea: Tj ETQq1 1 0.784314 rgBT /Overl Kingdom, 0, , 1-10.	0.4	0

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28351	<i>Eubacterium coprostanoligenes</i> and <i>Methanoculleus</i> identified as potential producers of metabolites that contribute to swine manure foaming. <i>Journal of Applied Microbiology</i> , 2022, 132, 2906-2924.	1.4	5
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28354	Exploring the Diversity of the Human Blood Virome. <i>Viruses</i> , 2021, 13, 2322.	1.5	13
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28356	Genome-Scale Data Reveal Deep Lineage Divergence and a Complex Demographic History in the Texas Horned Lizard ( <i>Phrynosoma cornutum</i> ) throughout the Southwestern and Central United States. <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	15
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28360	Honey bee sHSP are responsive to diverse proteostatic stresses and potentially promising biomarkers of honey bee stress. <i>Scientific Reports</i> , 2021, 11, 22087.	1.6	15
28362	Translation stalling proline motifs are enriched in slow-growing, thermophilic, and multicellular bacteria. <i>ISME Journal</i> , 2022, 16, 1065-1073.	4.4	2
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28366	A Protocol for Horizontally Acquired Metabolic Gene Detection in Algae. <i>Methods in Molecular Biology</i> , 2022, 2396, 61-69.	0.4	0
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28368	Massive Infection of Lungs with Exo-Erythrocytic Meronts in European Robin <i>Erithacus rubecula</i> during Natural <i>Haemoproteus attenuatus</i> Haemoproteosis. <i>Animals</i> , 2021, 11, 3273.	1.0	8
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28372	Coupling Machine Learning and High Throughput Multiplex Digital PCR Enables Accurate Detection of Carbapenem-Resistant Genes in Clinical Isolates. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 775299.	1.6	16
28373	Genetic Architecture of Novel Sources for Reproductive Cold Tolerance in Sorghum. <i>Frontiers in Plant Science</i> , 2021, 12, 772177.	1.7	3
28374	Systematic Identification of Endogenous Retroviral Protein-Coding Genes Expressed in Canine Oral Malignant Melanoma. <i>Frontiers in Virology</i> , 2021, 1, .	0.7	0
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28381	Toxic Peptide From <i>Palythoa caribaeorum</i> Acting on the TRPV1 Channel Prevents Pentylentetrazol-Induced Epilepsy in Zebrafish Larvae. <i>Frontiers in Pharmacology</i> , 2021, 12, 763089.	1.6	1
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28383	The Cymbidium genome reveals the evolution of unique morphological traits. <i>Horticulture Research</i> , 2021, 8, 255.	2.9	33
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28386	Identification, evolutionary analysis and functional diversification of RAV gene family in cotton ( <i>G.</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.6	10
28387	Lupus gut microbiota transplants cause autoimmunity and inflammation. <i>Clinical Immunology</i> , 2021, 233, 108892.	1.4	25
28389	Nest parasitism, promiscuity, and relatedness among wood ducks. <i>PLoS ONE</i> , 2021, 16, e0257105.	1.1	0
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28403	Comparative chloroplast genomes of <i>Prunus</i> subgenus <i>Cerasus</i> (Rosaceae): insights into sequence variations and phylogenetic relationships. <i>Tree Genetics and Genomes</i> , 2021, 17, 1.	0.6	13
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28411	Substrate preferences, phylogenetic and biochemical properties of proteolytic bacteria present in the digestive tract of Nile tilapia ( <i>Oreochromis niloticus</i> ). <i>AIMS Microbiology</i> , 2021, 7, 528-545.	1.0	4



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28435	From pairwise to multiple spliced alignment. <i>Bioinformatics Advances</i> , 0, , .	0.9	0
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28439	<i>Hydrodroma angelieri</i> (Acari, Hydrachnidia: Hydrodromidae) a new water mite species from Corsica based on morphological and DNA barcode evidence. <i>Acarologia</i> , 2022, 62, 3-11.	0.2	3
28442	Generation and characterization of genetically and antigenically diverse infectious clones of dengue virus serotypes 1-4. <i>Emerging Microbes and Infections</i> , 2022, 11, 227-239.	3.0	13
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28452	Temporal and spatial variation of microbial communities in stored rice grains from two major depots in China. <i>Food Research International</i> , 2022, 152, 110876.	2.9	13
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28454	Recent advances in fungal serine protease inhibitors. <i>Biomedicine and Pharmacotherapy</i> , 2022, 146, 112523.	2.5	18

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28459	De novo transcriptome analysis of bamboo in vitro shoots for identification of genes differentiating juvenile and aged plants. <i>Industrial Crops and Products</i> , 2022, 176, 114353.	2.5	3
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28463	First report of <i>Nosomma monstrosus</i> ticks infesting Asian water buffaloes ( <i>Bubalus bubalis</i> ) in Pakistan. <i>Ticks and Tick-borne Diseases</i> , 2022, 13, 101899.	1.1	18
28464	Comparative phylotranscriptomics reveals putative sex differentiating genes across eight diverse bivalve species. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2022, 41, 100952.	0.4	7
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28466	DNA databases of a CITES listed species <i>Aquilaria malaccensis</i> (Thymelaeaceae) as the tracking tools for forensic identification and chain of custody certification. <i>Forensic Science International: Genetics</i> , 2022, 57, 102658.	1.6	5
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28472	Characterization of the mitochondrial genome of <i>Tetrameres grusi</i> and insights into the phylogeny of Spirurina. <i>International Journal for Parasitology: Parasites and Wildlife</i> , 2022, 17, 35-42.	0.6	4

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28478	Isolation and characterization of aerobic actinomycetes with probiotic properties in Nile tilapia. <i>Journal of Applied Pharmaceutical Science</i> , 0, , .	0.7	1
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28487	Alignment Free Sequence Similarity Estimation using Local Binary Pattern on DNA Trajectory Images. , 2021, , .		1
28488	A panel of diverse <i>Pseudomonas aeruginosa</i> clinical isolates for research and development. <i>JAC-Antimicrobial Resistance</i> , 2021, 3, dlab179.	0.9	13
28489	First DNA barcodes of <i>Bembidion</i> species (Coleoptera: Carabidae) from Iran. <i>Journal of Natural History</i> , 2021, 55, 2245-2260.	0.2	0
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28492	<i>Rhodobacter amnigenus</i> sp. nov. and <i>Rhodobacter ruber</i> sp. nov., isolated from freshwater habitats. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	8
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28516	<i>Halomonas profundus</i> sp. nov., isolated from deep-sea sediment of the Mariana Trench. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	8
28517	A tau class GST, OsGSTU5, interacts with VirE2 and modulates the <i>Agrobacterium</i> -mediated transformation in rice. <i>Plant Cell Reports</i> , 2022, 41, 873-891.	2.8	3
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28522	Phylogeny and age of cockroaches: a reanalysis of mitogenomes with selective fossil calibrations. <i>Mitteilungen Aus Dem Museum Fur Naturkunde in Berlin - Deutsche Entomologische Zeitschrift</i> , 2022, 69, 1-18.	0.3	5
28523	Chromosome-level genome assembly of the shuttles hopppfish, <i>Periophthalmus modestus</i> . <i>GigaScience</i> , 2022, 11, .	3.3	4
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28533	Genetic diversity in terrestrial subsurface ecosystems impacted by geological degassing. <i>Nature Communications</i> , 2022, 13, 284.	5.8	11
28534	The Role of ZntA in <i>Klebsiella pneumoniae</i> Zinc Homeostasis. <i>Microbiology Spectrum</i> , 2022, 10, e0177321.	1.2	12
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#	ARTICLE	IF	CITATIONS
28537	Description of <i>Aureibaculum luteum</i> sp. nov. and <i>Aureibaculum flavum</i> sp. nov. isolated from Antarctic intertidal sediments. <i>Antonie Van Leeuwenhoek</i> , 2022, 115, 391.	0.7	1
28538	Molecular data confirms the existence of distinct lineages within <i>Lumbricus friendi</i> (Cognetti 1904) and related "friends". <i>European Journal of Soil Biology</i> , 2022, 108, 103382.	1.4	1
28539	Activity-Based Protein Profiling for the Identification of Novel Carbohydrate-Active Enzymes Involved in Xylan Degradation in the Hyperthermophilic Euryarchaeon <i>Thermococcus</i> sp. Strain 2319x1E. <i>Frontiers in Microbiology</i> , 2021, 12, 734039.	1.5	6
28540	Correct Species Identification and Its Implications for Conservation Using Haplomiscidae (Crustacea). <i>Tj ETQq1 1 0.784314 rgBT /Over</i>	1.2	13
28541	A Peroxide-Responding sRNA Evolved from a Peroxidase mRNA. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	8
28542	Spatio-Temporal Dynamics in Physico-Chemical Properties, Phytoplankton and Bacterial Diversity as an Indication of the Bovan Reservoir Water Quality. <i>Water (Switzerland)</i> , 2022, 14, 391.	1.2	7
28543	HISAT2 Parallelization Method Based on Spark Cluster. <i>Journal of Physics: Conference Series</i> , 2022, 2179, 012038.	0.3	7
28544	Genome-resolved evidence for functionally redundant communities and novel nitrogen fixers in the deyin-1 hydrothermal field, Mid-Atlantic Ridge. <i>Microbiome</i> , 2022, 10, 8.	4.9	5
28545	Accurate long-read sequencing allows assembly of the duplicated RHD and RHCE genes harboring variants relevant to blood transfusion. <i>American Journal of Human Genetics</i> , 2022, 109, 180-191.	2.6	11
28546	The NGS Magic Pudding: A Nanopore-Led Long-Read Genome Assembly for the Commercial Australian Freshwater Crayfish, <i>Cherax destructor</i> . <i>Frontiers in Genetics</i> , 2021, 12, 695763.	1.1	1
28547	Chromosome-Level Assembly of the Chinese Hooksnout Carp ( <i>Opsariichthys bidens</i> ) Genome Using PacBio Sequencing and Hi-C Technology. <i>Frontiers in Genetics</i> , 2021, 12, 788547.	1.1	3
28548	The gut microbiota of chickens in a commercial farm treated with a <i>Salmonella</i> phage cocktail. <i>Scientific Reports</i> , 2022, 12, 991.	1.6	15
28549	Dietary shifts and social interactions drive temporal fluctuations of the gut microbiome from wild redfronted lemurs. <i>ISME Communications</i> , 2022, 2, .	1.7	16
28550	Phylogenetic and Expression Analysis of CENH3 and APOLLO Genes in Sexual and Apomictic <i>Boechera</i> Species. <i>Plants</i> , 2022, 11, 387.	1.6	2
28551	Novel Phage Lysin Abp013 against <i>Acinetobacter baumannii</i> . <i>Antibiotics</i> , 2022, 11, 169.	1.5	11
28552	Whole-Genome Sequencing and RNA-Seq Reveal Differences in Genetic Mechanism for Flowering Response between Weedy Rice and Cultivated Rice. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1608.	1.8	4
28553	Ancestral sequence reconstruction and spatial structure analysis guided alteration of longer-chain substrate catalysis for <i>Thermomicrobium roseum</i> lipase. <i>Enzyme and Microbial Technology</i> , 2022, 156, 109989.	1.6	10
28554	Comparative transcriptomics reveal tissue level specialization towards diet in prickleback fishes. <i>Journal of Comparative Physiology B: Biochemical, Systemic, and Environmental Physiology</i> , 2022, 192, 275-295.	0.7	10

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28555	Novel Classes and Evolutionary Turnover of Histone H2B Variants in the Mammalian Germline. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	18
28556	Landscape genetics reveal low diversity and adaptive divergence in <i>Portulaca hatschbachii</i> (Portulacaceae): an endangered species endemic to rocky outcrops of the Atlantic Forest. <i>Botanical Journal of the Linnean Society</i> , 2022, 200, 116-141.	0.8	4
28557	The highly continuous reference genome of a leaf-chimeric red pineapple ( <i>Ananas comosus</i> var.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 60 2022, 12, .	0.8	1
28559	Pairs of Mutually Compensatory Frameshifting Mutations Contribute to Protein Evolution. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	7
28560	Rare toxin A-negative and toxin B-positive strain of <i>Clostridioides difficile</i> from Japan lacking a complete <i>tcdA</i> gene. <i>Journal of Infection and Chemotherapy</i> , 2022, 28, 651-656.	0.8	2
28561	Seaweed Fertilizer Prepared by EM-Fermentation Increases Abundance of Beneficial Soil Microbiome in Paddy ( <i>Oryzasativa</i> L.) during Vegetative Stage. <i>Fermentation</i> , 2022, 8, 46.	1.4	7
28562	Whole-genome analysis to determine the rate and patterns of intra-subtype reassortment among influenza type-A viruses in Africa. <i>Virus Evolution</i> , 2022, 8, veac005.	2.2	4
28563	A New Jasmine Virus C Isolate Identified by Nanopore Sequencing Is Associated to Yellow Mosaic Symptoms of <i>Jasminum officinale</i> in Italy. <i>Plants</i> , 2022, 11, 309.	1.6	5
28564	Gut microbiome alterations in hereditary angioedema. <i>Annals of Allergy, Asthma and Immunology</i> , 2022, , .	0.5	2
28565	Complete de novo assembly of <i>Wolbachia</i> endosymbiont of <i>Diaphorina citri</i> Kuwayama (Hemiptera:) Tj ETQq1 1 0.784314 rgBT /Overlock 1.6 14	1.6	14
28566	Mitochondrial genome sequencing of marine leukaemias reveals cancer contagion between clam species in the Seas of Southern Europe. <i>ELife</i> , 2022, 11, .	2.8	22
28568	Could Phylogenetic Analysis Be Used for Feline Leukemia Virus (FeLV) Classification?. <i>Viruses</i> , 2022, 14, 249.	1.5	3
28569	Detection and Molecular Characterization of a Novel Species of Circovirus in a Tawny Owl ( <i>Strix</i> ) Tj ETQq0 0 0 rgBT /Overlock 1.0 2 Tf 50 20	1.0	2
28571	Evolutionary and mechanistic diversity of Type I-F CRISPR-associated transposons. <i>Molecular Cell</i> , 2022, 82, 616-628.e5.	4.5	36
28572	Mutational analysis of <i>Aedes aegypti</i> Dicer 2 provides insights into the biogenesis of antiviral exogenous small interfering RNAs. <i>PLoS Pathogens</i> , 2022, 18, e1010202.	2.1	6
28573	Complete Genome Sequences of Five <i>Burkholderia</i> Strains with Biocontrol Activity against Various Lettuce Pathogens. <i>Microbiology Resource Announcements</i> , 2022, 11, e0112021.	0.3	4
28574	Finding and Characterizing Repeats in Plant Genomes. <i>Methods in Molecular Biology</i> , 2022, 2443, 327-385.	0.4	2
28575	Diversity, phylogeny and evolution of the rapidly evolving genus <i>Psidium</i> L. (Myrtaceae, Myrteae). <i>Annals of Botany</i> , 2022, 129, 367-388.	1.4	8



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28578	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
28579	Assembly and comparative analysis of the first complete mitochondrial genome of <i>Acer truncatum</i> Bunge: a woody oil-tree species producing nervonic acid. <i>BMC Plant Biology</i> , 2022, 22, 29.	1.6	31
28580	Activity- and Enrichment-Based Metaproteomics Insights into Active Urease from the Rumen Microbiota of Cattle. <i>International Journal of Molecular Sciences</i> , 2022, 23, 817.	1.8	1
28581	Comparative Genomics of <i>Pseudomonas stutzeri</i> Complex: Taxonomic Assignments and Genetic Diversity. <i>Frontiers in Microbiology</i> , 2021, 12, 755874.	1.5	6
28582	Assessment of Genetic Diversity and Relatedness in an Andean Potato Collection from Argentina by High-Density Genotyping. <i>Horticulturae</i> , 2022, 8, 54.	1.2	3
28583	Breaking antimicrobial resistance by disrupting extracytoplasmic protein folding. <i>ELife</i> , 2022, 11, .	2.8	14
28585	Alterations in intestinal microbiota composition coincide with impaired intestinal morphology and dysfunctional ileal immune response in growing-finishing pigs under constant chronic heat stress. <i>Journal of Animal Science and Biotechnology</i> , 2022, 13, 1.	2.1	29
28586	Comparative genomics reveals electron transfer and syntrophic mechanisms differentiating methanotrophic and methanogenic archaea. <i>PLoS Biology</i> , 2022, 20, e3001508.	2.6	62
28587	The changes of microbial diversity and flavor compounds during the fermentation of millet Huangjiu, a traditional Chinese beverage. <i>PLoS ONE</i> , 2022, 17, e0262353.	1.1	16
28588	Structural insights into how vacuolar sorting receptors recognize the sorting determinants of seed storage proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	8
28589	Rhizosphere analysis of field-grown <i>Panax ginseng</i> with different degrees of red skin provides the basis for preventing red skin syndrome. <i>BMC Microbiology</i> , 2022, 22, 12.	1.3	6
28590	A chromosome-scale genome assembly for the holly ( <i>Ilex polyneura</i> ) provides insights into genomic adaptations to elevation in Southwest China. <i>Horticulture Research</i> , 2022, 9, .	2.9	12
28591	Enteric virome negatively affects seroconversion following oral rotavirus vaccination in a longitudinally sampled cohort of Ghanaian infants. <i>Cell Host and Microbe</i> , 2022, 30, 110-123.e5.	5.1	23
28592	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
28593	<i>Gracilaria parva</i> sp. nov. (Gracilariales, Rhodophyta) a Diminutive Species from the Tropical Eastern Pacific. <i>Taxonomy</i> , 2022, 2, 48-56.	0.4	1
28594	In the Search of Marine Pestiviruses: First Case of <i>Phocoena Pestivirus</i> in a Belt Sea Harbour Porpoise. <i>Viruses</i> , 2022, 14, 161.	1.5	3
28595	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

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28596	Exogenous Production of N-acetylmuramyl-L Alanine Amidase (LysM2) from Siphoviridae Phage Affecting Anti-Gram-Negative Bacteria: Evaluation of Its Structure and Function. <i>Avicenna Journal of Medical Biotechnology</i> , 2022, 14, 46-53.	0.2	1
28597	Seasonal succession of bacterial communities in cultured <i>Caulerpa lentillifera</i> detected by high-throughput sequencing. <i>Open Life Sciences</i> , 2022, 17, 10-21.	0.6	4
28598	A chromosome-scale reference genome assembly of yellow mangrove ( <i>Bruguiera parviflora</i> ) reveals a whole genome duplication event associated with the Rhizophoraceae lineage. <i>Molecular Ecology Resources</i> , 2022, 22, 1939-1953.	2.2	13
28599	A Superior Contiguous Whole Genome Assembly for Shrimp ( <i>Penaeus indicus</i> ). <i>Frontiers in Marine Science</i> , 2022, 8, .	1.2	6
28601	The Discovery of a New Mimivirus Isolate in Association with Virophage-Transposon Elements in Brazil Highlights the Main Genomic and Evolutionary Features of This Tripartite System. <i>Viruses</i> , 2022, 14, 206.	1.5	4
28602	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
28604	Parkinson's Disease Medication Alters Small Intestinal Motility and Microbiota Composition in Healthy Rats. <i>MSystems</i> , 2022, 7, e0119121.	1.7	13
28605	Microbial Consortia Involved in Traditional Sicilian Sourdough: Characterization of Lactic Acid Bacteria and Yeast Populations. <i>Microorganisms</i> , 2022, 10, 283.	1.6	13
28606	Insights into the systematics of Old World taenitoid ferns (Pteridoideae; Pteridaceae): evidence from phylogeny and micromorphology. <i>Botanical Journal of the Linnean Society</i> , 2022, 200, 165-193.	0.8	3
28607	Assessment of marine benthic diatom communities: insights from a combined morphological and metabarcoding approach in Mediterranean shallow coastal waters. <i>Marine Pollution Bulletin</i> , 2022, 174, 113183.	2.3	13
28608	Diversification in and around the Atlas Mountains: Insights into the systematics and biogeography of the genus <i>Thalpomena</i> (Orthoptera: Acrididae: Oedipodinae). <i>Systematic Entomology</i> , 2022, 47, 402-419.	1.7	5
28609	A new subgenus of <i>Epeorus</i> and its five species from China (Ephemeroptera: Heptageniidae). <i>Insect Systematics and Evolution</i> , 2022, -1, 1-40.	0.2	2
28610	Genome-wide analysis of VPE family in four <i>Gossypium</i> species and transcriptional expression of VPEs in the upland cotton seedlings under abiotic stresses. <i>Functional and Integrative Genomics</i> , 2022, 22, 179-192.	1.4	14
28611	Draft Genome Sequence of Isolate POC01, a Novel Anaerobic Member of the Oscillospiraceae Family, Isolated from Human Feces. <i>Microbiology Resource Announcements</i> , 2022, 11, e0113421.	0.3	0
28612	Perspectives in Myrtaceae evolution from plastomes and nuclear phylogenies. <i>Genetics and Molecular Biology</i> , 2022, 45, e20210191.	0.6	4
28613	<i>Enterocytozoon schreckii</i> n. sp. Infects the Enterocytes of Adult Chinook Salmon ( <i>Oncorhynchus tshawytscha</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 e0090821.	1.3	8
28614	Patterns and Predictors of Small Mammal Phylogenetic and Functional Diversity in Contrasting Elevational Gradients in Kenya. <i>Frontiers in Ecology and Evolution</i> , 2022, 9, .	1.1	5
28615	CANT-HYD: A Curated Database of Phylogeny-Derived Hidden Markov Models for Annotation of Marker Genes Involved in Hydrocarbon Degradation. <i>Frontiers in Microbiology</i> , 2021, 12, 764058.	1.5	21

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28616	Unrecognized Ant Megadiversity in Monsoonal Australia: Diversity and Its Distribution in the Hyperdiverse <i>Monomorium nigrius</i> Forel Group. <i>Diversity</i> , 2022, 14, 46.	0.7	7
28617	Geography and climate drive the distribution and diversification of the cosmopolitan cyanobacterium <i>Microcoleus</i> (Oscillatoriales, Cyanobacteria). <i>European Journal of Phycology</i> , 2022, 57, 396-405.	0.9	5
28618	DNA barcoding and morphological identification of spiny lobsters in South Korean waters: a new record of <i>Panulirus longipes</i> and <i>Panulirus homarus homarus</i> . <i>PeerJ</i> , 2022, 10, e12744.	0.9	2
28619	Dynamic genetic differentiation drives the widespread structural and functional convergent evolution of snake venom proteinaceous toxins. <i>BMC Biology</i> , 2022, 20, 4.	1.7	17
28620	Gallic Acid Alleviates Gut Dysfunction and Boosts Immune and Antioxidant Activities in Puppies Under Environmental Stress Based on Microbiomeâ€“Metabolomics Analysis. <i>Frontiers in Immunology</i> , 2021, 12, 813890.	2.2	27
28621	Intestinal Claudin-7 deficiency impacts the intestinal microbiota in mice with colitis. <i>BMC Gastroenterology</i> , 2022, 22, 24.	0.8	8
28622	Prevalence of genetically similar <i>Flavobacterium columnare</i> phages across aquaculture environments reveals a strong potential for pathogen control. <i>Environmental Microbiology</i> , 2022, 24, 2404-2420.	1.8	5
28623	Bacterial community structures and functional gene diversity of toluene denitrifying degraders in coking contaminated enrichments. <i>International Journal of Environmental Science and Technology</i> , 0, 1.	1.8	0
28625	Metagenomic Analysis of Bacterial Communities and Antibiotic Resistance Genes in <i>Penaeus monodon</i> Biofloc-Based Aquaculture Environments. <i>Frontiers in Marine Science</i> , 2022, 8, .	1.2	6
28626	Limited Diversity and Frequency of Ectomycorrhizal Inoculum in 16-11,000-Year-Old Extirpated Piñon Stands. <i>SSRN Electronic Journal</i> , 0, .	0.4	0
28627	Habitat Adaptation Drives Speciation of a <i>Streptomyces</i> Species with Distinct Habitats and Disparate Geographic Origins. <i>MBio</i> , 2022, 13, e0278121.	1.8	15
28628	The Species-Specific 282 Residue in the PB2 Subunit of the Polymerase Regulates RNA Synthesis and Replication of Influenza A Viruses Infecting Bat and Nonbat Hosts. <i>Journal of Virology</i> , 2022, 96, jvi0219021.	1.5	2
28629	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
28630	Elevational Constraints on the Composition and Genomic Attributes of Microbial Communities in Antarctic Soils. <i>MSystems</i> , 2022, 7, e0133021.	1.7	9
28631	The Diversity of <i>Passalora fulva</i> Isolates Collected from Tomato Plants in U.S. High Tunnels. <i>Phytopathology</i> , 2022, 112, 1350-1360.	1.1	3
28632	Pleistocene mitogenomes reconstructed from the environmental DNA of permafrost sediments. <i>Current Biology</i> , 2022, 32, 851-860.e7.	1.8	13
28633	Clues to reaction specificity in <i>PLP</i> -dependent fold type I aminotransferases of monosaccharide biosynthesis. <i>Proteins: Structure, Function and Bioinformatics</i> , 2022, 90, 1247-1258.	1.5	0
28634	Diversification by CofC and Control by CofD Govern Biosynthesis and Evolution of Coenzyme F <sub>420</sub> and Its Derivative 3PG-F <sub>420</sub> . <i>MBio</i> , 2022, 13, e0350121.	1.8	2

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28636	Modular evolution of secretion systems and virulence plasmids in a bacterial species complex. <i>BMC Biology</i> , 2022, 20, 16.	1.7	16
28637	Characterisation of tetraspanins from <i>Schistosoma haematobium</i> and evaluation of their potential as novel diagnostic markers. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010151.	1.3	5
28638	Genetic Evidence of an Isolation Barrier between Flea Subspecies of <i>Citellophilus tesquorum</i> (Wagner, 1901) and <i>C. r. r.</i> <i>Journal of Biogeography</i> , 2022, 49, 1078-1091.	1.0	1
28639	Genome-wide identification of auxin response factor (ARF) gene family and the miR160-ARF18-mediated response to salt stress in peanut ( <i>Arachis hypogaea</i> L.). <i>Genomics</i> , 2022, 114, 171-184.	1.3	30
28640	Three new species of <i>Helicometroides</i> Yamaguti, 1934 from Japan and Australia, with new molecular evidence of a widespread species. <i>Parasitology</i> , 2022, , 1-18.	0.7	3
28641	Glutamine synthetase evolutionary history revisited: Tracing back beyond the Last Universal Common Ancestor. <i>Evolution; International Journal of Organic Evolution</i> , 2022, 76, 605-622.	1.1	8
28642	<i>Schistosoma mansoni</i> Î±-N-acetylgalactosaminidase (SmNAGAL) regulates coordinated parasite movement and egg production. <i>PLoS Pathogens</i> , 2022, 18, e1009828.	2.1	14
28643	Neofunctionalization of Glycolytic Enzymes: An Evolutionary Route to Plant Parasitism in the Oomycete <i>Phytophthora nicotianae</i> . <i>Microorganisms</i> , 2022, 10, 281.	1.6	3
28644	Molecular characterisation and updated description of <i>Neoechinorhynchus aldrichettae</i> Edmonds, 1971 (Acanthocephala: Neoechinorhynchidae), based on material from <i>Aldrichetta forsteri</i> (Valenciennes) collected in Tasmania, Australia. <i>Systematic Parasitology</i> , 2022, 99, 241.	0.5	2
28645	The hidden world within plants: metatranscriptomics unveils the complexity of wood microbiomes. <i>Journal of Experimental Botany</i> , 2022, 73, 2682-2697.	2.4	24
28646	<i>Agromyces agglutinans</i> sp. nov., isolated from saline lake sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	4
28647	Interaction between MAPKs and MKPs in hexaploid chrysanthemum illuminates functional paralogue diversification in polyploids. <i>Horticultural Plant Journal</i> , 2023, 9, 158-168.	2.3	1
28648	Nanos Is Expressed in Somatic and Germline Tissue during Larval and Post-Larval Development of the Annelid <i>Alitta virens</i> . <i>Genes</i> , 2022, 13, 270.	1.0	6
28650	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
28651	Genome analysis of <i>Pseudomonas</i> sp. 14A reveals metabolic capabilities to support epiphytic behavior. <i>World Journal of Microbiology and Biotechnology</i> , 2022, 38, 49.	1.7	1
28652	New finding of peridomestic <i>Triatoma infestans</i> (Klug, 1834) (Hemiptera: Reduviidae) in Mexico: Molecular approach using cytochrome B and cytochrome oxidase I. <i>Infection, Genetics and Evolution</i> , 2022, 97, 105187.	1.0	2
28653	Evolution of two-component quorum sensing systems. <i>Access Microbiology</i> , 2022, 4, 000303.	0.2	6

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28657	Sequence determination and bioinformatic comparison of ten venom serine proteases of <i>Trimeresurus gracilis</i> , a Taiwanese endemic pitviper with controversial taxonomy. <i>Toxicon</i> , 2022, 206, 28-37.	0.8	4
28658	Genome Characterization and Probiotic Potential of <i>Corynebacterium amycolatum</i> Human Vaginal Isolates. <i>Microorganisms</i> , 2022, 10, 249.	1.6	11
28659	In-depth analysis of amino acid and nucleotide sequences of Hsp60: How conserved is this protein?. <i>Proteins: Structure, Function and Bioinformatics</i> , 2022, 90, 1119-1141.	1.5	2
28660	Mitogenomic phylogeny resolves <i>Cuneopsis</i> (Bivalvia: Unionidae) as polyphyletic: The description of two new genera and a new species. <i>Zoologica Scripta</i> , 2022, 51, 173-184.	0.7	8
28661	Genomic and phenotypic analysis of SspH1 identifies a new <i>Salmonella</i> effector, SspH3. <i>Molecular Microbiology</i> , 2022, 117, 770-789.	1.2	3
28662	Identification of <i>Pueraria</i> spp. through DNA barcoding and comparative transcriptomics. <i>BMC Plant Biology</i> , 2022, 22, 10.	1.6	7
28663	Metagenomics-Guided Assessment of Water Quality and Predicting Pathogenic Load. Impact of Meat Consumption on Health and Environmental Sustainability, 2022, , 71-91.	0.4	1
28664	San-Huang-Yi-Shen Capsule Ameliorates Diabetic Nephropathy in Rats Through Modulating the Gut Microbiota and Overall Metabolism. <i>Frontiers in Pharmacology</i> , 2021, 12, 808867.	1.6	23
28665	Selective Isolation of <i>Eggerthella lenta</i> from Human Faeces and Characterisation of the Species Prophage Diversity. <i>Microorganisms</i> , 2022, 10, 195.	1.6	9
28667	RNA Viroisphere in a Marine Zooplankton Community in the Subtropical Western North Pacific. <i>Microbes and Environments</i> , 2022, 37, n/a.	0.7	3
28668	Genotype-specific features reduce the susceptibility of South American yellow fever virus strains to vaccine-induced antibodies. <i>Cell Host and Microbe</i> , 2022, 30, 248-259.e6.	5.1	11
28669	Clonally expanded B cells in multiple sclerosis bind EBV EBNA1 and GialCAM. <i>Nature</i> , 2022, 603, 321-327.	13.7	343
28670	Phylogenetic placement of <i>Trifolium kentuckiense</i> (Fabaceae), a new member of the native eastern North American clover clade. <i>Castanea</i> , 2022, 86, .	0.2	0
28671	Long-read transcriptome sequencing provides insight into lignan biosynthesis during fruit development in <i>Schisandra chinensis</i> . <i>BMC Genomics</i> , 2022, 23, 17.	1.2	10
28672	Another plea for "best practice" in molecular approaches to trematode systematics: <i>Diplostomum</i> sp. clade Q identified as <i>Diplostomum baeri</i> Dubois, 1937 in Europe. <i>Parasitology</i> , 2022, 149, 503-518.	0.7	8
28673	Regional and temporal coordinated mutation patterns in SARS-CoV-2 spike protein revealed by a clustering and network analysis. <i>Scientific Reports</i> , 2022, 12, 1128.	1.6	28
28675	Computational Medicinal Chemistry to Target GPCRs. , 2022, , 84-114.		3

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28676	The <i>Ixodes scapularis</i> Symbiont <i>Rickettsia buchneri</i> Inhibits Growth of Pathogenic Rickettsiaceae in Tick Cells: Implications for Vector Competence. <i>Frontiers in Veterinary Science</i> , 2021, 8, 748427.	0.9	11
28678	Microbial Depolymerization of Epoxy Resins: A Novel Approach to a Complex Challenge. <i>Applied Sciences (Switzerland)</i> , 2022, 12, 466.	1.3	3
28681	Acquisition of the arginine deiminase system benefits epiparasitic <i>Saccharibacteria</i> and their host bacteria in a mammalian niche environment. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	30
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28684	<i>Mucisphaera calidilacus</i> gen. nov., sp. nov., a novel planctomycete of the class <i>Phycisphaerae</i> isolated in the shallow sea hydrothermal system of the Lipari Islands. <i>Antonie Van Leeuwenhoek</i> , 2022, 115, 407.	0.7	8
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28686	Evidence from <i>Drosophila</i> Supports Higher Duplicability of Faster Evolving Genes. <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	4
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28689	Morphological and molecular data reveal the conspecificity of the spider mites <i>Tetranychus gloveri</i> and <i>T. okinawanus</i> (Acari: Trombidiformes: Tetranychidae). <i>Systematic and Applied Acarology</i> , 0, , .	0.5	1
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28707	The Barley and Wheat Pan-Genomes. <i>Methods in Molecular Biology</i> , 2022, 2443, 147-159.	0.4	2
28708	Isolation of a Dissimilatory Iodate-Reducing <i>Aromatoleum</i> sp. From a Freshwater Creek in the San Francisco Bay Area. <i>Frontiers in Microbiology</i> , 2021, 12, 804181.	1.5	2
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28738	BepiTBR: T-B reciprocity enhances B cell epitope prediction. <i>IScience</i> , 2022, 25, 103764.	1.9	9
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28741	Taxonomical Evaluation of Plant Chloroplastic Markers by Bayesian Classifier. <i>Frontiers in Plant Science</i> , 2021, 12, 782663.	1.7	2
28742	A novel C-terminal DxRSDxE motif in ceramide synthases involved in dimer formation. <i>Journal of Biological Chemistry</i> , 2022, 298, 101517.	1.6	12
28743	A glimpse on metazoan ZNFX1 helicases, ancient players of antiviral innate immunity. <i>Fish and Shellfish Immunology</i> , 2022, 121, 456-466.	1.6	6
28744	Lack of Genetic Structure Among Populations of Striped Flea Beetle <i>Phyllotreta striolata</i> (Coleoptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 2	1.1	0
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28749	Hybrid sequencing reveals the full-length <i>Nephila pilipes</i> pyriform spidroin 1 (PySp1). <i>International Journal of Biological Macromolecules</i> , 2022, 200, 362-369.	3.6	4
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28751	Two new pseudocryptic species in the medium-sized common European land snails, <i>Fruticicola</i> Held, 1838; as a result of phylogeographic analysis of <i>Fruticicola fruticum</i> (O. F. MÃ¼ller, 1774) (Gastropoda: Tj ETQq1 1.0.7843 14 rgBT /Ov	1.2	6
28752	Characterization of IL-17/IL-17R gene family in <i>Sebastes schlegelii</i> and their expression profiles under <i>Aeromonas salmonicida</i> and <i>Edwardsiella piscicida</i> infections. <i>Aquaculture</i> , 2022, 551, 737901.	1.7	4
28753	Phylogenomic analysis of evolutionary relationships in <i>Ranitomeya</i> poison frogs (Family) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 2 107389.	1.2	6
28754	A new microbothriid monogenean <i>Dermopristis pterophilus</i> n. sp. from the skin of the Critically Endangered green sawfish <i>Pristis zijsron</i> Bleeker, 1851 (Batoidea: Pristidae) in Western Australia. <i>International Journal for Parasitology: Parasites and Wildlife</i> , 2022, 17, 185-193.	0.6	0
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28757	The first report of the <i>bla</i> IMP-10 gene and complete sequence of the IMP-10-encoding plasmid p12NE515 from <i>Pseudomonas aeruginosa</i> in China. <i>Acta Tropica</i> , 2022, 228, 106326.	0.9	3

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28760	Molecular characterization of <i>Dipetalonema yatesi</i> from the black-faced spider monkey ( <i>Ateles</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 66 <i>International Journal for Parasitology: Parasites and Wildlife</i> , 2022, 17, 152-157.	0.6	4
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28773	OUP accepted manuscript. <i>DNA Research</i> , 2022, , .	1.5	4
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28781	Known allosteric proteins have central roles in genetic disease. <i>PLoS Computational Biology</i> , 2022, 18, e1009806.	1.5	2
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28783	An unexpected tenant: contamination in a <i>Physeter catodon</i> (Physeteridae, Artiodactyla) genome indicates undescribed species of <i>Sarcocystis</i> Lankester, 1882 (Sarcocystidae, Eucoccidiorida) in the marine environment. <i>Folia Parasitologica</i> , 2022, 69, .	0.7	1
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28799	Molecular markers and SEM imaging reveal pseudocryptic diversity within the Ponto-Caspian low-profile amphipod invader <i>Dikerogammarus bispinosus</i> . , 2022, 89, 94-108.		9
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28805	Gene Overlapping as a Modulator of Begomovirus Evolution. <i>Microorganisms</i> , 2022, 10, 366.	1.6	5
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28985	Using rDNA sequences to define dinoflagellate species. <i>PLoS ONE</i> , 2022, 17, e0264143.	1.1	8
28987	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
28988	COX4-like, a Nuclear-Encoded Mitochondrial Gene Duplicate, Is Essential for Male Fertility in <i>Drosophila melanogaster</i> . <i>Genes</i> , 2022, 13, 424.	1.0	5
28989	Active anaerobic methane oxidation and sulfur disproportionation in the deep terrestrial subsurface. <i>ISME Journal</i> , 2022, 16, 1583-1593.	4.4	16
28990	Community Structure and Functional Annotations of the Skin Microbiome in Healthy and Diseased Catfish, <i>Heteropneustes fossilis</i> . <i>Frontiers in Microbiology</i> , 2022, 13, 856014.	1.5	4

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28993	Reference genome of lumpfish <i>Cyclopterus lumpus</i> Linnaeus provides evidence of male heterogametic sex determination through the AMH pathway. <i>Molecular Ecology Resources</i> , 2022, 22, 1427-1439.	2.2	16
28994	Survey for Virus Diversity in Common Bean ( <i>Phaseolus vulgaris</i> ) Fields and the Detection of a Novel Strain of Cowpea polerovirus 1 in Zambia. <i>Plant Disease</i> , 2022, 106, 2380-2391.	0.7	0
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28996	Association of Leeches with the Endangered Houston Toad. <i>Southeastern Naturalist</i> , 2022, 21, .	0.2	1
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28999	In silico analyses of maleidride biosynthetic gene clusters. <i>Fungal Biology and Biotechnology</i> , 2022, 9, 2.	2.5	4
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29001	Circumscription and Phylogenetic Position of Two Propagulose Species of <i>Syntrichia</i> (Pottiaceae), Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.6	2
29002	Distribution of Alleles of PRNP Gene Associated with Chronic Wasting Disease in Wild and Domesticated Reindeer <i>Rangifer tarandus</i> in Russia. <i>Russian Journal of Genetics</i> , 2022, 58, 158-163.	0.2	1
29003	Microbiome structure and response to watering in rhizosphere of <i>Nitrosalsola vermiculata</i> and surrounding bulk soil. <i>Notulae Botanicae Horti Agrobotanici Cluj-Napoca</i> , 2022, 50, 12567.	0.5	1
29004	Comparative Genome Analysis of <i>Candidatus Phytoplasma luffae</i> ™ Reveals the Influential Roles of Potential Mobile Units in <i>Phytoplasma</i> Evolution. <i>Frontiers in Microbiology</i> , 2022, 13, 773608.	1.5	15
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29006	The Genome of <i>Rhyzopertha dominica</i> (Fab.) (Coleoptera: Bostrichidae): Adaptation for Success. <i>Genes</i> , 2022, 13, 446.	1.0	10
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29011	An investigation of spatial-temporal patterns and predictions of the coronavirus 2019 pandemic in Colombia, 2020–2021. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010228.	1.3	8
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29013	Genome-Wide Identification and Expression Analysis of the R2R3-MYB Transcription Factor Family Revealed Their Potential Roles in the Flowering Process in Longan ( <i>Dimocarpus longan</i> ). <i>Frontiers in Plant Science</i> , 2022, 13, 820439.	1.7	8
29014	Structure of a cereal purple acid phytase provides new insights to phytate degradation in plants. <i>Plant Communications</i> , 2022, 3, 100305.	3.6	5
29015	Phylogenetic Relationships of <i>Guimaraesiella</i> and <i>Priceiella</i> (Phthiraptera: Ischnocera) from Babblers and Non-Babblers (Passeriformes). <i>Journal of Parasitology</i> , 2022, 108, 107-121.	0.3	2
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29018	Evolutionary history of the p53 family DNA-binding domain: insights from an <i>Alvinella pompejana</i> homolog. <i>Cell Death and Disease</i> , 2022, 13, 214.	2.7	10
29019	Survey of nonconventional yeasts for lipid and hydrocarbon biotechnology. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2022, 49, .	1.4	2
29020	Associating life stages and sexes of Nearctic <i>Polycentropus</i> Curtis, 1835 (Trichoptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 342	0.8	5
29021	A severe microsporidian disease in cultured Atlantic Bluefin Tuna ( <i>Thunnus thynnus</i> ). <i>IMA Fungus</i> , 2022, 13, 5.	1.7	0
29022	Cervicovaginal DNA Virome Alterations Are Associated with Genital Inflammation and Microbiota Composition. <i>MSystems</i> , 2022, 7, e0006422.	1.7	14
29023	Molecular Characterization, Evolutionary Analysis, and Expression Profiling of BOR Genes in Important Cereals. <i>Plants</i> , 2022, 11, 911.	1.6	14
29024	Comparison of <i>Auxenochlorella protothecoides</i> and <i>Chlorella</i> spp. Chloroplast Genomes: Evidence for Endosymbiosis and Horizontal Virus-like Gene Transfer. <i>Life</i> , 2022, 12, 458.	1.1	0
29025	Evolutionary and Association Analysis of Buffalo FABP Family Genes Reveal Their Potential Role in Milk Performance. <i>Genes</i> , 2022, 13, 600.	1.0	7
29026	A Novel Network Science and Similarity-Searching-Based Approach for Discovering Potential Tumor-Homing Peptides from Antimicrobials. <i>Antibiotics</i> , 2022, 11, 401.	1.5	6
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29035	A Decomposition and Dominance-Based Multiobjective Artificial Bee Colony Algorithm for Multiple Sequence Alignment. <i>Mobile Information Systems</i> , 2022, 2022, 1-13.	0.4	1
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29037	Genomic adaptations for arboreal locomotion in Asian flying treefrogs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2116342119.	3.3	6
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29039	The Use and Limitations of the 16S rRNA Sequence for Species Classification of <i>Anaplasma</i> Samples. <i>Microorganisms</i> , 2022, 10, 605.	1.6	17
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29041	Draft Genome Sequence of a Novel Calicivirus from a Brown Bullhead ( <i>Ameiurus nebulosus</i> ) from Lake Memphremagog, Vermont/Quebec. <i>Microbiology Resource Announcements</i> , 2022, 11, e0118821.	0.3	1
29042	Associations between inflammation-related LL-37 with subgingival microbial dysbiosis in rheumatoid arthritis patients. <i>Clinical Oral Investigations</i> , 2022, 26, 4161-4172.	1.4	4
29043	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
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29046	<i>Hymenostylium chapadense</i> M.J.Cano & J.A.Jiménez (Pottiaceae), a new species from Brazil and its phylogenetic position based on molecular data. <i>Journal of Bryology</i> , 0, , 1-11.	0.4	0

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29048	Taxonomical identification of Chinese cabbage yellows inhibitory fungus isolated from disease suppressive soil. <i>Journal of General Plant Pathology</i> , 0, , 1.	0.6	2
29049	<i>Sporobolomyces lactucae</i> sp. nov. (Pucciniomycotina, Microbotryomycetes, Sporidiobolales): An Abundant Component of Romaine Lettuce Phylloplanes. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 302.	1.5	0
29050	African climate and geomorphology drive evolution and ghost introgression in sable antelope. <i>Molecular Ecology</i> , 2022, 31, 2968-2984.	2.0	8
29052	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
29053	<i>Pseudomonas germanica</i> sp. nov., isolated from <i>Iris germanica</i> rhizomes. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	4
29054	Membrane Interactions and Uncoating of Aichi Virus, a Picornavirus That Lacks a VP4. <i>Journal of Virology</i> , 2022, 96, e0008222.	1.5	2
29055	The oxytocin signaling complex reveals a molecular switch for cation dependence. <i>Nature Structural and Molecular Biology</i> , 2022, 29, 274-281.	3.6	29
29056	Mucospheres produced by a mixotrophic protist impact ocean carbon cycling. <i>Nature Communications</i> , 2022, 13, 1301.	5.8	27
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29062	Chromosome-Level Genome Assembly for <i>Acer pseudosieboldianum</i> and Highlights to Mechanisms for Leaf Color and Shape Change. <i>Frontiers in Plant Science</i> , 2022, 13, 850054.	1.7	7
29063	A chromosome-level genome assembly of <i>Paracymoriza distinctalis</i> (Lepidoptera: Crambidae). <i>Tj ETQq0 0 0 rgBT /Overlock 10 T</i>	0.6	0
29064	Patterns of selection in the evolution of a transposable element. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	3
29065	Ensifer meliloti L6-AK89, an Effective Inoculant of Medicago lupulina Varieties: Phenotypic and Deep-Genome Screening. <i>Agronomy</i> , 2022, 12, 766.	1.3	8
29067	Cell-wall damage activates DOF transcription factors to promote wound healing and tissue regeneration in <i>Arabidopsis thaliana</i> . <i>Current Biology</i> , 2022, 32, 1883-1894.e7.	1.8	31



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29070	Host Shift Speciation of the Ectomycorrhizal Genus <i>Suillus</i> (Suillineae, Boletales) and Biogeographic Comparison With Its Host Pinaceae. <i>Frontiers in Microbiology</i> , 2022, 13, 831450.	1.5	4
29071	The Facts and Family Secrets of Plasmids That Replicate via the Rolling-Circle Mechanism. <i>Microbiology and Molecular Biology Reviews</i> , 2022, 86, e0022220.	2.9	10
29072	Abundance of integrons in halophilic bacteria. <i>Canadian Journal of Microbiology</i> , 2022, , 1-11.	0.8	0
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29075	Environmental Potential for Microbial 1,4-Dioxane Degradation Is Sparse despite Mobile Elements Playing a Role in Trait Distribution. <i>Applied and Environmental Microbiology</i> , 2022, 88, e0209121.	1.4	8
29076	Identification and functional expression of a new xylose isomerase from the goat rumen microbiome in <i>Saccharomyces cerevisiae</i> . <i>Letters in Applied Microbiology</i> , 2022, 74, 941-948.	1.0	4
29077	Draft Genome Sequence of <i>Polaromonas eurypsychrophila</i> AER18D-145, Isolated from a Uranium Tailings Management Facility in Northern Saskatchewan, Canada. <i>Microbiology Resource Announcements</i> , 2022, 11, e0001322.	0.3	1
29079	Biological Control of Diamondback Moth Increased Efficacy with Mixtures of <i>Beauveria</i> Fungi. <i>Microorganisms</i> , 2022, 10, 646.	1.6	5
29080	The ectomycorrhizal association of <i>Tricholoma matsutake</i> and two allied species, <i>T. bakamatsutake</i> and <i>T. fulvocastaneum</i> , with native hosts in subtropical China. <i>Mycologia</i> , 2022, 114, 303-318.	0.8	6
29082	Identification of <i>Clostridium innocuum</i> hypothetical protein that is cross-reactive with <i>C. difficile</i> anti-toxin antibodies. <i>Anaerobe</i> , 2022, 75, 102555.	1.0	10
29083	Investigation of cross-regional spread and evolution of equine influenza H3N8 at US and global scales using Bayesian phylogeography based on balanced subsampling. <i>Transboundary and Emerging Diseases</i> , 2022, 69, .	1.3	2
29084	Metabolomic and Transcriptional Profiling of Oleuropein Bioconversion into Hydroxytyrosol during Table Olive Fermentation by <i>Lactiplantibacillus plantarum</i> . <i>Applied and Environmental Microbiology</i> , 2022, 88, AEM0201921.	1.4	2
29086	The first molecular detection of <i>Anaplasma capra</i> in domestic ruminants in the central part of Turkey, with genetic diversity and genotyping of <i>Anaplasma capra</i> . <i>Tropical Animal Health and Production</i> , 2022, 54, 129.	0.5	14
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29088	Temperature Extremes and Sex-Related Physiology, Not Environmental Variability, Are Key in Explaining Thermal Sensitivity of Bimodal-Breathing Intertidal Crabs. <i>Frontiers in Marine Science</i> , 2022, 9, .	1.2	2
29089	Isolation and characterisation of monoclonal picocyanobacterial strains from contrasting New Zealand lakes. <i>Inland Waters</i> , 2022, 12, 383-396.	1.1	1

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29091	Molecular and Morphological Analysis Supports the Separation of <i>Robrichia</i> as a Genus Distinct from <i>Enterolobium</i> (Leguminosae: Caesalpinioideae: Mimosoid Clade). Systematic Botany, 2022, 47, 268-277.	0.2	3
29092	DNA Barcoding and New Records of Odonates (Insecta: Odonata) from Para�ba State, Brazil. Diversity, 2022, 14, 203.	0.7	3
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29095	Host species is linked to pathogen genotype for the amphibian chytrid fungus ( <i>Batrachochytrium</i> ) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	1.1	4
29097	Multiple Profile Models Extract Features from Protein Sequence Data and Resolve Functional Diversity of Very Different Protein Families. Molecular Biology and Evolution, 2022, 39, .	3.5	7
29098	Can fractal dimensions objectivize gastropod shell morphometrics? A case study from Lake Lugu (SW) Tj ETQq0 0 0 rgBT /Overlock 10 T	0.8	4
29099	Innovation and Emerging Roles of <i>Populus trichocarpa</i> TEOSINTE BRANCHED1/CYCLOIDEA/PROLIFERATING CELL FACTOR Transcription Factors in Abiotic Stresses by Whole-Genome Duplication. Frontiers in Plant Science, 2022, 13, 850064.	1.7	6
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29103	Genome Sequence and Analysis of the Flavinogenic Yeast <i>Candida membranifaciens</i> IST 626. Journal of Fungi (Basel, Switzerland), 2022, 8, 254.	1.5	1
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29106	Phage-encoded ribosomal protein S21 expression is linked to late-stage phage replication. ISME Communications, 2022, 2, .	1.7	10
29107	Analysis of biodiversity data suggests that mammal species are hidden in predictable places. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2103400119.	3.3	13
29108	Observation of the Gut Microbiota Profile in BALB/c Mice Induced by <i>Plasmodium yoelii</i> 17XL Infection. Frontiers in Microbiology, 2022, 13, 858897.	1.5	6
29109	The Common Bean V Gene Encodes Flavonoid 3-Hydroxylase: A Major Mutational Target for Flavonoid Diversity in Angiosperms. Frontiers in Plant Science, 2022, 13, 869582.	1.7	7
29110	Identifying strawberry DOF family transcription factors and their expressions in response to crown rot. Notulae Botanicae Horti Agrobotanici Cluj-Napoca, 2022, 50, 12640.	0.5	0

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29112	Developing new genetic algorithm based on integer programming for multiple sequence alignment. <i>Soft Computing</i> , 2022, 26, 3863-3870.	2.1	0
29113	Aerobic and anaerobic methane oxidation in a seasonally anoxic basin. <i>Limnology and Oceanography</i> , 2022, 67, 1257-1273.	1.6	8
29114	Strain-Level Variation and Diverse Host Bacterial Responses in Episymbiotic Saccharibacteria. <i>MSystems</i> , 2022, 7, e0148821.	1.7	6
29115	Comparative Genomic Analysis of <i>Xanthomonas campestris</i> pv. <i>campestris</i> Isolates BJSJQ20200612 and GSXT20191014 Provides Novel Insights Into Their Genetic Variability and Virulence. <i>Frontiers in Microbiology</i> , 2022, 13, 833318.	1.5	3
29116	Novel Low Pathogenic Avian Influenza H6N1 in Backyard Chicken in Easter Island (Rapa Nui), Chilean Polynesia. <i>Viruses</i> , 2022, 14, 718.	1.5	2
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29118	Functional analysis of the ScAG and ScAGL11 MADS-box transcription factors for anthocyanin biosynthesis and bicolour pattern formation in <i>Senecio cruentus</i> ray florets. <i>Horticulture Research</i> , 2022, 9, .	2.9	18
29120	AutoCoE – A High-Throughput In Silico Pipeline for Predicting Inter-Protein Coevolution. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3351.	1.8	1
29122	Comparative genomic analysis of vertebrate mitochondrial reveals a differential of rearrangements rate between taxonomic class. <i>Scientific Reports</i> , 2022, 12, 5479.	1.6	13
29123	Development of Real-Time Molecular Assays for the Detection of Wesselsbron Virus in Africa. <i>Microorganisms</i> , 2022, 10, 550.	1.6	1
29124	<i>Thiomicrobacterium heinhorstiae</i> sp. nov. and <i>Thiomicrobacterium cannonii</i> sp. nov.: novel sulphur-oxidizing chemolithoautotrophs isolated from the chemocline of Hospital Hole, an anchialine sinkhole in Spring Hill, Florida, USA. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	13
29126	PacRAT: a program to improve barcode-variant mapping from PacBio long reads using multiple sequence alignment. <i>Bioinformatics</i> , 2022, 38, 2927-2929.	1.8	5
29127	DNA barcoding the Lake Edward basin: high taxonomic coverage of a tropical freshwater ichthyofauna. <i>Hydrobiologia</i> , 2022, 849, 1743-1762.	1.0	3
29129	Crystal structures of bacterial small multidrug resistance transporter EmrE in complex with structurally diverse substrates. <i>ELife</i> , 2022, 11, .	2.8	13
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29289	Cleavage activation and functional comparison of <i>Manduca sexta</i> serine protease homologs SPH1a, SPH1b, SPH4, and SPH101 in conjunction with SPH2. <i>Insect Biochemistry and Molecular Biology</i> , 2022, 144, 103762.	1.2	10
29290	The evolution of microtubule associated proteins – a reference proteomic perspective. <i>BMC Genomics</i> , 2022, 23, 266.	1.2	4
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29294	Establishment of the Y-linked Dmrt1Y as the candidate sex determination gene in spotbanded scat ( <i>Selenotoca multifasciata</i> ). <i>Aquaculture Reports</i> , 2022, 23, 101085.	0.7	0
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29299	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
29300	A multidisciplinary study of Iberian Chalcolithic dogs. <i>Journal of Archaeological Science: Reports</i> , 2022, 42, 103338.	0.2	0
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29307	Phylogenetic conservatism of mycoparasitism and its contribution to pathogen antagonism. <i>Molecular Ecology</i> , 2022, 31, 3018-3030.	2.0	7
29308	De novo genome assembly of <i>Bradysia cellarum</i> (Diptera: Sciaridae), a notorious pest in traditional special vegetables in China. <i>Insect Molecular Biology</i> , 2022, 31, 508-518.	1.0	3

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29312	Discovery of Novel Tyrosine Ammonia Lyases for the Enzymatic Synthesis of <i>p</i> -Coumaric Acid. <i>ChemBioChem</i> , 2022, 23, .	1.3	8
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29317	Evolution of toll-like receptor gene family in amphibians. <i>International Journal of Biological Macromolecules</i> , 2022, 208, 463-474.	3.6	11
29318	Genomics divergence of <i>Lactococcus lactis</i> subsp. <i>lactis</i> isolated from naturally fermented dairy products. <i>Food Research International</i> , 2022, 155, 111108.	2.9	9
29319	Evaluations of two glutathione S-transferase epsilon genes for their contributions to metabolism of three selected insecticides in <i>Locusta migratoria</i> . <i>Pesticide Biochemistry and Physiology</i> , 2022, 183, 105084.	1.6	7
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29323	A mixed blessing of viruses in wastewater treatment plants. <i>Water Research</i> , 2022, 215, 118237.	5.3	21
29324	Ancient DNA confirms crossbreeding of domestic South American camelids in two pre-conquest archaeological sites. <i>Journal of Archaeological Science</i> , 2022, 141, 105593.	1.2	1
29325	Genome-based taxonomy of genera <i>Halomicrobium</i> and <i>Halosiccatus</i> , and description of <i>Halomicrobium salinisoli</i> sp. nov. <i>Systematic and Applied Microbiology</i> , 2022, 45, 126308.	1.2	24
29326	Molecular data confirm <i>Triatoma pallidipennis</i> Stål, 1872 (Hemiptera: Reduviidae: Triatominae) as a novel cryptic species complex. <i>Acta Tropica</i> , 2022, 229, 106382.	0.9	9
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29333	Knockout of SLALKBH2 weakens the DNA damage repair ability of tomato. Plant Science, 2022, 319, 111266.	1.7	1
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29341	Heterologous expression, biochemical characterisation and computational analysis of Bacteroides fragilis enolase. Computational Biology and Chemistry, 2022, 98, 107658.	1.1	0
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29351	Genetic Variability and the Potential Range of <i>Darevskia rostombekowi</i> in Transcaucasia. <i>Biology Bulletin</i> , 2021, 48, 681-692.	0.1	2
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29353	High-Quality Genome Assembly of Oleaginous Red Yeast <i>Sporobolomyces roseus</i> CGMCC 2.4355. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	1
29354	Cofactor-independent RNA editing by a synthetic S-type PPR protein. <i>Synthetic Biology</i> , 2022, 7, ysab034.	1.2	12
29355	<i>N</i> -glycans from <i>Paramecium bursaria</i> chloroella virus MA-1D: Re-evaluation of the oligosaccharide common core structure. <i>Glycobiology</i> , 2022, 32, 260-273.	1.3	2
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29357	Biodiversity and Enzyme Activity of Marine Fungi with 28 New Records from the Tropical Coastal Ecosystems in Vietnam. <i>Mycobiology</i> , 2021, 49, 559-581.	0.6	10
29358	New Dothideomycetes from Freshwater Habitats in Spain. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 1102.	1.5	7
29359	Improving phylogenetic resolution of the Lamiales using the complete plastome sequences of six <i>Penstemon</i> species. <i>PLoS ONE</i> , 2021, 16, e0261143.	1.1	3
29360	Novel strain of <i>Pseudoruminococcus massiliensis</i> possesses traits important in gut adaptation and host-microbe interactions. <i>Gut Microbes</i> , 2022, 14, 2013761.	4.3	0
29361	Neotropical niche evolution of <i>Otoba</i> trees in the context of global biogeography of the nutmeg family. <i>Journal of Biogeography</i> , 2022, 49, 156-170.	1.4	6
29362	A DNA barcode library for the water mites of Montenegro. <i>Biodiversity Data Journal</i> , 2021, 9, e78311.	0.4	10
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29367	ArfX2 GTPase Regulates Trafficking From the Trans-Golgi to Lysosomes and Is Necessary for Liver Abscess Formation in the Protozoan Parasite <i>Entamoeba histolytica</i> . Frontiers in Cellular and Infection Microbiology, 2021, 11, 794152.	1.8	3
29368	<i>Sabulicella rubraurantiaca</i> gen. nov., sp. nov., a new member of the family Acetobacteraceae, isolated from desert soil. Archives of Microbiology, 2022, 204, 1.	1.0	44
29369	Unique roles of vaginal <i>Megasphaera</i> phylotypes in reproductive health. Microbial Genomics, 2021, 7, .	1.0	6
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29371	Molecular Detection of <i>Nosema</i> spp. in Honey in Bulgaria. Veterinary Sciences, 2022, 9, 10.	0.6	4
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29379	<i>Haloprofundus salilacus</i> sp. nov., <i>Haloprofundus halobius</i> sp. nov. and <i>Haloprofundus salinisoli</i> sp. nov.: three extremely halophilic archaea isolated from salt lake and saline soil. Extremophiles, 2022, 26, 6.	0.9	23
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29383	Morphological and molecular investigations of the rhizocephalan barnacle <i>Peltogaster lineata</i> Shiino, 1943 in the northern part of the species range (Peter the Great Bay, the Sea of Japan). Marine Biodiversity, 2021, 51, 1.	0.3	2
29384	Comprehensive Transcriptome Sequencing of Tanaidacea with Proteomic Evidences for Their Silk. Genome Biology and Evolution, 2021, 13, .	1.1	8
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29387	<i>dnal</i> : a New Approach to Identify Species within the Genus Enterobacter. Microbiology Spectrum, 2021, 9, e0124221.	1.2	3
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29402	Virome Characterization in Commercial Bovine Serum Batches – A Potentially Needed Testing Strategy for Biological Products. Viruses, 2021, 13, 2425.	1.5	5
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29411	Comparative Genomic Study of Vinyl Chloride Cluster and Description of Novel Species, <i>Mycobacterium vinylchloridicum</i> sp. nov.. <i>Frontiers in Microbiology</i> , 2021, 12, 767895.	1.5	2
29412	The Imaginal Characters of <i>Cincticostella gosei</i> (Allen, 1975) linking the genus <i>Cincticostella</i> Allen, 1971 to <i>Ephacera</i> Paclt, 1994 (Ephemeroptera: Ephemerellidae). <i>Zootaxa</i> , 2021, 5081, 131-140.	0.2	1
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29415	Understanding molecular relationships in <i>Campomanesia Ruiz &amp; Pav.</i> (Myrtaceae): emphasizing the <i>C. xanthocarpa</i> complex based on multiple accessions. <i>Revista Brasileira De Botanica</i> , 2021, 44, 917-927.	0.5	1
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29418	Phylogenetic re-assessment of the delimitation of <i>Plocama</i> and its species relationships and limits (Rubiaceae, Putorieae): resurrection of the monospecific genus <i>Aitchisonia</i> and a description of trib. nov. <i>Aitchisonieae</i> . <i>Plant Systematics and Evolution</i> , 2022, 308, 1.	0.3	2
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29558	Phylogeny of <i>Amphidinium</i> (Dinophyceae) from Guam and Okinawa, with descriptions of <i>A. pagoense</i> sp. nov. and <i>A. uduigamense</i> sp. nov. <i>Phycologia</i> , 0, , 1-14.	0.6	1
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31443	The Complete Mitochondrial Genome of <i>Stichopus naso</i> (Aspidochirotida: Stichopodidae: Stichopus) and Its Phylogenetic Position. <i>Genes</i> , 2022, 13, 825.	1.0	2
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31445	Spatial heterogeneity of knockdown resistance mutations in the dengue vector <i>Aedes albopictus</i> in Guangzhou, China. <i>Parasites and Vectors</i> , 2022, 15, 156.	1.0	2
31446	Third Generation Genome Sequencing Reveals That Endobacteria in Nematophagous Fungi <i>Esteya vermicola</i> Contain Multiple Genes Encoding for Nematicidal Proteins. <i>Frontiers in Microbiology</i> , 2022, 13, 842684.	1.5	1
31447	New cyanobacterial genus <i>Argonema</i> is hiding in soil crusts around the world. <i>Scientific Reports</i> , 2022, 12, 7203.	1.6	6
31449	Unveiling an enigma from the Cerrado: taxonomic revision of two sympatric species of <i>Apostolepis Cope, 1862</i> (Dipsadidae: Xenodontinae: Elapomorhini) from central Brazil. <i>European Journal of Taxonomy</i> , 0, 817, .	0.6	0
31450	SPIN enables high throughput species identification of archaeological bone by proteomics. <i>Nature Communications</i> , 2022, 13, 2458.	5.8	31
31451	Elucidation of host and symbiont contributions to peptidoglycan metabolism based on comparative genomics of eight aphid subfamilies and their <i>Buchnera</i> . <i>PLoS Genetics</i> , 2022, 18, e1010195.	1.5	11
31452	Revision of the African cichlid fish genus <i>Ctenochromis</i> (Teleostei, Cichliformes), including a description of the new genus <i>Shuja</i> from Lake Tanganyika and the new species <i>Ctenochromis scatebra</i> from northern Tanzania. <i>European Journal of Taxonomy</i> , 0, 819, 23-54.	0.6	2
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31454	Tolypoclamamide H and the Proposed Tolypoclamamide NRPS in <i>Tolypocladium</i> Species. <i>Journal of Natural Products</i> , 2022, 85, 1363-1373.	1.5	10
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31456	Rampant nuclear-mitochondrial-plastid phylogenomic discordance in globally distributed calcifying microalgae. <i>New Phytologist</i> , 2022, 235, 1394-1408.	3.5	11
31457	Distribution and Diversity of Prunus Necrotic Ringspot Virus, Prune Dwarf Virus, and Peach Latent Mosaic Viroid in Wild <i>Prunus</i> spp. in South Carolina and Georgia. <i>PhytoFrontiers</i> , 2022, 2, 363-370.	0.8	4
31458	Cryptic Genes for Interbacterial Antagonism Distinguish <i>Rickettsia</i> Species Infecting Blacklegged Ticks From Other <i>Rickettsia</i> Pathogens. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 880813.	1.8	8
31459	Functional Diversity of the Lepidopteran ATP-Binding Cassette Transporters. <i>Journal of Molecular Evolution</i> , 2022, 90, 258-270.	0.8	3
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31462	Evolution of osmosensing OSCA1 Ca <sup>2+</sup> channel family coincident with plant transition from water to land. <i>Plant Genome</i> , 2022, 15, e20198.	1.6	5
31463	Neither <i>Seseli</i> nor <i>Eriocyclus</i> : a new Iranian relict genus <i>Shomalina</i> (Apiaceae), related to <i>Azilia</i> . <i>Plant Systematics and Evolution</i> , 2022, 308, .	0.3	2
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31465	A comparative analysis depicting the disease characteristics and phylogenetic signature of human cytomegalovirus infection in Human Immunodeficiency Virus 1 seropositive patients with end-organ retinitis and gastro-enteric diseases. <i>Scientific Reports</i> , 2022, 12, 7617.	1.6	1
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31469	On the presence of the giant freshwater prawn, <i>Macrobrachium rosenbergii</i> , in French Guiana confirmed by citizen science and genetic analyses. , 2022, 1, 100039.		1
31470	Exploring the microbial influence on seasonal nitrous oxide concentration in a full-scale wastewater treatment plant using metagenome assembled genomes. <i>Water Research</i> , 2022, 219, 118563.	5.3	5
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31472	Phylogeography of the freshwater rotifer <i>Brachionus calyciflorus</i> species complex in China. <i>Hydrobiologia</i> , 2022, 849, 2813-2829.	1.0	4
31473	The role of gilts in transmission dynamics of swine influenza virus and impacts of vaccination strategies and quarantine management. <i>Porcine Health Management</i> , 2022, 8, 19.	0.9	3
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31475	CRISPR/Cas9-mediated tetraallelic mutation of the "Green Revolution" SEMIDWARF1 ( <i>SD1</i> ) gene confers lodging resistance in <i>Eragrostis tef</i> . <i>Plant Biotechnology Journal</i> , 2022, 20, 1716-1729.	4.1	16
31476	In-Depth Satellitome Analyses of 37 <i>Drosophila</i> Species Illuminate Repetitive DNA Evolution in the <i>Drosophila</i> Genus. <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	16
31477	Genome-Wide Identification and Evolution Analysis of the Gibberellin Oxidase Gene Family in Six Gramineae Crops. <i>Genes</i> , 2022, 13, 863.	1.0	9
31479	Estimated Divergence Times of <i>Lecanicillium</i> in the Family Cordycipitaceae Provide Insights Into the Attribution of <i>Lecanicillium</i> . <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	6

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31481	Widespread Sterol Methyltransferase Participates in the Biosynthesis of Both C <sub>41</sub> - and C <sub>42</sub> -Methyl Sterols. <i>Journal of the American Chemical Society</i> , 2022, 144, 9023-9032.	6.6	9
31482	Reconstruction of full-length LINE-1 progenitors from ancestral genomes. <i>Genetics</i> , 2022, 221, .	1.2	6
31483	High-Resolution Metagenomics of Human Gut Microbiota Generated by Nanopore and Illumina Hybrid Metagenome Assembly. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	4
31484	The Luminal Microbiota Varies Biogeographically in the Gastrointestinal Tract of Rhesus Macaques. <i>Microbiology Spectrum</i> , 2022, 10, e0034322.	1.2	2
31486	Genome and transcriptome mechanisms driving cephalopod evolution. <i>Nature Communications</i> , 2022, 13, 2427.	5.8	47
31487	Hybrid Sequencing Resolved Inverted Terminal Repeats in the Genome of Megavirus Baoshan. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	3
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31489	The flying spider-monkey tree fern genome provides insights into fern evolution and arborescence. <i>Nature Plants</i> , 2022, 8, 500-512.	4.7	42
31490	<i>Copranaerobaculum intestinale</i> gen. nov., sp. nov., a novel anaerobic bacterium isolated from human faeces. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	6
31491	Assembly of a hybrid mangrove, <i>Bruguiera hainesii</i> , and its two ancestral contributors, <i>Bruguiera cylindrica</i> and <i>Bruguiera gymnorhiza</i> . <i>Genomics</i> , 2022, 114, 110382.	1.3	5
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31493	Genomic features of the polyphagous cotton leafworm <i>Spodoptera littoralis</i> . <i>BMC Genomics</i> , 2022, 23, 353.	1.2	2
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31495	The curious case of Charles Darwin's frog, <i>Rana charlesdarwini</i> Das, 1998: Phylogenetic position and generic placement, with taxonomic insights on other minervaryan frogs (Dicroglossidae: Minervarya) in the Andaman and Nicobar Archipelago. <i>Vertebrate Zoology</i> , 0, 72, 169-199.	2.0	1
31496	Identification and Comparative Genomic Analysis of Type VI Secretion Systems and Effectors in <i>Klebsiella pneumoniae</i> . <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	8
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31500	Ten <i>Ostreobium</i> (Ulvophyceae) strains from Great Barrier Reef corals as a resource for algal endolith biology and genomics. <i>Phycologia</i> , 2022, 61, 452-458.	0.6	6

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31503	Fifteen complete chloroplast genomes of <i>Trapa</i> species (Trapaceae): insight into genome structure, comparative analysis and phylogenetic relationships. <i>BMC Plant Biology</i> , 2022, 22, 230.	1.6	11
31504	<i>icaR</i> and <i>icaT</i> are Ancient Chromosome Genes Encoding Substrates of the Type III Secretion Apparatus in <i>Shigella flexneri</i> . <i>MSphere</i> , 2022, 7, e0011522.	1.3	2
31505	Palaeogenomic analysis of black rat ( <i>Rattus rattus</i> ) reveals multiple European introductions associated with human economic history. <i>Nature Communications</i> , 2022, 13, 2399.	5.8	12
31506	PANDORA: A Fast, Anchor-Restrained Modelling Protocol for Peptide: MHC Complexes. <i>Frontiers in Immunology</i> , 2022, 13, .	2.2	14
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31510	Haemogregarines of the Genera <i>Haemogregarina</i> , <i>Hemolivia</i> , and <i>Hepatozoon</i> Infecting Vietnamese Freshwater Turtles, with Additional Notes on Primer Specificity and Primer-template Mismatches Affecting Diagnostic Success. <i>Protist</i> , 2022, 173, 125884.	0.6	4
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31513	<i>Paenibacillus</i> sp. Strain OL15 Immobilized in Agar as a Potential Bioremediator for Waste Lubricating Oil-Contaminated Soils and Insights into Soil Bacterial Communities Affected by Inoculations of the Strain and Environmental Factors. <i>Biology</i> , 2022, 11, 727.	1.3	5
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31517	Uncovering early thyroid hormone signalling events through temperature-mediated activation of molecular memory in the cultured bullfrog tadpole tail fin. <i>General and Comparative Endocrinology</i> , 2022, 323-324, 114047.	0.8	2
31518	<i>Aspergillus terreus</i> , <i>Penicillium</i> sp. and <i>Bacillus</i> sp. isolated from mangrove soil having laccase and peroxidase role in depolymerization of polyethylene bags. <i>Process Biochemistry</i> , 2022, 118, 215-226.	1.8	10
31519	GPP (composition of <i>Ganoderma lucidum</i> polysaccharides and <i>Polyporus umbellatus</i> polysaccharides) protects against DSS-induced murine colitis by enhancing immune function and regulating intestinal flora. <i>Food Science and Human Wellness</i> , 2022, 11, 795-805.	2.2	10

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31522	Population changes in a whale breeding ground revealed by citizen science noninvasive genetics. <i>Global Ecology and Conservation</i> , 2022, 37, e02141.	1.0	2
31523	Engineering of the chloroaniline-catabolic plasmid pDCA-1 and its potential for genetic bioaugmentation. <i>International Biodeterioration and Biodegradation</i> , 2022, 172, 105435.	1.9	3
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31525	<i>Tuber eburneum</i> and <i>Tuber mujicii</i> : New pine-associated <i>Tuber</i> species from eastern North America. <i>Mycologia</i> , 2022, 114, 575-586.	0.8	1
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31527	Electrophoretic and molecular profile of the hemoglobinopathies in newborns at a reference hospital in Mozambique. <i>Rendiconti Lincei</i> , 2022, 33, 283-293.	1.0	1
31528	Correlations between dominant vegetation type and composition and diversity of soil bacterial communities in a subtropical forest. <i>Soil Science Society of America Journal</i> , 0, , .	1.2	2
31529	New insights from the virome of <i>Halyomorpha halys</i> (Stål, 1855). <i>Virus Research</i> , 2022, 316, 198802.	1.1	3
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31531	Uncovering overlooked diversity using molecular phylogenetic approach: A case of Japanese sphaeriid clams ( <i>Bivalvia</i> : <i>Sphaeriidae</i> ). <i>Molecular Phylogenetics and Evolution</i> , 2022, 173, 107508.	1.2	5
31532	The invasion biology of tomato begomoviruses in Costa Rica reveals neutral synergism that may lead to increased disease pressure and economic loss. <i>Virus Research</i> , 2022, 317, 198793.	1.1	6
31533	Genomic Analyses of SUT and TST Sugar Transporter Families in Low and High Sugar Accumulating Sugarcane Species ( <i>Saccharum spontaneum</i> and <i>Saccharum officinarum</i> ). <i>Tropical Plant Biology</i> , 2022, 15, 181-196.	1.0	3
31534	Between a rock and a dry place: phylogenomics, biogeography, and systematics of ridge-tailed monitors ( <i>Squamata</i> : <i>Varanidae</i> : <i>Varanus acanthurus</i> complex). <i>Molecular Phylogenetics and Evolution</i> , 2022, 173, 107516.	1.2	5
31535	Benefits of alignment quality control processing steps and an Angiosperms353 phylogenomics pipeline applied to the <i>Celastrales</i> . <i>Cladistics</i> , 2022, 38, 595-611.	1.5	1
31536	Identification and genome characterization of novel parechovirus sequences from <i>Hipposideros armiger</i> in China. <i>Virology Journal</i> , 2022, 19, 80.	1.4	0
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31542	Possible new Arkansas endemic plant revealed by DNA sequence analysis, A. <i>Journal of the Arkansas Academy of Science</i> , 0, 66, .	0.0	0
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31546	Analysis of rhodopsin G protein-coupled receptor orthologs reveals semiochemical peptides for parasite ( <i>Schistosoma mansoni</i> ) and host ( <i>Biomphalaria glabrata</i> ) interplay. <i>Scientific Reports</i> , 2022, 12, 8243.	1.6	5
31548	Temperature and Geographic Location Impact the Distribution and Diversity of Photoautotrophic Gene Variants in Alkaline Yellowstone Hot Springs. <i>Microbiology Spectrum</i> , 2022, 10, e0146521.	1.2	7
31549	Phylogeny of NF-YA trans-activation splicing isoforms in vertebrate evolution. <i>Genomics</i> , 2022, 114, 110390.	1.3	4
31550	Lack of Association between Fluconazole Susceptibility and ERG11 Nucleotide Polymorphisms in <i>Cryptococcus neoformans</i> Clinical Isolates from Uganda. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 508.	1.5	5
31551	The phylogeographical pattern of the Amur minnow <i>Rhynchocypris lagowskii</i> (Cypriniformes: Cyprinidae). <i>Journal of Herpetology</i> , 2022, 56, 108-114.	0.8	2
31552	<i>Streptomyces benahoarensis</i> sp. nov. Isolated From a Lava Tube of La Palma, Canary Islands, Spain. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	3
31553	Plastid phylogenomic analyses of the <i>Selaginella sanguinolenta</i> group (Selaginellaceae) reveal conflict signatures resulting from sequence types, outlier genes, and pervasive RNA editing. <i>Molecular Phylogenetics and Evolution</i> , 2022, 173, 107507.	1.2	7
31554	A genome-wide scan of wastewater <i>E. coli</i> for genes under positive selection: focusing on mechanisms of antibiotic resistance. <i>Scientific Reports</i> , 2022, 12, 8037.	1.6	5
31555	WITCH: Improved Multiple Sequence Alignment Through Weighted Consensus Hidden Markov Model Alignment. <i>Journal of Computational Biology</i> , 2022, , .	0.8	10
31556	Synergy of Dietary Quercetin and Vitamin E Improves Cecal Microbiota and Its Metabolite Profile in Aged Breeder Hens. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	1
31557	High DDT resistance without apparent association to <i>kdr</i> and Glutathione-S-transferase ( <i>GST</i> ) gene mutations in <i>Aedes aegypti</i> population at hotel compounds in Zanzibar. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010355.	1.3	3

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31559	The Proteobacterial Methanotroph <i>Methylosinus trichosporium</i> OB3b Remodels Membrane Lipids in Response to Phosphate Limitation. <i>MBio</i> , 2022, 13, e0024722.	1.8	2
31560	Identification of epitranscriptomic methylation marker genes in <i>Arabidopsis</i> and their expression profiling in response to developmental, anatomical, and environmental modulations. <i>Current Plant Biology</i> , 2022, , 100247.	2.3	3
31561	Databases, Knowledgebases, and Software Tools for Virus Informatics. <i>Advances in Experimental Medicine and Biology</i> , 2022, 1368, 1-19.	0.8	0
31562	Thermoadaptation in an Ancestral Diterpene Cyclase by Altered Loop Stability. <i>Journal of Physical Chemistry B</i> , 2022, 126, 3809-3821.	1.2	5
31563	Origins of glycan selectivity in streptococcal Siglec-like adhesins suggest mechanisms of receptor adaptation. <i>Nature Communications</i> , 2022, 13, 2753.	5.8	4
31564	Hmx gene conservation identifies the origin of vertebrate cranial ganglia. <i>Nature</i> , 2022, 605, 701-705.	13.7	15
31565	Conformational spread drives the evolution of the calcium-calmodulin protein kinase II. <i>Scientific Reports</i> , 2022, 12, 8499.	1.6	1
31566	ENPP1's regulation of extracellular cGAMP is a ubiquitous mechanism of attenuating STING signaling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2119189119.	3.3	30
31567	kmer2vec: A Novel Method for Comparing DNA Sequences by word2vec Embedding. <i>Journal of Computational Biology</i> , 2022, 29, 1001-1021.	0.8	8
31568	Chromosome-level assembly, annotation and phylome of <i>Pelobates cultripes</i> , the western spadefoot toad. <i>DNA Research</i> , 2022, 29, .	1.5	1
31569	The assembled and annotated genome of the masked palm civet ( <i>Paguma larvata</i> ). <i>GigaScience</i> , 2022, 11, .	3.3	2
31570	<i>Methanococcoides orientis</i> sp. nov., a methylotrophic methanogen isolated from sediment of the East China Sea. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	9
31571	The chromosome-level genome assembly of the Japanese yellowtail jack <i>Seriola aureovittata</i> provides insights into genome evolution and efficient oxygen transport. <i>Molecular Ecology Resources</i> , 2022, 22, 2701-2712.	2.2	5
31572	Nanopore sequencing of full <i>scp</i> rRNA operon improves resolution in mycobiome analysis and reveals high diversity in both human gut and environments. <i>Molecular Ecology</i> , 2023, 32, 6330-6344.	2.0	10
31573	Epistatic drift causes gradual decay of predictability in protein evolution. <i>Science</i> , 2022, 376, 823-830.	6.0	38
31574	Complete Genome Sequence of Tea Plant Necrotic Ring Blotch Virus Detected from a Tea Plant in Japan. <i>Microbiology Resource Announcements</i> , 2022, 11, e0032322.	0.3	4
31575	Genome-wide identification of sugar transporter gene family in Brassicaceae crops and an expression analysis in the radish. <i>BMC Plant Biology</i> , 2022, 22, 245.	1.6	1

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31577	Molecular and genomic investigation of an urban outbreak of dengue virus serotype 2 in Angola, 2017–2019. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010255.	1.3	9
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31579	Detection and Identification of Novel Intracellular Bacteria Hosted in Strains CBS 648.67 and CFCC 80795 of Biocontrol Fungi & Metarhizium. <i>Microbes and Environments</i> , 2022, 37, n/a.	0.7	0
31583	The involvement of CYP1A2 in biodegradation of dioxins in pigs. <i>PLoS ONE</i> , 2022, 17, e0267162.	1.1	2
31584	The Impact of Chromate on <i>Pseudomonas aeruginosa</i> Molybdenum Homeostasis. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	4
31587	Multicopper oxidase enzymes from <i>Chrysosporthe cubensis</i> improve the saccharification yield of sugarcane bagasse. <i>Process Biochemistry</i> , 2022, 119, 68-81.	1.8	2
31589	<i>Natrinema halophilum</i> sp. nov., <i>Natrinema salinisoli</i> sp. nov., <i>Natrinema amylolyticum</i> sp. nov. and <i>Haloterrigena alkaliphila</i> sp. nov., four extremely halophilic archaea isolated from salt mine, saline soil and salt lake. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	21
31590	Genome Assembly and Population Resequencing Reveal the Geographical Divergence of Shanmei ( <i>Rubus</i> ) Tj ETQq0,0,0 rgBT /Overlock 1	3.0	3
31591	<i>Synbranchus</i> of the Middle to Lower Xingu Basin, Brazil, with the description of a new rheophilic species, <i>S. royal</i> ( <i>Synbranchiformes: Synbranchidae</i> ). <i>Proceedings of the Academy of Natural Sciences of Philadelphia</i> , 2022, 166, .	1.3	2
31592	Crystal structure of thermally stable homodimeric cytochrome <i>c</i> from <i>Thermus thermophilus</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2022, 78, 217-225.	0.4	4
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31596	Localization of a TORC1-eIF4F translation complex during CD8+ T cell activation drives divergent cell fate. <i>Molecular Cell</i> , 2022, 82, 2401-2414.e9.	4.5	14
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31600	Ancient proteins resolve controversy over the identity of <i>Genyornis</i> eggshell. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	14
31602	HIV Transmembrane Glycoprotein Conserved Domains and Genetic Markers Across HIV-1 and HIV-2 Variants. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	2



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31604	<i>Fordiophyton tereticaule</i> (Melastomataceae), a new species from China. <i>PhytoKeys</i> , 0, 197, 59-69.	0.4	0
31606	Is <i>Hyperdermium</i> Congeneric with <i>Ascopolyporus</i> ? Phylogenetic Relationships of <i>Ascopolyporus</i> spp. (Cordycipitaceae, Hypocreales) and a New Genus <i>Neohyperdermium</i> on Scale Insects in Thailand. <i>Journal of Fungi</i> (Basel, Switzerland), 2022, 8, 516.	1.5	3
31607	Monocot diet sources drive diversity of gut bacterial communities in <i>Spodoptera frugiperda</i> (Lepidoptera: Noctuidae) larvae. <i>Journal of Applied Entomology</i> , 2022, 146, 942-956.	0.8	6
31608	Contrasting Patterns of Genetic Diversity and Divergence Between Landlocked and Migratory Populations of Fish <i>Galaxias maculatus</i> , Evaluated Through Mitochondrial DNA Sequencing and Nuclear DNA Microsatellites. <i>Frontiers in Genetics</i> , 2022, 13, .	1.1	4
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31611	The first draft genome assembly and data analysis of the Malaysian mahseer ( <i>Tor tambroides</i> ). <i>Aquaculture and Fisheries</i> , 2022, , .	1.2	2
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31617	Characterization of Glucokinases from Pathogenic Free-Living Amoebae. <i>Antimicrobial Agents and Chemotherapy</i> , 2022, 66, .	1.4	2
31618	Invasion History of the Pinewood Nematode <i>Bursaphelenchus xylophilus</i> Influences the Abundance of <i>Serratia</i> sp. in Pupal Chambers and Tracheae of Insect-Vector <i>Monochamus alternatus</i> . <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	9
31620	Comparison of the performance of raw and <i>Lactobacillus paracasei</i> fermented soybean meal in diets for turbot ( <i>Scophthalmus maximus</i> L.): Growth, intestinal morphology, apoptosis, tight junction, and microbiota. <i>Aquaculture Reports</i> , 2022, 24, 101184.	0.7	2
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31622	Bulk Sequencing from mRNA with UMI for Evaluation of B-Cell Isotype and Clonal Evolution: A Method by the AIRR Community. <i>Methods in Molecular Biology</i> , 2022, , 345-377.	0.4	1
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31625	Plant pathogens provide clues to the potential origin of bat white-nose syndrome <i>Pseudogymnoascus destructans</i> . <i>Virulence</i> , 2022, 13, 1020-1031.	1.8	6

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31627	Selection and Development of Nontoxic Nonproteolytic <i>Clostridium botulinum</i> Surrogate Strains for Food Challenge Testing. <i>Foods</i> , 2022, 11, 1577.	1.9	6
31628	SeBPPI: A Sequence-Based Proteinâ€œProtein Binding Predictor. <i>Journal of Computational Biophysics and Chemistry</i> , 2022, 21, 729-737.	1.0	2
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31632	Transcriptome analysis of <i>Mythimna separata</i> : De novo assembly and detection of genes related to betaâ€œcypermethrin resistance. <i>Archives of Insect Biochemistry and Physiology</i> , 2022, 111, .	0.6	1
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31637	Complete Genome Sequence of Clover Yellow Mosaic Virus Isolated from White Clover in Japan. <i>Microbiology Resource Announcements</i> , 0, , .	0.3	0
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31639	Characterization of <i>Pseudomonas viridiflava</i> isolates associated with a new leaf spot disease in <i>Cichorium</i> species. , 2022, 104, 1061-1070.		2
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31642	Declining Population Sizes and Loss of Genetic Diversity in Commercial Fishes: A Simple Method for a First Diagnostic. <i>Frontiers in Marine Science</i> , 2022, 9, .	1.2	7
31644	Confirmation of <i>Tylototriton ziegleri</i> Nishikawa, Matsui &amp; Nguyen, 2013 in China, with discussion on the relationship between <i>T. verrucosus</i> Anderson, 1871 and <i>T. panwaensis</i> Grismer, Wood, Quah, Thura, Espinoza &amp; Murdoch, 2019 (Caudata, Salamandridae). <i>Biodiversity Data Journal</i> , 0, 10, .	0.4	0
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31651	Evolution of a <i>cis</i> -Acting SNP That Controls Type VI Secretion in <i>Vibrio cholerae</i> . <i>MBio</i> , 2022, 13, .	1.8	3
31653	New Insights into the Taxonomy of Bacteria in the Genomic Era and a Case Study with Rhizobia. <i>International Journal of Microbiology</i> , 2022, 2022, 1-19.	0.9	12
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31660	Isolation and characterization of <i>Bradyrhizobium elkanii</i> as a root nodule symbiont of red sword bean <i>Canavalia gladiata</i> var. <i>gladiata</i> . <i>Soil Science and Plant Nutrition</i> , 0, , 1-8.	0.8	0
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31668	Effects of amino acid composition of yeast extract on the microbiota and aroma quality of fermented soy sauce. <i>Food Chemistry</i> , 2022, 393, 133289.	4.2	23
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31685	P Starvation in Roses Leads to Strongly Genotype-Dependent Induction of P-Transporter Genes during Black Spot Leaf Disease. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 549.	1.5	0
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31689	De Novo Assembly of <i>Plasmodium knowlesi</i> Genomes From Clinical Samples Explains the Counterintuitive Intrachromosomal Organization of Variant SICAv and kir Multiple Gene Family Members. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	3
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31703	A glimpse into the past: phylogenesis and protein domain analysis of the group XIV of C-type lectins in vertebrates. <i>BMC Genomics</i> , 2022, 23, .	1.2	1
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31710	The chromosome-level genome for <i>Toxicodendron vernicifluum</i> provides crucial insights into Anacardiaceae evolution and urushiol biosynthesis. <i>IScience</i> , 2022, 25, 104512.	1.9	6
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31713	Metabarcoding analysis of different portions of the digestive tract of scorpions (Scorpiones,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 187	3.1	2
31714	Genome Wide Identification and Expression Profiling Indicate Expansion of Family 184 Protease Inhibitor via Gene Tandem Duplication and Divergence in Razor Clam <i>Sinonovacula constricta</i> . <i>Frontiers in Immunology</i> , 0, 13, .	2.2	0
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31749	The Genetic Adaptations of Toxoptera Aurantia Facilitated its Rapid Multiple Plant Hosts Dispersal and Invasion. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
31750	Overlooked for over a century: <i>Ophioderma occultum</i> sp. nov. (Echinodermata), a new species of brittle star from the Eastern Pacific. <i>Journal of Natural History</i> , 2022, 56, 365-384.	0.2	2
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#	ARTICLE	IF	CITATIONS
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31756	Rediscovery and phylogenetic analysis of the Shelta Cave Crayfish ( <i>Orconectes sheltae</i> Cooper) Tj ETQq1 1 0.784314 rgBT /Overlook Alabama, USA. <i>Subterranean Biology</i> , 0, 43, 11-31.	5.0	1
31757	Methodology-Centered Review of Molecular Modeling, Simulation, and Prediction of SARS-CoV-2. <i>Chemical Reviews</i> , 2022, 122, 11287-11368.	23.0	38
31759	Metagenomic Screening for Lipolytic Genes Reveals an Ecology-Clustered Distribution Pattern. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
31760	Clarifying the taxonomy of some cryptic blennies (Blenniidae) in their native and introduced range. <i>Scientific Reports</i> , 2022, 12, .	1.6	6
31763	Comparative Analysis and Ancestral Sequence Reconstruction of Bacterial Sortase Family Proteins Generates Functional Ancestral Mutants with Different Sequence Specificities. , 2022, 1, 121-135.		4
31764	A nucleotide signature for the identification of <i>Pinelliae</i> Rhizoma ( <i>Banxia</i> ) and its products. <i>Molecular Biology Reports</i> , 2022, 49, 7753-7763.	1.0	4
31765	Anatomy and Symbiosis of the Digestive System of the Vent Shrimp <i>Rimicaris Exoculata</i> and <i>Rimicaris Chacei</i> Revealed Through Imaging Approaches. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	2
31766	On the role of metaheuristic optimization in bioinformatics. <i>International Transactions in Operational Research</i> , 2023, 30, 2909-2944.	1.8	6
31767	Drought-induced forest dieback increases taxonomic, functional, and phylogenetic diversity of saproxylic beetles at both local and landscape scales. <i>Landscape Ecology</i> , 2022, 37, 2025-2043.	1.9	12
31768	A functionally conserved STORR gene fusion in <i>Papaver</i> species that diverged 16.8 million years ago. <i>Nature Communications</i> , 2022, 13, .	5.8	7
31769	Four new members of the family Cytophagaceae: <i>Chryseosolibacter histidini</i> gen. nov., sp. nov., <i>Chryseosolibacter indicus</i> gen. nov., sp. nov., <i>Dawidia cretensis</i> , gen. nov., sp. nov., and <i>Dawidia soli</i> , gen. nov., sp. nov. isolated from diverse habitat. <i>Antonie Van Leeuwenhoek</i> , 2022, 115, 1059-1072.	0.7	1
31770	Optimizing Molecular Detection for the Hop Downy Mildew Pathogen <i>Pseudoperonospora humuli</i> in Plant Tissue. <i>Phytopathology</i> , 2022, 112, 2426-2439.	1.1	1
31771	Evaluating Starter Feeding on Ruminant Function in Yak Calves: Combined 16S rRNA Sequencing and Metabolomics. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	5
31772	A Reduced F <sub>420</sub> -Dependent Nitrite Reductase in an Anaerobic Methanotrophic Archaeon. <i>Journal of Bacteriology</i> , 2022, 204, .	1.0	3
31773	Expansion of a retrovirus lineage in the koala genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	3
31774	<i>Photobacterium arenosum</i> WH24, Isolated from the Gill of Pacific Oyster <i>Crassostrea gigas</i> from the North Sea of Germany: Co-cultivation and Prediction of Virulence. <i>Current Microbiology</i> , 2022, 79, .	1.0	2
31775	Population structure, phylogeography and demographic history of <i>Tenulosa ilisha</i> populations in the Indian Ocean region inferred from mitochondrial DNA sequence variation. <i>Regional Studies in Marine Science</i> , 2022, , 102478.	0.4	1

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31778	Trematodes of Genera <i>Gyrabascus</i> and <i>Parabascus</i> from Bats in European Russia: Morphology and Molecular Phylogeny. <i>Biology</i> , 2022, 11, 878.	1.3	3
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31780	Vision-related convergent gene losses reveal SERPINE3's unknown role in the eye. <i>ELife</i> , 0, 11, .	2.8	9
31781	A New Record of the Introduced Species <i>Triatoma infestans</i> (Hemiptera: Reduviidae) in Mexico. <i>Journal of Medical Entomology</i> , 2022, 59, 2150-2157.	0.9	6
31782	Characterization of inositol lipid metabolism in gut-associated Bacteroidetes. <i>Nature Microbiology</i> , 2022, 7, 986-1000.	5.9	19
31783	Structure of human NADK2 reveals atypical assembly and regulation of NAD kinases from animal mitochondria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	3
31784	Transcriptome-Guided Identification of Pectin Methyl-Esterase-Related Enzymes and Novel Molecular Processes Effectuating the Hard-to-Cook Defect in Common Bean ( <i>Phaseolus vulgaris</i> L.). <i>Foods</i> , 2022, 11, 1692.	1.9	3
31785	<i>Neokomagataea anthophila</i> sp. nov., an osmotolerant acetic acid bacterium isolated in Thailand and emended description of the genus <i>Neokomagataea</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	5
31786	Phylogenetic analysis of current <i>Porcine circovirus 4</i> sequences: does the porcine circoviruses evolutionary history repeat itself?. <i>Transboundary and Emerging Diseases</i> , 0, , .	1.3	3
31787	Is Coloburiscidae (Ephemeroptera) Monophyletic? A Comparison of Datasets. <i>Diversity</i> , 2022, 14, 505.	0.7	1
31788	<i>Blastococcus tunisiensis</i> sp. nov., isolated from limestone collected in Tunisia. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	5
31789	Batch alignment via retention orders for preprocessing large-scale multi-batch LC-MS experiments. <i>Bioinformatics</i> , 2022, 38, 3759-3767.	1.8	1
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31791	Population genetic structure and phenotypic diversity of <i>Aspidodera railletii</i> (Nematoda: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 187 Td ( Parasites and Vectors, 2022, 15, .	1.0	2
31792	Change of Gut Microbiota in PRRSV-Resistant Pigs and PRRSV-Susceptible Pigs from Tongcheng Pigs and Large White Pigs Crossed Population upon PRRSV Infection. <i>Animals</i> , 2022, 12, 1504.	1.0	6
31793	A new giant keelback slug of the genus <i>Limax</i> from the Balkans, described by citizen scientists. <i>Biodiversity Data Journal</i> , 0, 10, .	0.4	1
31794	Ancestrally Reconstructed von Willebrand Factor Reveals Evidence for Trench Warfare Coevolution between Opossums and Pit Vipers. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	4



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31796	NOMAD: metagenomic characterisation of the viral pathogen composition in outbreaks of non-malaria acute febrile illness cases. , 0, 5, 24.		0
31797	Comparisons of cell proliferation and cell death from tornaria larva to juvenile worm in the hemichordate <i>Schizocardium californicum</i> . <i>EvoDevo</i> , 2022, 13, .	1.3	6
31798	Transcriptional Basis for Haustorium Formation and Host Establishment in Hemiparasitic <i>Psittacanthus schiedeanus</i> Mistletoes. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	4
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31802	Evolutionary action of mutations reveals antimicrobial resistance genes in <i>Escherichia coli</i> . <i>Nature Communications</i> , 2022, 13, .	5.8	11
31803	Enzymatic browning and genome-wide polyphenol oxidase gene identification in three contrasting avocado accessions. <i>Plant Biotechnology Reports</i> , 0, , .	0.9	0
31804	Thousands of small, novel genes predicted in global phage genomes. <i>Cell Reports</i> , 2022, 39, 110984.	2.9	21
31805	Global and seasonal variation of marine phosphonate metabolism. <i>ISME Journal</i> , 2022, 16, 2198-2212.	4.4	22
31806	Isolation and Whole-Genome Sequencing of Four Antibiotic-Producing <i>Pseudomonas</i> Strains. <i>Microbiology Resource Announcements</i> , 0, , .	0.3	0
31807	Detection of Multiple Lineages of PRRSV in Breeding and Growing Swine Farms. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	10
31808	Metagenomic profiles of the early life microbiome of Indonesian inpatient neonates and their influence on clinical characteristics. <i>Scientific Reports</i> , 2022, 12, .	1.6	3
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31810	DeepHageTP: a convolutional neural network framework for identifying phage-specific proteins from metagenomic sequencing data. <i>PeerJ</i> , 0, 10, e13404.	0.9	3
31811	Structural insights into the lysophospholipid brain uptake mechanism and its inhibition by syncytin-2. <i>Nature Structural and Molecular Biology</i> , 2022, 29, 604-612.	3.6	20
31812	A gene deriving from the ancestral sex chromosomes was lost from the X and retained on the Y chromosome in eutherian mammals. <i>BMC Biology</i> , 2022, 20, .	1.7	2

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31814	Multigene phylogeny and haplotype analysis reveals predominance of oomycetous fungus, <i>Phytophthora meadii</i> (McRae) associated with fruit rot disease of arecanut in India. Saudi Journal of Biological Sciences, 2022, 29, 103341.	1.8	4
31815	An efficient numerical representation of genome sequence: natural vector with covariance component. PeerJ, 0, 10, e13544.	0.9	1
31816	Z-RNA and the Flipside of the SARS Nsp13 Helicase: Is There a Role for Flipons in Coronavirus-Induced Pathology?. Frontiers in Immunology, 0, 13, .	2.2	6
31817	Deciphering the Multi-Chromosomal Mitochondrial Genome of <i>Populus simonii</i> . Frontiers in Plant Science, 0, 13, .	1.7	23
31818	<i>Halomonas jincaotanensis</i> sp. nov., isolated from the Pamir Plateau degrading polycyclic aromatic hydrocarbon. Archives of Microbiology, 2022, 204, .	1.0	4
31819	To kill or to be killed: pangenome analysis of <i>Escherichia coli</i> strains reveals a tailocin specific for pandemic ST131. BMC Biology, 2022, 20, .	1.7	10
31820	Haplotype-resolved powdery mildew resistance loci reveal the impact of heterozygous structural variation on NLR genes in <i>Muscadinia rotundifolia</i> . G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	7
31821	Phylogenetic study of the New Caledonian endemic genus <i>Adenodaphne</i> (Lauraceae) confirms its synonymy with <i>Litsea</i> . Botany Letters, 2023, 170, 479-487.	0.7	1
31822	Gene Conversion Explains Elevated Diversity in the Immunity Modulating APL1 Gene of the Malaria Vector <i>Anopheles funestus</i> . Genes, 2022, 13, 1102.	1.0	2
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31826	Microbial community roles and chemical mechanisms in the parasitic development of <i>Orobancha cumana</i> . , 0, , .		3
31827	CView: A network based tool for enhanced alignment visualization. PLoS ONE, 2022, 17, e0259726.	1.1	1
31828	Correlations Between the Metabolome and the Endophytic Fungal Metagenome Suggests Importance of Various Metabolite Classes in Community Assembly in Horseradish ( <i>Armoracia rusticana</i> ), Tj ETQq1 1 0.784314 ngBT /Overclock 10 Tf		
31829	Interference of bio-control <i>Trichoderma</i> to enhance physical and physiological strength of sugarcane during Pokkah boeng infection. World Journal of Microbiology and Biotechnology, 2022, 38, .	1.7	1
31830	Characterization of <i>Kordiimonas marina</i> sp. nov. and <i>Kordiimonas laminariae</i> sp. nov. and Comparative Genomic Analysis of the Genus <i>Kordiimonas</i> , A Marine-Adapted Taxon. Frontiers in Marine Science, 0, 9, .	1.2	11
31832	<i>N</i> -Acetylglucosamine Promotes Tomato Plant Growth by Shaping the Community Structure and Metabolism of the Rhizosphere Microbiome. Microbiology Spectrum, 2022, 10, .	1.2	6
31833	<i>Enenterum kyphosi</i> Yamaguti, 1970 and <i>Enenterum petrae</i> n. sp. (Digenea: Enenteridae) from kyphosid fishes (Centrarchiformes: Kyphosidae) collected in marine waters off eastern Australia. Zootaxa, 2022, 5154, 271-288.	0.2	3

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31836	Substrates and Loaded Iron Ions Relative Position Influence the Catalytic Characteristics of the Metalloenzymes <i>Angelica archangelica</i> Flavone Synthase I and <i>Camellia sinensis</i> Flavonol Synthase. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	2
31837	Investigation of active site amino acid influence on carbon and chlorine isotope fractionation during reductive dechlorination. <i>FEMS Microbiology Ecology</i> , 2022, 98, .	1.3	6
31838	Complete Genome Sequencing of Tick-Borne Encephalitis Virus Directly from Clinical Samples: Comparison of Shotgun Metagenomic and Targeted Amplicon-Based Sequencing. <i>Viruses</i> , 2022, 14, 1267.	1.5	5
31839	Fourteen new Polynucleobacter species: <i>P. brandtiae</i> sp. nov., <i>P. kasalickyi</i> sp. nov., <i>P. antarcticus</i> sp. nov., <i>P. arcticus</i> sp. nov., <i>P. tropicus</i> sp. nov., <i>P. bastaniensis</i> sp. nov., <i>P. corsicus</i> sp. nov., <i>P. finlandensis</i> sp. nov., <i>P. ibericus</i> sp. nov., <i>P. hallstattensis</i> sp. nov., <i>P. alcilacus</i> sp. nov., <i>P. nymphae</i> sp. nov., <i>P. paludilacus</i> sp. nov. and <i>P. parvulilacunae</i> sp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	47
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31841	Computer-Aided Analysis of West Sub-Saharan Africa Snakes Venom towards the Design of Epitope-Based Poly-Specific Antivenoms. <i>Toxins</i> , 2022, 14, 418.	1.5	4
31843	Evolution of Multiple Domains of the HIV-1 Envelope Glycoprotein during Coreceptor Switch with CCR5 Antagonist Therapy. <i>Microbiology Spectrum</i> , 0, , .	1.2	1
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31846	In-depth comparative analysis of <i>Tritrichomonas foetus</i> transcriptomics reveals novel genes linked with adaptation to feline host. <i>Scientific Reports</i> , 2022, 12, .	1.6	3
31847	Characterization of the complete chloroplast genome of <i>Cycas ferruginea</i> , a vulnerable species. <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 1048-1049.	0.2	2
31848	Re-terrestrialization in the phylogeny of epiphytic plant lineages: Microsoroid ferns as a case study. <i>Journal of Systematics and Evolution</i> , 2023, 61, 613-626.	1.6	6
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31852	The CRISPR/Cas Machinery Evolution and Gene Flow in the Hot Spring Cyanobacterium <i>Thermotichus</i> . <i>Diversity</i> , 2022, 14, 502.	0.7	2
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31855	Differentiated Evolutionary Strategies of Genetic Diversification in Atlantic and Pacific Thaumarchaeal Populations. <i>MSystems</i> , 2022, 7, .	1.7	3
31857	Mitochondrial Phylogenomics of <i>Cuscuta</i> (Convolvulaceae) Reveals a Potentially Functional Horizontal Gene Transfer from the Host. <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	9
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31861	<i>Thylacopteris minuta</i> (Polypodiaceae), a new fern species from Myanmar. <i>PhytoKeys</i> , 0, 199, 141-153.	0.4	0
31863	A molecular-genetics perspective on the systematics of the parthenogenetic flowerpot blindsnake <i>Indotyphlops braminus</i> (Daudin, 1803) (Squamata: Serpentes: Typhlopidae). <i>Systematics and Biodiversity</i> , 2022, 20, 1-16.	0.5	1
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31867	Detection of non-reference porcine endogenous retrovirus loci in the Vietnamese native pig genome. <i>Scientific Reports</i> , 2022, 12, .	1.6	2
31869	Draft Genome Sequences of <i>Erysipelothrix</i> sp. Strains Isolated from Stranded Septic Bottlenose Dolphins in Alabama, USA. <i>Microbiology Resource Announcements</i> , 2022, 11, .	0.3	2
31870	Transcription Start Site Heterogeneity and Preferential Packaging of Specific Full-Length RNA Species Are Conserved Features of Primate Lentiviruses. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	8
31871	Filogeografía de <i>Tigridia durangensis</i> (Tigridieae: Iridaceae), una especie endémica de la Zona de Transición Mexicana. <i>Botanical Sciences</i> , 2022, 100, 1040-1057.	0.3	1
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31874	Characterization of <i>Stenotrophomonas maltophilia</i> phage AXL1 as a member of the genus Pamexvirus encoding resistance to trimethoprim-sulfamethoxazole. <i>Scientific Reports</i> , 2022, 12, .	1.6	5
31875	Expression of a novel mycobacterial phosphodiesterase successfully lowers cAMP levels resulting in reduced tolerance to cell wall-targeting antimicrobials. <i>Journal of Biological Chemistry</i> , 2022, 298, 102151.	1.6	12
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31878	Molecular characterization of a flatworm <i>Girardia</i> isolate from Guanajuato, Mexico. <i>Developmental Biology</i> , 2022, 489, 165-177.	0.9	1
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31882	Draft genome sequence and functional analysis of <i>Lysinibacillus xylanilyticus</i> t26, a plant growth-promoting bacterium isolated from <i>Capsicum chinense</i> rhizosphere. <i>Journal of Biosciences</i> , 2022, 47, .	0.5	2
31883	Phylogenomic and functional characterization of an evolutionary conserved cytochrome P450-based insecticide detoxification mechanism in bees. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	31
31884	New Complex of Cryptic Species Discovered in Genus <i>Biblis</i> (Papilionoidea: Nymphalidae: Biblidinae) in Mexico. <i>Neotropical Entomology</i> , 2022, 51, 557-569.	0.5	1
31885	Contextual Constraints: Dynamic Evolution of Snake Venom Phospholipase A2. <i>Toxins</i> , 2022, 14, 420.	1.5	7
31886	DNA-assisted inventory and community structure of benthic marine algae in Taiping Island (or Itu Aba) Tj ETQq1 1 0,784314 rgBT /Over 0,4 6		
31887	Mapping immunogenic epitopes of an adhesin-like protein from <i>Methanobrevibacter ruminantium</i> M1 and comparison of empirical data with in silico prediction methods. <i>Scientific Reports</i> , 2022, 12, .	1.6	5
31888	Ancestral reconstruction of duplicated signaling proteins reveals the evolution of signaling specificity. <i>ELife</i> , 0, 11, .	2.8	13
31889	The complete mitochondrial genome of <i>Acanthopagrus pacificus</i> (Perciformes, Sparidae) from Iriomotejima Island, Okinawa, Japan. <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 1027-1029.	0.2	1
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31892	Bacterial Associates of a Desert Specialist Fungus-Growing Ant Antagonize Competitors with a Nocamycin Analog. <i>ACS Chemical Biology</i> , 2022, 17, 1824-1830.	1.6	6
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31894	<i>Corallococcus soli</i> sp. Nov., a Soil Myxobacterium Isolated from Subtropical Climate, Chalus County, Iran, and Its Potential to Produce Secondary Metabolites. <i>Microorganisms</i> , 2022, 10, 1262.	1.6	7

#	ARTICLE	IF	CITATIONS
31895	Transcriptional response of <i>Meloidogyne incognita</i> to non-fumigant nematicides. <i>Scientific Reports</i> , 2022, 12, .	1.6	5
31896	Combining Traditional and Molecular Techniques Supports the Discovery of a Novel <i>Legionella</i> Species During Environmental Surveillance in a Healthcare Facility. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
31897	Highly Specialized Carbohydrate Metabolism Capability in <i>Bifidobacterium</i> Strains Associated with Intestinal Barrier Maturation in Early Preterm Infants. <i>MBio</i> , 2022, 13, .	1.8	10
31898	Chromosome-level genome assemblies of four wild peach species provide insights into genome evolution and genetic basis of stress resistance. <i>BMC Biology</i> , 2022, 20, .	1.7	13
31899	Identification of <i>nosZ</i> -expressing microorganisms consuming trace N <sub>2</sub> O in microaerobic chemostat consortia dominated by an uncultured <i>Burkholderiales</i> . <i>ISME Journal</i> , 2022, 16, 2087-2098.	4.4	12
31900	Mining therapeutic targets from the antibiotic-resistant <i>Campylobacter coli</i> and virtual screening of natural product inhibitors against its riboflavin synthase. <i>Molecular Diversity</i> , 2023, 27, 793-810.	2.1	7
31901	Antidepressant Shugan Jieyu Capsule Alters Gut Microbiota and Intestinal Microbiome Function in Rats With Chronic Unpredictable Mild Stress -Induced Depression. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	9
31902	Revision of the taxonomic position of <i>Pseudocypretta</i> Klie, 1932 (Ostracoda: Cyprididae), with a redescription of <i>P. maculata</i> Klie, 1932. <i>Journal of Crustacean Biology</i> , 2022, 42, .	0.3	3
31903	<i>Sisubiotus hakaiensis</i> sp. nov. (Tardigrada, Macrobiotidae), a new tardigrade species from Calvert Island (British Columbia, Canada). <i>European Journal of Taxonomy</i> , 0, 823, .	0.6	1
31904	The chromosome-scale assembly of endive ( <i>Cichorium endivia</i> ) genome provides insights into the sesquiterpenoid biosynthesis. <i>Genomics</i> , 2022, 114, 110400.	1.3	6
31905	The taxonomic position of brooding limpets of the genera <i>Erginus</i> and <i>Rhodopetala</i> (Patellogastropoda). <i>Zoologischer Anzeiger</i> , 2022, 299, 200-206.	0.4	1
31906	Loci underlying leaf agronomic traits identified by re-sequencing celery accessions based on an assembled genome. <i>IScience</i> , 2022, 25, 104565.	1.9	6
31907	Genome-Wide Analysis of von Willebrand Factor A Gene Family in Rice for Its Role in Imparting Biotic Stress Resistance with Emphasis on Rice Blast Disease. <i>Rice Science</i> , 2022, 29, 375-384.	1.7	3
31908	Probing the structure and function of polymerase $\hat{\iota}$ , helicase-like domain. <i>DNA Repair</i> , 2022, 116, 103358.	1.3	2
31909	Population structure and reproduction of the alvinocaridid shrimp <i>Rimicaris exoculata</i> on the Mid-Atlantic Ridge: Variations between habitats and vent fields. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2022, 186, 103827.	0.6	3
31910	Phylogenetic analysis of human parainfluenza type 3 virus strains responsible for the outbreak during the COVID-19 pandemic in Seoul, South Korea. <i>Journal of Clinical Virology</i> , 2022, 153, 105213.	1.6	5
31911	An acceleration of carotenoid production and growth of <i>Haematococcus lacustris</i> induced by host-microbiota network interaction. <i>Microbiological Research</i> , 2022, 262, 127097.	2.5	4
31912	Discovery of deoxyribonuclease II-like proteins in bacteria. <i>Molecular Phylogenetics and Evolution</i> , 2022, 174, 107554.	1.2	0

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31914	Diversity of begomoviruses infecting crops and weeds in the Caribbean and Latin America. , 2022, , 139-158.		0
31915	The Manchurian Walnut Genome: Insights into Juglone and Lipid Biosynthesis. <i>GigaScience</i> , 2022, 11, .	3.3	13
31916	Update and elucidation of Plasmodium kinomes: Prioritization of kinases as potential drug targets for malaria. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 3708-3717.	1.9	0
31917	Evolutionary Characteristics of Mobile DNA Elements in the Chromosome of <i>Klebsiella Pneumoniae</i> Harboring Multidrug Resistance and Virulence Factors. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
31918	A Retrospective Analysis of Wastewater Confirms Dominant Circulation of SARS-CoV-2 Delta Variant in Nairobi, Kenya, between April 2021 and August 2021. <i>American Journal of Molecular Biology</i> , 2022, 12, 109-121.	0.1	0
31919	Lignin-Oxidizing Vibrios Involved in the Mineralization of Plant Detritus in the Continental Slope. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
31920	Mitochondrial diversity and population structure of grass carp ( <i>Ctenopharyngodon idella</i> ) in the Pearl River after anthropogenic release. <i>Knowledge and Management of Aquatic Ecosystems</i> , 2022, , 14.	0.5	1
31921	A remarkable new species of the genus <i>Hydaticus</i> from Madagascar, with an identification key for Malagasy species of the genus (Coleoptera: Dytiscidae: Dytiscinae). <i>Annales De La Societe Entomologique De France</i> , 2022, 58, 197-214.	0.4	0
31922	A new species of <i>Calamaria</i> (Squamata: Colubridae) from Guangdong Province, southern China. <i>Vertebrate Zoology</i> , 0, 72, 433-444.	2.0	0
31923	Ongoing Positive Selection Drives the Evolution of SARS-CoV-2 Genomes. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 1214-1223.	3.0	9
31924	<i>Neoroseomonas marina</i> sp. nov., Isolated from a Beach Sand. <i>Current Microbiology</i> , 2022, 79, .	1.0	1
31925	DIP2 is a unique regulator of diacylglycerol lipid homeostasis in eukaryotes. <i>ELife</i> , 0, 11, .	2.8	5
31926	Conserved secreted effectors contribute to endophytic growth and multihost plant compatibility in a vascular wilt fungus. <i>Plant Cell</i> , 2022, 34, 3214-3232.	3.1	20
31927	Predicting interactions of the frass-associated yeast <i>Hyphopichia heimii</i> with <i>Olea europaea</i> subsp. <i>cuspidata</i> and twig-boring bark beetles. <i>Folia Microbiologica</i> , 0, , .	1.1	1
31928	Genome-Guided Analysis of Seven Weed Species Reveals Conserved Sequence and Structural Features of Key Gene Targets for Herbicide Development. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
31929	Morphological and molecular evidence of the hybrid origin of <i>Crepidiastrum muratagenii</i> in Korea. <i>Korean Journal of Plant Taxonomy</i> , 2022, 52, 85-96.	0.3	0
31930	Morphological and Phylogenetic Evidences Reveal Four New Species of <i>Cantharellus</i> Subgenus <i>Cantharellus</i> (Hydnaceae, Cantharellales) From China. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	7

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31932	Genome sequences of 38 <i>Fusarium oxysporum</i> strains. <i>BMC Research Notes</i> , 2022, 15, .	0.6	1
31933	Phylogeography of the economic seaweeds <i>Chondrus</i> (Gigartinales). <i>Journal of Applied Phycology</i> , 2022, 37, 135-147.	0.9	6
31934	Exploring the interaction of influenza A subtypes H1N1 and H3N2 based on an evolution-driven transmission model. <i>Nonlinear Dynamics</i> , 0, , .	2.7	0
31935	The structure of EXTL3 helps to explain the different roles of bi-domain exostosins in heparan sulfate synthesis. <i>Nature Communications</i> , 2022, 13, .	5.8	14
31937	In-depth characterization of denitrifier communities across different soil ecosystems in the tundra. <i>Environmental Microbiomes</i> , 2022, 17, .	2.2	25
31938	Phylogenetic Assessment of Two Antarctic Representatives of <i>Paralepidapedon</i> Shimazu & Shimura, 1984 (Trematoda: Lepidapedidae). <i>Russian Journal of Marine Biology</i> , 2022, 48, 202-212.	0.2	1
31939	<i>Umbilicaria phaea</i> var. <i>coccinea</i> : conservation status, variety rank, and secondary chemistry. <i>Bryologist</i> , 2022, 125, .	0.1	0
31940	<i>Rhizocarpon ozsoyae</i> sp. nova (Rhizocarpaceae, lichenized Ascomycetes) from James Ross Island (Antarctic Peninsula). <i>Herzogia</i> , 2022, 35, .	0.1	1
31941	Comparative genomics of <i>Acinetobacter baumannii</i> and therapeutic bacteriophages from a patient undergoing phage therapy. <i>Nature Communications</i> , 2022, 13, .	5.8	20
31942	Resurrection of <i>Neocardiochiles Szpligetj</i> , 1908 (Hymenoptera, Braconidae, Cardiochilinae) with descriptions of five new species from the Neotropical region. <i>Journal of Hymenoptera Research</i> , 0, 91, 41-68.	0.8	1
31944	The essential <i>Rhodobacter sphaeroides</i> CenKR two-component system regulates cell division and envelope biosynthesis. <i>PLoS Genetics</i> , 2022, 18, e1010270.	1.5	7
31945	A chromosome-level genome of <i>Brachymystax tsinlingensis</i> provides resources and insights into salmonids evolution. <i>G3: Genes, Genomes, Genetics</i> , 0, , .	0.8	0
31946	Proposal for transfer <i>Bacillus alkalicola</i> to the genus <i>Evansella</i> as <i>Evansella alkalicola</i> comb. nov. <i>Archives of Microbiology</i> , 2022, 204, .	1.0	0
31948	A critical evaluation of <i>Mycobacterium bovis</i> pangenomics, with reference to its utility in outbreak investigation. <i>Microbial Genomics</i> , 2022, 8, .	1.0	7
31949	Low Intra-host and Inter-host Genetic Diversity of Carnivore Protoparvovirus 1 in Domestic Cats during a Feline Panleukopenia Outbreak. <i>Viruses</i> , 2022, 14, 1412.	1.5	1
31950	A new bellflower, <i>Campanula dersimensis</i> (Campanulaceae), from E Anatolia, Turkey. <i>Willdenowia</i> , 2022, 52, .	0.5	2
31951	RNA Cleavage Properties of Nucleobase-Specific RNase MC1 and Cusativin Are Determined by the Dinucleotide-Binding Interactions in the Enzyme-Active Site. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7021.	1.8	1



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31954	Identification and Functional Characterisation of Two Oat UDP-Glucosyltransferases Involved in Deoxynivalenol Detoxification. <i>Toxins</i> , 2022, 14, 446.	1.5	5
31955	The genome of <i>Prunus humilis</i> provides new insights to drought adaption and population diversity. <i>DNA Research</i> , 2022, 29, .	1.5	4
31956	Highly distinct genetic programs for peripheral nervous system formation in chordates. <i>BMC Biology</i> , 2022, 20, .	1.7	3
31957	The Tracking of Moist Habitats Allowed Aiphanes (Arecaceae) to Cover the Elevation Gradient of the Northern Andes. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3
31958	The Galapagos giant tortoise <i>Chelonoidis phantasticus</i> is not extinct. <i>Communications Biology</i> , 2022, 5, .	2.0	3
31959	Genomes of six viruses that infect Asgard archaea from deep-sea sediments. <i>Nature Microbiology</i> , 2022, 7, 953-961.	5.9	17
31960	Molecular evolutionary trends and biosynthesis pathways in the Oribatida revealed by the genome of <i>Archeogozetes longisetosus</i> . <i>Acarologia</i> , 2022, 62, 532-573.	0.2	3
31961	The neuropeptide Y receptor gene repository, phylogeny and comparative expression in allotetraploid common carp. <i>Scientific Reports</i> , 2022, 12, .	1.6	0
31962	Craniodental Morphology and Phylogeny of Marsupials. <i>Bulletin of the American Museum of Natural History</i> , 2022, 457, .	1.2	35
31963	Genome sequence and pathogenicity of <i>Vibrio vulnificus</i> strain MCCC 1A08743 isolated from contaminated prawns. <i>Biology Open</i> , 2022, 11, .	0.6	2
31964	Addition to the known diversity of Chinese freshwater planarians: integrative description of a new species of <i>Dugesia</i> Girard, 1850 (Platyhelminthes, Tricladida, Dugesiidae). <i>Zoosystematics and Evolution</i> , 2022, 98, 233-243.	0.4	2
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31967	DNA Barcoding and Distribution of Gastropods and Malacostracans in the Lower Danube Region. <i>Diversity</i> , 2022, 14, 533.	0.7	1
31968	Multiple <i>Alr</i> genes exhibit allorecognition-associated variation in the colonial cnidarian <i>Hydractinia</i> . <i>Immunogenetics</i> , 2022, 74, 559-581.	1.2	2
31969	Comparison of CpG- and UpA-mediated restriction of RNA virus replication in mammalian and avian cells and investigation of potential ZAP-mediated shaping of host transcriptome compositions. <i>Rna</i> , 2022, 28, 1089-1109.	1.6	6
31970	Insights into the Antimicrobial Activities and Metabolomes of <i>Aquimarina</i> (Flavobacteriaceae). <i>Frontiers in Microbiology</i> , 2022, 13, 978882.	2.2	11
31971	The asexual morph and molecular phylogeny of endemic <i>Phyllactinia verruculosa</i> on <i>Indigofera tinctoria</i> . <i>Mycoscience</i> , 2022, , .	0.3	0

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31973	<i>Fusarium abutilonis</i> and <i>F. guadeloupense</i> , two novel species in the <i>Fusarium buharicum</i> clade supported by multilocus molecular phylogenetic analyses. <i>Mycologia</i> , 2022, 114, 682-696.	0.8	4
31974	Fungal Flora in Adult Females of the Rearing Population of Ambrosia Beetle <i>Euwallacea interjectus</i> (Blandford) (Coleoptera: Curculionidae: Scolytinae): Does It Differ from the Wild Population? <i>Diversity</i> , 2022, 14, 535.	0.7	3
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31976	Lichen speciation is sparked by a substrate requirement shift and reproduction mode differentiation. <i>Scientific Reports</i> , 2022, 12, .	1.6	1
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31978	<i>Lagena</i> —an overlooked oomycete genus with a wide range of hosts. <i>Mycological Progress</i> , 2022, 21, .	0.5	3
31979	Long-term survival of <i>Dehalococcoides mccartyi</i> strains in mixed cultures under electron acceptor and ammonium limitation. <i>FEMS Microbes</i> , 2022, 3, .	0.8	4
31980	Molecular Phylogeny of Selected Kenyan Eucalyptus Species Inferred from MatK, rbcL and TrnL-F Genes and Their Suitability for Power Transmission Poles. <i>Diversity</i> , 2022, 14, 563.	0.7	1
31982	<i>Myriophyllum rubricaulis</i> sp. nov., a M. aquaticum look-alike only known in cultivation. <i>European Journal of Taxonomy</i> , 0, 828, 1-15.	0.6	1
31983	<i>Curvularia brachyspora</i> causing leaf spot on <i>Cucurbita argyrosperma</i> in Mexico. <i>Journal of General Plant Pathology</i> , 0, , .	0.6	0
31984	Incomplete denitrification phenotypes in diverse <i>Thermus</i> species from diverse geothermal spring sediments and adjacent soils in southwest China. <i>Extremophiles</i> , 2022, 26, .	0.9	4
31985	An integrative phylogenetic approach for inferring relationships of fossil gobioids (Teleostei: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 262 T	1.1	6
31986	Origin of Hawaiian ferns of the genus <i>Ctenitis</i> (Dryopteridaceae). <i>Botany Letters</i> , 0, , 1-15.	0.7	0
31987	Morphological and Molecular Identification of <i>Culicoides</i> (Diptera: Ceratopogonidae) Species of the Southern California Desert. <i>Journal of Medical Entomology</i> , 2022, 59, 1589-1600.	0.9	5
31988	The First Genome Survey and De Novo Assembly of the Short Mackerel ( <i>Rastrelliger brachysoma</i> ) and Indian Mackerel ( <i>Rastrelliger kanagurta</i> ). <i>Animals</i> , 2022, 12, 1769.	1.0	0
31989	Chromosome-scale assembly and annotation of the perennial ryegrass genome. <i>BMC Genomics</i> , 2022, 23, .	1.2	17
31990	The <code>RadOrgMiner</code> pipeline: Automated genotyping of organellar loci from <code>RADseq</code> data. <i>Methods in Ecology and Evolution</i> , 2022, 13, 1962-1975.	2.2	2

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31993	Structure of cytosine transport protein CodB provides insight into nucleobaseâ€cation symporter 1 mechanism. <i>EMBO Journal</i> , 2022, 41, .	3.5	5
31994	Historical and future climate change fosters expansion of Australian harvester termites, <i>Drepanotermes</i>. <i>Evolution; International Journal of Organic Evolution</i> , 2022, 76, 2145-2161.	1.1	0
31995	CLIBASIA_00460 Disrupts Hypersensitive Response and Interacts with Citrus Rad23 Proteins. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7846.	1.8	4
31997	Molecular Variation and Phylogeny within <i>Fusarium avenaceum</i> and Related Species. <i>Diversity</i> , 2022, 14, 574.	0.7	3
31998	Reference genome assemblies reveal the origin and evolution of allohexaploid oat. <i>Nature Genetics</i> , 2022, 54, 1248-1258.	9.4	45
31999	Structure Prediction, Evaluation, and Validation of GPR18 Lipid Receptor Using Free Programs. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7917.	1.8	0
32000	The complete mitochondrial genome of the edible mushroom <i>Pleurotus giganteus</i> (Agaricales). <i>Tj ETQq1 1 0.784314 rgBT /Overlock</i>	0.2	2
32001	Transcriptomic comparison sheds new light on regulatory networks for dimorphic flower development in response to photoperiod in <i>Viola prionantha</i> . <i>BMC Plant Biology</i> , 2022, 22, .	1.6	3
32002	Systematics and Plastome Evolution in Schizaeaceae. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	0
32003	Addition to Swedenâ€™s freshwater sponge fauna and a phylogeographic study of <i>Spongilla lacustris</i> (Spongillida, Porifera) in southern Sweden. <i>European Journal of Taxonomy</i> , 0, 828, .	0.6	0
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32005	Identification and characterization of transposable element AhMITE1 in the genomes of cultivated and two wild peanuts. <i>BMC Genomics</i> , 2022, 23, .	1.2	3
32006	Comparative phylogeny and evolutionary analysis of Dicer-like protein family in two plant monophyletic lineages. <i>Journal of Genetic Engineering and Biotechnology</i> , 2022, 20, 103.	1.5	0
32007	Genome Sequence of Feline Papillomavirus Strain P20 Assembled from Metagenomic Data from the Skin of a House Cat Owner. <i>Microbiology Resource Announcements</i> , 0, , .	0.3	0
32008	Lilac ( <i>Syringa oblata</i> ) genome provides insights into its evolution and molecular mechanism of petal color change. <i>Communications Biology</i> , 2022, 5, .	2.0	13
32009	Diversity of <i>Fusarium</i> community assembly shapes mycotoxin accumulation of diseased wheat heads. <i>Molecular Ecology</i> , 2023, 32, 2504-2518.	2.0	7
32010	Molecular Characterization of Kunitz-Type Protease Inhibitors from Blister Beetles (Coleoptera). <i>Tj ETQq1 1 0.784314 rgBT /Overlock</i>	1.8	1

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32014	New records of water mites from Turkey and Iran revealed by DNA barcoding, with the description of a new species (Acari, Hydrachnidia). <i>Systematic and Applied Acarology</i> , 0, , .	0.5	5
32015	Bioremediation of quinclorac injury on tobacco by a rhizosphere bacterium. <i>World Journal of Microbiology and Biotechnology</i> , 2022, 38, .	1.7	1
32016	Genetic origin and differentiation of ten paddy field-farmed <i>Cyprinus carpio</i> strains in China. <i>Aquaculture</i> , 2022, 561, 738573.	1.7	0
32017	Demographic Expansions and the Emergence of Host Specialization in Genetically Distinct Ecotypes of the Tick-Transmitted Bacterium <i>Anaplasma phagocytophilum</i> . <i>Applied and Environmental Microbiology</i> , 0, , .	1.4	2
32018	Genomic Characterization of <i>Lactiplantibacillus plantarum</i> Strains Possessing Differential Antiviral Immunomodulatory Activities. , 2022, 1, 136-160.		8
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32022	High-quality ice plant reference genome analysis provides insights into genome evolution and allows exploration of genes involved in the transition from C3 to CAM pathways. <i>Plant Biotechnology Journal</i> , 2022, 20, 2107-2122.	4.1	17
32023	Characteristics of Gut Microbiota in Patients With Clear Cell Renal Cell Carcinoma. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	9
32024	In silico analyses of leptin and leptin receptor of spotted snakehead <i>Channa punctata</i> . <i>PLoS ONE</i> , 2022, 17, e0270881.	1.1	2
32025	Stability profile of the neuronal SNARE complex reflects its potency to drive fast membrane fusion. <i>Biophysical Journal</i> , 2022, 121, 3081-3102.	0.2	3
32027	Evolutionary analysis of globin domains from kinetoplastids. <i>Archives of Microbiology</i> , 2022, 204, .	1.0	0
32028	A chromosome-level genome assembly of the jade perch ( <i>Scortum barcoo</i> ). <i>Scientific Data</i> , 2022, 9, .	2.4	3
32029	First representative complete mitochondrial genome of the <i>Taphozous melanopogon</i> Temminck, 1841 (Chiroptera: Emballonuridae) from China. <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 1291-1293.	0.2	0
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32034	A DNA barcode reference library for endemic Ponto-Caspian amphipods. <i>Scientific Reports</i> , 2022, 12, .	1.6	16
32035	<i>Erysipelothrix anatis</i> sp. nov., <i>Erysipelothrix aquatica</i> sp. nov. and <i>Erysipelothrix urinaevulpis</i> sp. nov., three novel species of the genus, and emended description of <i>Erysipelothrix</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	20
32036	Comparative Genomics of Thaumarchaeota From Deep-Sea Sponges Reveal Their Niche Adaptation. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
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32777	Size-fractionated microbiome observed during an eight-month long sampling in Jiaozhou Bay and the Yellow Sea. <i>Scientific Data</i> , 2022, 9, .	2.4	0
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32799	Analysis of the genome of grapevine red blotch virus and related grabloviruses indicates diversification prior to the arrival of <i>Vitis vinifera</i> in North America. <i>Journal of General Virology</i> , 2022, 103, .	1.3	5
32800	Chlorine redox chemistry is widespread in microbiology. <i>ISME Journal</i> , 2023, 17, 70-83.	4.4	1
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32802	Development and validation of a quantitative PCR for the detection of Guinea worm ( <i>Dracunculus</i> ) Tj ETQq1 1 0.784314 rgBT <sub>1</sub> /Overlo	1.3	1
32803	Phylogenomics of a <i>Saccharomyces cerevisiae</i> cocoa strain reveals adaptation to a West African fermented food population. <i>IScience</i> , 2022, 25, 105309.	1.9	1
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33272	Deep ecomorphological and genetic divergence in Steller's Jays ( <i>Cyanocitta stelleri</i> , Aves) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5</i>	0.8	8
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33278	Widespread convergent evolution of alpha-neurotoxin resistance in African mammals. <i>Biology Letters</i> , 2022, 18, .	1.0	1
33279	The Macaronesian Liverwort <i>Riccia boumanii</i> Dirkse, Losada & M.Stech (Marchantiophyta) <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 5</i>	0.1	1
33280	Genome-wide identification and expression analysis of the GRAS gene family in <i>Dendrobium chrysotoxum</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	7
33281	Three new species of <i>Diploderma</i> Hallowell, 1861 (Squamata, Agamidae) from the Hengduan Mountain Region, south-western China. <i>ZooKeys</i> , 0, 1131, 1-30.	0.5	1
33282	Revisiting the morphological species groups of West-Palearctic <i>Aphaenogaster</i> ants (Hymenoptera) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5</i>	5.5	7
33283	Phylogenetic position of <i>Ptychaphelenchus eucalypticola</i> Hodda, 2009 within the Aphelenchoidoidea <i>Skarbilovich, 1947 (Siddiqi, 1980) inferred from partial 18S and 28S rDNA gene sequences. Nematology</i> , 2022, 25, 59-76.	0.2	2
33284	Ancient endosymbiont-mediated transmission of a selfish gene provides a model for overcoming barriers to gene transfer into animal mitochondrial genomes. <i>BioEssays</i> , 2023, 45, .	1.2	1
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33286	Microbiota Community Structure and Interaction Networks within <i>Dermacentor silvarum</i> , <i>Ixodes persulcatus</i> , and <i>Haemaphysalis concinna</i> . <i>Animals</i> , 2022, 12, 3237.	1.0	0
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33295	First Report on Colletotrichum sansevieriae Causing Anthracnose of Sansevieria trifasciata in Germany. Gesunde Pflanzen, 2023, 75, 61-66.	1.7	1
33296	Pandemic <i>Vibrio cholerae</i> acquired competitive traits from an environmental <i>Vibrio</i> species. Life Science Alliance, 2023, 6, e202201437.	1.3	3
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33340	Geographical distribution and phylogenic relationships of <i>Hirschmanniella diversa</i> Sher (Nematoda: Tj ETQq1 1 0.784314 rgBT /Overlaid	0.2	0
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33439	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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33531	Identification of NPF Family Genes in <i>Brassica rapa</i> Reveal Their Potential Functions in Pollen Development and Response to Low Nitrate Stress. <i>International Journal of Molecular Sciences</i> , 2023, 24, 754.	1.8	3

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33828	Genome-wide identification of papain-like cysteine protease family genes in cultivated peanut ( <i>Arachis</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 T. <i>Environmental and Experimental Botany</i> , 2023, 209, 105272.	2.0	2
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33873	Pine has two glutamine synthetase paralogs, GS1b.1 and GS1b.2, exhibiting distinct biochemical properties. <i>Plant Journal</i> , 2023, 113, 1330-1347.	2.8	1
33874	Sugars and sucrose transporters in pollinia of <i>Phalaenopsis aphrodite</i> ( <i>Orchidaceae</i> ). <i>Journal of Experimental Botany</i> , 2023, 74, 2556-2571.	2.4	1
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33885	Effects of Continuous Straw Returning on Soil Functional Microorganisms and Microbial Communities. <i>Journal of Microbiology</i> , 2023, 61, 49-62.	1.3	3
33886	MAMMLE: A Framework for Phylogeny Estimation Based on Multiobjective Application-aware Multiple Sequence Alignment and Maximum Likelihood Ensemble. <i>Journal of Computational Biology</i> , 2023, 30, 245-249.	0.8	0
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33891	High Levels of Diversity in Anopheles Subgenus Kerteszia Revealed by Species Delimitation Analyses. <i>Genes</i> , 2023, 14, 344.	1.0	1
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33893	A novel, non-neuronal acetylcholinesterase of schistosome parasites is essential for definitive host infection. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	3
33894	Rebound HIV-1 in cerebrospinal fluid after antiviral therapy interruption is mainly clonally amplified R5 T cell-tropic virus. <i>Nature Microbiology</i> , 0, .	5.9	6
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33910	<i>Salvinia</i> plants in trade: what species are we actually talking about?. <i>EPPO Bulletin</i> , 2023, 53, 108-116.	0.6	0
33911	Plant Growth Promotion, Phytohormone Production and Genomics of the Rhizosphere-Associated Microalga, <i>Micractinium rhizosphaerae</i> sp. nov.. <i>Plants</i> , 2023, 12, 651.	1.6	4
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33914	Diversification of spiny-throated reed frogs ( <i>Anura: Hyperoliidae</i> ) with the description of a new, range-restricted species from the Ukaguru Mountains, Tanzania. <i>PLoS ONE</i> , 2023, 18, e0277535.	1.1	1
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33917	Centromere repositioning and shifts in wheat evolution. <i>Plant Communications</i> , 2023, 4, 100556.	3.6	16
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33919	Gene Profiling of the Ascorbate Oxidase Family Genes under Osmotic and Cold Stress Reveals the Role of AnAO5 in Cold Adaptation in <i>Ammopiptanthus nanus</i> . <i>Plants</i> , 2023, 12, 677.	1.6	6
33920	Genomics discovery of giant fungal viruses from subsurface oceanic crustal fluids. <i>ISME Communications</i> , 2023, 3, .	1.7	6
33921	The heparan sulfate modification enzyme, Hs6st1, governs <i>Xenopus</i> neuroectodermal patterning by regulating distributions of Fgf and Noggin. <i>Developmental Biology</i> , 2023, 496, 87-94.	0.9	2
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33926	Deep resilience: An evolutionary perspective on calcification in an age of ocean acidification. <i>Frontiers in Physiology</i> , 0, 14, .	1.3	1
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33931	StrainSelect: A novel microbiome reference database that disambiguates all bacterial strains, genome assemblies and extant cultures worldwide. <i>Heliyon</i> , 2023, 9, e13314.	1.4	0
33932	HPV and molecular mimicry in systemic lupus erythematosus and an impact of compiling B-cell epitopes and MHC-class II binding profiles with <i>in silico</i> evidence. <i>Journal of Biomolecular Structure and Dynamics</i> , 0, , 1-9.	2.0	0

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33945	Quaternary glucocorticoid receptor structure highlights allosteric interdomain communication. <i>Nature Structural and Molecular Biology</i> , 2023, 30, 286-295.	3.6	5
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34026	High-throughput microbial culturomics using automation and machine learning. <i>Nature Biotechnology</i> , 2023, 41, 1424-1433.	9.4	39
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34035	Impacts of dietary supplementation of bamboo vinegar and charcoal powder on growth performance, intestinal morphology, and gut microflora of large-scale loach <i>Paramisgurnus dabryanus</i> . <i>Journal of Oceanology and Limnology</i> , 2023, 41, 1187-1196.	0.6	1
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34072	Thermophilin 13: In Silico Analysis Provides New Insight in Genes Involved in Bacteriocin Production. <i>Microorganisms</i> , 2023, 11, 611.	1.6	1
34073	Molecular exploration of fossil eggshell uncovers hidden lineage of giant extinct bird. <i>Nature Communications</i> , 2023, 14, .	5.8	2
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34079	Complete genome sequences of newly discovered <i>Dioscorea</i> bacilliform AL virus and <i>Dioscorea</i> bacilliform SN virus isolates from <i>Dioscorea bulbifera</i> L. in northeastern Brazil. <i>European Journal of Plant Pathology</i> , 0, , .	0.8	0
34080	Novel strains of <i>Campylobacter</i> cause diarrheal outbreak in Rhesus macaques ( <i>Macaca mulatta</i> ) of Kathmandu Valley. <i>PLoS ONE</i> , 2023, 18, e0270778.	1.1	1

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34087	Sticky decisions: The multilayered regulation of adhesin production by bacteria. <i>PLoS Genetics</i> , 2023, 19, e1010648.	1.5	2
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34090	Evolutionary ecology of microbial populations inhabiting deep sea sediments associated with cold seeps. <i>Nature Communications</i> , 2023, 14, .	5.8	9
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