

T-REX: a web server for inferring, validating and visualizing networks

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Hippo pathway genes developed varied exon numbers and coevolved functional domains in metazoans for species specific growth control. BMC Evolutionary Biology, 2013, 13, 76.	3.2	7
2	Elucidating the origin of the ExbBD components of the TonB system through Bayesian inference and maximum-likelihood phylogenies. Molecular Phylogenetics and Evolution, 2013, 69, 674-686.	1.2	9
3	Triton's trident: cryptic Neogene divergences in a marine clam (<i>L. asaea australis</i>) correspond to Australia's three temperate biogeographic provinces. Molecular Ecology, 2013, 22, 1933-1946.	2.0	29
4	Inferring ancient divergences requires genes with strong phylogenetic signals. Nature, 2013, 497, 327-331.	13.7	541
5	<i>Azadinium dalianense</i> , a new dinoflagellate species from the Yellow Sea, China. Phycologia, 2013, 52, 625-636.	0.6	27
6	The Origin of Parasitism Gene in Nematodes: Evolutionary Analysis through the Construction of Domain Trees. Evolutionary Bioinformatics, 2013, 9, EBO.S13032.	0.6	0
7	Inferring explicit weighted consensus networks to represent alternative evolutionary histories. BMC Evolutionary Biology, 2013, 13, 274.	3.2	5
8	Are phylogenetic trees suitable for chemogenomics analyses of bioactivity data sets: the importance of shared active compounds and choosing a suitable data embedding method, as exemplified on Kinases. Journal of Cheminformatics, 2013, 5, 49.	2.8	12
9	Structural and Functional Characterization of DUF1471 Domains of Salmonella Proteins SrfN, YdgH/SssB, and YahO. PLoS ONE, 2014, 9, e101787.	1.1	13
10	Anterior Foregut Microbiota of the Glassy-Winged Sharpshooter Explored Using Deep 16S rRNA Gene Sequencing from Individual Insects. PLoS ONE, 2014, 9, e106215.	1.1	23
11	Use of Bioinformatics Tools in Different Spheres of Life Sciences. Journal of Data Mining in Genomics & Proteomics, 2014, 05, .	0.5	16
12	Mycobacterial Phylogenomics: An Enhanced Method for Gene Turnover Analysis Reveals Uneven Levels of Gene Gain and Loss among Species and Gene Families. Genome Biology and Evolution, 2014, 6, 1454-1465.	1.1	13
13	Alternative oxidase: Distribution, induction, properties, structure, regulation, and functions. Biochemistry (Moscow), 2014, 79, 1615-1634.	0.7	42
14	Arabidopsis thaliana phytochelatin synthase 2 is constitutively active in vivo and can rescue the growth defect of the PCS1-deficient cad1-3 mutant on Cd-contaminated soil. Journal of Experimental Botany, 2014, 65, 4241-4253.	2.4	81
15	Vallisneria spiralis and Egeria densa (Hydrocharitaceae) in arctic and subarctic Iceland. New Journal of Botany, 2014, 4, 85-89.	0.2	7
16	A New Approach for Phylogenetic Tree Construction Based on Minimal Absent Words. , 2014, , .		0
17	A new efficient algorithm for inferring explicit hybridization networks following the Neighbor-joining principle. Journal of Bioinformatics and Computational Biology, 2014, 12, 1450024.	0.3	5
18	Sexual dimorphism and intraspecific variation in wing size and shape of <i>T. ongeia fischeri</i> (Lepidoptera: Ycaenidae). Entomological Science, 2014, 17, 342-353.	0.3	8

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19	Genomic and Phenotypic Characterization of a Wild Medaka Population: Towards the Establishment of an Isogenic Population Genetic Resource in Fish. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 433-445.	0.8	54
20	Characterization of the GPI-anchored lipid transfer proteins in the moss <i>Physcomitrella patens</i> . <i>Plant Physiology and Biochemistry</i> , 2014, 75, 55-69.	2.8	37
21	The binary protein-protein interaction landscape of <i>Escherichia coli</i> . <i>Nature Biotechnology</i> , 2014, 32, 285-290.	9.4	218
22	New dinoflagellate species <i>Pteroperidinium haizhouense</i> sp. nov. (<i>Pteroperidinales</i> , <i>Dinophyceae</i>), its cyst theca relationship and phylogenetic position within the <i>Micronovela</i> group. <i>Phycological Research</i> , 2014, 62, 109-124.	0.8	14
23	Ionome Changes in <i>Xylella fastidiosa</i> Infected <i>Nicotiana tabacum</i> Correlate With Virulence and Discriminate Between Subspecies of Bacterial Isolates. <i>Molecular Plant-Microbe Interactions</i> , 2014, 27, 1048-1058.	1.4	36
24	Novel genotypes of <i>Trypanosoma binneyi</i> from wild platypuses (<i>Ornithorhynchus anatinus</i>) and identification of a leech as a potential vector. <i>Experimental Parasitology</i> , 2014, 145, 42-50.	0.5	26
25	Phylogeography and species delimitation in the New Zealand endemic, genetically hypervariable harvestman species, <i>Aoraki denticulata</i> (Arachnida, Opiliones, Cyphophthalmi). <i>Invertebrate Systematics</i> , 2014, 28, 401.	0.5	29
26	Genome and transcriptome sequencing identifies breeding targets in the orphan crop <i>tef</i> (<i>Eragrostis tef</i>). <i>PLoS ONE</i> , 2014, 9, e102113.	1.2	133
27	An abundant <i>Candidatus Phytoplasma solani</i> tuf b strain is associated with grapevine, stinging nettle and <i>Hyalesthes obsoletus</i> . <i>European Journal of Plant Pathology</i> , 2014, 140, 213-227.	0.8	66
28	Molecular and functional characterization of <i>Anopheles gambiae</i> inward rectifier potassium (Kir1) channels: A novel role in egg production. <i>Insect Biochemistry and Molecular Biology</i> , 2014, 51, 10-19.	1.2	27
29	Combining spatial and chemical information for clustering pharmacophores. <i>BMC Bioinformatics</i> , 2014, 15, S5.	1.2	7
30	Repurposed Transcriptomic Data Facilitate Discovery of Innate Immunity Toll-Like Receptor (TLR) Genes Across Lophotrochozoa. <i>Biological Bulletin</i> , 2014, 227, 201-209.	0.7	22
31	Phylogenetic Diversity of <i>Peltigera</i> Cyanolichens and Their Photobionts in Southern Chile and Antarctica. <i>Microbes and Environments</i> , 2015, 30, 172-179.	0.7	26
32	Opposite nucleotide usage biases in different parts of the <i>Corynebacterium diphtheriae</i> <i>spaC</i> gene. <i>International Journal of Bioinformatics Research and Applications</i> , 2015, 11, 347.	0.1	4
34	Morphology, ultrastructure, and phylogeny of <i>Protodinium simplex</i> and <i>Biecheleriopsis cf. adriatica</i> (<i>Dinophyceae</i>) from the China Sea. <i>Nova Hedwigia</i> , 2015, 101, 251-268.	0.2	7
35	Hidden biodiversity in an ancient lake: phylogenetic congruence between Lake Tanganyika trophic cichlids and their monogenean flatworm parasites. <i>Scientific Reports</i> , 2015, 5, 13669.	1.6	59
36	Comprehensive genome-wide analysis reveals different classes of enigmatic old yellow enzyme in fungi. <i>Scientific Reports</i> , 2014, 4, 4013.	1.6	25
37	Cyst motile stage relationship, morphology, ultrastructure, and molecular phylogeny of the gymnodinoid dinoflagellate <i>Barrufeta resplendens</i> comb. nov., formerly known as <i>Gyrodinium resplendens</i> , isolated from the Gulf of Mexico. <i>Journal of Phycology</i> , 2015, 51, 990-999.	1.0	9

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38	Peridiniopsis jiulongensis, a new freshwater dinoflagellate with a diatom endosymbiont from China. Nova Hedwigia, 2015, 101, 313-326.	0.2	10
39	Four new species of Pyropia (Bangiales, Rhodophyta) from the west coast of North America: the Pyropia lanceolata species complex updated. PhytoKeys, 2015, 52, 1-22.	0.4	22
40	Deep sequencing revealed molecular signature of horizontal gene transfer of plant like transcripts in the mosquito Anopheles culicifacies: an evolutionary puzzle. F1000Research, 2015, 4, 1523.	0.8	9
41	Identification of novel esterase-active enzymes from hot environments by use of the host bacterium Thermus thermophilus. Frontiers in Microbiology, 2015, 6, 275.	1.5	65
42	Analysis of virus genomes from glacial environments reveals novel virus groups with unusual host interactions. Frontiers in Microbiology, 2015, 6, 656.	1.5	65
44	Distinct molecular features facilitating ice-binding mechanisms in hyperactive antifreeze proteins closely related to an Antarctic sea ice bacterium. Journal of Biomolecular Structure and Dynamics, 2015, 33, 1424-1441.	2.0	2
45	Acetylcholinesterase 1 in populations of organophosphate-resistant North American strains of the cattle tick, Rhipicephalus microplus (Acari: Ixodidae). Parasitology Research, 2015, 114, 3027-3040.	0.6	11
46	Molecular phylogenetics and floral evolution in the sarracenioid clade (Actinidiaceae, Roridulaceae) Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.4	10
47	An update to polyketide synthase and non-ribosomal synthetase genes and nomenclature in Fusarium. Fungal Genetics and Biology, 2015, 75, 20-29.	0.9	123
48	Evolution of FOXRED1, an FAD-dependent oxidoreductase necessary for NADH:ubiquinone oxidoreductase (Complex I) assembly. Biochimica Et Biophysica Acta - Bioenergetics, 2015, 1847, 451-457.	0.5	16
49	Genetic and phenotypic diversity of Larix cajanderi Mayr in the north of the Russian Far East. Contemporary Problems of Ecology, 2015, 8, 9-20.	0.3	3
50	Cystâ€“theca relationship and phylogenetic positions of <i>Protoperidinium</i> (Peridinales,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 of <i>Protoperidinium shanghaiense</i> sp. nov.. Phycologia, 2015, 54, 49-66.	0.6	22
51	The Pseudomonas aeruginosa antimetabolite L -2-amino-4-methoxy-trans-3-butenoic acid (AMB) is made from glutamate and two alanine residues via a thiotemplate-linked tripeptide precursor. Frontiers in Microbiology, 2015, 6, 170.	1.5	52
52	Parallelization of genetic algorithms for sorting permutations by reversals over biological data. International Journal of Hybrid Intelligent Systems, 2015, 12, 53-64.	0.9	3
53	Cystâ€“theca relationship and phylogenetic positions of the diplopsalioideans (Peridinales,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 182 T	0.6	21
54	Mutational dynamics between primary and relapse neuroblastomas. Nature Genetics, 2015, 47, 872-877.	9.4	253
55	Selection and Spread of Artemisinin-Resistant Alleles in Thailand Prior to the Global Artemisinin Resistance Containment Campaign. PLoS Pathogens, 2015, 11, e1004789.	2.1	85
56	Cystâ€“theca relationships and phylogenetic positions of <sc>P</sc>eridinales (<sc>D</sc>inophyceae) with two anterior intercalary plates, with description of <i><sc>A</sc>rchaeperidinium bailongense</i> sp. nov. and <i><sc>P</sc>rotoperidinium fuzhouense</i> sp. nov. Phycological Research, 2015, 63, 134-151.	0.8	20

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57	Classification of bioinformatics workflows using weighted versions of partitioning and hierarchical clustering algorithms. BMC Bioinformatics, 2015, 16, 68.	1.2	13
58	Sequencing of historic and modern specimens reveals cryptic diversity in <i>Nothogenia</i> (Scinaiceae, Rhodophyta). Phycologia, 2015, 54, 97-108.	0.6	22
59	Structural and functional analysis of two universal stress proteins YdaA and YnaF from <i>Salmonella typhimurium</i> : possible roles in microbial stress tolerance. Journal of Structural Biology, 2015, 189, 238-250.	1.3	13
60	Phylogeny, Diversity, Distribution, and Host Specificity of <i>Haemoproteus</i> spp. (Apicomplexa: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 670-678.	0.8	16
61	Marker-trait association study for sucrose and yield contributing traits in sugarcane (<i>Saccharum</i> spp.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 0.6	0.6	33
62	Phylogenetic analysis of She population from Fujian Province in China based on 26 Y-STR Loci*. Forensic Science International: Genetics Supplement Series, 2015, 5, e520-e523.	0.1	0
63	Visualizing genome and systems biology: technologies, tools, implementation techniques and trends, past, present and future. GigaScience, 2015, 4, 38.	3.3	84
64	Comparative phylogeography and population genetic structure of three widespread mollusc species in the Mediterranean and near Atlantic. Marine Ecology, 2015, 36, 701-715.	0.4	25
65	Comprehensive Phylogenetic Analysis of Bovine Non-aureus Staphylococci Species Based on Whole-Genome Sequencing. Frontiers in Microbiology, 2016, 7, 1990.	1.5	49
66	Reassessment of Species Diversity of the Subfamily Denticollinae (Coleoptera: Elateridae) through DNA Barcoding. PLoS ONE, 2016, 11, e0148602.	1.1	27
67	Computational Analysis of the Predicted Evolutionary Conservation of Human Phosphorylation Sites. PLoS ONE, 2016, 11, e0152809.	1.1	9
68	Molecular ecology and phylogenetics of the water beetle genus <i>Ochthebius</i> revealed multiple independent shifts to marine rockpools lifestyle. Zoologica Scripta, 2016, 45, 175-186.	0.7	17
69	Compression-based distance methods as an alternative to statistical methods for constructing phylogenetic trees. , 2016, , .		0
70	Draft genome sequencing and secretome analysis of fungal phytopathogen <i>Ascochyta rabiei</i> provides insight into the necrotrophic effector repertoire. Scientific Reports, 2016, 6, 24638.	1.6	57
71	The evolutionary origin of CIPK16: A gene involved in enhanced salt tolerance. Molecular Phylogenetics and Evolution, 2016, 100, 135-147.	1.2	10
72	Unexpected Interfarm Transmission Dynamics during a Highly Pathogenic Avian Influenza Epidemic. Journal of Virology, 2016, 90, 6401-6411.	1.5	14
73	Genomic Comparison of <i>Campylobacter</i> spp. and Their Potential for Zoonotic Transmission between Birds, Primates, and Livestock. Applied and Environmental Microbiology, 2016, 82, 7165-7175.	1.4	73
74	The phylogenomic forest of bird trees contains a hard polytomy at the root of Neoaves. Zoologica Scripta, 2016, 45, 50-62.	0.7	122

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75	A plant biologists' guide to phylogenetic analysis of biological macromolecule sequences. <i>Biologia Plantarum</i> , 2016, 60, 619-627.	1.9	1
76	Molecular genetic identification of a new <i>Tisochrysis lutea</i> (Bendif et Probert, 2013) strain isolated from the Russian coastal waters of the Sea of Japan. <i>Microbiology</i> , 2016, 85, 325-332.	0.5	3
77	<i>Huia caspica</i> gen. & comb. nov., a dinoflagellate species that recently crossed the marine-freshwater boundary. <i>Phycological Research</i> , 2016, 64, 251-258.	0.8	9
78	Analysis of genetic admixture in Uyghur using the 26 Y-STR loci system. <i>Scientific Reports</i> , 2016, 6, 19998.	1.6	30
79	Using hybridization networks to retrace the evolution of Indo-European languages. <i>BMC Evolutionary Biology</i> , 2016, 16, 180.	3.2	11
80	Insect phylogenetics in the digital age. <i>Current Opinion in Insect Science</i> , 2016, 18, 48-52.	2.2	2
81	Biosystematic study in the genus <i>Cousinia</i> Cass. (Asteraceae), section <i>Cousinia</i> . <i>Biochemical Systematics and Ecology</i> , 2016, 69, 252-260.	0.6	12
82	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
83	Several steps of lateral gene transfer followed by events of "birth-and-death" evolution shaped a fungal sorbicillinoid biosynthetic gene cluster. <i>BMC Evolutionary Biology</i> , 2016, 16, 269.	3.2	33
84	ANIttools web: a web tool for fast genome comparison within multiple bacterial strains. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw084.	1.4	59
85	Influence of Host Ecology and Behavior on <i>Campylobacter jejuni</i> Prevalence and Environmental Contamination Risk in a Synanthropic Wild Bird Species. <i>Applied and Environmental Microbiology</i> , 2016, 82, 4811-4820.	1.4	33
86	Phylogenetic and Genomic Analyses Resolve the Origin of Important Plant Genes Derived from Transposable Elements. <i>Molecular Biology and Evolution</i> , 2016, 33, 1937-1956.	3.5	26
87	W-IQ-TREE: a fast online phylogenetic tool for maximum likelihood analysis. <i>Nucleic Acids Research</i> , 2016, 44, W232-W235.	6.5	3,039
88	Evolview v2: an online visualization and management tool for customized and annotated phylogenetic trees. <i>Nucleic Acids Research</i> , 2016, 44, W236-W241.	6.5	610
89	PHYLOViZ Online: web-based tool for visualization, phylogenetic inference, analysis and sharing of minimum spanning trees. <i>Nucleic Acids Research</i> , 2016, 44, W246-W251.	6.5	152
90	Oral fairy tale or literary fake? Investigating the origins of <i>Little Red Riding Hood</i> using phylogenetic network analysis. <i>Digital Scholarship in the Humanities</i> , 2016, 31, 611-636.	0.4	14
91	The fungal community changes over time in developing wheat heads. <i>International Journal of Food Microbiology</i> , 2016, 222, 30-39.	2.1	45
92	Cyst-theca relationship and phylogenetic positions of <i>Scrippsiella plana</i> sp. nov. and <i>S. spinifera</i> (Peridinales, Dinophyceae). <i>European Journal of Phycology</i> , 2016, 51, 188-202.	0.9	18

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93	Chitosan enhances parasitism of <i>Meloidogyne javanica</i> eggs by the nematophagous fungus <i>Pochonia chlamydosporia</i> . <i>Fungal Biology</i> , 2016, 120, 572-585.	1.1	51
94	Morphology, molecular phylogeny and azaspiracid profile of <i>Azadinium poporum</i> (Dinophyceae) from the Gulf of Mexico. <i>Harmful Algae</i> , 2016, 55, 56-65.	2.2	24
95	Identification of the non-ribosomal peptide synthetase responsible for biosynthesis of the potential anti-cancer drug sansalvamide in <i>Fusarium solani</i> . <i>Current Genetics</i> , 2016, 62, 799-807.	0.8	22
96	Analyses of methyltransferases across the pathogenicity spectrum of different mycobacterial species point to an extremophile connection. <i>Molecular BioSystems</i> , 2016, 12, 1615-1625.	2.9	21
97	Diversification patterns in cosmopolitan earthworms: similar mode but different tempo. <i>Molecular Phylogenetics and Evolution</i> , 2016, 94, 701-708.	1.2	27
98	A Visual Interface for Querying Heterogeneous Phylogenetic Databases. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017, 14, 131-144.	1.9	5
99	The cyst-theca relationship of the dinoflagellate cyst <i>Trinovantedinium pallidifulum</i> , with erection of <i>Protoperidinium lousianensis</i> sp. nov. and their phylogenetic position within the <i>Conica</i> group. <i>Palynology</i> , 2017, 41, 183-202.	0.7	20
100	Missing something? Codon aversion as a new character system in phylogenetics. <i>Cladistics</i> , 2017, 33, 545-556.	1.5	14
101	Biogeography and diversification dynamics of the African woodpeckers. <i>Molecular Phylogenetics and Evolution</i> , 2017, 108, 88-100.	1.2	14
102	Multiple introductions of <i>Sirex noctilio</i> (Hymenoptera: Siricidae) in northeastern North America based on microsatellite genotypes, and implications for biological control. <i>Biological Invasions</i> , 2017, 19, 1431-1447.	1.2	10
103	Genetic and genomic evidence of niche partitioning and adaptive radiation in mountain pine beetle fungal symbionts. <i>Molecular Ecology</i> , 2017, 26, 2077-2091.	2.0	52
104	Genotyping-by-sequencing provides the first well-resolved phylogeny for coffee (<i>Coffea</i>) and insights into the evolution of caffeine content in its species. <i>Molecular Phylogenetics and Evolution</i> , 2017, 109, 351-361.	1.2	59
105	Identification of alternatively spliced transcripts of rice phytochelatin synthase 2 gene <i>OsPCS2</i> involved in mitigation of cadmium and arsenic stresses. <i>Plant Molecular Biology</i> , 2017, 94, 167-183.	2.0	77
106	Uncovering the mask of the <i>Simulium feuerborni</i> complex (Diptera: Simuliidae): Description of a new pseudocryptic species <i>Simulium pairoti</i> from Malaysia. <i>Acta Tropica</i> , 2017, 169, 133-141.	0.9	13
107	Cystâ€Theca Relationship and Phylogenetic Position of <i>Impagidinium caspiense</i> Incubated from Caspian Sea Surface Sediments: Relation to <i>Gonyaulax baltica</i> and Evidence for Heterospory within Gonyaulacoid Dinoflagellates. <i>Journal of Eukaryotic Microbiology</i> , 2017, 64, 829-842.	0.8	25
108	In silico screening for candidate chassis strains of free fatty acid-producing cyanobacteria. <i>BMC Genomics</i> , 2017, 18, 33.	1.2	11
109	Therapeutically targeting guanylate cyclase-C: computational modeling of plecanatide, a uroguanylin analog. <i>Pharmacology Research and Perspectives</i> , 2017, 5, e00295.	1.1	23
110	Adding new pieces to the <i>Azadinium</i> (Dinophyceae) diversity and biogeography puzzle: Non-toxicogenic <i>Azadinium zhuanum</i> sp. nov. from China, toxicogenic <i>A. poporum</i> from the Mediterranean, and a non-toxicogenic <i>A. dalianense</i> from the French Atlantic. <i>Harmful Algae</i> , 2017, 66, 65-78.	2.2	30

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111	Cryptic diversity within the harmful dinoflagellate <i>Akashiwo sanguinea</i> in coastal Chinese waters is related to differentiated ecological niches. <i>Harmful Algae</i> , 2017, 66, 88-96.	2.2	24
112	DLTree: efficient and accurate phylogeny reconstruction using the dynamical language method. <i>Bioinformatics</i> , 2017, 33, 2214-2215.	1.8	8
113	Substrates of <i>Peltigera</i> Lichens as a Potential Source of Cyanobionts. <i>Microbial Ecology</i> , 2017, 74, 561-569.	1.4	25
114	Morphology, molecular phylogeny and okadaic acid production of epibenthic <i>Prorocentrum</i> (Dinophyceae) species from the northern South China Sea. <i>Algal Research</i> , 2017, 22, 14-30.	2.4	50
115	First record of resting cysts of the benthic dinoflagellate <i>Prorocentrum leucomiscum</i> in a natural reservoir in Gujanâ€Mestras, Gironde, France. <i>Journal of Phycology</i> , 2017, 53, 1193-1205.	1.0	15
116	Phenetic Comparison of Prokaryotic Genomes Using k-mers. <i>Molecular Biology and Evolution</i> , 2017, 34, 2716-2729.	3.5	20
117	Intracellular cargo transport by kinesin-3 motors. <i>Biochemistry (Moscow)</i> , 2017, 82, 803-815.	0.7	54
118	Cystâ€motile stage relationship and molecular phylogeny of a new freshwater dinoflagellate <i>Gymnodinium plasticum</i> from <i>Plastic Lake, Canada</i> . <i>Phycological Research</i> , 2017, 65, 312-321.	0.8	5
119	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
120	The complete mitogenome of the rockweed <i>Fucus distichus</i> (Fucaceae, Phaeophyceae). <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 203-204.	0.2	3
121	Put3 Positively Regulates Proline Utilization in <i>Candida albicans</i> . <i>MSphere</i> , 2017, 2, .	1.3	17
122	The malate sensing two-component system MaeKR is a non-canonical class of sensory complex for C4-dicarboxylates. <i>Scientific Reports</i> , 2017, 7, 2708.	1.6	5
123	A Critical Review on the Use of Support Values in Tree Viewers and Bioinformatics Toolkits. <i>Molecular Biology and Evolution</i> , 2017, 34, 1535-1542.	3.5	28
124	Detecting consistent patterns of directional adaptation using differential selection codon models. <i>BMC Evolutionary Biology</i> , 2017, 17, 147.	3.2	12
125	Analysis of the lipid body proteome of the oleaginous alga <i>Lobosphaera incisa</i> . <i>BMC Plant Biology</i> , 2017, 17, 98.	1.6	44
126	Post-translational regulation by structural changes of 4-dihydromethyltrisporate dehydrogenase, a key enzyme in sexual and parasitic communication mediated by the trisporic acid pheromone system, of the fungal fusion parasite <i>Parasitella parasitica</i> . <i>Journal of Theoretical Biology</i> , 2017, 413, 50-57.	0.8	2
127	The Anatoliaâ€Balkan phylogeographic fault: a snapshot from the genus <i>Isophya</i> (Orthoptera). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf</i>	0.7	28
128	Engineering cell sensing and responses using a GPCR-coupled CRISPR-Cas system. <i>Nature Communications</i> , 2017, 8, 2212.	5.8	81

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129	Transmission dynamics of co-endemic <i>Plasmodium vivax</i> and <i>P. falciparum</i> in Ethiopia and prevalence of antimalarial resistant genotypes. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005806.	1.3	57
130	MimiLook: A Phylogenetic Workflow for Detection of Gene Acquisition in Major Orthologous Groups of Megavirales. <i>Viruses</i> , 2017, 9, 72.	1.5	2
131	Origin and Evolution of RNA-Dependent RNA Polymerase. <i>Frontiers in Genetics</i> , 2017, 8, 125.	1.1	61
132	HPV8-E6 Interferes with Syntenin-2 Expression through Deregulation of Differentiation, Methylation and Phosphatidylinositide-Kinase Dependent Mechanisms. <i>Frontiers in Microbiology</i> , 2017, 8, 1724.	1.5	5
133	Research Article Evolution of the genus Mimivirus based on translation protein homology and its implication in the tree of life.. <i>Genetics and Molecular Research</i> , 2017, 16, .	0.3	6
134	Umbilicariaceae (lichenized Ascomycota) – Trait evolution and a new generic concept. <i>Taxon</i> , 2017, 66, 1282-1303.	0.4	30
135	The complete mitochondrial genome of the horned lizard <i>Phrynosoma blainvillii</i> (Squamata: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.2	0
136	Legionella Becoming a Mutualist: Adaptive Processes Shaping the Genome of Symbiont in the Louse <i>Polyplax serrata</i> . <i>Genome Biology and Evolution</i> , 2017, 9, 2946-2957.	1.1	47
137	Biogeography of Amazonian fishes: deconstructing river basins as biogeographic units. <i>Neotropical Ichthyology</i> , 2017, 15, .	0.5	78
138	Discovery and Biosynthesis of the Antibiotic Bicyclomycin in Distantly Related Bacterial Classes. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	36
139	Ancient Evolution of Mammarenaviruses: Adaptation via Changes in the L Protein and No Evidence for Host-Virus Codivergence. <i>Genome Biology and Evolution</i> , 2018, 10, 863-874.	1.1	22
140	Parallel evolution of Batesian mimicry supergene in two <i>Papilio</i> butterflies, <i>P. polytes</i> and <i>P. memnon</i> . <i>Science Advances</i> , 2018, 4, eaao5416.	4.7	48
141	Geographic population structure in an outcrossing plant invasion after centuries of cultivation and recent founding events. <i>AoB PLANTS</i> , 2018, 10, 020.	1.2	1
142	Transferring the freshwater dinoflagellate <i>Peridinium wisconsinense</i> (Dinophyceae) to the family Thoracosphaeraceae, with the description of <i>Fusiperidinium</i> gen. nov.. <i>Phycological Research</i> , 2018, 66, 137-148.	0.8	2
143	Polycomb group protein Suz12 is regulated by a novel miRNA-like small RNA. <i>Scientific Reports</i> , 2018, 8, 1720.	1.6	3
144	Phylogenomics. <i>Methods in Molecular Biology</i> , 2018, 1704, 103-187.	0.4	15
145	A Novel <i>Glaesserella</i> sp. Isolated from Pigs with Severe Respiratory Infections Has a Mosaic Genome with Virulence Factors Putatively Acquired by Horizontal Transfer. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	17
146	Comparative analysis of <i>Campylobacter</i> isolates from wild birds and chickens using MALDI-TOF MS, biochemical testing, and DNA sequencing. <i>Journal of Veterinary Diagnostic Investigation</i> , 2018, 30, 354-361.	0.5	20

#	ARTICLE	IF	CITATIONS
147	Atomic-level evidence for packing and positional amyloid polymorphism by segment from TDP-43 RRM2. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 311-319.	3.6	89
148	The fate of mitochondria after infection of the Mucoralean fungus <i>Absidia glauca</i> by the fusion parasite <i>Parasitella parasitica</i> : comparison of mitochondrial genomes in zygomycetes. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2018, 29, 113-120.	0.7	3
149	Is there genetic connectivity among the critically endangered White-winged Flufftail (<i>Sarothrura</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 18	0.4	1
150	Hiding in broad daylight: molecular and morphological data reveal a new ocean sunfish species (Tetraodontiformes: Molidae) that has eluded recognition. <i>Zoological Journal of the Linnean Society</i> , 2018, 182, 631-658.	1.0	24
151	Paleobiogeography of an Iberian endemic species, <i>Luciobarbus sclateri</i> (Günther, 1868) (Actinopterygii, Cyprinidae), inferred from mitochondrial and nuclear markers. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2018, 56, 127-147.	0.6	10
152	The cereal pathogen <i>Fusarium pseudograminearum</i> produces a new class of active cytokinins during infection. <i>Molecular Plant Pathology</i> , 2018, 19, 1140-1154.	2.0	37
153	<i>Adenoides sinensis</i> , a new sand-dwelling dinoflagellate species from China and reexamination of <i>Adenoides eludens</i> from an Atlantic strain. <i>Phycologia</i> , 2018, 57, 179-190.	0.6	2
154	Revisiting <i>Chaetoceros subtilis</i> and <i>C. subtilis</i> var. <i>abnormis</i> (Bacillariophyceae), reinstating the latter as <i>C. abnormis</i> . <i>Phycologia</i> , 2018, 57, 659-673.	0.6	4
155	Comparative Analyses of Cytochrome P450s and Those Associated with Secondary Metabolism in <i>Bacillus</i> Species. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3623.	1.8	19
157	Mitogenome analysis of a green tide forming <i>Ulva</i> from California, USA confirms its identity as <i>Ulva expansa</i> (Ulvaceae, Chlorophyta). <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 1302-1303.	0.2	29
158	Genome-wide analysis of horizontally acquired genes in the genus <i>Mycobacterium</i> . <i>Scientific Reports</i> , 2018, 8, 14817.	1.6	21
159	Ankyrin domain encoding genes from an ancient horizontal transfer are functionally integrated into <i>Nasonia</i> developmental gene regulatory networks. <i>Genome Biology</i> , 2018, 19, 148.	3.8	9
160	Inhibition of HIV-1 infection by human pegivirus type 1-derived peptides is affected by human pegivirus type 1 genotype and HIV-1 coreceptor tropism. <i>Aids</i> , 2018, 32, 1951-1957.	1.0	4
161	Agro-morphological description, genetic diversity and population structure of sugarcane varieties from sub-tropical India. <i>3 Biotech</i> , 2018, 8, 469.	1.1	2
162	Analysis of the complete organellar genomes of the rockweed <i>Fucus spiralis</i> (Fucaceae,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 18 Mitochondrial DNA Part B: Resources, 2018, 3, 482-483.	0.2	2
163	Integration of Bioinformatics in Bioremediation. <i>International Journal of Biomedical Data Mining</i> , 2018, 07, .	0.1	1
164	Microbial Interkingdom Interactions in Roots Promote <i>Arabidopsis</i> Survival. <i>Cell</i> , 2018, 175, 973-983.e14.	13.5	707
165	Engineering highly functional thermostable proteins using ancestral sequence reconstruction. <i>Nature Catalysis</i> , 2018, 1, 878-888.	16.1	106

#	ARTICLE	IF	CITATIONS
166	Thermophilic biodesulfurization and its application in oil desulfurization. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 9089-9103.	1.7	60
167	Profiling of 3696 Nuclear Receptor–Coregulator Interactions: A Resource for Biological and Clinical Discovery. <i>Endocrinology</i> , 2018, 159, 2397-2407.	1.4	27
168	Classification of Complete Proteomes of Different Organisms and Protein Sets Based on Their Protein Distributions in Terms of Some Key Attributes of Proteins. <i>International Journal of Genomics</i> , 2018, 2018, 1-12.	0.8	3
169	Massive lateral transfer of genes encoding plant cell wall-degrading enzymes to the mycoparasitic fungus <i>Trichoderma</i> from its plant-associated hosts. <i>PLoS Genetics</i> , 2018, 14, e1007322.	1.5	143
170	Analysis of Reptarenavirus genomes indicates different selective forces acting on the S and L segments and recent expansion of common genotypes. <i>Infection, Genetics and Evolution</i> , 2018, 64, 212-218.	1.0	6
171	<scp>PMERGE</scp>: Computational filtering of paralogous sequences from <scp>RAD</scp>–seq data. <i>Ecology and Evolution</i> , 2018, 8, 7002-7013.	0.8	15
172	Co-speciation in bedbug <i>Wolbachia</i> parallel the pattern in nematode hosts. <i>Scientific Reports</i> , 2018, 8, 8797.	1.6	43
173	Genomics reveals abundant speciation in the coral reef building alga <i>Porolithon onkodes</i> (Corallinales, Rhodophyta). <i>Journal of Phycology</i> , 2018, 54, 429-434.	1.0	87
174	Morpho-molecular diversity and phylogeny of <i>Bysmatrum</i> (Dinophyceae) from the South China Sea and France. <i>European Journal of Phycology</i> , 2018, 53, 318-335.	0.9	7
175	Computational Strategies for Dissecting the High-Dimensional Complexity of Adaptive Immune Repertoires. <i>Frontiers in Immunology</i> , 2018, 9, 224.	2.2	164
177	<i>Karodinium zhouanum</i> , a new dinoflagellate species from China, and molecular phylogeny of <i>Karenia digitata</i> and <i>Karenia longicanalis</i> (Gymnodiniales, Dinophyceae). <i>Phycologia</i> , 2018, 57, 401-412.	0.6	36
178	Optimizing Phylogenetic Queries for Performance. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 1-1.	1.9	0
179	A new fast method for inferring multiple consensus trees using k-medoids. <i>BMC Evolutionary Biology</i> , 2018, 18, 48.	3.2	20
180	Morphology, ultrastructure, and molecular phylogeny of <i>Wangodinium sinense</i> gen. et sp. nov. (Gymnodiniales, Dinophyceae) and revisiting of <i>Gymnodinium dorsalisulcum</i> and <i>Gymnodinium impudicum</i> . <i>Journal of Phycology</i> , 2018, 54, 744-761.	1.0	11
181	Sympatric occurrence of two <i>Azadinium poporum</i> ribotypes in the Eastern Mediterranean Sea. <i>Harmful Algae</i> , 2018, 78, 75-85.	2.2	19
182	Odonates, gregarines and water mites: why are the same host species infected by both parasites?. <i>Ecological Entomology</i> , 2018, 43, 591-600.	1.1	10
183	The Messinian imprint on the evolution of freshwater fishes of the genus <i>Luciobarbus</i> Heckel, 1843 (Teleostei, Cyprinidae) in the western Mediterranean. <i>Journal of Biogeography</i> , 2018, 45, 1593-1603.	1.4	12
184	Visualization of Biomedical Networks. , 2019, , 1016-1035.		2

#	ARTICLE	IF	CITATIONS
185	Inference of Horizontal Gene Transfer: Gaining Insights Into Evolution via Lateral Acquisition of Genetic Material. , 2019, , 953-964.		2
186	Horizontal Gene Transfer and Genome Evolution in the Phylum Actinobacteria. , 2019, , 155-174.		9
187	Properties of the generalized Robinson-Foulds metric. , 2019, , .		2
188	Bioinformatics Tools for Microbial Diversity Analysis. , 2019, , 23-47.		1
189	Characterizing the Twitter network of prominent politicians and SPLC-defined hate groups in the 2016 US presidential election. Social Network Analysis and Mining, 2019, 9, 1.	1.9	14
190	A Suggestion of Converting Protein Intrinsic Disorder to Structural Entropy Using Shannon's Information Theory. Entropy, 2019, 21, 591.	1.1	2
191	A new species of penzigoid <i>Xylaria</i> (Xylariaceae) from the cloud forest in eastern Mexico revealed through morphological and phylogenetic analyses. Botany, 2019, 97, 381-389.	0.5	3
192	191 Early weaning in pigs induces long-term alterations in intestinal nutrient transporter function and expression partially via beta adrenergic enteric neural receptors. Journal of Animal Science, 2019, 97, 112-113.	0.2	0
193	Automated methods for the investigation of language contact, with a focus on lexical borrowing. Language and Linguistics Compass, 2019, 13, e12355.	1.3	13
194	Domestic sheep and bighorn sheep carry distinct gammaherpesviruses belonging to the genus Macavirus. Virus Research, 2019, 272, 197729.	1.1	5
195	Occurrence and distribution of Amphidomataceae (Dinophyceae) in Danish coastal waters of the North Sea, the Limfjord and the Kattegat/Belt area. Harmful Algae, 2019, 88, 101637.	2.2	16
196	Phylogeny and phylogeography of the genus <i>Luciobarbus</i> (Haeckel, 1843) in Algeria inferred from mitochondrial DNA sequence variation. Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2019, 30, 332-344.	0.7	6
197	Introducing a new Austropotamobius crayfish species (Crustacea, Decapoda, Astacidae): A Miocene endemism of the Apuseni Mountains, Romania. Zoologischer Anzeiger, 2019, 279, 94-102.	0.4	24
198	Distribution and Diversity of Cytochrome P450 Monooxygenases in the Fungal Class Tremellomycetes. International Journal of Molecular Sciences, 2019, 20, 2889.	1.8	12
199	Using INC Within Divide-and-Conquer Phylogeny Estimation. Lecture Notes in Computer Science, 2019, , 167-178.	1.0	5
200	Evolview v3: a webserver for visualization, annotation, and management of phylogenetic trees. Nucleic Acids Research, 2019, 47, W270-W275.	6.5	564
201	Yap1b, a divergent Yap/Taz family member, cooperates with yap1 in survival and morphogenesis via common transcriptional targets. Development (Cambridge), 2019, 146, .	1.2	10
202	Evolution and functional differentiation of recently diverged phytochelatin synthase genes from <i>Arundo donax</i> L.. Journal of Experimental Botany, 2019, 70, 5391-5405.	2.4	15

#	ARTICLE	IF	CITATIONS
203	NGPhylogeny.fr: new generation phylogenetic services for non-specialists. <i>Nucleic Acids Research</i> , 2019, 47, W260-W265.	6.5	489
204	Cytochrome P450 Monooxygenase CYP139 Family Involved in the Synthesis of Secondary Metabolites in 824 Mycobacterial Species. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2690.	1.8	13
205	Cryptic speciation in <i>Protoceratium reticulatum</i> (Dinophyceae): Evidence from morphological, molecular and ecophysiological data. <i>Harmful Algae</i> , 2019, 88, 101610.	2.2	32
207	Morphology, ultrastructure and molecular phylogeny of cyst-producing <i>Caladoa arcachonensis</i> gen. et sp. nov. (Peridinales, Dinophyceae) from France and Indonesia. <i>European Journal of Phycology</i> , 2019, 54, 235-248.	0.9	11
208	The complete mitochondrial genome of the kelp fly <i>Fucellia costalis</i> (Diptera: Anthomyiidae) from Pacific Grove, California. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 162-163.	0.2	1
209	Different Evolutionary Trajectories of Two Insect-Specific Paralogous Proteins Involved in Stabilizing Muscle Myofibrils. <i>Genetics</i> , 2019, 212, 743-755.	1.2	13
210	The complete mitogenome of the invasive Japanese mud snail <i>Batillaria attramentaria</i> (Gastropoda: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 4031-4032.	0.2	2
211	Multilocus Sequence Typing (MLST) and Random Polymorphic DNA (RAPD) Comparisons of Geographic Isolates of <i>Neoparamoeba perurans</i> , the Causative Agent of Amoebic Gill Disease. <i>Pathogens</i> , 2019, 8, 244.	1.2	1
212	Genetic Diversity and Structure of Channel Catfish from Continental Waters of Mexico. <i>North American Journal of Aquaculture</i> , 2019, 81, 74-80.	0.7	2
213	A bacterial [4Fe 4S] ferredoxin as redox partner of the plastidic-type ferredoxin-NADP+ reductase from <i>Leptospira interrogans</i> . <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2019, 1863, 651-660.	1.1	4
214	Phylogenomics and multigene phylogenies decipher two new cryptic marine algae from California, <i>Gelidium gabrielsonii</i> and <i>G. Akathyanniae</i> (Gelidiales, Rhodophyta). <i>Journal of Phycology</i> , 2019, 55, 160-172.	1.0	22
215	There it is! <i>Fusarium pseudograminearum</i> did not lose the fusaristatin gene cluster after all. <i>Fungal Biology</i> , 2019, 123, 10-17.	1.1	12
216	Patterns of mutation within an emerging endemic lineage of HEV. <i>Journal of Viral Hepatitis</i> , 2019, 26, 191-198.	1.0	5
217	Elucidation of conformational diversity of druggable enzymes and classification of chemical modulators based on inhibitor-bound structures. <i>Journal of Biomolecular Structure and Dynamics</i> , 2019, 37, 4563-4568.	2.0	2
218	Taxonomic revision, phylogeny, and cyst wall composition of the dinoflagellate cyst genus <i>Votadinium</i> Reid (Dinophyceae, Peridinales, Protoperidiniaceae). <i>Palynology</i> , 2020, 44, 310-335.	0.7	12
219	Phylogenetic determinants of toxin gene distribution in genomes of <i>Brevibacillus laterosporus</i> . <i>Genomics</i> , 2020, 112, 1042-1053.	1.3	19
220	Characterization of the unarmored dinoflagellate <i>Pseliodinium pirum</i> (Ceratoperidiniaceae) from Jiaozhou Bay, China. <i>Phycological Research</i> , 2020, 68, 3-13.	0.8	7
221	Attributing <i>Ceratocorys</i> , <i>Pentaplaconium</i> and <i>Protoceratium</i> to Protoceratiaceae (Dinophyceae), with descriptions of <i>Ceratocorys malayensis</i> sp. nov. and <i>Pentaplaconium usupianum</i> sp. nov. <i>Phycologia</i> , 2020, 59, 6-23.	0.6	10

#	ARTICLE	IF	CITATIONS
222	Proof of homothally of Pheopolykrikos hartmannii and details of cyst germination process. Journal of Oceanology and Limnology, 2020, 38, 114-123.	0.6	5
223	The origin of chromosomal histones in a 30S ribosomal protein. Gene, 2020, 726, 144155.	1.0	1
224	The in silico characterization of neutral alpha-glucosidase C (GANC) and its evolution from GANAB. Gene, 2020, 726, 144192.	1.0	0
225	Evolutionary relationships among bifidobacteria and their hosts and environments. BMC Genomics, 2020, 21, 26.	1.2	26
226	Subsurface Stappia: Success Through Defence, Specialisation and Putative Pressure-Dependent Carbon Fixation. Microbial Ecology, 2020, 80, 34-46.	1.4	9
227	Amphidomataceae (Dinophyceae) in the western Greenland area, including description of <i>Azadinium perforatum</i> sp. nov. Phycologia, 2020, 59, 63-88.	0.6	16
228	Visualization of evolutionary relationships through geologic time in Timescale Creator. Applied Computing and Geosciences, 2020, 8, 100037.	1.0	3
229	More P450s Are Involved in Secondary Metabolite Biosynthesis in Streptomyces Compared to Bacillus, Cyanobacteria, and Mycobacterium. International Journal of Molecular Sciences, 2020, 21, 4814.	1.8	20
230	In silico functional and evolutionary analyses of rubber oxygenases (RoxA and RoxB). 3 Biotech, 2020, 10, 376.	1.1	2
231	Counting phylogenetic networks of level 1 and 2. Journal of Mathematical Biology, 2020, 81, 1357-1395.	0.8	13
232	Evolution of Poecilimon jonicus group (Orthoptera: Tettigoniidae): a history linked to the Aegean Neogene paleogeography. Organisms Diversity and Evolution, 2020, 20, 803-819.	0.7	6
233	The tree of life of polyamine oxidases. Scientific Reports, 2020, 10, 17858.	1.6	12
234	Impact of lifestyle on cytochrome P450 monooxygenase repertoire is clearly evident in the bacterial phylum Firmicutes. Scientific Reports, 2020, 10, 13982.	1.6	22
235	Next generation sequencing-aided comprehensive geographic coverage sheds light on the status of rare and extinct populations of <i>Aporia</i> butterflies (Lepidoptera: Pieridae). Scientific Reports, 2020, 10, 13970.	1.6	4
236	Differences in the Formation Mechanism of Giant Colonies in Two <i>Phaeocystis globosa</i> Strains. International Journal of Molecular Sciences, 2020, 21, 5393.	1.8	11
237	Comparative analyses and structural insights of new class glutathione transferases in <i>Cryptosporidium</i> species. Scientific Reports, 2020, 10, 20370.	1.6	4
238	Reclassification of <i>Gonyaulax verior</i> (Gonyaulacales, Dinophyceae) as <i>Sourniaea diacantha</i> gen. et comb. nov. Phycologia, 2020, 59, 246-260.	0.6	7
239	Task partitioning in ants lacking discrete morphological worker subcastes. Behavioral Ecology and Sociobiology, 2020, 74, 1.	0.6	7

#	ARTICLE	IF	CITATIONS
240	Optimizing taxon addition order and branch lengths in the construction of phylogenetic trees using maximum likelihood. <i>Journal of Bioinformatics and Computational Biology</i> , 2020, 18, 2050003.	0.3	4
241	Transposon activation is a major driver in the genome evolution of cultivated olive trees (<i>Olea</i> Tj ETQq1 1 0.784314 rgBT/Overlo 1.6 54	1.6	54
242	Genetic differentiation and phylogenetic potential of <i>Ty3/Gypsy</i> LTR retrotransposon markers in soil and plant pathogenic fungi. <i>Journal of Basic Microbiology</i> , 2020, 60, 508-516.	1.8	1
243	GenomeScope 2.0 and Smudgeplot for reference-free profiling of polyploid genomes. <i>Nature Communications</i> , 2020, 11, 1432.	5.8	660
244	Morpho-Physiological and Genomic Evaluation of Juglans Species Reveals Regional Maladaptation to Cold Stress. <i>Frontiers in Plant Science</i> , 2020, 11, 229.	1.7	6
245	Characterization of Tanzanian Avocado Using Morphological Traits. <i>Diversity</i> , 2020, 12, 64.	0.7	7
246	The complete mitochondrial and plastid genomes of the invasive marine red alga <i>Caulacanthus okamurae</i> (Caulacanthaceae, Rhodophyta) from Moss Landing, California, USA. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2067-2069.	0.2	2
247	Comparative Analysis, Structural Insights, and Substrate/Drug Interaction of CYP128A1 in <i>Mycobacterium tuberculosis</i> . <i>International Journal of Molecular Sciences</i> , 2020, 21, 4816.	1.8	7
248	Transfer index, NetUniFrac and some useful shortest path-based distances for community analysis in sequence similarity networks. <i>Bioinformatics</i> , 2020, 36, 2740-2749.	1.8	2
249	Characterization and diversity of the complete set of GH family 3 enzymes from <i>Rhodothermus marinus</i> DSM 4253. <i>Scientific Reports</i> , 2020, 10, 1329.	1.6	9
250	Comprehensive Analyses of Cytochrome P450 Monooxygenases and Secondary Metabolite Biosynthetic Gene Clusters in Cyanobacteria. <i>International Journal of Molecular Sciences</i> , 2020, 21, 656.	1.8	21
251	Taxogenomic assessment and genomic characterisation of <i>Weissella cibaria</i> strain 92 able to metabolise oligosaccharides derived from dietary fibres. <i>Scientific Reports</i> , 2020, 10, 5853.	1.6	15
252	A Widely Distributed Thraustochytrid Parasite of Diatoms Isolated from the Arctic Represents a gen. and sp. nov.. <i>Journal of Eukaryotic Microbiology</i> , 2020, 67, 480-490.	0.8	11
253	The Evolutionary and Functional Paradox of Cerato-platanins in Fungi. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	22
254	De novo assembly of the olive fruit fly (<i>Bactrocera oleae</i>) genome with linked-reads and long-read technologies minimizes gaps and provides exceptional Y chromosome assembly. <i>BMC Genomics</i> , 2020, 21, 259.	1.2	21
255	Distance-based phylogenetic inference from typing data: a unifying view. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	8
256	Morphology, ultrastructure and molecular phylogeny of <i>Johsia chumphonensis</i> gen. et sp. nov. and <i>Parvodinium parvulum</i> comb. nov. (Peridiniopsidaceae, Dinophyceae). <i>European Journal of Phycology</i> , 2021, 56, 324-336.	0.9	4
257	Multiple New Strains of Amphidomataceae (Dinophyceae) from the North Atlantic Revealed a High Toxin Profile Variability of <i>Azadinium spinosum</i> and a New Non-Toxicogenic <i>Az. cf. spinosum</i> . <i>Microorganisms</i> , 2021, 9, 134.	1.6	11

#	ARTICLE	IF	CITATIONS
258	Roles of Bioinformatics in Reproductive Science. , 2021, , 203-228.		2
259	Horizontal gene transfer and recombination analysis of SARS-CoV-2 genes helps discover its close relatives and shed light on its origin. BMC Ecology and Evolution, 2021, 21, 5.	0.7	44
261	Evolutionary Constraint on Visual and Nonvisual Mammalian Opsins. Journal of Biological Rhythms, 2021, 36, 109-126.	1.4	22
262	Crystal structure of the 6-phosphogluconate dehydrogenase from <i>Gluconobacter oxydans</i> reveals tetrameric 6PGDHs as the crucial intermediate in the evolution of structure and cofactor preference in the 6PGDH family. Wellcome Open Research, 0, 6, 48.	0.9	2
264	In Silico Analysis of P450s and Their Role in Secondary Metabolism in the Bacterial Class Gammaproteobacteria. Molecules, 2021, 26, 1538.	1.7	11
265	VERSO: A comprehensive framework for the inference of robust phylogenies and the quantification of intra-host genomic diversity of viral samples. Patterns, 2021, 2, 100212.	3.1	26
266	Descripci3n de la segunda especie del g3nero <i>Euacanth</i> (Scortechiniaceae, Coronophorales), de 3reas verdes urbanas y periurbanas de Xalapa, M3xico. Acta Botanica Mexicana, 2021, , .	0.1	2
267	Non-canonical substrates for terpene synthases in bacteria are synthesized by a new family of methyltransferases. FEMS Microbiology Reviews, 2021, 45, .	3.9	3
268	Ancient Bacterial Class Alphaproteobacteria Cytochrome P450 Monooxygenases Can Be Found in Other Bacterial Species. International Journal of Molecular Sciences, 2021, 22, 5542.	1.8	9
269	At least three families of hyphosphere small secreted cysteine-rich proteins can optimize surface properties to a moderately hydrophilic state suitable for fungal attachment. Environmental Microbiology, 2021, 23, 5750-5768.	1.8	12
270	The occurrence of Nematoda in coastal sea ice on Svalbard (European Arctic) determined with the 18S small subunit rRNA gene. Polar Biology, 2021, 44, 1153-1162.	0.5	4
271	A comprehensive molecular approach to the detection of drug-type versus fiber-type hemp varieties. Forensic Science International: Genetics, 2021, 52, 102464.	1.6	4
272	Diversity and distribution of harmful microalgae in the Gulf of Thailand assessed by DNA metabarcoding. Harmful Algae, 2021, 106, 102063.	2.2	18
273	The complete mitochondrial genome of the strawberry aphid <i>Chaetosiphon fragaefolii</i> Cockerell, 1901 (Hemiptera: Aphididae) from California, USA. Mitochondrial DNA Part B: Resources, 2021, 6, 2373-2375.	0.2	1
274	Experimental and Genomic Evaluation of the Oestrogen Degrading Bacterium <i>Rhodococcus equi</i> ATCC13557. Frontiers in Microbiology, 2021, 12, 670928.	1.5	2
275	Cyst-theca relationships of <i>Spiniferites bentorii</i> , <i>S. hyperacanthus</i> , <i>S. ramosus</i> , <i>S. scabratus</i> and molecular phylogenetics of <i>Spiniferites</i> and <i>Tectatodinium</i> (Gonyaulacales,) Tj ETQq1 1 0.784314 rgBtdOverlock 10 Tf 50		
276	Phylogenetic placement of <i>Flacillula</i> Strand, 1932 with seven new species from Sri Lanka (Araneae: Salticidae). Journal of Zoological Systematics and Evolutionary Research, 2021, 59, 1255-1272.	0.6	1
278	Reinstatement of Indian Ocean <i>Porolithon coarctatum</i> and <i>P. Agardineri</i> based on sequencing type specimens, and <i>P. Aepiphyticum</i> <i>sp. nov.</i> (Corallinales, Rhodophyta), with comments on subfamilies Hydrolithoideae and Metagoniolithoideae. Botanica Marina, 2021, 64, 363-377.	0.6	3

#	ARTICLE	IF	CITATIONS
279	Crystal structure of restriction endonuclease Kpn2I of CCGG-family. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2021, 1865, 129926.	1.1	0
280	Review of the cardinalfishes of the genus <i>Cercamia</i> (Percomorpha: Apogonidae) of the Red Sea and Indian Ocean with descriptions of three new species. <i>Zootaxa</i> , 2021, 5039, 363-394.	0.2	0
281	Dynamics of the Toxic Dinoflagellate <i>Alexandrium pacificum</i> in the Taiwan Strait and Its Linkages to Surrounding Populations. <i>Water (Switzerland)</i> , 2021, 13, 2681.	1.2	6
282	The maintenance of polymorphism in an ancient social supergene. <i>Molecular Ecology</i> , 2021, 30, 6246-6258.	2.0	13
283	Evolutionary Subdivision of Domestic Chickens: Implications for Local Breeds as Assessed by Phenotype and Genotype in Comparison to Commercial and Fancy Breeds. <i>Agriculture (Switzerland)</i> , 2021, 11, 914.	1.4	14
285	Morphological and molecular characterization of multiple new <i>Azadinium</i> strains revealed a high diversity of non-toxic species of <i>Amphidomataceae</i> (Dinophyceae) including two new <i>Azadinium</i> species in Irish waters, North East Atlantic. <i>Phycological Research</i> , 2021, 69, 88-115.	0.8	9
286	Influence of expertise on semantic categorization of wine odors. <i>Food Quality and Preference</i> , 2020, 83, 103923.	2.3	12
287	Global landscape of cell envelope protein complexes in <i>Escherichia coli</i> . <i>Nature Biotechnology</i> , 2018, 36, 103-112.	9.4	110
289	Phylogeny affects host's weight, immune response and parasitism in damselflies and dragonflies. <i>Royal Society Open Science</i> , 2016, 3, 160421.	1.1	19
297	Phylogenetic Relatedness of Circulating HIV-1C Variants in Mochudi, Botswana. <i>PLoS ONE</i> , 2013, 8, e80589.	1.1	33
298	Echinococcus P29 Antigen: Molecular Characterization and Implication on Post-Surgery Follow-Up of CE Patients Infected with Different Species of the <i>Echinococcus granulosus</i> Complex. <i>PLoS ONE</i> , 2014, 9, e98357.	1.1	29
299	Assessment of Species Diversity and Distribution of an Ancient Diatom Lineage Using a DNA Metabarcoding Approach. <i>PLoS ONE</i> , 2014, 9, e103810.	1.1	39
300	Impact of the choice of reference genome on the ability of the core genome SNV methodology to distinguish strains of <i>Salmonella enterica</i> serovar Heidelberg. <i>PLoS ONE</i> , 2018, 13, e0192233.	1.1	18
301	Genetic analysis of the endangered Cleveland Bay horse: A century of breeding characterised by pedigree and microsatellite data. <i>PLoS ONE</i> , 2020, 15, e0240410.	1.1	6
302	Habitat conditions drive phylogenetic structure of dominant bacterial phyla of microbialite communities from different locations in Mexico. <i>Revista De Biologia Tropical</i> , 2016, 64, 1057-65.	0.1	7
303	Fat storage-inducing transmembrane (FIT or FITM) proteins are related to lipid phosphatase/phosphotransferase enzymes. <i>Microbial Cell</i> , 2018, 5, 88-103.	1.4	46
304	The In Silico Drug Discovery Toolbox: Applications in Lead Discovery and Optimization. <i>Current Medicinal Chemistry</i> , 2019, 26, 3838-3873.	1.2	47
305	DEAD/DEXH-Box RNA Helicases in Selected Human Parasites. <i>Korean Journal of Parasitology</i> , 2015, 53, 583-595.	0.5	17

#	ARTICLE	IF	CITATIONS
306	Genetic and Pharmacological Inhibition of Autophagy Increases the Monoubiquitination of Non-Photosynthetic Phosphoenolpyruvate Carboxylase. <i>Plants</i> , 2021, 10, 12.	1.6	4
307	Morphometrics and phylogeography of the cave-obligate land snail <i>Helicodiscus barri</i> (Gastropoda,) Tj ETQq1 1 0.784314 rgBT/Overlock 10	3.0	10
308	At home at least: the taxonomic position of some north African <i>Xerocrassa</i> species (Pulmonata,) Tj ETQq0 0 0 rgBT/Overlock 5 10 Tf 50 6	0.5	5
309	Multilocus genetic and morphological phylogenetic analysis reveals a radiation of shiny South Asian jumping spiders (Araneae, Salticidae). <i>ZooKeys</i> , 2019, 839, 1-81.	0.5	7
310	Phylogenetic analysis of cubilin (CUBN) gene. <i>Bioinformatics</i> , 2013, 9, 29-36.	0.2	5
311	ASPEN, a methodology for reconstructing protein evolution with improved accuracy using ensemble models. <i>ELife</i> , 2019, 8, .	2.8	4
312	Diversification of Ferredoxins across Living Organisms. <i>Current Issues in Molecular Biology</i> , 2021, 43, 1374-1390.	1.0	9
313	Retrospective Genotyping and Whole Genome Sequencing of a Canine Parvovirus Outbreak in Bangladesh. <i>Pathogens</i> , 2021, 10, 1373.	1.2	0
314	Ion transporters and their exploration for conferring abiotic stress tolerance in plants. <i>Plant Growth Regulation</i> , 2022, 96, 1-23.	1.8	6
319	Adapting Reproducible Research Capabilities to Resilient Distributed Calculations. <i>International Journal of Grid and High Performance Computing</i> , 2016, 8, 58-69.	0.7	0
324	Brotherhoods of relative entropy, boolean operators and principle component analysis for a gradient of living communities. <i>Turkish Journal of Forestry Türkiye Ormancılık Dergisi</i> , 0, , 130-137.	0.1	0
325	Minimum-Width Drawings of Phylogenetic Trees. <i>Lecture Notes in Computer Science</i> , 2019, , 39-55.	1.0	2
330	Cultivation of a vampire: <i>Candidatus Absconditicoccus praedator</i> ™. <i>Environmental Microbiology</i> , 2022, 24, 30-49.	1.8	30
331	Phylogenetic relationships and systematics of the jumping spider genus <i>Colopsus</i> with the description of eight new species from Sri Lanka (Araneae: Salticidae). <i>Journal of Natural History</i> , 2020, 54, 2763-2814.	0.2	7
332	Characterisation of a putative M23-domain containing protein in <i>Mycobacterium tuberculosis</i> . <i>PLoS ONE</i> , 2021, 16, e0259181.	1.1	4
333	Morphological and molecular identification of new records and new host plants of powdery mildews (Erysiphaceae) from Mexico. <i>Botany</i> , 0, , .	0.5	1
335	Characterization of <i>Amphidinium</i> (Amphidinales, Dinophyceae) species from the China Sea based on morphological, molecular, and pigment data. <i>Journal of Oceanology and Limnology</i> , 0, , 1.	0.6	2
336	Unraveling the <i>Gonyaulax baltica</i> Species Complex: Cystotheca Relationship of <i>Impagidinium variaseptum</i> , <i>Spiniferites pseudodelicatus</i> sp. nov. and <i>S. ristingensis</i> (Gonyaulacaceae, Dinophyceae), With Descriptions of <i>Gonyaulax bohaiensis</i> sp. nov., <i>G. amoyensis</i> sp. nov. and <i>G. portimonensis</i> sp. nov., <i>Journal of Phycology</i> , 2022, 58, 465-486.	1.0	7

#	ARTICLE	IF	CITATIONS
337	Two toxigenic <i>Ostreopsis</i> species, <i>O. cf. ovata</i> and <i>O. siamensis</i> (Dinophyceae), from the South China Sea, tropical Western Pacific. <i>Harmful Algae</i> , 2022, 113, 102206.	2.2	5
338	Genomic Insights into the Distribution of Peptidases and Proteolytic Capacity among <i>Prevotella</i> and <i>Paraprevotella</i> Species. <i>Microbiology Spectrum</i> , 2022, 10, e0218521.	1.2	10
339	Characterization and distribution of kisspeptins, kisspeptin receptors, GnIH, and GnRH1 in the brain of the protogynous bluehead wrasse (<i>Thalassoma bifasciatum</i>). <i>Journal of Chemical Neuroanatomy</i> , 2022, 121, 102087.	1.0	3
340	Occurrence of parasitic infections in a <i>Margalefidinium polykrikoides</i> (Dinophyceae) bloom in the Taiwan Strait in 2018. <i>Journal of Sea Research</i> , 2022, 183, 102190.	0.6	0
341	Complete Genome Sequence, Molecular Characterization and Phylogenetic Relationships of a Novel Tern Atadenovirus. <i>Microorganisms</i> , 2022, 10, 31.	1.6	3
342	<i>Amphidinium stirisquamum</i> sp. nov. (Dinophyceae), a new marine sand-dwelling dinoflagellate with a novel type of body scale. <i>Algae</i> , 2021, 36, 241-261.	0.9	5
343	Caseinolytic Proteins (Clp) in the Genus <i>Klebsiella</i> : Special Focus on ClpK. <i>Molecules</i> , 2022, 27, 200.	1.7	2
344	Well-Behaved Variants Seldom Make the Apparatus: Stemmata and Apparatus in Digital Research. <i>Digital Medievalist</i> , 2021, 14, .	0.1	4
345	Draft Genome Sequence of <i>Desulfovibrio</i> sp. Strain CSMB_222, Isolated from Coal Seam Formation Water. <i>Microbiology Resource Announcements</i> , 2021, 10, e0056421.	0.3	2
349	Building alternative consensus trees and supertrees using <i>k</i> -means and Robinson and Foulds distance. <i>Bioinformatics</i> , 2022, 38, 3367-3376.	1.8	2
350	An Unprecedented Number of Cytochrome P450s Are Involved in Secondary Metabolism in <i>Salinispora</i> Species. <i>Microorganisms</i> , 2022, 10, 871.	1.6	8
351	Contrasting Health Effects of Bacteroidetes and Firmicutes Lies in Their Genomes: Analysis of P450s, Ferredoxins, and Secondary Metabolite Clusters. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5057.	1.8	17
352	Phylogenetic placement of <i>Carrhotus</i> Thorell, 1891 with three new species from Sri Lanka (Araneae: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 0.6	0.6	1
353	Co-occurrence of <i>Alexandrium minutum</i> (Dinophyceae) ribotypes from the Chinese and Malaysian coastal waters and their toxin production. <i>Harmful Algae</i> , 2022, 115, 102238.	2.2	5
355	Lifestyles Shape the Cytochrome P450 Repertoire of the Bacterial Phylum Proteobacteria. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5821.	1.8	7
356	Genomic analysis of a Nile tilapia strain selected for salinity tolerance shows signatures of selection and hybridization with blue tilapia (<i>Oreochromis aureus</i>). <i>Aquaculture</i> , 2022, 560, 738527.	1.7	11
357	Isolation of <i>Listeria ivanovii</i> from Bulk-Tank Milk of Sheep and Goat Farms—From Clinical Work to Bioinformatics Studies: Prevalence, Association with Milk Quality, Antibiotic Susceptibility, Predictors, Whole Genome Sequence and Phylogenetic Relationships. <i>Biology</i> , 2022, 11, 871.	1.3	3
358	Endosymbiont population genomics sheds light on transmission mode, partner specificity, and stability of the scaly-foot snail holobiont. <i>ISME Journal</i> , 2022, 16, 2132-2143.	4.4	6

#	ARTICLE	IF	CITATIONS
359	The CRISPR/Cas Machinery Evolution and Gene Flow in the Hot Spring Cyanobacterium <i>Thermotrichus</i> . <i>Diversity</i> , 2022, 14, 502.	0.7	2
360	New Reports of <i>Phytophthora</i> Species in Plant Nurseries in Spain. <i>Pathogens</i> , 2022, 11, 826.	1.2	7
361	Establishing a taxonomy of metal subgenres based on quantitative musical and thematic features. <i>Metal Music Studies</i> , 2022, 8, 183-203.	0.9	2
362	Morphologic and phylogenic characterization of two bloom-forming planktonic <i>Prorocentrum</i> (Dinophyceae) species and their potential distribution in the China Sea. <i>Algal Research</i> , 2022, 66, 102788.	2.4	4
363	De novo determination of mosquitocidal Cry11Aa and Cry11Ba structures from naturally-occurring nanocrystals. <i>Nature Communications</i> , 2022, 13, .	5.8	9
364	Semicyptic Diversity around <i>Chaetoceros elegans</i> (Bacillariophyta, Mediophyceae), and the Description of Two New Species. <i>Diversity</i> , 2022, 14, 676.	0.7	1
365	Molecular Phylogenetic Analysis of Salt-Tolerance-Related Genes in Root-Nodule Bacteria Species <i>Sinorhizobium meliloti</i> . <i>Agronomy</i> , 2022, 12, 1968.	1.3	3
366	<i>Desulfuromonas</i> sp. 'CSMB_57â€™™, isolation and genomic insights from the most abundant bacterial taxon in eastern Australian coals. <i>Microbial Genomics</i> , 2022, 8, .	1.0	0
367	Morphological and molecular characterization of the genus <i>Coolia</i> (Dinophyceae) from Bah� de La Paz, southwest Gulf of California. <i>Algae</i> , 2022, 37, 185-204.	0.9	4
368	virDTL: Viral Recombination Analysis Through Phylogenetic Reconciliation and Its Application to Sarbecoviruses and SARS-CoV-2. <i>Journal of Computational Biology</i> , 2023, 30, 3-20.	0.8	0
369	Using Genomes and Evolutionary Analyses to Screen for Host-Specificity and Positive Selection in the Plant Pathogen <i>Xylella fastidiosa</i> . <i>Applied and Environmental Microbiology</i> , 2022, 88, .	1.4	6
371	A new marine epipsammic diatom species, <i>Ambo dajingensis</i> sp. nov. (Bacillariophyceae), from the coast of Southeast China. <i>PhytoKeys</i> , 0, 210, 23-34.	0.4	0
372	Genome Comparison on Succinct Colored de Bruijn Graphs. <i>Lecture Notes in Computer Science</i> , 2022, , 165-177.	1.0	0
373	Comparative Analysis of Molecular RFLP and SNP Markers in Assessing and Understanding the Genetic Diversity of Various Chicken Breeds. <i>Genes</i> , 2022, 13, 1876.	1.0	3
374	Cryptic speciation of benthic <i>Prorocentrum</i> (Dinophyceae) species and their potential as ecological indicators. <i>Journal of Sea Research</i> , 2022, , 102304.	0.6	1
375	<i>Pentaplaconium lapazense</i> sp. nov. from Central and Southern Gulf of California, a new non-toxic gonyaulaclean resembling <i>Protoceratium reticulatum</i> . <i>Marine Micropaleontology</i> , 2023, 178, 102187.	0.5	2
376	Combined Culture and DNA Metabarcoding Analysis of Cyanobacterial Community Structure in Response to Coral Reef Health Status in the South China Sea. <i>Journal of Marine Science and Engineering</i> , 2022, 10, 1984.	1.2	4
377	More than Just Protein Degradation: The Regulatory Roles and Moonlighting Functions of Extracellular Proteases Produced by Fungi Pathogenic for Humans. <i>Journal of Fungi (Basel)</i> , 2022, 7, 1075.	0.784314	10

#	ARTICLE	IF	CITATIONS
378	Unraveling signatures of chicken genetic diversity and divergent selection in breed-specific patterns of early myogenesis, nitric oxide metabolism and post-hatch growth. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1
380	Metabarcoding revealed a high diversity of Amphidomataceae (Dinophyceae) and the seasonal distribution of their toxigenic species in the Taiwan Strait. <i>Harmful Algae</i> , 2023, 124, 102404.	2.2	2
381	HexSE: Simulating evolution in overlapping reading frames. <i>Virus Evolution</i> , 2023, 9, .	2.2	0
382	Evolution of Cytochrome P450 Enzymes and Their Redox Partners in Archaea. <i>International Journal of Molecular Sciences</i> , 2023, 24, 4161.	1.8	8
383	GPTree Cluster: phylogenetic tree cluster generator in the context of supertree inference. <i>Bioinformatics Advances</i> , 2023, 3, .	0.9	0
384	Genetic Structure Analysis of 155 Transboundary and Local Populations of Cattle (<i>Bos taurus</i> , <i>Bos</i>) Tj ETQq1 1 0.784314 rgBT /Overl... 24, 5061.	1.8	1
385	A complete theoretical framework for inferring horizontal gene transfers using partial order sets. <i>PLoS ONE</i> , 2023, 18, e0281824.	1.1	1
386	Genome Organization of Four Brazilian <i>Xanthomonas albilineans</i> Strains Does Not Correlate with Aggressiveness. <i>Microbiology Spectrum</i> , 0, , .	1.2	1
395	Phylogenetic Analysis of Reticulate Software Evolution. , 2023, , .		0
399	Inferring Multiple Consensus Trees and Supertrees Using Clustering: A Review. <i>Springer Optimization and Its Applications</i> , 2023, , 191-213.	0.6	0
400	Phylogenomics using Compression Distances: Incorporating Rate Heterogeneity and Amino Acid Properties. , 2023, , .		0