

# RAxML-III: a fast program for maximum likelihood-based trees

Bioinformatics

21, 456-463

DOI: [10.1093/bioinformatics/bti191](https://doi.org/10.1093/bioinformatics/bti191)

Citation Report

#	ARTICLE	IF	CITATIONS
1	Parallel and Distributed Computation of Large Phylogenetic Trees. , 2005, , 325-346.		3
2	Shortest triplet clustering: reconstructing large phylogenies using representative sets. BMC Bioinformatics, 2005, 6, 92.	1.2	34
5	Improving the efficiency of SPR moves in phylogenetic tree search methods based on maximum likelihood. Bioinformatics, 2005, 21, 4338-4347.	1.8	209
6	RAxML-OMP: An Efficient Program for Phylogenetic Inference on SMPs. Lecture Notes in Computer Science, 2005, , 288-302.	1.0	80
7	Phylogenetic diversity and ecology of environmental Archaea. Current Opinion in Microbiology, 2005, 8, 638-642.	2.3	120
8	Obesity alters gut microbial ecology. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 11070-11075.	3.3	5,247
9	Phylogenomics. Annual Review of Ecology, Evolution, and Systematics, 2005, 36, 541-562.	3.8	303
12	Phylogenetic models of rate heterogeneity: a high performance computing perspective. , 2006, , .		211
13	Phylogenetic Analyses of Parasites in the New Millennium. Advances in Parasitology, 2006, 63, 1-124.	1.4	35
14	DISTRIBUTION AND EVOLUTION OF GENETIC CASTE DETERMINATION IN Pogonomyrmex SEED-HARVESTER ANTS. Ecology, 2006, 87, 2171-2184.	1.5	58
15	Getting a Tree Fast: Neighbor Joining, FastME, and Distance-Based Methods. , 2006, Chapter 6, Unit 6.3.		25
16	Unexpected Diversity and Complexity of the Guerrero Negro Hypersaline Microbial Mat. Applied and Environmental Microbiology, 2006, 72, 3685-3695.	1.4	435
17	PBPI: a High Performance Implementation of Bayesian Phylogenetic Inference. , 2006, , .		17
18	Greengenes, a Chimera-Checked 16S rRNA Gene Database and Workbench Compatible with ARB. Applied and Environmental Microbiology, 2006, 72, 5069-5072.	1.4	9,859
19	Molecular characterization of phospholipid hydroperoxide glutathione peroxidases from Hydra vulgaris. Gene, 2006, 381, 1-12.	1.0	14
20	A five-gene phylogeny of Pezizomycotina. Mycologia, 2006, 98, 1018-1028.	0.8	280
21	RAxML-VI-HPC: maximum likelihood-based phylogenetic analyses with thousands of taxa and mixed models. Bioinformatics, 2006, 22, 2688-2690.	1.8	14,675
22	A genome-wide survey of the evolutionarily conserved Wnt pathways in the sea urchin Strongylocentrotus purpuratus. Developmental Biology, 2006, 300, 121-131.	0.9	76

#	ARTICLE	IF	CITATIONS
23	Lineage-specific expansions provide genomic complexity among sea urchin GTPases. <i>Developmental Biology</i> , 2006, 300, 165-179.	0.9	8
24	Eurotiomycetes: Eurotiomycetidae and Chaetothyriomycetidae. <i>Mycologia</i> , 2006, 98, 1053-1064.	0.8	91
25	A five-gene phylogeny of Pezizomycotina. <i>Mycologia</i> , 2006, 98, 1018-1028.	0.8	283
26	A molecular phylogeny of the flagellated fungi (Chytridiomycota) and description of a new phylum (Blastocladiomycota). <i>Mycologia</i> , 2006, 98, 860-871.	0.8	224
27	Identification of Three Distinct Phylogenetic Groups of CAX Cation/Proton Antiporters. <i>Journal of Molecular Evolution</i> , 2006, 63, 815-825.	0.8	166
28	UniFrac—an online tool for comparing microbial community diversity in a phylogenetic context. <i>BMC Bioinformatics</i> , 2006, 7, 371.	1.2	1,321
29	Phylogenetic Supermatrix Analysis of GenBank Sequences from 2228 Papilionoid Legumes. <i>Systematic Biology</i> , 2006, 55, 818-836.	2.7	148
30	Accomplishments and Challenges in High Performance Computing for Computational Biology. <i>Current Bioinformatics</i> , 2006, 1, 185-195.	0.7	1
31	Computational Grand Challenges in Assembling the Tree of Life: Problems and Solutions. <i>Advances in Computers</i> , 2006, , 127-176.	1.2	18
32	Biology—PBPI. , 2006, , .		14
33	Efficient Likelihood Computations with Nonreversible Models of Evolution. <i>Systematic Biology</i> , 2006, 55, 756-768.	2.7	132
34	Eurotiomycetes: Eurotiomycetidae and Chaetothyriomycetidae. <i>Mycologia</i> , 2006, 98, 1053-1064.	0.8	158
35	Evidence of Multiple Maximum Likelihood Points for a Phylogenetic Tree. , 2006, , .		2
36	Phylospaces: reconstructing evolutionary trees in tuple space. , 2006, , .		0
37	A molecular phylogeny of the flagellated fungi (Chytridiomycota) and description of a new phylum (Blastocladiomycota). <i>Mycologia</i> , 2006, 98, 860-871.	0.8	357
38	The sister group relation of Parmeliaceae (Lecanorales, Ascomycota). <i>Mycologia</i> , 2007, 99, 42-49.	0.8	20
39	Large-scale maximum likelihood-based phylogenetic analysis on the IBM BlueGene/L. , 2007, , .		84
40	Dynamic multigrain parallelization on the cell broadband engine. , 2007, , .		46

#	ARTICLE	IF	CITATIONS
41	Phylogeny Reconstruction. , 0, , 83-128.		1
42	MultiPhyl: a high-throughput phylogenomics webserver using distributed computing. <i>Nucleic Acids Research</i> , 2007, 35, W33-W37.	6.5	59
43	Phylogenomic Analysis Supports the Monophyly of Cryptophytes and Haptophytes and the Association of Rhizaria with Chromalveolates. <i>Molecular Biology and Evolution</i> , 2007, 24, 1702-1713.	3.5	218
44	Increasing the Efficiency of Searches for the Maximum Likelihood Tree in a Phylogenetic Analysis of up to 150 Nucleotide Sequences. <i>Systematic Biology</i> , 2007, 56, 988-1010.	2.7	65
45	New Approaches to Phylogenetic Tree Search and Their Application to Large Numbers of Protein Alignments. <i>Systematic Biology</i> , 2007, 56, 727-740.	2.7	30
46	PlantTribes: a gene and gene family resource for comparative genomics in plants. <i>Nucleic Acids Research</i> , 2007, 36, D970-D976.	6.5	93
47	Multiple Evolutionary Mechanisms Drive Papillomavirus Diversification. <i>Molecular Biology and Evolution</i> , 2007, 24, 1242-1258.	3.5	101
48	The sister group relation of Parmeliaceae (Lecanorales, Ascomycota). <i>Mycologia</i> , 2007, 99, 42-49.	0.8	29
49	Linking of Digital Images to Phylogenetic Data Matrices Using a Morphological Ontology. <i>Systematic Biology</i> , 2007, 56, 283-294.	2.7	84
50	Host origin of plastid solute transporters in the first photosynthetic eukaryotes. <i>Genome Biology</i> , 2007, 8, R212.	13.9	116
51	RAxML-Cell: Parallel Phylogenetic Tree Inference on the Cell Broadband Engine. , 2007, , .		30
52	Improving the Efficiency of p-ECR Moves in Evolutionary TreeSearch Methods Based on Maximum Likelihood by Neighbor Joining. , 2007, , .		9
53	Building the Tree of Life on Terascale Systems. , 2007, , .		11
54	Distributed and Generic Maximum Likelihood Evaluation. , 2007, , .		6
55	Quantitative and Qualitative $\hat{\Pi}^2$ Diversity Measures Lead to Different Insights into Factors That Structure Microbial Communities. <i>Applied and Environmental Microbiology</i> , 2007, 73, 1576-1585.	1.4	2,418
56	Varying the Sample Number for Monte Carlo Localization in Mobile Sensor Networks. , 2007, , .		8
57	Cytinaceae are sister to Muntingiaceae (Malvales). <i>Taxon</i> , 2007, 56, 1129-1135.	0.4	25
58	Construction and annotation of large phylogenetic trees. <i>Australian Systematic Botany</i> , 2007, 20, 287.	0.3	19

#	ARTICLE	IF	CITATIONS
59	Phylogenetic classification of Cordyceps and the clavicipitaceous fungi. <i>Studies in Mycology</i> , 2007, 57, 5-59.	4.5	800
60	Efficient Tree Searches with Available Algorithms. <i>Evolutionary Bioinformatics</i> , 2007, 3, 117693430700300.	0.6	41
61	Phylogenetic analysis of beta-papillomaviruses as inferred from nucleotide and amino acid sequence data. <i>Molecular Phylogenetics and Evolution</i> , 2007, 42, 213-222.	1.2	35
62	Phylogenetic comparison of protein-coding versus ribosomal RNA-coding sequence data: A case study of the Lecanoromycetes (Ascomycota). <i>Molecular Phylogenetics and Evolution</i> , 2007, 44, 412-426.	1.2	144
63	A multi-locus chloroplast phylogeny for the Cucurbitaceae and its implications for character evolution and classification. <i>Molecular Phylogenetics and Evolution</i> , 2007, 44, 553-577.	1.2	163
64	New methods for inferring population dynamics from microbial sequences. <i>Infection, Genetics and Evolution</i> , 2007, 7, 24-43.	1.0	18
65	Phylogenetic systematics of microorganisms inhabiting thermal environments. <i>Biochemistry (Moscow)</i> , 2007, 72, 1299-1312.	0.7	32
66	Metagenomic and functional analysis of hindgut microbiota of a wood-feeding higher termite. <i>Nature</i> , 2007, 450, 560-565.	13.7	1,181
67	Orthology prediction at scalable resolution by phylogenetic tree analysis. <i>BMC Bioinformatics</i> , 2007, 8, 83.	1.2	117
68	A Multigene Analysis of <i>Corallomyxa tenera</i> sp. nov. Suggests its Membership in a Clade that Includes <i>Gromia</i> , <i>Haplosporidia</i> and <i>Foraminifera</i> . <i>Protist</i> , 2007, 158, 457-472.	0.6	28
69	Marine fungal lineages in the Hypocreomycetidae. <i>Mycological Research</i> , 2007, 111, 154-162.	2.5	29
70	Using a multigene phylogenetic analysis to assess generic delineation and character evolution in Verrucariaceae (Verrucariales, Ascomycota). <i>Mycological Research</i> , 2007, 111, 1145-1168.	2.5	151
71	A 567â€œTaxon Data Set for Angiosperms: The Challenges Posed by Bayesian Analyses of Large Data Sets. <i>International Journal of Plant Sciences</i> , 2007, 168, 137-157.	0.6	143
72	Using Confidence Set Heuristics During Topology Search Improves the Robustness of Phylogenetic Inference. <i>Journal of Molecular Evolution</i> , 2007, 64, 80-89.	0.8	0
73	Exploring New Search Algorithms and Hardware for Phylogenetics: RAxML Meets the IBM Cell. <i>Journal of Signal Processing Systems</i> , 2007, 48, 271-286.	1.0	128
74	Gene Duplication in Early Vertebrates Results in Tissue-Specific Subfunctionalized Adaptor Proteins: CASP and GRASP. <i>Journal of Molecular Evolution</i> , 2008, 67, 168-178.	0.8	5
75	Strong mitochondrial DNA support for a Cretaceous origin of modern avian lineages. <i>BMC Biology</i> , 2008, 6, 6.	1.7	208
76	An even â€œnewerâ€œ animal phylogeny. <i>BioEssays</i> , 2008, 30, 1043-1047.	1.2	22

#	ARTICLE	IF	CITATIONS
77	Evolution of four BK virus subtypes. <i>Infection, Genetics and Evolution</i> , 2008, 8, 632-643.	1.0	43
78	Phylogenetic placement of diverse amoebae inferred from multigene analyses and assessment of clade stability within "Amoebozoa" upon removal of varying rate classes of SSU-rDNA. <i>Molecular Phylogenetics and Evolution</i> , 2008, 47, 339-352.	1.2	82
79	The oldest fossil evidence of animal parasitism by fungi supports a Cretaceous diversification of fungal-arthropod symbioses. <i>Molecular Phylogenetics and Evolution</i> , 2008, 49, 495-502.	1.2	189
80	Diversification of unicellular eukaryotes: cryptomonad colonizations of marine and fresh waters inferred from revised 18S rRNA phylogeny. <i>Environmental Microbiology</i> , 2008, 10, 2635-2644.	1.8	79
81	Environmental distribution and population biology of <i>Candidatus</i> <i>Accumulibacter</i> , a primary agent of biological phosphorus removal. <i>Environmental Microbiology</i> , 2008, 10, 2692-2703.	1.8	102
82	Molecular phylogenetics of Vespoidea indicate paraphyly of the superfamily and novel relationships of its component families and subfamilies. <i>Zoologica Scripta</i> , 2008, 37, 539-560.	0.7	120
83	Lineage diversification and historical demography of a sky island salamander, <i>Plethodon ouachitae</i> , from the Interior Highlands. <i>Molecular Ecology</i> , 2008, 17, 5315-5335.	2.0	87
84	A novel rodent papillomavirus isolated from anogenital lesions in its natural host. <i>Virology</i> , 2008, 374, 186-197.	1.1	40
85	XplorSeq: A software environment for integrated management and phylogenetic analysis of metagenomic sequence data. <i>BMC Bioinformatics</i> , 2008, 9, 420.	1.2	47
86	A topological transformation in evolutionary tree search methods based on maximum likelihood combining p-ECR and neighbor joining. <i>BMC Bioinformatics</i> , 2008, 9, S4.	1.2	3
87	Broadly sampled multigene trees of eukaryotes. <i>BMC Evolutionary Biology</i> , 2008, 8, 14.	3.2	130
88	Evolution of C2H2-zinc finger genes and subfamilies in mammals: Species-specific duplication and loss of clusters, genes and effector domains. <i>BMC Evolutionary Biology</i> , 2008, 8, 176.	3.2	112
89	Evolution of a family of metazoan active-site-serine enzymes from penicillin-binding proteins: a novel facet of the bacterial legacy. <i>BMC Evolutionary Biology</i> , 2008, 8, 26.	3.2	35
90	Using ESTs for phylogenomics: can one accurately infer a phylogenetic tree from a gappy alignment?. <i>BMC Evolutionary Biology</i> , 2008, 8, 95.	3.2	106
91	Molecular phylogeny and systematics of <i>Polyblastia</i> (Verrucariaceae, Eurotiomycetes) and allied genera. <i>Mycological Research</i> , 2008, 112, 1307-1318.	2.5	32
92	Empirical evaluation of a prior for Bayesian phylogenetic inference. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2008, 363, 4031-4039.	1.8	35
93	Inferring Trees. <i>Methods in Molecular Biology</i> , 2008, 452, 287-309.	0.4	13
95	Inference of Phylogenetic Trees. <i>Lecture Notes in Mathematics</i> , 2008, , 1-38.	0.1	3

#	ARTICLE	IF	CITATIONS
96	Functions, structure, and read-through alternative splicing of feline APOBEC3 genes. <i>Genome Biology</i> , 2008, 9, R48.	13.9	116
97	Methods for Analyzing Viral Evolution. , 2008, , 165-204.		5
98	A Phylogenomic Investigation into the Origin of Metazoa. <i>Molecular Biology and Evolution</i> , 2008, 25, 664-672.	3.5	259
99	A Rapid Bootstrap Algorithm for the RAxML Web Servers. <i>Systematic Biology</i> , 2008, 57, 758-771.	2.7	6,439
100	A rock-inhabiting ancestor for mutualistic and pathogen-rich fungal lineages. <i>Studies in Mycology</i> , 2008, 61, 111-119.	4.5	178
101	Short Quartet Puzzling: A New Quartet-Based Phylogeny Reconstruction Algorithm. <i>Journal of Computational Biology</i> , 2008, 15, 91-103.	0.8	33
102	An outlook into ultra-scale visualization of large-scale biological data. , 2008, , .		4
103	Phylogenetic reconstruction with disk-covering and Bayesian approaches. , 2008, , .		0
104	Mitochondrial cob and cox1 Genes and Editing of the Corresponding mRNAs in <i>Dinophysis acuminata</i> from Narragansett Bay, with Special Reference to the Phylogenetic Position of the Genus <i>Dinophysis</i> . <i>Applied and Environmental Microbiology</i> , 2008, 74, 1546-1554.	1.4	40
105	A new araphid diatom genus <i>Psammoneis</i> gen. nov. (Plagiogrammaceae, Bacillariophyta) with three new species based on SSU and LSU rDNA sequence data and morphology. <i>Phycologia</i> , 2008, 47, 510-528.	0.6	22
106	<i>Pseudostriatella</i> (Bacillariophyta): a description of a new araphid diatom genus based on observations of frustule and auxospore structure and 18S rDNA phylogeny. <i>Phycologia</i> , 2008, 47, 371-391.	0.6	38
107	Molecular phylogeny of choanoflagellates, the sister group to Metazoa. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 16641-16646.	3.3	204
108	A Bayesian Perspective on a Non-parsimonious Parsimony Model. <i>Systematic Biology</i> , 2008, 57, 406-419.	2.7	28
109	Probabilistic Phylogenetic Inference with Insertions and Deletions. <i>PLoS Computational Biology</i> , 2008, 4, e1000172.	1.5	51
110	Group II introns in Eubacteria and Archaea: ORF-less introns and new varieties. <i>Rna</i> , 2008, 14, 1704-1713.	1.6	81
111	<i>Spirochaeta cellobiosiphila</i> sp. nov., a facultatively anaerobic, marine spirochaete. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2008, 58, 2762-2768.	0.8	32
112	Cytological Characterization of YpsB, a Novel Component of the <i>Bacillus subtilis</i> Divisome. <i>Journal of Bacteriology</i> , 2008, 190, 7096-7107.	1.0	48
113	Improvement of molecular phylogenetic inference and the phylogeny of Bilateria. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2008, 363, 1463-1472.	1.8	167

#	ARTICLE	IF	CITATIONS
114	Description of a new divergent lineage and three new species of Honduran salamanders of the genus <i>Oedipina</i> (Caudata, Plethodontidae). <i>Zootaxa</i> , 2008, 1930, 1-17.	0.2	9
115	Emergence of Xin Demarcates a Key Innovation in Heart Evolution. <i>PLoS ONE</i> , 2008, 3, e2857.	1.1	23
116	Large-Scale Phylogenetic Analysis on Current HPC Architectures. <i>Scientific Programming</i> , 2008, 16, 255-270.	0.5	14
118	Origin of Saxitoxin Biosynthetic Genes in Cyanobacteria. <i>PLoS ONE</i> , 2009, 4, e5758.	1.1	110
119	Load Balance in the Phylogenetic Likelihood Kernel. , 2009, , .		9
120	Fine-grain Parallelism Using Multi-core, Cell/BE, and GPU Systems: Accelerating the Phylogenetic Likelihood Function. , 2009, , .		37
121	Many-core algorithms for statistical phylogenetics. <i>Bioinformatics</i> , 2009, 25, 1370-1376.	1.8	380
122	Evolutionary History and Stress Regulation of Plant Receptor-Like Kinase/Pelle Genes. <i>Plant Physiology</i> , 2009, 150, 12-26.	2.3	340
123	Diversity and Evolution of Effector Loci in Natural Populations of the Plant Pathogen <i>Melampsora lini</i> . <i>Molecular Biology and Evolution</i> , 2009, 26, 2499-2513.	3.5	130
124	RAMI: a tool for identification and characterization of phylogenetic clusters in microbial communities. <i>Bioinformatics</i> , 2009, 25, 736-742.	1.8	54
125	Ensemble dispatching on an IBM Blue Gene/L for a bioinformatics knowledge environment. , 2009, , .		3
126	Comparative genomic analyses of the human fungal pathogens <i>Coccidioides</i> and their relatives. <i>Genome Research</i> , 2009, 19, 1722-1731.	2.4	295
127	An Evolutionary Model-Based Algorithm for Accurate Phylogenetic Breakpoint Mapping and Subtype Prediction in HIV-1. <i>PLoS Computational Biology</i> , 2009, 5, e1000581.	1.5	151
128	Restriction of Equine Infectious Anemia Virus by Equine APOBEC3 Cytidine Deaminases. <i>Journal of Virology</i> , 2009, 83, 7547-7559.	1.5	41
129	GRASSIUS: A Platform for Comparative Regulatory Genomics across the Grasses. <i>Plant Physiology</i> , 2009, 149, 171-180.	2.3	260
130	Genome Sequences of Three <i>Agrobacterium</i> Biovars Help Elucidate the Evolution of Multichromosome Genomes in Bacteria. <i>Journal of Bacteriology</i> , 2009, 191, 2501-2511.	1.0	220
131	Towards a new classification of the Arthoniales (Ascomycota) based on a three-gene phylogeny focussing on the genus <i>Opegrapha</i> . <i>Mycological Research</i> , 2009, 113, 141-152.	2.5	63
132	On the evolution of the Hysteriaceae and Mytiliniaceae (Pleosporomycetidae, Dothideomycetes.) <i>Tj ETQq1 1 0.784314 rgBT /Overlock</i>	2.5	68



#	ARTICLE	IF	CITATIONS
133	Multigene Evidence for the Placement of a Heterotrophic Amoeboid Lineage Leukarachnion sp. among Photosynthetic Stramenopiles. <i>Protist</i> , 2009, 160, 376-385.	0.6	36
134	Comparative analysis of plant genomes allows the definition of the "Phytolongins": a novel non-SNARE longin domain protein family. <i>BMC Genomics</i> , 2009, 10, 510.	1.2	23
135	Phylogeny of the CDC25 homology domain reveals rapid differentiation of Ras pathways between early animals and fungi. <i>Cellular Signalling</i> , 2009, 21, 1579-1585.	1.7	21
136	The Evolutionary History of Lysine Biosynthesis Pathways Within Eukaryotes. <i>Journal of Molecular Evolution</i> , 2009, 69, 240-248.	0.8	32
137	The Biogeography of Ammonia-Oxidizing Bacterial Communities in Soil. <i>Microbial Ecology</i> , 2009, 58, 435-445.	1.4	128
138	A putative azoreductase gene is involved in the <i>Shewanella oneidensis</i> response to heavy metal stress. <i>Applied Microbiology and Biotechnology</i> , 2009, 82, 1131-1141.	1.7	36
139	Phylogeographic and demographic effects of Pleistocene climatic fluctuations in a montane salamander, <i>Plethodon fourchensis</i> . <i>Molecular Ecology</i> , 2009, 18, 2243-2262.	2.0	84
140	Fine structure and 18S rDNA phylogeny of a marine araphid pennate diatom <i>Plagiosiriata gorensis</i> gen. et sp. nov. (Bacillariophyta). <i>Phycological Research</i> , 2009, 57, 25-35.	0.8	9
141	Convergence in trophic morphology and feeding performance among piscivorous natricine snakes. <i>Journal of Evolutionary Biology</i> , 2009, 22, 1203-1211.	0.8	46
142	A small population of planktonic <i>Flavobacteria</i> with disproportionately high growth during the spring phytoplankton bloom in a prealpine lake. <i>Environmental Microbiology</i> , 2009, 11, 2676-2686.	1.8	80
143	Eyespot evolution: phylogenetic insights from <i>Junonia</i> and related butterfly genera (Nymphalidae: Junoniini). <i>Evolution &amp; Development</i> , 2009, 11, 489-497.	1.1	55
144	Labyrinthulomycetes phylogeny and its implications for the evolutionary loss of chloroplasts and gain of ectoplasmic gliding. <i>Molecular Phylogenetics and Evolution</i> , 2009, 50, 129-140.	1.2	104
145	Rapid radiation of Impatiens (Balsaminaceae) during Pliocene and Pleistocene: Result of a global climate change. <i>Molecular Phylogenetics and Evolution</i> , 2009, 52, 806-824.	1.2	161
146	Phylogenetic positions of Glaucophyta, green plants (Archaeplastida) and Haptophyta (Chromalveolata) as deduced from slowly evolving nuclear genes. <i>Molecular Phylogenetics and Evolution</i> , 2009, 53, 872-880.	1.2	62
147	Phylogeny of rock-inhabiting fungi related to Dothideomycetes. <i>Studies in Mycology</i> , 2009, 64, 123-133.	4.5	202
148	Locating Large-Scale Gene Duplication Events through Reconciled Trees: Implications for Identifying Ancient Polyploidy Events in Plants. <i>Journal of Computational Biology</i> , 2009, 16, 1071-1083.	0.8	21
149	Molecular differentiation of the <i>Psytalia concolor</i> ( <i>Szpliget</i> ) species complex (Hymenoptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 Biological Control, 2009, 49, 17-26.	1.4	56
150	Simple and fast classification of non-LTR retrotransposons based on phylogeny of their RT domain protein sequences. <i>Gene</i> , 2009, 448, 207-213.	1.0	86

#	ARTICLE	IF	CITATIONS
152	Embedded Computer Systems: Architectures, Modeling, and Simulation. Lecture Notes in Computer Science, 2009, , .	1.0	1
153	Phylogenetic-Signal Dissection of Nuclear Housekeeping Genes Supports the Paraphyly of Sponges and the Monophyly of Eumetazoa. Molecular Biology and Evolution, 2009, 26, 2261-2274.	3.5	158
154	The Ultramicrobacterium <i>Elusimicrobium minutum</i> gen. nov., sp. nov., the First Cultivated Representative of the Termite Group 1 Phylum. Applied and Environmental Microbiology, 2009, 75, 2831-2840.	1.4	162
155	A Large-Scale Phylogeny of Polygonaceae Based on Molecular Data. International Journal of Plant Sciences, 2009, 170, 1044-1055.	0.6	69

157

#	ARTICLE	IF	CITATIONS
172	Phylogenetic affiliation of the desert truffles <i>Picoa juniperi</i> and <i>Picoa lefebvrei</i> . <i>Antonie Van Leeuwenhoek</i> , 2010, 98, 429-436.	0.7	20
173	Deep Phylogeny and Evolution of Slime Moulds (Mycetozoa). <i>Protist</i> , 2010, 161, 55-70.	0.6	122
174	MetaPIGA v2.0: maximum likelihood large phylogeny estimation using the metapopulation genetic algorithm and other stochastic heuristics. <i>BMC Bioinformatics</i> , 2010, 11, 379.	1.2	89
175	The evolutionary diversification of LSF and Grainyhead transcription factors preceded the radiation of basal animal lineages. <i>BMC Evolutionary Biology</i> , 2010, 10, 101.	3.2	37
176	Evolution of nectarivory in phyllostomid bats (Phyllostomidae Gray, 1825, Chiroptera: Mammalia). <i>BMC Evolutionary Biology</i> , 2010, 10, 165.	3.2	117
177	A phylogenetic mosaic plastid proteome and unusual plastid-targeting signals in the green-colored dinoflagellate <i>Lepidodinium chlorophorum</i> . <i>BMC Evolutionary Biology</i> , 2010, 10, 191.	3.2	62
178	Assembling networks of microbial genomes using linear programming. <i>BMC Evolutionary Biology</i> , 2010, 10, 360.	3.2	4
179	Functional evolution of the trace amine associated receptors in mammals and the loss of TAAR1 in dogs. <i>BMC Evolutionary Biology</i> , 2010, 10, 51.	3.2	31
180	Genome analysis and comparative genomics of a <i>Giardia intestinalis</i> assemblage E isolate. <i>BMC Genomics</i> , 2010, 11, 543.	1.2	125
181	Molecular phylogeny of the Calyptratae (Diptera: Cyclorrhapha) with an emphasis on the superfamily Oestroidea and the position of Mystacinobiidae and McAlpine's fly. <i>Systematic Entomology</i> , 2010, 35, 614-635.	1.7	151
182	The Hawaiian Rhodophyta Biodiversity Survey (2006-2010): a summary of principal findings. <i>BMC Plant Biology</i> , 2010, 10, 258.	1.6	105
183	The RAD51 and DMC1 homoeologous genes of bread wheat: cloning, molecular characterization and expression analysis. <i>BMC Research Notes</i> , 2010, 3, 245.	0.6	35
184	Identification of the mitochondrial carrier that provides <i>Yarrowia lipolytica</i> with a fatty acid-induced and nucleotide-sensitive uncoupling protein-like activity. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2010, 1797, 81-88.	0.5	20
185	Nucleotide substitution rates for the full set of mitochondrial protein-coding genes in Coleoptera. <i>Molecular Phylogenetics and Evolution</i> , 2010, 56, 796-807.	1.2	141
186	Identification of new molecular markers for assembling the eukaryotic tree of life. <i>Molecular Phylogenetics and Evolution</i> , 2010, 55, 1177-1182.	1.2	14
187	A phylogeny of Vetigastropoda and other "archaeogastropods" reorganizing old gastropod clades. <i>Invertebrate Biology</i> , 2010, 129, 220-240.	0.3	54
188	A Description of a New "Amoebozoan" Isolated from the American Lobster, <i>Homarus americanus</i> . <i>Journal of Eukaryotic Microbiology</i> , 2010, 57, 40-47.	0.8	17
189	Evolution of Distorted Pellicle Patterns in Rigid Photosynthetic Euglenids ( <i>Phacus</i> Dujardin). <i>Journal of Eukaryotic Microbiology</i> , 2010, 57, 19-32.	0.8	6

#	ARTICLE	IF	CITATIONS
190	Conserved Meiotic Genes Point to Sex in the Choanoflagellates. <i>Journal of Eukaryotic Microbiology</i> , 2010, 57, 56-62.	0.8	36
191	Invalidation of <i>Hyperamoeba</i> by Transferring its Species to Other Genera of Myxogastria. <i>Journal of Eukaryotic Microbiology</i> , 2010, 57, 189-196.	0.8	25
192	RECONSTRUCTING RETICULATION HISTORY IN A PHYLOGENETIC FRAMEWORK AND THE POTENTIAL OF ALLOPATRIC SPECIATION DRIVEN BY POLYPLOIDY IN AN AGAMIC COMPLEX IN CRATAEGUS (ROSACEAE). Evolution; <i>International Journal of Organic Evolution</i> , 2010, 64, 3593-3608.	1.1	46
193	<i>Phytophthora andina</i> sp. nov., a newly identified heterothallic pathogen of solanaceous hosts in the Andean highlands. <i>Plant Pathology</i> , 2010, 59, 613-625.	1.2	48
194	A phylogeographical study of the toxic benthic dinoflagellate genus <i>Ostreopsis</i> Schmidt. <i>Journal of Biogeography</i> , 2010, 37, 830-841.	1.4	130
195	Diversity and abundance of <i>Korarchaeota</i> in terrestrial hot springs of Iceland and Kamchatka. <i>ISME Journal</i> , 2010, 4, 346-356.	4.4	61
196	Karst pools in subsurface environments: collectors of microbial diversity or temporary residence between habitat types. <i>Environmental Microbiology</i> , 2010, 12, 1061-1074.	1.8	55
197	Phylogenetic diversity and metagenomics of candidate division OP3. <i>Environmental Microbiology</i> , 2010, 12, 1218-1229.	1.8	90
198	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
199	Identification of the dominant sulfate-reducing bacterial partner of anaerobic methanotrophs of the ANME-2 clade. <i>Environmental Microbiology</i> , 2010, 12, 2327-2340.	1.8	153
200	Phylogenetic position, systematic status, and divergence time of the Procarididea (Crustacea: Tj ETQq0 0 0 rGT /Overlock 10 Tf 50 342	0.7	55
201	Phylogenetics and evolution of <i>Capitata</i> (Cnidaria: Hydrozoa), and the systematics of <i>Corynidae</i> . <i>Zoologica Scripta</i> , 2010, 39, 290-304.	0.7	271
202	Testing hybridization hypotheses and evaluating the evolutionary potential of hybrids in mangrove plant species. <i>Journal of Evolutionary Biology</i> , 2010, 23, 2249-2261.	0.8	31
203	New insights into the origin of two new epiphytic <i>Impatiens</i> species (Balsaminaceae) from West Central Africa based on molecular phylogenetic analyses. <i>Taxon</i> , 2010, 59, 1508-1518.	0.4	17
204	An Insect Herbivore Microbiome with High Plant Biomass-Degrading Capacity. <i>PLoS Genetics</i> , 2010, 6, e1001129.	1.5	213
205	Mitochondrial Cox1 Sequence Data Reliably Uncover Patterns of Insect Diversity But Suffer from High Lineage-Idiosyncratic Error Rates. <i>PLoS ONE</i> , 2010, 5, e14448.	1.1	90
206	Maximum Likelihood Analyses of 3,490 rbcL Sequences: Scalability of Comprehensive Inference versus Group-Specific Taxon Sampling. <i>Evolutionary Bioinformatics</i> , 2010, 6, EBO.S4528.	0.6	6
207	The genome of pseudocowpoxvirus: comparison of a reindeer isolate and a reference strain. <i>Journal of General Virology</i> , 2010, 91, 1560-1576.	1.3	76

#	ARTICLE	IF	CITATIONS
208	The evolution of phototransduction from an ancestral cyclic nucleotide gated pathway. Proceedings of the Royal Society B: Biological Sciences, 2010, 277, 1963-1969.	1.2	75
209	<i>Halarchaeum acidiphilum</i> gen. nov., sp. nov., a moderately acidophilic haloarchaeon isolated from commercial solar salt. International Journal of Systematic and Evolutionary Microbiology, 2010, 60, 2513-2516.	0.8	74
210	Adaptation to herbivory by the Tammar wallaby includes bacterial and glycoside hydrolase profiles different from other herbivores. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 14793-14798.	3.3	234
211	Searching for Mesophilic <i>Thermotogales</i> Bacteria: "Mesotogas" in the Wild. Applied and Environmental Microbiology, 2010, 76, 4896-4900.	1.4	44
212	Unifying Vertical and Nonvertical Evolution: A Stochastic ARG-based Framework. Systematic Biology, 2010, 59, 27-41.	2.7	53
213	A photoactivatable green-fluorescent protein from the phylum Ctenophora. Proceedings of the Royal Society B: Biological Sciences, 2010, 277, 1155-1160.	1.2	27
214	<i>Geomicrobium halophilum</i> gen. nov., sp. nov., a moderately halophilic and alkaliphilic bacterium isolated from soil. International Journal of Systematic and Evolutionary Microbiology, 2010, 60, 990-995.	0.8	26
215	Phylogenetic placement of some morphologically unusual members of Verrucariales. Mycologia, 2010, 102, 835-846.	0.8	28
216	Repeated loss of coloniality and symbiosis in scleractinian corals. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 11877-11882.	3.3	105
217	Unifying stream based and reconfigurable computing to design application accelerators. , 2010, , .		0
218	The systematic position of <i>Diopsina</i> Curran, 1928 (Diptera: Diopsidae) inferred from DNA sequence data. Insect Systematics and Evolution, 2010, 41, 295-302.	0.2	4
219	Broadly Sampled Multigene Analyses Yield a Well-Resolved Eukaryotic Tree of Life. Systematic Biology, 2010, 59, 518-533.	2.7	212
220	SATCHMO-JS: a webserver for simultaneous protein multiple sequence alignment and phylogenetic tree construction. Nucleic Acids Research, 2010, 38, W29-W34.	6.5	26
221	Ancient Protostome Origin of Chemosensory Ionotropic Glutamate Receptors and the Evolution of Insect Taste and Olfaction. PLoS Genetics, 2010, 6, e1001064.	1.5	680
222	<i>Remototrachyna</i> , a newly recognized tropical lineage of lichens in the Hypotrachyna clade (Parmeliaceae, Ascomycota), originated in the Indian subcontinent. American Journal of Botany, 2010, 97, 579-590.	0.8	61
223	Evolution of Human Papillomavirus Carcinogenicity. Advances in Virus Research, 2010, 77, 41-62.	0.9	29
224	Highlights of the Didymellaceae: A polyphasic approach to characterise <i>Phoma</i> and related pleosporalean genera. Studies in Mycology, 2010, 65, 1-60.	4.5	455
225	Phylogenetic Trees From Sequences. , 2010, , 101-124.		0

#	ARTICLE	IF	CITATIONS
226	Halostagnicola kamekurae sp. nov., an extremely halophilic archaeon from solar salt. International Journal of Systematic and Evolutionary Microbiology, 2010, 60, 2828-2831.	0.8	19
227	FPGA acceleration of the phylogenetic likelihood function for Bayesian MCMC inference methods. BMC Bioinformatics, 2010, 11, 184.	1.2	44
228	Decreased HIV diversity after allogeneic stem cell transplantation of an HIV-1 infected patient: a case report. Virology Journal, 2010, 7, 55.	1.4	8
229	Floral symmetry genes and the origin and maintenance of zygomorphy in a plant-pollinator mutualism. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 6388-6393.	3.3	134
230	New Heuristic Methods for Joint Species Delimitation and Species Tree Inference. Systematic Biology, 2010, 59, 59-73.	2.7	241
231	Natronoarchaeum mannanyticum gen. nov., sp. nov., an aerobic, extremely halophilic archaeon isolated from commercial salt. International Journal of Systematic and Evolutionary Microbiology, 2010, 60, 2529-2534.	0.8	43
232	Bayesian Phylogenetics and Its Influence on Insect Systematics. Annual Review of Entomology, 2010, 55, 189-206.	5.7	42
233	Phylogeny of Asian primate malaria parasites inferred from apicoplast genome-encoded genes with special emphasis on the positions of Plasmodium vivax and P. fragile. Gene, 2010, 450, 32-38.	1.0	25
234	Monitoring associations between clade-level variation, overall community structure and ecosystem function in enhanced biological phosphorus removal (EBPR) systems using terminal-restriction fragment length polymorphism (T-RFLP). Water Research, 2010, 44, 4908-4923.	5.3	51
235	Phylogenetic relationships within the suborder Dermanyssina (Acari: Parasitiformes) and a test of dermanyssoid monophyly. International Journal of Acarology, 2010, 36, 299-312.	0.3	33
236	Why barcode? High-throughput multiplex sequencing of mitochondrial genomes for molecular systematics. Nucleic Acids Research, 2010, 38, e197-e197.	6.5	152
237	The taxonomic status and phylogenetic relationships of the genus <i>Aenigmomphiscola</i> Kruglov and Starobogatov, 1981 (Gastropoda: Pulmonata: Lymnaeidae). Journal of Natural History, 2011, 45, 2049-2068.	0.2	23
238	Diversity of the desert truffle <i>Terfezia boudieri</i> Chatin. in southern Tunisia. Canadian Journal of Microbiology, 2011, 57, 599-605.	0.8	9
240	<i>Cantharellus texensis</i> sp. nov. from Texas, a southern lookalike of <i>C. cinnabarinus</i> revealed by <i>tef-1</i> sequence data. Mycologia, 2011, 103, 1037-1046.	0.8	38
241	<i>Penicillium araracuarensis</i> sp. nov., <i>Penicillium elleniae</i> sp. nov., <i>Penicillium penarajense</i> sp. nov., <i>Penicillium vanderhammenii</i> sp. nov. and <i>Penicillium wotroi</i> sp. nov., isolated from leaf litter. International Journal of Systematic and Evolutionary Microbiology, 2011, 61, 1462-1475.	0.8	44
243	Genetic Structure of Two Protist Species (Myxogastria, Amoebozoa) Suggests Asexual Reproduction in Sexual Amoebae. PLoS ONE, 2011, 6, e22872.	1.1	47
244	<i>Acremonium</i> phylogenetic overview and revision of <i>Gliomastix</i> , <i>Sarocladium</i> , and <i>Trichothecium</i> . Studies in Mycology, 2011, 68, 139-162.	4.5	208
245	Crawling through time: Transition of snails to slugs dating back to the Paleozoic, based on mitochondrial phylogenomics. Marine Genomics, 2011, 4, 51-59.	0.4	52

#	ARTICLE	IF	CITATIONS
246	Phylogenetic Analysis of Protein Sequence Data Using the Randomized Accelerated Maximum Likelihood (<scp>RAXML</scp>) Program. <i>Current Protocols in Molecular Biology</i> , 2011, 96, Unit19.11.	2.9	43
247	Rock-inhabiting fungi originated during periods of dry climate in the late Devonian and middle Triassic. <i>Fungal Biology</i> , 2011, 115, 987-996.	1.1	102
248	Molecular Systematics of the Leptodeirini (Colubroidea: Dipsadidae) Revisited: Species-tree Analyses and Multi-locus Data. <i>Copeia</i> , 2011, 2011, 407-417.	1.4	17
249	Phylogenetic Relationships of <i>Muehlenbeckia</i> , <i>Fallopia</i> , and <i>Reynoutria</i> (Polygonaceae) Investigated with Chloroplast and Nuclear Sequence Data. <i>International Journal of Plant Sciences</i> , 2011, 172, 1053-1066.	0.6	29
250	MEGA5: Molecular Evolutionary Genetics Analysis Using Maximum Likelihood, Evolutionary Distance, and Maximum Parsimony Methods. <i>Molecular Biology and Evolution</i> , 2011, 28, 2731-2739.	3.5	36,550
251	Targeted Amplicon Sequencing (TAS): A Scalable Next-Gen Approach to Multilocus, Multitaxa Phylogenetics. <i>Genome Biology and Evolution</i> , 2011, 3, 1312-1323.	1.1	196
252	Isolation of Succinivibrionaceae Implicated in Low Methane Emissions from Tammar Wallabies. <i>Science</i> , 2011, 333, 646-648.	6.0	179
253	Phylogeny and palaeoecology of <i>Polyommatus</i> blue butterflies show Beringia was a climate-regulated gateway to the New World. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2011, 278, 2737-2744.	1.2	98
254	<i>Chthonomonas calidirosea</i> gen. nov., sp. nov., an aerobic, pigmented, thermophilic micro-organism of a novel bacterial class, <i>Chthonomonadetes classis nov.</i> , of the newly described phylum <i>Armatimonadetes</i> originally designated candidate division OP10. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2011, 61, 2482-2490.	0.8	75
255	<i>Halostagnicola alkaliphila</i> sp. nov., an alkaliphilic haloarchaeon from commercial rock salt. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2011, 61, 1149-1152.	0.8	20
256	Phylogenetic position of the brown algae-associated lichenized fungus <i>Verrucaria tavaresiae</i> (Verrucariaceae). <i>Bryologist</i> , 2011, 114, 563.	0.1	14
257	Revisiting photobiont diversity in the lichen family Verrucariaceae (Ascomycota). <i>European Journal of Phycology</i> , 2011, 46, 399-415.	0.9	148
258	Phylogeny of Polygoneae (Polygonaceae: Polygonoideae). <i>Taxon</i> , 2011, 60, 1653-1666.	0.4	44
259	GROWTH AND DEVELOPMENT SYMPOSIUM: Promoting healthier humans through healthier livestock: Animal agriculture enters the metagenomics era <sup>12</sup> . <i>Journal of Animal Science</i> , 2011, 89, 835-844.	0.2	12
260	The Use of Bioinformatics for Studying HIV Evolutionary and Epidemiological History in South America. <i>AIDS Research and Treatment</i> , 2011, 2011, 1-13.	0.3	12
261	The iPlant Collaborative: Cyberinfrastructure for Plant Biology. <i>Frontiers in Plant Science</i> , 2011, 2, 34.	1.7	396
262	Multilocus Genotyping of Human <i>Giardia</i> Isolates Suggests Limited Zoonotic Transmission and Association between Assemblage B and Flatulence in Children. <i>PLoS Neglected Tropical Diseases</i> , 2011, 5, e1262.	1.3	118
263	Global Distribution of <i>Polaromonas</i> Phylotypes - Evidence for a Highly Successful Dispersal Capacity. <i>PLoS ONE</i> , 2011, 6, e23742.	1.1	125



#	ARTICLE	IF	CITATIONS
264	Uncultivated Microbial Eukaryotic Diversity: A Method to Link ssu rRNA Gene Sequences with Morphology. <i>PLoS ONE</i> , 2011, 6, e28158.	1.1	7
265	Comparative Transcriptomics of Eastern African Cichlid Fishes Shows Signs of Positive Selection and a Large Contribution of Untranslated Regions to Genetic Diversity. <i>Genome Biology and Evolution</i> , 2011, 3, 443-455.	1.1	56
266	Massive Genomic Decay in <i>Serratia symbiotica</i> , a Recently Evolved Symbiont of Aphids. <i>Genome Biology and Evolution</i> , 2011, 3, 195-208.	1.1	186
267	Population structure of two crayfish with diverse physiological requirements. <i>Crustacean Issues</i> , 2011, , 323-343.	0.9	3
268	Fish Farming Affects the Abundance and Diversity of the Mercury Resistance Gene <i>merA</i> in Marine Sediments. <i>Microbes and Environments</i> , 2011, 26, 205-211.	0.7	11
269	Evolutionary trade-offs among decomposers determine responses to nitrogen enrichment. <i>Ecology Letters</i> , 2011, 14, 933-938.	3.0	84
270	Seasonal differences in bacterial community composition following nutrient additions in a eutrophic lake. <i>Environmental Microbiology</i> , 2011, 13, 887-899.	1.8	87
271	Another step towards understanding the slit limpets (Fissurellidae, Fissurelloidea, Vetigastropoda,) Tj ETQq1 1 0.784314 rgBT /Overlook	0.7	17
272	Fungal community composition and function after long-term exposure of northern forests to elevated atmospheric CO <sub>2</sub> and tropospheric O <sub>3</sub> . <i>Global Change Biology</i> , 2011, 17, 2184-2195.	4.2	45
273	A phylogeographic, demographic and historical analysis of the short-tailed pit viper ( <i>Gloydius</i> ) Tj ETQq1 1 0.784314 rgBT /Overlook <i>Ecology</i> , 2011, 20, 1905-1922.	2.0	65
274	An exceptionally high nucleotide and haplotype diversity and a signature of positive selection for the <i>elf4E</i> resistance gene in barley are revealed by allele mining and phylogenetic analyses of natural populations. <i>Molecular Ecology</i> , 2011, 20, no-no.	2.0	48
275	Stage-specific requirement for <i>Isa1</i> and <i>Isa2</i> proteins in the mitochondrion of <i>Trypanosoma brucei</i> and heterologous rescue by human and <i>Blastocystis</i> orthologues. <i>Molecular Microbiology</i> , 2011, 81, 1403-1418.	1.2	36
276	BARRUFETA BRAVENSIS GEN. NOV. SP. NOV. (DINOPHYCEAE): A NEW BLOOM-FORMING SPECIES FROM THE NORTHWEST MEDITERRANEAN SEA1. <i>Journal of Phycology</i> , 2011, 47, 375-392.	1.0	29
277	Differentiating between effects of invasion and diversity: impacts of aboveground plant communities on belowground fungal communities. <i>New Phytologist</i> , 2011, 189, 526-535.	3.5	28
278	A multigenic perspective on phylogenetic relationships in the largest family of salamanders, the Plethodontidae. <i>Molecular Phylogenetics and Evolution</i> , 2011, 59, 623-635.	1.2	70
279	Parallel evolution and phenotypic divergence in lichenized fungi: A case study in the lichen-forming fungal family Graphidaceae (Ascomycota: Lecanoromycetes: Ostropales). <i>Molecular Phylogenetics and Evolution</i> , 2011, 61, 45-63.	1.2	82
280	Monophyly and interrelationships of Snook and Barramundi (Centropomidae sensu Greenwood) and five new markers for fish phylogenetics. <i>Molecular Phylogenetics and Evolution</i> , 2011, 60, 463-471.	1.2	44
281	The genome of woodland strawberry ( <i>Fragaria vesca</i> ). <i>Nature Genetics</i> , 2011, 43, 109-116.	9.4	1,091



#	ARTICLE	IF	CITATIONS
282	Ancestral polyploidy in seed plants and angiosperms. <i>Nature</i> , 2011, 473, 97-100.	13.7	1,862
283	The radiation of Satyrini butterflies (Nymphalidae: Satyrinae): a challenge for phylogenetic methods. <i>Zoological Journal of the Linnean Society</i> , 2011, 161, 64-87.	1.0	68
284	Oral and Poster Manuscripts. <i>Influenza and Other Respiratory Viruses</i> , 2011, 5, 54-442.	1.5	5
285	Evolutionary dynamics of influenza A nucleoprotein (NP) lineages revealed by large-scale sequence analyses. <i>Infection, Genetics and Evolution</i> , 2011, 11, 2125-2132.	1.0	21
286	Directed next generation sequencing for phylogenetics: An example using Decapoda (Crustacea). <i>Zoologischer Anzeiger</i> , 2011, 250, 497-506.	0.4	21
287	The Novel Marine Gliding Zooflagellate Genus <i>Mantamonas</i> (Mantamonadida ord. n.: Apusozoa). <i>Protist</i> , 2011, 162, 207-221.	0.6	49
288	Potential pitfalls of modelling ribosomal RNA data in phylogenetic tree reconstruction: Evidence from case studies in the Metazoa. <i>BMC Evolutionary Biology</i> , 2011, 11, 146.	3.2	53
289	Tree-based delimitation of morphologically ambiguous taxa: A study of the lizard malaria parasites on the Caribbean island of Hispaniola. <i>International Journal for Parasitology</i> , 2011, 41, 967-980.	1.3	22
290	The early origin of melanocortin receptors, agouti-related peptide, agouti signalling peptide, and melanocortin receptor-accessory proteins, with emphasis on pufferfishes, elephant shark, lampreys, and amphioxus. <i>European Journal of Pharmacology</i> , 2011, 660, 61-69.	1.7	54
291	Evaluation of HVAC filters as a sampling mechanism for indoor microbial communities. <i>Atmospheric Environment</i> , 2011, 45, 338-346.	1.9	75
292	Single origin and subsequent diversification of central Andean endemic <i>Umbilicaria</i> species. <i>Mycologia</i> , 2011, 103, 45-56.	0.8	24
293	The 18S and 28S rDNA identity and phylogeny of the common lotic chrysophyte <i>Hydrurus foetidus</i> . <i>European Journal of Phycology</i> , 2011, 46, 282-291.	0.9	39
294	Using genetic distances in addition to ITS molecular phylogeny to identify potential species in the <i>Parmotrema reticulatum</i> complex: a case study. <i>Lichenologist</i> , 2011, 43, 569-583.	0.5	25
295	Convergent evolution of a symbiotic duet: The case of the lichen genus <i>Polychidium</i> (Peltigerales, Ascomycota). <i>American Journal of Botany</i> , 2011, 98, 1647-1656.	0.8	39
296	Correlations Between Bacterial Ecology and Mobile DNA. <i>Current Microbiology</i> , 2011, 62, 198-208.	1.0	93
297	Evolution of the TOR Pathway. <i>Journal of Molecular Evolution</i> , 2011, 73, 209-220.	0.8	118
298	The new hyphomycete genera <i>Brachyalaria</i> and <i>Infundichalara</i> , the similar <i>Exochalara</i> and species of <i>Phialophora</i> sect. <i>Catenulatae</i> (Leotiomyces). <i>Fungal Diversity</i> , 2011, 46, 67-86.	4.7	40
299	The contribution of <i>tef-1</i> sequences to species delimitation in the <i>Cantharellus cibarius</i> complex in the southeastern USA. <i>Fungal Diversity</i> , 2011, 49, 35-46.	4.7	58

#	ARTICLE	IF	CITATIONS
300	The phylogenetic position of the lichenicolous ascomycete <i>Capronia peltigerae</i> . <i>Fungal Diversity</i> , 2011, 49, 225-233.	4.7	29
301	New insights into the systematics and phylogeny of the genus <i>Jattaea</i> and similar fungi of the Calosphaeriales. <i>Fungal Diversity</i> , 2011, 49, 167-198.	4.7	30
302	Functional specialization in nucleotide sugar transporters occurred through differentiation of the gene cluster <i>EamA</i> (DUF6) before the radiation of Viridiplantae. <i>BMC Evolutionary Biology</i> , 2011, 11, 123.	3.2	37
303	Site-specific time heterogeneity of the substitution process and its impact on phylogenetic inference. <i>BMC Evolutionary Biology</i> , 2011, 11, 17.	3.2	54
304	Islands beneath islands: phylogeography of a groundwater amphipod crustacean in the Balearic archipelago. <i>BMC Evolutionary Biology</i> , 2011, 11, 221.	3.2	30
305	A dated phylogeny and collection records reveal repeated biome shifts in the African genus <i>Coccinia</i> (Cucurbitaceae). <i>BMC Evolutionary Biology</i> , 2011, 11, 28.	3.2	56
306	Genomic lineages of <i>Rhizobium etli</i> revealed by the extent of nucleotide polymorphisms and low recombination. <i>BMC Evolutionary Biology</i> , 2011, 11, 305.	3.2	40
307	Genetic Structure of <i>Graphocephala atropunctata</i> (Hemiptera: Cicadellidae) Populations Across Its Natural Range in California Reveals Isolation by Distance. <i>Journal of Economic Entomology</i> , 2011, 104, 279-287.	0.8	9
308	Evolution of the Ras-like small GTPases and their regulators. <i>Small GTPases</i> , 2011, 2, 4-16.	0.7	54
309	On the variability of spore ornamentation in <i>Laccaria tortilis</i> ( <i>Basidiomycota</i> ), Tj ETQq1 1 0.784314 rgBT /Overlock 10 T 5 0.1 2	0.1	2
310	Characterization of <i>Salmonella enterica</i> Serovar Typhimurium Isolates Harboring a Chromosomally Encoded CMY-2 $\beta$ -Lactamase Gene Located on a Multidrug Resistance Genomic Island. <i>Antimicrobial Agents and Chemotherapy</i> , 2011, 55, 4114-4121.	1.4	37
311	Why do leafcutter bees cut leaves? New insights into the early evolution of bees. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2011, 278, 3593-3600.	1.2	93
312	Niche Partitioning of Marine Group I Crenarchaeota in the Euphotic and Upper Mesopelagic Zones of the East China Sea. <i>Applied and Environmental Microbiology</i> , 2011, 77, 7469-7478.	1.4	53
313	Reverse Evolution in RH1 for Adaptation of Cichlids to Water Depth in Lake Tanganyika. <i>Molecular Biology and Evolution</i> , 2011, 28, 1769-1776.	3.5	33
314	Diversification at Transcription Factor Binding Sites within a Species and the Implications for Environmental Adaptation. <i>Molecular Biology and Evolution</i> , 2011, 28, 3331-3344.	3.5	5
315	Ortholog identification in the presence of domain architecture rearrangement. <i>Briefings in Bioinformatics</i> , 2011, 12, 413-422.	3.2	28
316	Whole-Genome Analysis of <i>Salmonella enterica</i> Serovar Typhimurium T000240 Reveals the Acquisition of a Genomic Island Involved in Multidrug Resistance via IS1 Derivatives on the Chromosome. <i>Antimicrobial Agents and Chemotherapy</i> , 2011, 55, 623-630.	1.4	49
317	Portrayal of <i>Impatiens nzabiana</i> (Balsaminaceae): a Morphological, Molecular and Biogeographic Study of a New Gabonese Species. <i>Systematic Botany</i> , 2011, 36, 440-448.	0.2	14

#	ARTICLE	IF	CITATIONS
318	Restriction of Porcine Endogenous Retrovirus by Porcine APOBEC3 Cytidine Deaminases. <i>Journal of Virology</i> , 2011, 85, 3842-3857.	1.5	25
319	<i>Salarchaeum japonicum</i> gen. nov., sp. nov., an aerobic, extremely halophilic member of the Archaea isolated from commercial salt. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2011, 61, 2266-2270.	0.8	35
320	Soil rotifer communities are extremely diverse globally but spatially autocorrelated locally. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 4406-4410.	3.3	90
321	Result verification, code verification and computation of support values in phylogenetics. <i>Briefings in Bioinformatics</i> , 2011, 12, 270-279.	3.2	5
322	A Bayesian Approach for Fast and Accurate Gene Tree Reconstruction. <i>Molecular Biology and Evolution</i> , 2011, 28, 273-290.	3.5	110
323	Survey of Branch Support Methods Demonstrates Accuracy, Power, and Robustness of Fast Likelihood-based Approximation Schemes. <i>Systematic Biology</i> , 2011, 60, 685-699.	2.7	912
324	A New Species of <i>Neophylax</i> from Northern Virginia, USA (Trichoptera: Uenoidae). <i>Proceedings of the Entomological Society of Washington</i> , 2011, 113, 7-13.	0.0	2
325	Unity in Variety--The Pan-Genome of the Chlamydiae. <i>Molecular Biology and Evolution</i> , 2011, 28, 3253-3270.	3.5	184
326	VERIFICATION OF PHYLOGENETIC INFERENCE PROGRAMS USING METAMORPHIC TESTING. <i>Journal of Bioinformatics and Computational Biology</i> , 2011, 09, 729-747.	0.3	10
327	MrBayes on a Graphics Processing Unit. <i>Bioinformatics</i> , 2011, 27, 1255-1261.	1.8	55
328	Dynamic Evolution of Pathogenicity Revealed by Sequencing and Comparative Genomics of 19 <i>Pseudomonas syringae</i> Isolates. <i>PLoS Pathogens</i> , 2011, 7, e1002132.	2.1	413
329	Performance, Accuracy, and Web Server for Evolutionary Placement of Short Sequence Reads under Maximum Likelihood. <i>Systematic Biology</i> , 2011, 60, 291-302.	2.7	476
330	Emergence of a Globally Dominant IncHI1 Plasmid Type Associated with Multiple Drug Resistant Typhoid. <i>PLoS Neglected Tropical Diseases</i> , 2011, 5, e1245.	1.3	114
331	A First Attempt to Bring Computational Biology into Advanced High School Biology Classrooms. <i>PLoS Computational Biology</i> , 2011, 7, e1002244.	1.5	26
332	Temporal Fluctuation of Multidrug Resistant <i>Salmonella</i> Typhi Haplotypes in the Mekong River Delta Region of Vietnam. <i>PLoS Neglected Tropical Diseases</i> , 2011, 5, e929.	1.3	47
333	<i>Lanonia</i> (Arecaceae: Palmae), a New Genus from Asia, with a Revision of the Species. <i>Systematic Botany</i> , 2011, 36, 883-895.	0.2	13
334	The Permian--Triassic mass extinction forces the radiation of the modern marine phytoplankton. <i>Phycologia</i> , 2011, 50, 684-693.	0.6	14
335	Resolving Difficult Phylogenetic Questions: Why More Sequences Are Not Enough. <i>PLoS Biology</i> , 2011, 9, e1000602.	2.6	932

#	ARTICLE	IF	CITATIONS
336	Genomic Transition to Pathogenicity in Chytrid Fungi. <i>PLoS Pathogens</i> , 2011, 7, e1002338.	2.1	99
337	Interspecific Sex in Grass Smuts and the Genetic Diversity of Their Pheromone-Receptor System. <i>PLoS Genetics</i> , 2011, 7, e1002436.	1.5	70
338	Virus Pathogen Database and Analysis Resource (ViPR): A Comprehensive Bioinformatics Database and Analysis Resource for the Coronavirus Research Community. <i>Viruses</i> , 2012, 4, 3209-3226.	1.5	156
339	Common Coinfections of <i>Giardia intestinalis</i> and <i>Helicobacter pylori</i> in Non-Symptomatic Ugandan Children. <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1780.	1.3	71
340	Transmission of Equine Influenza Virus during an Outbreak Is Characterized by Frequent Mixed Infections and Loose Transmission Bottlenecks. <i>PLoS Pathogens</i> , 2012, 8, e1003081.	2.1	57
341	Revised Phylogeny and Novel Horizontally Acquired Virulence Determinants of the Model Soft Rot Phytopathogen <i>Pectobacterium wasabiae</i> SCC3193. <i>PLoS Pathogens</i> , 2012, 8, e1003013.	2.1	93
342	Evolution of an Eurasian Avian-like Influenza Virus in Naïve and Vaccinated Pigs. <i>PLoS Pathogens</i> , 2012, 8, e1002730.	2.1	79
343	Multiple Horizontal Gene Transfers of Ammonium Transporters/Ammonia Permeases from Prokaryotes to Eukaryotes: Toward a New Functional and Evolutionary Classification. <i>Molecular Biology and Evolution</i> , 2012, 29, 51-60.	3.5	75
344	The multiple fuzzy origins of woodiness within Balsaminaceae using an integrated approach. Where do we draw the line?. <i>Annals of Botany</i> , 2012, 109, 783-799.	1.4	34
345	ViPR: an open bioinformatics database and analysis resource for virology research. <i>Nucleic Acids Research</i> , 2012, 40, D593-D598.	6.5	610
346	Miocene Dispersal Drives Island Radiations in the Palm Tribe Trachycarpeae (Arecaceae). <i>Systematic Biology</i> , 2012, 61, 426-442.	2.7	77
347	Unified modeling of gene duplication, loss, and coalescence using a locus tree. <i>Genome Research</i> , 2012, 22, 755-765.	2.4	153
348	FastML: a web server for probabilistic reconstruction of ancestral sequences. <i>Nucleic Acids Research</i> , 2012, 40, W580-W584.	6.5	295
349	Evolutionary Dynamics of Local Pandemic H1N1/2009 Influenza Virus Lineages Revealed by Whole-Genome Analysis. <i>Journal of Virology</i> , 2012, 86, 11-18.	1.5	101
350	Correlating microbial community profiles with geochemical data in highly stratified sediments from the Arctic Mid-Ocean Ridge. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E2846-55.	3.3	282
351	Phylogenomic datasets provide both precision and accuracy in estimating the timescale of placental mammal phylogeny. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2012, 279, 3491-3500.	1.2	449
352	<i>Malmographina</i> , a new genus for <i>Graphina malmei</i> (Ascomycota: Ostropales) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	0.5	16
353	Detection of a Possible Bioterrorism Agent, <i>Francisella</i> sp., in a Clinical Specimen by Use of Next-Generation Direct DNA Sequencing. <i>Journal of Clinical Microbiology</i> , 2012, 50, 1810-1812.	1.8	38

#	ARTICLE	IF	CITATIONS
354	Bacterial Communities in Women with Bacterial Vaginosis: High Resolution Phylogenetic Analyses Reveal Relationships of Microbiota to Clinical Criteria. <i>PLoS ONE</i> , 2012, 7, e37818.	1.1	545
355	Lack of Methylation in the Upstream Region of Human Papillomavirus Type 6 from Aerodigestive Tract Papillomas. <i>Journal of Virology</i> , 2012, 86, 13790-13794.	1.5	8
356	Estimating the Distribution of Selection Coefficients from Phylogenetic Data Using Sitewise Mutation-Selection Models. <i>Genetics</i> , 2012, 190, 1101-1115.	1.2	114
357	A Single Ancient Origin for Prototypical Serine/Arginine-Rich Splicing Factors $\hat{A}$ $\hat{A}$ . <i>Plant Physiology</i> , 2012, 158, 546-560.	2.3	28
358	The steppe relics: taxonomic study on two lymnaeid species endemic to the former USSR (Gastropoda: Tj ETQq0 0.0 rgBT /Oyerlock 10	0.0	0
359	Phylogenetic revision of <i>Backhousieae</i> (Myrtaceae): Neogene divergence, a revised circumscription of <i>Backhousia</i> and two new species. <i>Australian Systematic Botany</i> , 2012, 25, 404.	0.3	11
360	A new species of <i>Leptobrachium</i> from Myanmar (Anura: Megophryidae). <i>Zootaxa</i> , 2012, 3415, .	0.2	12
361	Phylogenetic classification of <i>Pleurothecium</i> and <i>Pleurotheciella</i> gen. nov. and its dactylaria-like anamorph (Sordariomycetes) based on nuclear ribosomal and protein-coding genes. <i>Mycologia</i> , 2012, 104, 1299-1314.	0.8	45
362	<i>Rhizobium etli</i> taxonomy revised with novel genomic data and analyses. <i>Systematic and Applied Microbiology</i> , 2012, 35, 353-358.	1.2	59
363	Regulation of archaella expression by the FHA and von Willebrand domain-containing proteins ArnA and ArnB in <i>Sulfolobus acidocaldarius</i> . <i>Molecular Microbiology</i> , 2012, 86, 24-36.	1.2	72
364	Diversity Among <i>Ralstonia solanacearum</i> Strains Isolated from the Southeastern United States. <i>Phytopathology</i> , 2012, 102, 924-936.	1.1	50
365	Phylogenetic and Phylogeographic Patterns of the HIV Type 1 Subtype F1 Parenteral Epidemic in Romania. <i>AIDS Research and Human Retroviruses</i> , 2012, 28, 1161-1166.	0.5	9
366	Population dynamics of DENV-1 genotype V in Brazil is characterized by co-circulation and strain/lineage replacement. <i>Archives of Virology</i> , 2012, 157, 2061-2073.	0.9	42
367	Sexual transmission of predicted CXCR4-tropic HIV-1 likely originating from the source partner's seminal cells. <i>Virology</i> , 2012, 434, 2-4.	1.1	8
368	Species status and population structure of mussels (Mollusca: Bivalvia: <i>Mytilus</i> spp.) in the Wadden Sea of Lower Saxony (Germany). <i>Organisms Diversity and Evolution</i> , 2012, 12, 387-402.	0.7	10
369	Microbial Communities Involved in Methane Production from Hydrocarbons in Oil Sands Tailings. <i>Environmental Science &amp; Technology</i> , 2012, 46, 9802-9810.	4.6	102
370	Fine-grain parallelism using multi-core, Cell/BE, and GPU Systems. <i>Parallel Computing</i> , 2012, 38, 365-390.	1.3	20
371	Molecular phylogeny and biogeography of Malagasy frogs of the genus <i>Gephyromantis</i> . <i>Molecular Phylogenetics and Evolution</i> , 2012, 62, 555-560.	1.2	27

#	ARTICLE	IF	CITATIONS
372	Expanded phylogenetic and dating analyses of the apples and their relatives (Pyreae, Rosaceae). <i>Molecular Phylogenetics and Evolution</i> , 2012, 63, 230-243.	1.2	115
373	RNA polymerase beta subunit ( <i>rpoB</i> ) gene and the 16Sâ€“23S rRNA intergenic transcribed spacer region (ITS) as complementary molecular markers in addition to the 16S rRNA gene for phylogenetic analysis and identification of the species of the family Mycoplasmataceae. <i>Molecular Phylogenetics and Evolution</i> , 2012, 62, 515-528.	1.2	72
374	Exploring diversity in cryptorhynchine weevils (Coleoptera) using distance-, character- and tree-based species delineation. <i>Molecular Phylogenetics and Evolution</i> , 2012, 63, 1-14.	1.2	57
375	Phylogenetics of Chondrichthyes and the problem of rooting phylogenies with distant outgroups. <i>Molecular Phylogenetics and Evolution</i> , 2012, 63, 365-373.	1.2	29
376	The Molecular Basis of Host Specialization in Bean Pathovars of <i>Pseudomonas syringae</i> . <i>Molecular Plant-Microbe Interactions</i> , 2012, 25, 877-888.	1.4	83
377	New molecular data on <i>Pyrenulaceae</i> from Sri Lanka reveal two well-supported groups within this family. <i>Lichenologist</i> , 2012, 44, 639-647.	0.5	30
378	Relative embryo length as an adaptation to habitat and life cycle in Apiaceae. <i>New Phytologist</i> , 2012, 195, 479-487.	3.5	49
379	Hydroxysteroid dehydrogenases (HSDs) in bacteria â€“ A bioinformatic perspective. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2012, 129, 31-46.	1.2	94
380	<i>Natribacillus halophilus</i> gen. nov., sp. nov., a moderately halophilic and alkalitolerant bacterium isolated from soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2012, 62, 289-294.	0.8	25
381	Phylogenetics links monster larva to deepâ€“sea shrimp. <i>Ecology and Evolution</i> , 2012, 2, 2367-2373.	0.8	37
382	Evaluating multiple criteria for species delimitation: an empirical example using Hawaiian palms (Arecaceae: <i>Pritchardia</i> ). <i>BMC Evolutionary Biology</i> , 2012, 12, 23.	3.2	42
383	Analysis of a comprehensive dataset of diversity generating retroelements generated by the program DiGrEF. <i>BMC Genomics</i> , 2012, 13, 430.	1.2	26
384	Subgenotype reclassification of genotype B hepatitis B virus. <i>BMC Gastroenterology</i> , 2012, 12, 116.	0.8	20
385	Phylogenomics supports microsporidia as the earliest diverging clade of sequenced fungi. <i>BMC Biology</i> , 2012, 10, 47.	1.7	182
386	Archaeal origin of tubulin. <i>Biology Direct</i> , 2012, 7, 10.	1.9	91
387	Phylogeography of the Teiid Lizard <i>Kentropyx calcarata</i> and the Sphaerodactylid <i>Gonatodes humeralis</i> (Reptilia: Squamata): Testing A Geological Scenario for the Lower Amazonâ€“Tocantins Basins, Amazonia, Brazil. <i>Herpetologica</i> , 2012, 68, 272.	0.2	11
388	Defining evolutionary boundaries across parapatric ecomorphs of <i>B</i> lack <i>S</i> alamanders ( <i>A</i> neides flavipunctatus) with conservation implications. <i>Molecular Ecology</i> , 2012, 21, 5745-5761.	2.0	21
389	Evolutionary Dynamics of the <i>Yersinia enterocolitica</i> Complex. <i>Advances in Experimental Medicine and Biology</i> , 2012, 954, 15-22.	0.8	5



#	ARTICLE	IF	CITATIONS
390	Cirrosporium novae-zelandiae, an enigmatic coelomycete with meristem arthroconidia, with ancestors in the Eurotiomycetes. Mycologia, 2012, 104, 1315-1324.	0.8	6
391	Frustule-related gene transcription and the influence of diatom community composition on silica precipitation in an iron-limited environment. Limnology and Oceanography, 2012, 57, 1619-1633.	1.6	37
392	Divergence and Phylogeny of Firmicutes from the Cuatro Ci�negas Basin, Mexico: A Window to an Ancient Ocean. Astrobiology, 2012, 12, 674-684.	1.5	50
393	Intact polar and core glycerol dibiphytanyl glycerol tetraether lipids in the Arabian Sea oxygen minimum zone: I. Selective preservation and degradation in the water column and consequences for the TEX86. Geochimica Et Cosmochimica Acta, 2012, 98, 228-243.	1.6	111
394	Comparison of two DNA sequence-based typing schemes for the Fusarium solani Species Complex and proposal of a new consensus method. Journal of Microbiological Methods, 2012, 91, 65-72.	0.7	17
395	Novel animal papillomavirus sequences and accurate phylogenetic placement. Molecular Phylogenetics and Evolution, 2012, 65, 883-891.	1.2	19
396	The Essentials of Computational Molecular Evolution. Methods in Molecular Biology, 2012, 855, 111-152.	0.4	28
397	Affinities of the Boletus chromapes group to Royoungia and the description of two new genera, Harrya and Australopilus. Australian Systematic Botany, 2012, 25, 418.	0.3	46
398	Insights into the bovine rumen plasmidome. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 5452-5457.	3.3	145
399	Sequencing of mitochondrial genomes of nine Aspergillus and Penicillium species identifies mobile introns and accessory genes as main sources of genome size variability. BMC Genomics, 2012, 13, 698.	1.2	131
400	Genome sequence of the necrotrophic fungus Penicillium digitatum, the main postharvest pathogen of citrus. BMC Genomics, 2012, 13, 646.	1.2	205
401	Unexpected discovery of a novel basidiolichen in the threatened Caatinga biome of northeastern Brazil. Bryologist, 2012, 115, 601.	0.1	13
402	A Deeply Branching Thermophilic Bacterium with an Ancient Acetyl-CoA Pathway Dominates a Subsurface Ecosystem. PLoS ONE, 2012, 7, e30559.	1.1	161
403	18S rDNA Phylogeny of Lamproderma and Allied Genera (Stemonitales, Myxomycetes, Amoebozoa). PLoS ONE, 2012, 7, e35359.	1.1	75
404	Integrated Analysis of Residue Coevolution and Protein Structure in ABC Transporters. PLoS ONE, 2012, 7, e36546.	1.1	14
405	Multi-Locus Phylogeographic and Population Genetic Analysis of Anolis carolinensis: Historical Demography of a Genomic Model Species. PLoS ONE, 2012, 7, e38474.	1.1	40
406	Evolutionary History and Phylodynamics of Influenza A and B Neuraminidase (NA) Genes Inferred from Large-Scale Sequence Analyses. PLoS ONE, 2012, 7, e38665.	1.1	31
407	Multiple Inter-Kingdom Horizontal Gene Transfers in the Evolution of the Phosphoenolpyruvate Carboxylase Gene Family. PLoS ONE, 2012, 7, e51159.	1.1	7

#	ARTICLE	IF	CITATIONS
408	Xin proteins and intercalated disc maturation, signaling and diseases. <i>Frontiers in Bioscience - Landmark</i> , 2012, 17, 2566.	3.0	43
409	Molecular phylogeny and systematics of the <i>Ocellularia</i> clade (Ascomycota: Ostropales). <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50</i>	0.4	45
410	<i>Anzia mahaelyensis</i> and <i>Anzia flavotenuis</i> , two new lichen species from Sri Lanka. <i>Lichenologist</i> , 2012, 44, 381-389.	0.5	14
411	Phototrophic Phylotypes Dominate Mesothermal Microbial Mats Associated with Hot Springs in Yellowstone National Park. <i>Microbial Ecology</i> , 2012, 64, 162-170.	1.4	25
412	Testing relationships among the vetigastropod taxa: a molecular approach. <i>Journal of Molluscan Studies</i> , 2012, 78, 12-27.	0.4	44
413	Microevolution of extensively drug-resistant tuberculosis in Russia. <i>Genome Research</i> , 2012, 22, 735-745.	2.4	173
414	Revival of Palaeoptera head characters support a monophyletic origin of Odonata and Ephemeroptera (Insecta). <i>Cladistics</i> , 2012, 28, 560-581.	1.5	71
415	A specific mix of generalists: bacterial symbionts in Mediterranean <i>Ircinia</i> spp.. <i>FEMS Microbiology Ecology</i> , 2012, 79, 619-637.	1.3	75
416	What genomes have to say about the evolution of the Earth. <i>Gondwana Research</i> , 2012, 21, 483-494.	3.0	18
417	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
418	A MOLECULAR PHYLOGENY OF <i>ACROCHAETE</i> AND OTHER ENDOPHYTIC GREEN ALGAE (ULVALES). <i>Tj ETQq0 0 0 rgBT /Overlock 16</i>	1.0	16
419	Utility of the DNA barcoding gene fragment for parasitic wasp phylogeny (Hymenoptera:). <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50</i>	2.2	46
420	Identification of novel inter-genotypic recombinants of human hepatitis B viruses by large-scale phylogenetic analysis. <i>Virology</i> , 2012, 427, 51-59.	1.1	44
421	DNA sequences corroborate <i>Soesiladeepakius</i> as a non-salticoid genus of jumping spiders: placement with lapsiines, phylogeny, and description of six new species (Araneae, Salticidae). <i>Zoological Journal of the Linnean Society</i> , 2012, 165, 274-295.	1.0	5
422	Parallel evolution in courtship songs of North American and European green lacewings (Neuroptera:). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50</i>	0.7	31
423	Phylogenomics of T4 cyanophages: lateral gene transfer in the "core" and origins of host genes. <i>Environmental Microbiology</i> , 2012, 14, 2113-2126.	1.8	114
424	<i>Staphylococcus</i> prevails in the skin microbiota of long-term immunodeficient mice. <i>Environmental Microbiology</i> , 2012, 14, 2087-2098.	1.8	13
425	Pseudoscorpion mitochondria show rearranged genes and genome-wide reductions of RNA gene sizes and inferred structures, yet typical nucleotide composition bias. <i>BMC Evolutionary Biology</i> , 2012, 12, 31.	3.2	29



#	ARTICLE	IF	CITATIONS
426	MRL and SuperFine+MRL: new supertree methods. <i>Algorithms for Molecular Biology</i> , 2012, 7, 3.	0.3	62
427	The Evolutionary Root of Flowering Plants. <i>Systematic Biology</i> , 2013, 62, 50-61.	2.7	71
428	Quantification and relative severity of inflated branch-support values generated by alternative methods: An empirical example. <i>Molecular Phylogenetics and Evolution</i> , 2013, 67, 277-296.	1.2	27
429	Phylogenetic diversity of nonmarine picocyanobacteria. <i>FEMS Microbiology Ecology</i> , 2013, 85, 293-301.	1.3	66
430	Bioinformatics Research and Applications. <i>Lecture Notes in Computer Science</i> , 2013, , .	1.0	0
431	<i>Marinococcus tarijensis</i> sp. nov., a moderately halophilic bacterium isolated from a salt mine. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013, 63, 3319-3323.	0.8	7
432	A comprehensive and integrative reconstruction of evolutionary history for Anomura (Crustacea): Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	3.2	113
433	High-throughput genome sequencing of lichenizing fungi to assess gene loss in the ammonium transporter/ammonia permease gene family. <i>BMC Genomics</i> , 2013, 14, 225.	1.2	41
434	High-resolution SAR11 ecotype dynamics at the Bermuda Atlantic Time-series Study site by phylogenetic placement of pyrosequences. <i>ISME Journal</i> , 2013, 7, 1322-1332.	4.4	191
435	Host specificity shapes population structure of pinworm parasites in Caribbean reptiles. <i>Molecular Ecology</i> , 2013, 22, 4576-4590.	2.0	33
436	Phylogeny and evolution of Planomonadida (Sulcozoa): Eight new species and new genera <i>Fabomonas</i> and <i>Nutomonas</i> . <i>European Journal of Protistology</i> , 2013, 49, 179-200.	0.5	19
437	Reduction and Expansion in Microsporidian Genome Evolution: New Insights from Comparative Genomics. <i>Genome Biology and Evolution</i> , 2013, 5, 2285-2303.	1.1	114
438	<i>Flavobacterium akiainvivens</i> sp. nov., from decaying wood of <i>Wikstroemia oahuensis</i> , Hawai'i, and emended description of the genus <i>Flavobacterium</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013, 63, 3280-3286.	0.8	90
439	Starting from scratch: Evolution of the lichen thallus in the basidiolichen <i>Dictyonema</i> (Agaricales): Tj ETQq1 1 0.784314 rgBT /Overlock 47	1.1	47
440	High-Throughput Genomic Data in Systematics and Phylogenetics. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2013, 44, 99-121.	3.8	434
441	Dating Phylogenies with Sequentially Sampled Tips. <i>Systematic Biology</i> , 2013, 62, 674-688.	2.7	79
442	Transcriptome deep-sequencing and clustering of expressed isoforms from <i>Favia</i> corals. <i>BMC Genomics</i> , 2013, 14, 546.	1.2	22
443	Explosive diversification following a benthic to pelagic shift in freshwater fishes. <i>BMC Evolutionary Biology</i> , 2013, 13, 272.	3.2	30

#	ARTICLE	IF	CITATIONS
444	Comparison of the <i>Legionella pneumophila</i> population structure as determined by sequence-based typing and whole genome sequencing. <i>BMC Microbiology</i> , 2013, 13, 302.	1.3	39
445	Fastphylo: Fast tools for phylogenetics. <i>BMC Bioinformatics</i> , 2013, 14, 334.	1.2	18
446	<i>Halarchaeum salinum</i> sp. nov., a moderately acidophilic haloarchaeon isolated from commercial sea salt. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013, 63, 1138-1142.	0.8	20
447	Advancing Our Understanding of the Human Microbiome Using QIIME. <i>Methods in Enzymology</i> , 2013, 531, 371-444.	0.4	553
448	<i>Youngia thunbergiana</i> (Crepidinae, Cichorieae, Asteraceae), a Species Overlooked in the North American Flora. <i>Castanea</i> , 2013, 78, 330-337.	0.2	6
449	PartFastTree: Constructing large phylogenetic trees and estimating their reliability. , 2013, , .		1
450	Toxic <i>Pseudo-nitzschia</i> spp. in the northwestern Adriatic Sea: characterization of species composition by genetic and molecular quantitative analyses. <i>Journal of Plankton Research</i> , 2013, 35, 352-366.	0.8	32
451	Insights into bilaterian evolution from three spiralian genomes. <i>Nature</i> , 2013, 493, 526-531.	13.7	564
452	Balancing a Cline by Influx of Migrants: A Genetic Transition in Water Frogs of Eastern Greece. <i>Journal of Heredity</i> , 2013, 104, 57-71.	1.0	13
453	Comparative Analysis of Bat Genomes Provides Insight into the Evolution of Flight and Immunity. <i>Science</i> , 2013, 339, 456-460.	6.0	522
454	Amoeba Stages in the Deepest Branching Heteroloboseans, Including <i>Pharyngomonas</i> : Evolutionary and Systematic Implications. <i>Protist</i> , 2013, 164, 272-286.	0.6	33
455	RNA secondary structure, an important bioinformatics tool to enhance multiple sequence alignment: a case study ( <i>Sordariomycetes</i> , Fungi). <i>Mycological Progress</i> , 2013, 12, 305-319.	0.5	11
456	Deconstructing <i>Mus gemischus</i> : advances in understanding ancestry, structure, and variation in the genome of the laboratory mouse. <i>Mammalian Genome</i> , 2013, 24, 1-20.	1.0	56
457	Deep metazoan phylogeny: When different genes tell different stories. <i>Molecular Phylogenetics and Evolution</i> , 2013, 67, 223-233.	1.2	242
458	Diversification rates have declined in the Malagasy herpetofauna. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2013, 280, 20131109.	1.2	28
459	Host range evolution in a selected group of osmiine bees (Hymenoptera: Megachilidae): the Boraginaceae-Fabaceae paradox. <i>Biological Journal of the Linnean Society</i> , 2013, 108, 35-54.	0.7	38
460	Molecular phylogeny of the bee genus <i>Hoplitis</i> (Megachilidae: Osmiini) - how does nesting biology affect biogeography?. <i>Zoological Journal of the Linnean Society</i> , 2013, 167, 28-42.	1.0	18
461	Phylogenetic congruence between <i>Mollitrichosiphum</i> (Aphididae: Greenideinae) and <i>Buchnera</i> indicates insect-bacteria parallel evolution. <i>Systematic Entomology</i> , 2013, 38, 81-92.	1.7	30

#	ARTICLE	IF	CITATIONS
462	Molecules, morphology and minute hooded beetles: a phylogenetic study with implications for the evolution and classification of Corylophidae (Coleoptera: Cucujoidea). <i>Systematic Entomology</i> , 2013, 38, 209-232.	1.7	23
463	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
464	Effects of ornamentation and phylogeny on the evolution of wing shape in stalk-eyed flies (Diopsidae). <i>Journal of Evolutionary Biology</i> , 2013, 26, 1281-1293.	0.8	10
465	A genomic portrait of the emergence, evolution, and global spread of a methicillin-resistant <i>Staphylococcus aureus</i> pandemic. <i>Genome Research</i> , 2013, 23, 653-664.	2.4	412
466	Phylogenetic Inferences Reveal a Large Extent of Novel Biodiversity in Chemically Rich Tropical Marine Cyanobacteria. <i>Applied and Environmental Microbiology</i> , 2013, 79, 1882-1888.	1.4	67
467	Interactions of Nitrifying Bacteria and Heterotrophs: Identification of a Micavibrio-Like Putative Predator of <i>Nitrospira</i> spp. <i>Applied and Environmental Microbiology</i> , 2013, 79, 2027-2037.	1.4	90
468	The toxicity and intraspecific variability of <i>Alexandrium andersonii</i> Balech. <i>Harmful Algae</i> , 2013, 25, 26-38.	2.2	16
469	The draft genome of sweet orange ( <i>Citrus sinensis</i> ). <i>Nature Genetics</i> , 2013, 45, 59-66.	9.4	837
470	Molecular phylogeny of black fungus gnats (Diptera: Sciaroidea: Sciaridae) and the evolution of larval habitats. <i>Molecular Phylogenetics and Evolution</i> , 2013, 66, 833-846.	1.2	56
471	The Lichen Connections of Black Fungi. <i>Mycopathologia</i> , 2013, 175, 523-535.	1.3	49
472	<i>Halobaculum magnesiophilum</i> sp. nov., a magnesium-dependent haloarchaeon isolated from commercial salt. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013, 63, 861-866.	0.8	23
473	Expanded taxon sampling disentangles evolutionary relationships and reveals a new family in Peltigerales (Lecanoromycetidae, Ascomycota). <i>Fungal Diversity</i> , 2013, 58, 171-184.	4.7	31
474	The African coelacanth genome provides insights into tetrapod evolution. <i>Nature</i> , 2013, 496, 311-316.	18.7	612
475	Nutritional physiology of a rock-inhabiting, model microcolonial fungus from an ancestral lineage of the Chaetothyriales (Ascomycetes). <i>Fungal Genetics and Biology</i> , 2013, 56, 54-66.	0.9	62
476	Molecular systematics of <i>Woswasia atropurpurea</i> gen. et sp. nov. (Sordariomycetidae), a fungicolous ascomycete with globose ascospores and holoblastic conidiogenesis. <i>Mycologia</i> , 2013, 105, 476-485.	0.8	14
477	TESTING THE MUSEUM VERSUS CRADLE TROPICAL BIOLOGICAL DIVERSITY HYPOTHESIS: PHYLOGENY, DIVERSIFICATION, AND ANCESTRAL BIOGEOGRAPHIC RANGE EVOLUTION OF THE ANTS. <i>Evolution; International Journal of Organic Evolution</i> , 2013, 67, 2240-2257.	1.1	290
478	Historical biogeography and phylogeny of <i>Typhlatya</i> cave shrimps (Decapoda: Atyidae) based on mitochondrial and nuclear data. <i>Journal of Biogeography</i> , 2013, 40, 594-607.	1.4	34
479	<i>Halomicroarcula pellucida</i> gen. nov., sp. nov., a non-pigmented, transparent-colony-forming, halophilic archaeon isolated from solar salt. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013, 63, 3556-3562.	0.8	39

#	ARTICLE	IF	CITATIONS
480	Salinisphaera japonica sp. nov., a moderately halophilic bacterium isolated from the surface of a deep-sea fish, Malacocottus gibber, and emended description of the genus Salinisphaera. International Journal of Systematic and Evolutionary Microbiology, 2013, 63, 2180-2185.	0.8	22
481	Journey from the West: Did tropical Graphidaceae (lichenized Ascomycota: Ostropales) evolve from a saxicolous ancestor along the American Pacific coast?. American Journal of Botany, 2013, 100, 844-856.	0.8	36
482	Population genomics of post-vaccine changes in pneumococcal epidemiology. Nature Genetics, 2013, 45, 656-663.	9.4	364
483	An artifact caused by undersampling optimal trees in supermatrix analyses of locally sampled characters. Molecular Phylogenetics and Evolution, 2013, 69, 265-275.	1.2	26
484	ORIGINS, EVOLUTION, AND DIVERSIFICATION OF CLEPTOPARASITIC LINEAGES IN LONG-TONGUED BEES. Evolution; International Journal of Organic Evolution, 2013, 67, n/a-n/a.	1.1	34
485	Conservation of Dark Recovery Kinetic Parameters and Structural Features in the Pseudomonadaceae "Short" Light, Oxygen, Voltage (LOV) Protein Family: Implications for the Design of LOV-Based Optogenetic Tools. Biochemistry, 2013, 52, 4460-4473.	1.2	15
486	Whole genome sequencing identifies zoonotic transmission of MRSA isolates with the novel <i>mecA</i> homologue <i>mecC</i> . EMBO Molecular Medicine, 2013, 5, 509-515.	3.3	192
487	Performance Evaluation of Computational Phylogeny Software in Parallel Computing Environment. Advances in Intelligent Systems and Computing, 2013, , 255-264.	0.5	0
488	A phylogenetic analysis of Sciomyzidae (Diptera) and some related genera. Cladistics, 2013, 29, 404-415.	1.5	11
489	The effects of model choice and mitigating bias on the ribosomal tree of life. Molecular Phylogenetics and Evolution, 2013, 69, 17-38.	1.2	53
490	Halarchaeum rubridurum sp. nov., a moderately acidophilic haloarchaeon isolated from commercial sea salt samples. International Journal of Systematic and Evolutionary Microbiology, 2013, 63, 3143-3147.	0.8	15
491	Natronoarchaeum philippinense sp. nov., a haloarchaeon isolated from commercial solar salt. International Journal of Systematic and Evolutionary Microbiology, 2013, 63, 920-924.	0.8	11
492	CHROMATOGATE: A TOOL FOR DETECTING BASE MIS-CALLS IN MULTIPLE SEQUENCE ALIGNMENTS BY SEMI-AUTOMATIC CHROMATOGRAM INSPECTION. Computational and Structural Biotechnology Journal, 2013, 6, e201303001.	1.9	9
494	The evolution and function of vessel and pit characters with respect to cavitation resistance across 10 Prunus species. Tree Physiology, 2013, 33, 684-694.	1.4	82
495	High-performance computing and the cloud. Xrds, 2013, 19, 52-57.	0.2	3
496	opm: an R package for analysing OmniLog <sup>®</sup> phenotype microarray data. Bioinformatics, 2013, 29, 1823-1824.	1.8	214
497	CodonPhyML: Fast Maximum Likelihood Phylogeny Estimation under Codon Substitution Models. Molecular Biology and Evolution, 2013, 30, 1270-1280.	3.5	99
498	Comparative Genomics of Blattabacterium cuenoti: The Frozen Legacy of an Ancient Endosymbiont Genome. Genome Biology and Evolution, 2013, 5, 351-361.	1.1	64

#	ARTICLE	IF	CITATIONS
499	Comparative Genomic Analysis of the Endosymbionts of Herbivorous Insects Reveals Eco-Environmental Adaptations: Biotechnology Applications. <i>PLoS Genetics</i> , 2013, 9, e1003131.	1.5	56
500	Exploring the origin and potential for spread of the 2013 dengue outbreak in Luanda, Angola. <i>Global Health Action</i> , 2013, 6, 21822.	0.7	35
501	An Epidemic of Dengue-1 in a Remote Village in Rural Laos. <i>PLoS Neglected Tropical Diseases</i> , 2013, 7, e2360.	1.3	31
502	Bioinformatics analysis of large-scale viral sequences. <i>Virulence</i> , 2013, 4, 97-106.	1.8	4
503	A TPR domain-containing N-terminal module of MPS1 is required for its kinetochore localization by Aurora B. <i>Journal of Cell Biology</i> , 2013, 201, 217-231.	2.3	119
504	<i>Rudaeicoccus suwonensis</i> gen. nov., sp. nov., an actinobacterium isolated from the epidermal tissue of a root of a <i>Phalaenopsis</i> orchid. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013, 63, 1291-1296.	0.8	13
505	Unexpected Genomic Variability in Clinical and Environmental Strains of the Pathogenic Yeast <i>Candida parapsilosis</i> . <i>Genome Biology and Evolution</i> , 2013, 5, 2382-2392.	1.1	62
506	Complete DNA Sequence of <i>Kuraishia capsulata</i> Illustrates Novel Genomic Features among Budding Yeasts ( <i>Saccharomycotina</i> ). <i>Genome Biology and Evolution</i> , 2013, 5, 2524-2539.	1.1	39
507	Mitochondrial and Nuclear Genes-Based Phylogeography of <i>Arvicanthis niloticus</i> (Murinae) and Sub-Saharan Open Habitats Pleistocene History. <i>PLoS ONE</i> , 2013, 8, e77815.	1.1	33
508	STRAW: Species TRee Analysis Web server. <i>Nucleic Acids Research</i> , 2013, 41, W238-W241.	6.5	93
509	Evolution of modular intraflagellar transport from a coatomer-like progenitor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 6943-6948.	3.3	144
510	<i>Halarchaeum nitrireducens</i> sp. nov., a moderately acidophilic haloarchaeon isolated from commercial sea salt. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013, 63, 4202-4206.	0.8	17
511	Novel Parallelization Schemes for Large-Scale Likelihood-based Phylogenetic Inference. , 2013, , .		29
512	Organic carbon transformations in high-Arctic peat soils: key functions and microorganisms. <i>ISME Journal</i> , 2013, 7, 299-311.	4.4	292
513	The complete mitochondrial genome of <i>Paracymoriza prodigalis</i> (Leech, 1889) (Lepidoptera), with a preliminary phylogenetic analysis of <i>Pyraloidea</i> . <i>Aquatic Insects</i> , 2013, 35, 71-88.	0.6	24
514	Host and viral features of human dengue cases shape the population of infected and infectious <i>Aedes aegypti</i> mosquitoes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 9072-9077.	3.3	220
515	Metagenomics uncovers a new group of low GC and ultra-small marine Actinobacteria. <i>Scientific Reports</i> , 2013, 3, 2471.	1.6	182
516	Surprisingly extensive mixed phylogenetic and ecological signals among bacterial Operational Taxonomic Units. <i>Nucleic Acids Research</i> , 2013, 41, 5175-5188.	6.5	121

#	ARTICLE	IF	CITATIONS
517	From $\hat{\alpha}$ - to $\hat{\beta}$ -Proteobacteria: The Origin and Evolution of Rhizobial Nodulation Genes nodJ. <i>Molecular Biology and Evolution</i> , 2013, 30, 2494-2508.	3.5	53
518	The Evolutionary Path to Extraintestinal Pathogenic, Drug-Resistant <i>Escherichia coli</i> Is Marked by Drastic Reduction in Detectable Recombination within the Core Genome. <i>Genome Biology and Evolution</i> , 2013, 5, 699-710.	1.1	45
519	Complete genome sequence of <i>Desulfocapsa sulfexigens</i> , a marine deltaproteobacterium specialized in disproportionating inorganic sulfur compounds. <i>Standards in Genomic Sciences</i> , 2013, 8, 58-68.	1.5	69
520	Novel Evolutionary Lineages Revealed in the Chaetothyriales (Fungi) Based on Multigene Phylogenetic Analyses and Comparison of ITS Secondary Structure. <i>PLoS ONE</i> , 2013, 8, e63547.	1.1	86
521	Amphitremida (Poche, 1913) Is a New Major, Ubiquitous Labyrinthulomycete Clade. <i>PLoS ONE</i> , 2013, 8, e53046.	1.1	48
522	Assembly of a Marine Viral Metagenome after Physical Fractionation. <i>PLoS ONE</i> , 2013, 8, e60604.	1.1	18
523	Two-Gene Phylogeny of Bright-Spored Myxomycetes (Slime Moulds, Superorder Lucisporidia). <i>PLoS ONE</i> , 2013, 8, e62586.	1.1	58
524	The Effect of Primer Choice and Short Read Sequences on the Outcome of 16S rRNA Gene Based Diversity Studies. <i>PLoS ONE</i> , 2013, 8, e71360.	1.1	121
525	Unraveling the Evolution of the Atlantic Cod's (Gadus morhua L.) Alternative Immune Strategy. <i>PLoS ONE</i> , 2013, 8, e74004.	1.1	64
526	Evolutionary Dynamics of Overlapped Genes in <i>Salmonella</i> . <i>PLoS ONE</i> , 2013, 8, e81016.	1.1	2
527	<b>Molecular phylogenetic reconstruction of the endemic Asian salamander family Hynobiidae (Amphibia, Caudata)</b> . <i>Zootaxa</i> , 2013, 3626, 77-93.	0.2	18
528	A New Species of Seed-harvester Ant, <i>Pogonomyrmex hoelldobleri</i> (Hymenoptera: Formicidae). <i>Open Access Journal of Entomology</i> , 2013, 1, 1-14.	0.2	2
529	<b>Vulcanolepas scotiaensis</b> , sp. nov., a new deep-sea scalpelliform barnacle (Eolepadidae: Neolepadinae) from hydrothermal vents in the Scotia Sea, Antarctica. <i>Zootaxa</i> , 2013, 3745, 551.	0.2	28
530	The Genome of <i>Nitrospina gracilis</i> Illuminates the Metabolism and Evolution of the Major Marine Nitrite Oxidizer. <i>Frontiers in Microbiology</i> , 2013, 4, 27.	1.5	243
531	An Analysis of Thaumarchaeota Populations from the Northern Gulf of Mexico. <i>Frontiers in Microbiology</i> , 2013, 4, 72.	1.5	89
532	Quantitative and phylogenetic study of the Deep Sea Archaeal Group in sediments of the Arctic mid-ocean spreading ridge. <i>Frontiers in Microbiology</i> , 2013, 4, 299.	1.5	45
533	Intraspecific morphological and genetic variability in the European freshwater snail <i>Radix labiata</i> (Rossmassler, 1835) (Gastropoda: Basommatophora: Lymnaeidae). <i>Contributions To Zoology</i> , 2013, 82, 55-68.	0.2	24
534	Shallow-Water Northern Hemisphere Jaera (Crustacea, Isopoda, Janiridae) Found on Whale Bones in the Southern Ocean Deep Sea: Ecology and Description of <i>Jaera tyleri</i> sp. nov. <i>PLoS ONE</i> , 2014, 9, e93018.	1.1	9



#	ARTICLE	IF	CITATIONS
535	The Impact of Modelling Rate Heterogeneity among Sites on Phylogenetic Estimates of Intraspecific Evolutionary Rates and Timescales. PLoS ONE, 2014, 9, e95722.	1.1	48
536	Rediscovery of an Endemic Vertebrate from the Remote Islas Revillagigedo in the Eastern Pacific Ocean: The Clari <sup>3</sup> n Nightsnake Lost and Found. PLoS ONE, 2014, 9, e97682.	1.1	14
537	First Reported Chikungunya Fever Outbreak in the Republic of Congo, 2011. PLoS ONE, 2014, 9, e115938.	1.1	58
538	<strong>Molecular phylogenetics of American snapping shrimps allied to <i>Alpheus floridanus</i> Kingsley, 1878 (Crustacea: Decapoda: Alpheidae)</strong> . Zootaxa, 2014, 3895, 492.	0.2	15
539	Classification of pmoA amplicon pyrosequences using BLAST and the lowest common ancestor method in MEGAN. Frontiers in Microbiology, 2012, 5, 34.	1.5	121
540	<i>Pinus flexilis</i> and <i>Picea engelmannii</i> share a simple and consistent needle endophyte microbiota with a potential role in nitrogen fixation. Frontiers in Microbiology, 2014, 5, 333.	1.5	81
541	Group 1 Allergen Genes in Two Species of House Dust Mites, <i>Dermatophagoides farinae</i> and <i>D. pteronyssinus</i> (Acari: Pyroglyphidae): Direct Sequencing, Characterization and Polymorphism. PLoS ONE, 2014, 9, e114636.	1.1	12
542	Fungal Genomics. Advances in Botanical Research, 2014, , 1-52.	0.5	25
543	FastMG: a simple, fast, and accurate maximum likelihood procedure to estimate amino acid replacement rate matrices from large data sets. BMC Bioinformatics, 2014, 15, 341.	1.2	16
544	<i>Bradomyces</i> gen. nov. (Chaetothyriales, Trichomeriaceae), a new ascomycete genus accommodating poorly differentiated melanized fungi. Antonie Van Leeuwenhoek, 2014, 106, 979-992.	0.7	28
545	Comparative genome analysis identifies few traits unique to the <i>Escherichia coli</i> ST131 H30Rx clade and extensive mosaicism at the capsule locus. BMC Genomics, 2014, 15, 830.	1.2	23
546	Frequent migration of introduced cucurbit-infecting begomoviruses among Middle Eastern countries. Virology Journal, 2014, 11, 181.	1.4	23
547	Reassessing evolutionary relationships in the filamentous cyanolichen genus <i>Spilonema</i> ( <i>Peltigerales</i> , Lecanoromycetes). Lichenologist, 2014, 46, 373-388.	0.5	14
548	New lichen-associated bulbil-forming species of Cantharellales (Basidiomycetes). Lichenologist, 2014, 46, 333-347.	0.5	15
549	Identification and activity of acetate-assimilating bacteria in diffuse fluids venting from two deep-sea hydrothermal systems. FEMS Microbiology Ecology, 2014, 90, 731-746.	1.3	21
550	Differential Expression of Conserved Germ Line Markers and Delayed Segregation of Male and Female Primordial Germ Cells in a Hermaphrodite, the Leech <i>Helobdella</i> . Molecular Biology and Evolution, 2014, 31, 341-354.	3.5	31
551	The taxonomy and diversity of <i>Platerodrilus</i> (Coleoptera, Lycidae) inferred from molecular data and morphology of adults and larvae. ZooKeys, 2014, 426, 29-63.	0.5	15
552	Gene Expansion Shapes Genome Architecture in the Human Pathogen <i>Lichtheimia corymbifera</i> : An Evolutionary Genomics Analysis in the Ancient Terrestrial Mucorales (Mucoromycotina). PLoS Genetics, 2014, 10, e1004496.	1.5	80

#	ARTICLE	IF	CITATIONS
553	Duplications and losses in gene families of rust pathogens highlight putative effectors. <i>Frontiers in Plant Science</i> , 2014, 5, 299.	1.7	44
554	A new species of the paper wasp genus <i>Polistes</i> (Hymenoptera, Vespidae, Polistinae) in Europe revealed by morphometrics and molecular analyses. <i>ZooKeys</i> , 2014, 400, 67-118.	0.5	14
555	Molecular tracing of the emergence, diversification, and transmission of <i>S. aureus</i> sequence type 8 in a New York community. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 6738-6743.	3.3	176
556	Mechanisms of Linezolid Resistance among Coagulase-Negative Staphylococci Determined by Whole-Genome Sequencing. <i>MBio</i> , 2014, 5, e00894-14.	1.8	35
557	A Shared Population of Epidemic Methicillin-Resistant <i>Staphylococcus aureus</i> 15 Circulates in Humans and Companion Animals. <i>MBio</i> , 2014, 5, e00985-13.	1.8	95
558	A Penalized-Likelihood Method to Estimate the Distribution of Selection Coefficients from Phylogenetic Data. <i>Genetics</i> , 2014, 197, 257-271.	1.2	55
559	Genomic insights into the rapid emergence and evolution of MDR in <i>Staphylococcus pseudintermedius</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2015, 70, 997-1007.	1.3	77
560	<i>Halorhabdus tiamatea</i> proteogenomics and glycosidase activity measurements identify the first cultivated euryarchaeon from a deep-sea anoxic brine lake as potential polysaccharide degrader. <i>Environmental Microbiology</i> , 2014, 16, 2525-2537.	1.8	41
561	BIOTYPE EXPRESSION AND INSECTICIDE RESPONSE OF <i>Bemisia tabaci</i> CHEMOSENSORY PROTEIN. <i>Archives of Insect Biochemistry and Physiology</i> , 2014, 85, 137-151.	0.6	64
562	Novel trophic niches drive variable progress towards ecological speciation within an adaptive radiation of pupfishes. <i>Molecular Ecology</i> , 2014, 23, 1846-1862.	2.0	64
563	Phylogeny and floral hosts of a predominantly pollen generalist group of mason bees (Megachilidae: Tj ETQq0 0 0 rBT /Overlock 10 Tf	0.7	64
564	Three new <i>Laccaria</i> species from Southwest China (Yunnan). <i>Mycological Progress</i> , 2014, 13, 1105.	0.5	24
565	Evidence for Soft Selective Sweeps in the Evolution of Pneumococcal Multidrug Resistance and Vaccine Escape. <i>Genome Biology and Evolution</i> , 2014, 6, 1589-1602.	1.1	112
566	Winter bloom of a rare betaproteobacterium in the Arctic Ocean. <i>Frontiers in Microbiology</i> , 2014, 5, 425.	1.5	43
567	The Holozoan <i>Capsaspora owczarzaki</i> Possesses a Diverse Complement of Active Transposable Element Families. <i>Genome Biology and Evolution</i> , 2014, 6, 949-963.	1.1	5
568	Acetic Acid Bacteria Genomes Reveal Functional Traits for Adaptation to Life in Insect Guts. <i>Genome Biology and Evolution</i> , 2014, 6, 912-920.	1.1	66
569	Rapid transcriptome sequencing of an invasive pest, the brown marmorated stink bug <i>Halyomorpha halys</i> . <i>BMC Genomics</i> , 2014, 15, 738.	1.2	62
570	Comparative genomics of the major fungal agents of human and animal Sporotrichosis: <i>Sporothrix schenckii</i> and <i>Sporothrix brasiliensis</i> . <i>BMC Genomics</i> , 2014, 15, 943.	1.2	121



#	ARTICLE	IF	CITATIONS
571	A comprehensive evaluation of rodent malaria parasite genomes and gene expression. BMC Biology, 2014, 12, 86.	1.7	251
572	Gene flow in environmental <i>Legionella pneumophila</i> leads to genetic and pathogenic heterogeneity within a Legionnairesâ€™ disease outbreak. Genome Biology, 2014, 15, 504.	3.8	36
573	Adaptive Change Inferred from Genomic Population Analysis of the ST93 Epidemic Clone of Community-Associated Methicillin-Resistant <i>Staphylococcus aureus</i> . Genome Biology and Evolution, 2014, 6, 366-378.	1.1	40
574	Phylogenomic Study Indicates Widespread Lateral Gene Transfer in <i>Entamoeba</i> and Suggests a Past Intimate Relationship with Parabasalids. Genome Biology and Evolution, 2014, 6, 2350-2360.	1.1	24
575	Molecular phylogeny and taxonomy of the endolithic lichen genus <i>Bagliettoa</i> (Ascomycota: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 34)	0.4	6
576	Gene Loss Rather Than Gene Gain Is Associated with a Host Jump from Monocots to Dicots in the Smut Fungus <i>Melanopsichium pennsylvanicum</i> . Genome Biology and Evolution, 2014, 6, 2034-2049.	1.1	146
577	Modularized Evolution in Archaeal Methanogens Phylogenetic Forest. Genome Biology and Evolution, 2014, 6, 3344-3359.	1.1	5
578	Genome Comparison of <i>Candida orthopsilosis</i> Clinical Strains Reveals the Existence of Hybrids between Two Distinct Subspecies. Genome Biology and Evolution, 2014, 6, 1069-1078.	1.1	138
579	Phylogeny and taxonomy of <i>Staurothele</i> ( <i>Verrucariaceae</i> , lichenized ascomycetes) from the karst of northern Vietnam. Lichenologist, 2014, 46, 515-533.	0.5	16
580	THE INFLUENCE OF SAMPLING DESIGN ON SPECIES TREE INFERENCE: A NEW RELATIONSHIP FOR THE NEW WORLD CHICKADEES (AVES: <i>POECILE</i> ). Evolution; International Journal of Organic Evolution, 2014, 68, 501-513.	1.1	34
581	One Alga to Rule them All: Unrelated Mixotrophic Testate Amoebae (Amoebozoa, Rhizaria and) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 34)	0.6	38
582	A multigene phylogeny reveals that <i>Ochroconis</i> belongs to the family Sympoventuriaceae (Venturiales, Tj ETQq1 1 0,784314,rgBT /Ove	4.7	27
583	Molecular data resolve a new order of Arthoniomycetes sister to the primarily lichenized Arthoniales and composed of black yeasts, lichenicolous and rock-inhabiting species. Fungal Diversity, 2014, 66, 113-137.	4.7	55
584	On the relationship between an Asian haplotype on chromosome 6 that reduces androstenone levels in boars and the differential expression of <i>SULT2A1</i> in the testis. BMC Genetics, 2014, 15, 4.	2.7	7
585	<i>Sporoschismopsis angustata</i> sp. nov., a new holomorph species in the Reticulascaceae (Glomerellales), and a reappraisal of <i>Sporoschismopsis</i> . Mycological Progress, 2014, 13, 671-681.	0.5	10
586	Primate phylogenetic relationships and divergence dates inferred from complete mitochondrial genomes. Molecular Phylogenetics and Evolution, 2014, 75, 165-183.	1.2	260
587	Divergent maximum-likelihood-branch-support values for polytomies. Molecular Phylogenetics and Evolution, 2014, 73, 87-96.	1.2	49
588	Lepidostromatales, a new order of lichenized fungi (Basidiomycota, Agaricomycetes), with two new genera, <i>Ertzia</i> and <i>Sulzbacheromyces</i> , and one new species, <i>Lepidostroma winklerianum</i> . Fungal Diversity, 2014, 64, 165-179.	4.7	36

#	ARTICLE	IF	CITATIONS
589	Global assessment of genetic variation and phenotypic plasticity in the lichen-forming species <i>Tephromela atra</i> . <i>Fungal Diversity</i> , 2014, 64, 233-251.	4.7	57
590	Transcriptome-wide evolutionary analysis on essential brown algae (Phaeophyceae) in China. <i>Acta Oceanologica Sinica</i> , 2014, 33, 13-19.	0.4	7
591	Multiple ITS Haplotypes in the Genome of the Lichenized Basidiomycete <i>Cora inversa</i> (Hygrophoraceae): Fact or Artifact?. <i>Journal of Molecular Evolution</i> , 2014, 78, 148-162.	0.8	31
592	The Use (and Misuse) of Phylogenetic Trees in Comparative Behavioral Analyses. <i>International Journal of Primatology</i> , 2014, 35, 32-54.	0.9	8
593	Reassortment patterns of avian influenza virus internal segments among different subtypes. <i>BMC Evolutionary Biology</i> , 2014, 14, 16.	3.2	77
594	The sooty moulds. <i>Fungal Diversity</i> , 2014, 66, 1-36.	4.7	417
595	Salt tolerance and polyphyly in the cyanobacterium <i>Croococcidiopsis</i> ( <i>leurocapsales</i> ). <i>Journal of Phycology</i> , 2014, 50, 472-482.	1.0	24
596	Enzymatic Synthesis of Bioinformatically Predicted Microcin C-Like Compounds Encoded by Diverse Bacteria. <i>MBio</i> , 2014, 5, e01059-14.	1.8	24
597	Evolution of the Cation Chloride Cotransporter Family: Ancient Origins, Gene Losses, and Subfunctionalization through Duplication. <i>Molecular Biology and Evolution</i> , 2014, 31, 434-447.	3.5	54
598	Genomic Support for a Moa "Tinamou Clade and Adaptive Morphological Convergence in Flightless Ratites. <i>Molecular Biology and Evolution</i> , 2014, 31, 1686-1696.	3.5	80
599	The Shape of Modern Tree Reconstruction Methods. <i>Systematic Biology</i> , 2014, 63, 436-441.	2.7	9
600	<i>Xylochrysis lucida</i> gen. et sp. nov., a new lignicolous ascomycete (Sordariomycetidae) with holoblastic conidiogenesis. <i>Mycologia</i> , 2014, 106, 564-572.	0.8	10
601	AmphoraNet: The webserver implementation of the AMPHORA2 metagenomic workflow suite. <i>Gene</i> , 2014, 533, 538-540.	1.0	98
602	Molecular phylogeny and evolutionary dynamics of influenza A nonstructural (NS) gene. <i>Infection, Genetics and Evolution</i> , 2014, 22, 192-200.	1.0	11
603	Evolution and transmission of drug-resistant tuberculosis in a Russian population. <i>Nature Genetics</i> , 2014, 46, 279-286.	9.4	451
604	Application of Mitochondrial DNA in Stock Identification. , 2014, , 257-295.		14
605	<i>Dictyonema huaorani</i> (Agaricales: Hygrophoraceae), a new lichenized basidiomycete from Amazonian Ecuador with presumed hallucinogenic properties. <i>Bryologist</i> , 2014, 117, 386-394.	0.1	15
606	Evidence of natural <i>Wolbachia</i> infections in field populations of <i>Anopheles gambiae</i> . <i>Nature Communications</i> , 2014, 5, 3985.	5.8	142

#	ARTICLE	IF	CITATIONS
607	Formal Revision of the <i>Alexandrium tamarense</i> Species Complex (Dinophyceae) Taxonomy: The Introduction of Five Species with Emphasis on Molecular-based (rDNA) Classification. <i>Protist</i> , 2014, 165, 779-804.	0.6	283
608	<i>Cautires apterus</i> , a New Species and the First Record of Wingless Male Lycidae (Coleoptera) Discovered in the North Pare Mountains, Tanzania. <i>Annales Zoologici</i> , 2014, 64, 1-7.	0.1	13
609	Photobiont selectivity leads to ecological tolerance and evolutionary divergence in a polymorphic complex of lichenized fungi. <i>Annals of Botany</i> , 2014, 114, 463-475.	1.4	94
610	Higher level molecular phylogeny of darkling beetles (Coleoptera: Tenebrionidae). <i>Journal of Molecular Evolution</i> , 2014, 78, 1074-1084.	1.7	74
611	Body size variation and caste ratios in geographically distinct populations of the invasive big-headed ant, <i>Pheidole megacephala</i> (Hymenoptera: Formicidae). <i>Biological Journal of the Linnean Society</i> , 2014, 113, 423-438.	0.7	23
612	Phylogenetic position of the bee genera <i>Ancyla</i> and <i>Tarsalia</i> (Hymenoptera: Apidae): A remarkable base compositional bias and an early Paleogene geodispersal from North America to the Old World. <i>Molecular Phylogenetics and Evolution</i> , 2014, 81, 258-270.	1.2	42
613	Genomic surveillance elucidates Ebola virus origin and transmission during the 2014 outbreak. <i>Science</i> , 2014, 345, 1369-1372.	6.0	1,083
614	Evolution of the mir-181 microRNA family. <i>Computers in Biology and Medicine</i> , 2014, 52, 82-87.	3.9	31
615	Bias in Tree Searches and its Consequences for Measuring Group Supports. <i>Systematic Biology</i> , 2014, 63, 851-861.	2.7	9
616	Getting Started with Microbiome Analysis: Sample Acquisition to Bioinformatics. <i>Current Protocols in Human Genetics</i> , 2014, 82, 18.8.1-29.	3.5	111
617	A novel hybrid SCCmec-mecC region in <i>Staphylococcus sciuri</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2014, 69, 911-918.	1.3	73
618	Expression Profiling of the Wheat Pathogen <i>Zymoseptoria tritici</i> Reveals Genomic Patterns of Transcription and Host-Specific Regulatory Programs. <i>Genome Biology and Evolution</i> , 2014, 6, 1353-1365.	1.1	92
619	A multilocus phylogeny reveals deep lineages within African galagids (Primates: Galagidae). <i>BMC Evolutionary Biology</i> , 2014, 14, 72.	3.2	80
620	The <i>Arabidopsis</i> Kinome: phylogeny and evolutionary insights into functional diversification. <i>BMC Genomics</i> , 2014, 15, 548.	1.2	116
621	Comparative genomics and transcriptomics in ants provide new insights into the evolution and function of odorant binding and chemosensory proteins. <i>BMC Genomics</i> , 2014, 15, 718.	1.2	82
622	Integrated Bayesian species delimitation and morphological diagnostics of chorioptic mange mites (Acariformes: Psoroptidae: Chorioptes). <i>Parasitology Research</i> , 2014, 113, 2603-2627.	0.6	31
623	Application of Diffusion Growth Chambers for the Cultivation of Marine Sponge-Associated Bacteria. <i>Marine Biotechnology</i> , 2014, 16, 594-603.	1.1	72
624	<i>Nitrolancea hollandica</i> gen. nov., sp. nov., a chemolithoautotrophic nitrite-oxidizing bacterium isolated from a bioreactor belonging to the phylum Chloroflexi. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2014, 64, 1859-1865.	0.8	82

#	ARTICLE	IF	CITATIONS
625	Another Look at the Root of the Angiosperms Reveals a Familiar Tale. <i>Systematic Biology</i> , 2014, 63, 368-382.	2.7	68
626	Numerical Computations with GPUs. , 2014, , .		15
627	Islands in ice: isolated populations of <i>Cryptopygus sverdrupi</i> (Collembola) among nunataks in the SÅr Rondane Mountains, Dronning Maud Land, Antarctica. <i>Biodiversity</i> , 2014, 15, 169-177.	0.5	14
628	New Insights into Dissemination and Variation of the Health Care-Associated Pathogen <i>Acinetobacter baumannii</i> from Genomic Analysis. <i>MBio</i> , 2014, 5, e00963-13.	1.8	184
629	A reappraisal of orders and families within the subclass Chaetothyriomycetidae (Eurotiomycetes.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.5	62
630	New â€œmissing linkâ€–genus of the colonial volvocine green algae gives insights into the evolution of oogamy. <i>BMC Evolutionary Biology</i> , 2014, 14, 37.	3.2	48
631	The Emergence of Lobsters: Phylogenetic Relationships, Morphological Evolution and Divergence Time Comparisons of an Ancient Group (Decapoda: Achelata, Astacidea, Glypheidea, Polychelida). <i>Systematic Biology</i> , 2014, 63, 457-479.	2.7	124
632	Compartmentalized microbial composition, oxygen gradients and nitrogen fixation in the gut of <i>Odontotaenius disjunctus</i> . <i>ISME Journal</i> , 2014, 8, 6-18.	4.4	80
633	Genomic analysis of the causative agents of coccidiosis in domestic chickens. <i>Genome Research</i> , 2014, 24, 1676-1685.	2.4	176
634	Evolutionary relationships of <i>Pemphigus</i> and allied genera (Hemiptera: Aphididae.) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	1.5	14
635	A taxonomic reâ€–evaluation reveals that <i>Phytophthora cinnamomi</i> and <i>Phytophthora cinnamomi</i> var. <i>parvispora</i> are separate species. <i>Forest Pathology</i> , 2014, 44, 1-20.	0.5	51
636	A novel papillomavirus isolated from a nasal neoplasia in an Italian free-ranging chamois ( <i>Rupicapra r.</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	0.8	10
637	<i>Cryptomarasmius</i> gen. nov. established in the Physalacriaceae to accommodate members of <i>Marasmius</i> section <i>Hygrometrici</i> . <i>Mycologia</i> , 2014, 106, 86-94.	0.8	23
638	Mobile elements and mitochondrial genome expansion in the soil fungus and potato pathogen <i>Rhizoctonia solani</i> AG-3. <i>FEMS Microbiology Letters</i> , 2014, 352, 165-173.	0.7	143
639	Incubator birds: biogeographical origins and evolution of underground nesting in megapodes (Galliformes: Megapodiidae). <i>Journal of Biogeography</i> , 2014, 41, 2045-2056.	1.4	36
640	Towards a mitogenomic phylogeny of Lepidoptera. <i>Molecular Phylogenetics and Evolution</i> , 2014, 79, 169-178.	1.2	185
641	Phylogenetic relationships among Synallaxini spinetails (Aves: Furnariidae) reveal a new biogeographic pattern across the Amazon and Parana river basins. <i>Molecular Phylogenetics and Evolution</i> , 2014, 78, 223-231.	1.2	12
642	A molecular phylogeny of <i>Phasmatodea</i> with emphasis on <i>Necrosiinae</i> , the most speciesâ€–rich subfamily of stick insects. <i>Systematic Entomology</i> , 2014, 39, 205-222.	1.7	81

#	ARTICLE	IF	CITATIONS
643	Diffusion of influenza viruses among migratory birds with a focus on the Southwest United States. <i>Infection, Genetics and Evolution</i> , 2014, 26, 185-193.	1.0	13
644	A first comprehensive census of fungi in soil reveals both hyperdiversity and fine-scale niche partitioning. <i>Ecological Monographs</i> , 2014, 84, 3-20.	2.4	293
645	The 2012 dengue outbreak in Madeira: exploring the origins. <i>Eurosurveillance</i> , 2014, 19, 20718.	3.9	80
646	A phylogenetic analysis of the southern African gecko genus <i>Afroedura</i> Loveridge (Squamata: Tj ETQq1 1 0.784314 rgBT /Overlock 10 South Africa. <i>Zootaxa</i> , 2014, 3846, 451-501.	0.2	22
647	New higher taxa in the lichen family Graphidaceae (lichenized Ascomycota: Ostropales) based on a three-gene skeleton phylogeny. <i>Phytotaxa</i> , 2014, 189, 39.	0.1	36
648	Revisiting the phylogeny of Ocellularieae, the second largest tribe within Graphidaceae (lichenized) Tj ETQq1 1 0.784314 rgBT /Overlock 28	0.1	28
649	Status, distribution, and genetics of Blair's fencing crayfish, <i>Faxonella blairi</i> (Decapoda: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 502	0.1	1
650	<i>Carajasia</i> (Rubiaceae), a new and endangered genus from Carajás mountain range, Pará, Brazil. <i>Phytotaxa</i> , 2015, 206, 14.	0.1	38
651	Cyanobacteria and the Great Oxidation Event: evidence from genes and fossils. <i>Palaeontology</i> , 2015, 58, 769-785.	1.0	207
652	Remarkable ancient divergences amongst neglected loriform primates. <i>Zoological Journal of the Linnean Society</i> , 2015, 175, 661-674.	1.0	71
653	Phylogeny and classification of <i>Cucujidae</i> and the recognition of a new superfamily <i>Cucujiformia</i> (Cucujidae: Cucujiformia). <i>Systematic Entomology</i> , 2015, 40, 745-778.	1.7	171
654	Functional conservation of an ancestral Pellino protein in helminth species. <i>Scientific Reports</i> , 2015, 5, 11687.	1.6	5
655	Revision of the <i>Verrucaria elaeomelaena</i> species complex and morphologically similar freshwater lichens (Verrucariaceae, Ascomycota). <i>Phytotaxa</i> , 2015, 197, 161.	0.1	24
656	The post-vaccine microevolution of invasive <i>Streptococcus pneumoniae</i> . <i>Scientific Reports</i> , 2015, 5, 14952.	1.6	36
657	Mitochondrial genomes of two phlebotomine sand flies, <i>Phlebotomus chinensis</i> and <i>Phlebotomus papatasi</i> (Diptera: Nematocera), the first representatives from the family Psychodidae. <i>Parasites and Vectors</i> , 2015, 8, 472.	1.0	14
658	<i>Pisorisporiales</i> , a new order of aquatic and terrestrial fungi for <i>Achroceratosphaeria</i> and <i>Pisorisporium</i> gen. nov. in the <i>Sordariomycetes</i> . <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2015, 34, 40-49.	1.6	12
659	Genomic dissection of the 1994 <i>Cronobacter sakazakii</i> outbreak in a French neonatal intensive care unit. <i>BMC Genomics</i> , 2015, 16, 750.	1.2	37
660	Molecular phylogeny of <i>Macrolycus</i> ( <i>Cucujidae</i> : <i>Lycidae</i> ) with description of new species from China. <i>Entomological Science</i> , 2015, 18, 319-329.	0.3	6

#	ARTICLE	IF	CITATIONS
661	Consequences of Common Topological Rearrangements for Partition Trees in Phylogenomic Inference. <i>Journal of Computational Biology</i> , 2015, 22, 1129-1142.	0.8	14
662	Using RAXML to Infer Phylogenies. <i>Current Protocols in Bioinformatics</i> , 2015, 51, 6.14.1-6.14.14.	25.8	215
663	Amino acid positions subject to multiple coevolutionary constraints can be robustly identified by their eigenvector network centrality scores. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 2293-2306.	1.5	23
664	Phylogeography of Influenza A(H3N2) Virus in Peru, 2010–2012. <i>Emerging Infectious Diseases</i> , 2015, 21, 1330-1338.	2.0	29
665	The evolution and expression of panarthropod frizzled genes. <i>Frontiers in Ecology and Evolution</i> , 2015, 3, .	1.1	20
666	Bacterial endophyte communities in the foliage of coast redwood and giant sequoia. <i>Frontiers in Microbiology</i> , 2015, 6, 1008.	1.5	49
667	Lake Tanganyika—A 'Melting Pot' of Ancient and Young Cichlid Lineages (Teleostei: Cichlidae)? <i>PLoS ONE</i> , 2015, 10, e0125043.	1.1	36
668	Identification of Habitat-Specific Biomes of Aquatic Fungal Communities Using a Comprehensive Nearly Full-Length 18S rRNA Dataset Enriched with Contextual Data. <i>PLoS ONE</i> , 2015, 10, e0134377.	1.1	62
669	Phytophthora infestans RXLR-WY Effector AVR3a Associates with Dynamin-Related Protein 2 Required for Endocytosis of the Plant Pattern Recognition Receptor FLS2. <i>PLoS ONE</i> , 2015, 10, e0137071.	1.1	78
670	Phylogenetic Reconstruction of the Calosphaerales and Togniniales Using Five Genes and Predicted RNA Secondary Structures of ITS, and <i>Flabellascus tenuirostris</i> gen. et sp. nov.. <i>PLoS ONE</i> , 2015, 10, e0144616.	1.1	26
671	New species of <i>Blaesodactylus</i> (Squamata: Gekkonidae) from Tsingy karstic outcrops in Ankarana National Park, northern Madagascar. <i>Zootaxa</i> , 2015, 3980, 406-16.	0.2	8
672	What Is <i>Peromyscus</i> ? Evidence from nuclear and mitochondrial DNA sequences suggests the need for a new classification. <i>Journal of Mammalogy</i> , 2015, 96, 708-719.	0.6	49
673	Gut-Associated Bacteria of <i>Dendroctonus valens</i> and their Involvement in Verbenone Production. <i>Microbial Ecology</i> , 2015, 70, 1012-1023.	1.4	91
674	Resolving the phylogeny of a speciose spider group, the family Linyphiidae (Araneae). <i>Molecular Phylogenetics and Evolution</i> , 2015, 91, 135-149.	1.2	23
675	The Inference of Gene Trees with Species Trees. <i>Systematic Biology</i> , 2015, 64, e42-e62.	2.7	226
676	Degeneration of the Nonrecombining Regions in the Mating-Type Chromosomes of the Anther-Smut Fungi. <i>Molecular Biology and Evolution</i> , 2015, 32, 928-943.	3.5	49
677	Molecular characterisation of hepatitis B virus in HIV-1 subtype C infected patients in Botswana. <i>BMC Infectious Diseases</i> , 2015, 15, 335.	1.3	16
678	A new time tree reveals Earth history's imprint on the evolution of modern birds. <i>Science Advances</i> , 2015, 1, e1501005.	4.7	303



#	ARTICLE	IF	CITATIONS
679	Strawberry Fruit Rot Caused by <i>Neopestalotiopsis iranensis</i> sp. nov., and <i>N. mesopotamica</i> . <i>Current Microbiology</i> , 2015, 72, 329-36.	1.0	20
680	Genome-scale phylogenetic analysis finds extensive gene transfer among fungi. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20140335.	1.8	77
681	The forest for the trees: evaluating molecular phylogenies with an emphasis on higher-level Decapoda. <i>Journal of Crustacean Biology</i> , 2015, 35, 577-592.	0.3	43
682	Morphology, molecular phylogenetics and biogeography of <i>Impatiens akomensis</i> (Balsaminaceae), a new species from Cameroon. <i>Plant Ecology and Evolution</i> , 2015, 148, 397-408.	0.3	6
683	Evolution of gamete attraction molecules: evidence for purifying selection in speract and its receptor, in the pantropical sea urchin <i>Diadema</i> . <i>Evolution &amp; Development</i> , 2015, 17, 92-108.	1.1	9
684	Increasing complexity and versatility: How the calcium signaling toolkit was shaped during plant land colonization. <i>Cell Calcium</i> , 2015, 57, 231-246.	1.1	122
685	Morphological and Molecular Diversification of Asian Endemic <i>Diffugia tuberspinifera</i> (Amoebozoa, Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.6	19
686	The role of real-time in biomedical science: A meta-analysis on computational complexity, delay and speedup. <i>Computers in Biology and Medicine</i> , 2015, 58, 73-84.	3.9	13
687	Divergence across diet, time and populations rules out parallel evolution in the gut microbiomes of Trinidadian guppies. <i>ISME Journal</i> , 2015, 9, 1508-1522.	4.4	133
689	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
690	Spatial Organization in Protein Kinase A Signaling Emerged at the Base of Animal Evolution. <i>Journal of Proteome Research</i> , 2015, 14, 2976-2987.	1.8	16
691	North-South Colonization Associated with Local Adaptation of the Wild Tomato Species <i>Solanum chilense</i> . <i>Molecular Biology and Evolution</i> , 2015, 32, 2932-2943.	3.5	47
692	Differential gene retention as an evolutionary mechanism to generate biodiversity and adaptation in yeasts. <i>Scientific Reports</i> , 2015, 5, 11571.	1.6	50
693	First insight into dead wood protistan diversity: a molecular sampling of bright-spored Myxomycetes (Amoebozoa, slime-moulds) in decaying beech logs. <i>FEMS Microbiology Ecology</i> , 2015, 91, .	1.3	23
694	<i>Halocalculus aciditolerans</i> gen. nov., sp. nov., an acid-tolerant haloarchaeon isolated from commercial salt. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 1640-1645.	0.8	17
695	<i>Halococcus agarilyticus</i> sp. nov., an agar-degrading haloarchaeon isolated from commercial salt. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 1634-1639.	0.8	12
696	<i>Halorubrum gandharaense</i> sp. nov., an alkaliphilic haloarchaeon from commercial rock salt. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 2345-2350.	0.8	13
697	Molecular systematics of <i>Barbatosphaeria</i> (&lt;I&gt;Sordariomycetes&lt;/I&gt;): multigene phylogeny and secondary ITS structure. <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2015, 35, 21-38.	1.6	13

#	ARTICLE	IF	CITATIONS
698	Phylogeny and species delineation in European species of the genus <i>Steganacarus</i> (Acari, Oribatida) using mitochondrial and nuclear markers. <i>Experimental and Applied Acarology</i> , 2015, 66, 173-186.	0.7	10
699	Diversifying Selection Analysis Predicts Antigenic Evolution of 2009 Pandemic H1N1 Influenza A Virus in Humans. <i>Journal of Virology</i> , 2015, 89, 5427-5440.	1.5	21
700	<i>Babela massiliensis</i> , a representative of a widespread bacterial phylum with unusual adaptations to parasitism in amoebae. <i>Biology Direct</i> , 2015, 10, 13.	1.9	71
701	Molecular data support establishment of a new genus for the lichenicolous species <i>Neobarya usneae</i> (Hypocreales). <i>Bryologist</i> , 2015, 118, 83-92.	0.1	8
702	Molecular and morphologic data reveal multiple species in <i>Peromyscus pectoralis</i> . <i>Journal of Mammalogy</i> , 2015, 96, 446-459.	0.6	8
703	<i>Halorubrum persicum</i> sp. nov., an extremely halophilic archaeon isolated from sediment of a hypersaline lake. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 1770-1778.	0.8	23
704	SISPA-Seq for rapid whole genome surveys of bacterial isolates. <i>Infection, Genetics and Evolution</i> , 2015, 32, 191-198.	1.0	16
705	The diversification of the genus <i>Monodelphis</i> and the chronology of Didelphidae (Didelphimorphia). <i>Zoological Journal of the Linnean Society</i> , 2015, 174, 414-427.	1.0	19
706	DNA-based species delimitation separates highly divergent populations within morphologically coherent clades of poorly dispersing beetles. <i>Zoological Journal of the Linnean Society</i> , 2015, 175, 59-72.	1.0	30
707	Elucidating Phylogenetic Relationships in the <i>Aechmea</i> Alliance: AFLP Analysis of <i>Portea</i> and the <i>Gravisia</i> Complex (Bromeliaceae, Bromelioideae). <i>Systematic Botany</i> , 2015, 40, 716-725.	0.2	30
708	Characterization of multiple isolates from an <i>Alexandrium ostenfeldii</i> bloom in The Netherlands. <i>Harmful Algae</i> , 2015, 49, 94-104.	2.2	59
709	Genomic sequence of the aflatoxigenic filamentous fungus <i>Aspergillus nomius</i> . <i>BMC Genomics</i> , 2015, 16, 551.	1.2	33
710	<i>Tuber turmericum</i> sp. nov., a Chinese truffle species based on morphological and molecular data. <i>Mycological Progress</i> , 2015, 14, 1.	0.5	10
711	Phylogenetic placement of the lichenicolous, anamorphic genus <i>Lichenodiplis</i> and its connection to <i>Muellerella</i> -like teleomorphs. <i>Fungal Biology</i> , 2015, 119, 1115-1128.	1.1	22
712	High multiple carriage and emergence of <i>Streptococcus pneumoniae</i> vaccine serotype variants in Malawian children. <i>BMC Infectious Diseases</i> , 2015, 15, 234.	1.3	56
713	DNA capture reveals transoceanic gene flow in endangered river sharks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 13302-13307.	3.3	65
714	The Food Web of Boiling Springs Lake Appears Dominated by the Heterolobosean <i>Tetramitus thermacidophilus</i> Strain <i>BSL</i> . <i>Journal of Eukaryotic Microbiology</i> , 2015, 62, 374-390.	0.8	6
715	Clinical Sequencing Uncovers Origins and Evolution of Lassa Virus. <i>Cell</i> , 2015, 162, 738-750.	13.5	230



#	ARTICLE	IF	CITATIONS
716	A revised infrageneric classification of the genus <i>Peperomia</i> (Piperaceae). <i>Taxon</i> , 2015, 64, 424-444.	0.4	35
717	High-level of viral genomic diversity in cervical cancers: A Brazilian study on human papillomavirus type 16. <i>Infection, Genetics and Evolution</i> , 2015, 34, 44-51.	1.0	22
718	Morphology-based phylogenetic binning to assess a taxonomic challenge: a case study in Graphidaceae (Ascomycota) requires a new generic name for the widespread <i>Lepidotrema wightii</i> . <i>Botanical Journal of the Linnean Society</i> , 2015, 179, 436-443.	0.8	11
719	Capturing the cloud of diversity reveals complexity and heterogeneity of MRSA carriage, infection and transmission. <i>Nature Communications</i> , 2015, 6, 6560.	5.8	105
720	Disentangling the complex of <i>Lichenothelia</i> species from rock communities in the desert. <i>Mycologia</i> , 2015, 107, 1233-1253.	0.8	23
721	Intelligent Computing Theories and Methodologies. <i>Lecture Notes in Computer Science</i> , 2015, , .	1.0	2
722	Complete genome sequence of <i>Propionibacterium freudenreichii</i> DSM 20271T. <i>Standards in Genomic Sciences</i> , 2015, 10, 83.	1.5	23
723	Community Shift from Phototrophic to Chemotrophic Sulfide Oxidation following Anoxic Holomixis in a Stratified Seawater Lake. <i>Applied and Environmental Microbiology</i> , 2015, 81, 298-308.	1.4	52
724	<i>Halostagnicola bangensis</i> sp. nov., an alkaliphilic haloarchaeon from a soda lake. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 754-759.	0.8	13
725	<i>Burkholderia pseudomallei</i> sequencing identifies genomic clades with distinct recombination, accessory, and epigenetic profiles. <i>Genome Research</i> , 2015, 25, 129-141.	2.4	61
726	Phylogenetic and transcriptomic analyses reveal the evolution of bioluminescence and light detection in marine deep-sea shrimps of the family Oplophoridae (Crustacea: Decapoda). <i>Molecular Phylogenetics and Evolution</i> , 2015, 83, 278-292.	1.2	41
727	Deciphering the human microbiome using next-generation sequencing data and bioinformatics approaches. <i>Methods</i> , 2015, 79-80, 52-59.	1.9	39
728	Computer science and parsimony: a reappraisal, with discussion of methods for poorly structured datasets. <i>Cladistics</i> , 2015, 31, 210-225.	1.5	7
729	<sc>POY</sc> version 5: phylogenetic analysis using dynamic homologies under multiple optimality criteria. <i>Cladistics</i> , 2015, 31, 189-196.	1.5	74
730	Origins of major archaeal clades correspond to gene acquisitions from bacteria. <i>Nature</i> , 2015, 517, 77-80.	13.7	238
731	Strains of the Morphospecies <i>Ploeotia costata</i> (Euglenozoa) Isolated from the Western North Pacific (Taiwan) Reveal Substantial Genetic Differences. <i>Journal of Eukaryotic Microbiology</i> , 2015, 62, 318-326.	0.8	6
732	A Beginners Guide to Estimating the Non-synonymous to Synonymous Rate Ratio of all Protein-Coding Genes in a Genome. <i>Methods in Molecular Biology</i> , 2015, 1201, 65-90.	0.4	105
733	Use of Whole-Genus Genome Sequence Data To Develop a Multilocus Sequence Typing Tool That Accurately Identifies <i>Yersinia</i> Isolates to the Species and Subspecies Levels. <i>Journal of Clinical Microbiology</i> , 2015, 53, 35-42.	1.8	45

#	ARTICLE	IF	CITATIONS
734	Multigene phylogeny resolves deep branching of Amoebozoa. <i>Molecular Phylogenetics and Evolution</i> , 2015, 83, 293-304.	1.2	84
735	Characterization of <i>Tulamoeba bucina</i> n. sp., an Extremely Halotolerant Amoeboflagellate Heterolobosean Belonging to the <i>Tulamoeba</i> "Pleurostomum" Clade (Tulamoebidae n. fam.). <i>Journal of Eukaryotic Microbiology</i> , 2015, 62, 227-238.	0.8	18
736	Systematics and phylogeny of <i>Sitana</i> (Reptilia: Agamidae) of Peninsular India, with the description of one new genus and five new species. <i>Contributions To Zoology</i> , 2016, 85, 67-111.	0.2	39
737	Sharpening the species boundaries in the <i>Cladonia mediterranea</i> complex (Cladoniaceae, Ascomycota). <i>Personia: Molecular Phylogeny and Evolution of Fungi</i> , 2016, 37, 1-12.	1.6	8
738	State aggregation for fast likelihood computations in molecular evolution. <i>Bioinformatics</i> , 2017, 33, 354-362.	1.8	7
739	AN INTRODUCTION TO MOLECULAR PHYLOGENETIC ANALYSIS. <i>Reviews in Agricultural Science</i> , 2016, 4, 36-45.	0.9	24
740	Genetic changes found in a distinct clade of Enterovirus D68 associated with paralysis during the 2014 outbreak. <i>Virus Evolution</i> , 2016, 2, vew015.	2.2	44
741	Evaluation of properties over phylogenetic trees using stochastic logics. <i>BMC Bioinformatics</i> , 2016, 17, 235.	1.2	3
742	PhyloBot: A Web Portal for Automated Phylogenetics, Ancestral Sequence Reconstruction, and Exploration of Mutational Trajectories. <i>PLoS Computational Biology</i> , 2016, 12, e1004976.	1.5	43
743	Combined Analysis of Variation in Core, Accessory and Regulatory Genome Regions Provides a Super-Resolution View into the Evolution of Bacterial Populations. <i>PLoS Genetics</i> , 2016, 12, e1006280.	1.5	177
744	Whole Genome Sequence Analysis of a Large Isoniazid-Resistant Tuberculosis Outbreak in London: A Retrospective Observational Study. <i>PLoS Medicine</i> , 2016, 13, e1002137.	3.9	77
745	Spatiotemporal Co-existence of Two <i>Mycobacterium ulcerans</i> Clonal Complexes in the Offin River Valley of Ghana. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004856.	1.3	7
746	The Genetic Diversity of Influenza A Viruses in Wild Birds in Peru. <i>PLoS ONE</i> , 2016, 11, e0146059.	1.1	24
747	From the Tunnels into the Treetops: New Lineages of Black Yeasts from Biofilm in the Stockholm Metro System and Their Relatives among Ant-Associated Fungi in the Chaetothyriales. <i>PLoS ONE</i> , 2016, 11, e0163396.	1.1	33
748	Variants Exported Blood-Stage Proteins Encoded by Plasmodium Multigene Families Are Expressed in Liver Stages Where They Are Exported into the Parasitophorous Vacuole. <i>PLoS Pathogens</i> , 2016, 12, e1005917.	2.1	56
749	Evolution of Epiphytism and Fruit Traits Act Unevenly on the Diversification of the Species-Rich Genus <i>Peperomia</i> (Piperaceae). <i>Frontiers in Plant Science</i> , 2016, 07, 1145.	1.7	12
750	Comparative Transcriptomics of Strawberries ( <i>Fragaria</i> spp.) Provides Insights into Evolutionary Patterns. <i>Frontiers in Plant Science</i> , 2016, 7, 1839.	1.7	33
751	Ecological and evolutionary variation in community nitrogen use traits during tropical dry forest secondary succession. <i>Ecology</i> , 2016, 97, 1194-1206.	1.5	20

#	ARTICLE	IF	CITATIONS
752	Phylogenetics of Pitcairnioideae (Bromeliaceae): evidence from nuclear and plastid DNA sequence data. <i>Botanical Journal of the Linnean Society</i> , 2016, 181, 323-342.	0.8	46
753	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
754	Climatic niche conservatism and ecological opportunity in the explosive radiation of arvicoline rodents (Arvicolinae, Cricetidae). <i>Evolution; International Journal of Organic Evolution</i> , 2016, 70, 1094-1104.	1.1	18
755	Out of South-East Asia: phylogeny and biogeography of the spiny ant genus <i>Polyrhachis</i> Smith (Hymenoptera: Formicidae). <i>Systematic Entomology</i> , 2016, 41, 369-378.	1.7	19
756	Function and evolution of a Lotus japonicus AP2/ERF family transcription factor that is required for development of infection threads. <i>DNA Research</i> , 2016, 24, dsw052.	1.5	36
757	Etiology and Epidemiological Conditions Promoting Fusarium Root Rot in Sweetpotato. <i>Phytopathology</i> , 2016, 106, 909-919.	1.1	25
758	A deep sequencing reveals significant diversity among dominant variants and evolutionary dynamics of avian leukosis viruses in two infectious ecosystems. <i>BMC Veterinary Research</i> , 2016, 12, 287.	0.7	9
759	A preliminary molecular phylogeny of the genus <i>Riccia</i> L. (Ricciaceae) in Australia. <i>Australian Systematic Botany</i> , 2016, 29, 197.	0.3	14
760	De novo sequencing and detection of secondary metabolite gene clusters of <i>Penicillium griseofulvum</i> . <i>Acta Horticulturae</i> , 2016, , 157-162.	0.1	0
761	Evolution of Australian <i>Cryptocarya</i> (Lauraceae) based on nuclear and plastid phylogenetic trees: evidence of recent landscape-level disjunctions. <i>Australian Systematic Botany</i> , 2016, 29, 157.	0.3	10
762	Determinants of FIV and HIV Vif sensitivity of feline APOBEC3 restriction factors. <i>Retrovirology</i> , 2016, 13, 46.	0.9	21
763	New records of crustose Teloschistaceae (lichens, Ascomycota) from the Murmansk region of Russia. <i>Polish Polar Research</i> , 2016, 37, 421-434.	0.9	5
764	Phylogenetic Data and Chemical Traits Characterize a New Species in the Lichen Genus <i>Tephromela</i> . <i>Herzogia</i> , 2016, 29, 383.	0.1	4
765	<i>Tuber shii</i> sp. nov., a sister species of <i>T. jinshajiangense</i> from China in <i>Puberulum</i> group. <i>Phytotaxa</i> , 2016, 269, 279.	0.1	4
766	Phylogenetic diversity of bulbil-forming lichenicolous fungi in Cantharellales including a new genus and species. <i>Bryologist</i> , 2016, 119, 341-349.	0.1	14
767	<i>Sulzbacheromyces caatingae</i> : notes on its systematics, morphology and distribution based on ITS barcoding sequences. <i>Lichenologist</i> , 2016, 48, 61-70.	0.5	9
768	The complete mitochondrial genome of the white-tailed tropicbird, <i>Phaethon lepturus</i> . <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 4259-4260.	0.7	1
769	Building a genomic framework for prospective MRSA surveillance in the United Kingdom and the Republic of Ireland. <i>Genome Research</i> , 2016, 26, 263-270.	2.4	63

#	ARTICLE	IF	CITATIONS
770	Metagenomics Reveals Dysbiosis and a Potentially Pathogenic <i>N. flavescens</i> Strain in Duodenum of Adult Celiac Patients. <i>American Journal of Gastroenterology</i> , 2016, 111, 879-890.	0.2	128
771	187-gene phylogeny of protozoan phylum Amoebozoa reveals a new class (Cutosea) of deep-branching, ultrastructurally unique, enveloped marine Lobosa and clarifies amoeba evolution. <i>Molecular Phylogenetics and Evolution</i> , 2016, 99, 275-296.	1.2	61
772	Binding interface change and cryptic variation in the evolution of protein-protein interactions. <i>BMC Evolutionary Biology</i> , 2016, 16, 40.	3.2	7
773	Two new lineages of aquatic ascomycetes: <i>Atractospora</i> gen. nov. and <i>Rubellisphaeria</i> gen. et sp. nov., and a sexual morph of <i>Myrmecidium montsegurinum</i> sp. nov.. <i>Mycological Progress</i> , 2016, 15, 1.	0.5	14
774	Terrace Aware Data Structure for Phylogenomic Inference from Supermatrices. <i>Systematic Biology</i> , 2016, 65, 997-1008.	2.7	1,453
775	Complete mitochondrial genome of <i>Pycnonotus xanthorrhous</i> (Passeriformes, Pycnonotidae) and phylogenetic consideration. <i>Biochemical Systematics and Ecology</i> , 2016, 69, 83-90.	0.6	0
776	Genomic diversification of marine cyanophages into stable ecotypes. <i>Environmental Microbiology</i> , 2016, 18, 4240-4253.	1.8	44
777	Family-Joining: A Fast Distance-Based Method for Constructing Generally Labeled Trees. <i>Molecular Biology and Evolution</i> , 2016, 33, 2720-2734.	3.5	4
778	Transmission of methicillin-resistant <i>Staphylococcus aureus</i> in long-term care facilities and their related healthcare networks. <i>Genome Medicine</i> , 2016, 8, 102.	3.6	30
779	The evolution of Ebola virus: Insights from the 2013â€“2016 epidemic. <i>Nature</i> , 2016, 538, 193-200.	13.7	264
780	Evolutionary genomics of yeast pathogens in the Saccharomycotina. <i>FEMS Yeast Research</i> , 2016, 16, fow064.	1.1	102
781	Three New, Seemingly-Cryptic Species in the Lichen Genus <i>Caloplaca</i> (Teloschistaceae) Distinguished in Two-Phase Phenotype Evaluation. <i>Annales Botanici Fennici</i> , 2016, 53, 243-262.	0.0	26
782	Genomic differentiation among wild cyanophages despite widespread horizontal gene transfer. <i>BMC Genomics</i> , 2016, 17, 930.	1.2	96
783	WGS analysis and molecular resistance mechanisms of azithromycin-resistant (MIC >2) <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50</i> Chemotherapy, 2016, 71, 3109-3116.	1.3	81
784	A new ant genus from southern Argentina and southern Chile, <i>Patagonomyrmex</i> (Hymenoptera:) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50</i>	0.2	7
785	Osmoadaptative Strategy and Its Molecular Signature in Obligately Halophilic Heterotrophic Protists. <i>Genome Biology and Evolution</i> , 2016, 8, 2241-2258.	1.1	53
786	Description of a new species of <i>Sitana</i> Cuvier, 1829 from southern India. <i>Zootaxa</i> , 2016, 4139, 167.	0.2	4
787	Phylogenetics of tribe Sabiceae (Ixoroideae, Rubiaceae) revisited, with a new subgeneric classification for <i>Sabicea</i> . <i>Botanical Journal of the Linnean Society</i> , 2016, 182, 551-580.	0.8	5

#	ARTICLE	IF	CITATIONS
788	Taxonomic classification of the reef coral family Lobophylliidae (Cnidaria: Anthozoa: Scleractinia). <i>Zoological Journal of the Linnean Society</i> , 2016, 178, 436-481.	1.0	33
789	The genome and transcriptome of <i>Trichormus</i> sp. NMC-1: insights into adaptation to extreme environments on the Qinghai-Tibet Plateau. <i>Scientific Reports</i> , 2016, 6, 29404.	1.6	33
790	Genomic resources for a unique, low-virulence <i>Babesia</i> taxon from China. <i>Parasites and Vectors</i> , 2016, 9, 564.	1.0	17
791	Mitochondrial genomes of praying mantises (Dictyoptera, Mantodea): rearrangement, duplication, and reassigment of tRNA genes. <i>Scientific Reports</i> , 2016, 6, 25634.	1.6	43
792	<i>Suillus foetidus</i> (Boletales, Basidiomycota), a new species from northeast China. <i>Phytotaxa</i> , 2016, 260, 167.	0.1	5
793	Transcriptome sequencing of <i>Crucihimalaya himalaica</i> (Brassicaceae) reveals how <i>Arabidopsis</i> close relative adapt to the Qinghai-Tibet Plateau. <i>Scientific Reports</i> , 2016, 6, 21729.	1.6	47
794	A Transcriptome-based Perspective of Cell Cycle Regulation in Dinoflagellates. <i>Protist</i> , 2016, 167, 610-621.	0.6	14
795	Ebola Virus Glycoprotein with Increased Infectivity Dominated the 2013–2016 Epidemic. <i>Cell</i> , 2016, 167, 1088-1098.e6.	13.5	173
796	Newly recognised lineages of perithecial ascomycetes: the new orders <i>Conioscyphales</i> and <i>Pleurotheciales</i> . <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2016, 37, 57-81.	1.6	41
797	Genotypic distribution of HHV-8 in AIDS individuals without and with Kaposi sarcoma. <i>Medicine (United States)</i> , 2016, 95, e5291.	0.4	22
798	Systematic Surveillance Detects Multiple Silent Introductions and Household Transmission of Methicillin-Resistant <i>Staphylococcus aureus</i> USA300 in the East of England. <i>Journal of Infectious Diseases</i> , 2016, 214, 447-453.	1.9	45
799	Horizontal acquisition of toxic alkaloid synthesis in a clade of plant associated fungi. <i>Fungal Genetics and Biology</i> , 2016, 86, 71-80.	0.9	26
800	Characterization of novel human papillomavirus types 157, 158 and 205 from healthy skin and recombination analysis in genus $\beta^3$ -Papillomavirus. <i>Infection, Genetics and Evolution</i> , 2016, 42, 20-29.	1.0	17
801	Assessing parallel gene histories in viral genomes. <i>BMC Evolutionary Biology</i> , 2016, 16, 32.	3.2	10
802	Genome sequencing and secondary metabolism of the postharvest pathogen <i>Penicillium griseofulvum</i> . <i>BMC Genomics</i> , 2016, 17, 19.	1.2	70
803	Identifying the effect of patient sharing on between-hospital genetic differentiation of methicillin-resistant <i>Staphylococcus aureus</i> . <i>Genome Medicine</i> , 2016, 8, 18.	3.6	20
804	The influenza A virus NS genome segment displays lineage-specific patterns in predicted RNA secondary structure. <i>BMC Research Notes</i> , 2016, 9, 279.	0.6	12
805	Phylogenetic position of the house dust mite subfamily <i>Guatemalichinae</i> (Acariformes: Pyroglyphidae) based on integrated molecular and morphological analyses and different measures of support. <i>Cladistics</i> , 2016, 32, 261-275.	1.5	4

#	ARTICLE	IF	CITATIONS
806	Phylogenomics of "Discosea": A new molecular phylogenetic perspective on Amoebozoa with flat body forms. <i>Molecular Phylogenetics and Evolution</i> , 2016, 99, 144-154.	1.2	38
807	Subfamilial and tribal relationships of Ranunculaceae: evidence from eight molecular markers. <i>Plant Systematics and Evolution</i> , 2016, 302, 419-431.	0.3	38
808	A new <i>Laccaria</i> species from cloud forest of Fortuna, Panama. <i>Mycological Progress</i> , 2016, 15, 1.	0.5	16
809	Extremotolerant fungi from alpine rock lichens and their phylogenetic relationships. <i>Fungal Diversity</i> , 2016, 76, 119-142.	4.7	69
810	HIV infection and hepatitis C virus genotype 1a are associated with phylogenetic clustering among people with recently acquired hepatitis C virus infection. <i>Infection, Genetics and Evolution</i> , 2016, 37, 252-258.	1.0	13
812	Making sense of genomes of parasitic worms: Tackling bioinformatic challenges. <i>Biotechnology Advances</i> , 2016, 34, 663-686.	6.0	30
813	Genome dynamics of multidrug-resistant <i>Acinetobacter baumannii</i> during infection and treatment. <i>Genome Medicine</i> , 2016, 8, 26.	3.6	77
814	Mating type markers reveal high levels of heterothallism in <i>Leptographium sensu lato</i> . <i>Fungal Biology</i> , 2016, 120, 538-546.	1.1	9
815	Ortholog-Finder: A Tool for Constructing an Ortholog Data Set. <i>Genome Biology and Evolution</i> , 2016, 8, 446-457.	1.1	18
816	Myxozoan infections of caecilians demonstrate broad host specificity and indicate a link with human activity. <i>International Journal for Parasitology</i> , 2016, 46, 375-381.	1.3	14
817	Molecular phylogeny of the tropical lichen family Pyrenulaceae: contribution from dried herbarium specimens and FTA card samples. <i>Mycological Progress</i> , 2016, 15, 1.	0.5	27
818	Molecular analysis of Chinese truffles resembling <i>Tuber californicum</i> in morphology reveals a rich pattern of species diversity with emphasis on four new species. <i>Mycologia</i> , 2016, 108, 344-353.	0.8	13
819	Phylogenetic analyses of Chinese <i>Tuber</i> species that resemble <i>T. borchii</i> reveal the existence of the new species <i>T. hubeiense</i> and <i>T. wumengense</i> . <i>Mycologia</i> , 2016, 108, 354-362.	0.8	9
820	From one to six: unrecognized species diversity in the genus <i>Acantholichen</i> (lichenized) Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.8	18
821	Multiple taxa in the <i>Phoma</i> -complex associate with black elder ( <i>Sambucus nigra</i> L.). <i>Fungal Biology</i> , 2016, 120, 43-50.	1.1	3
822	Comparison of Whole-Genome Sequencing and Molecular-Epidemiological Techniques for <i>Clostridium difficile</i> Strain Typing. <i>Journal of the Pediatric Infectious Diseases Society</i> , 2016, 5, 329-332.	0.6	12
823	Increase in bacteraemia cases in the East Midlands region of the UK due to MDREscherichia coliST73: high levels of genomic and plasmid diversity in causative isolates. <i>Journal of Antimicrobial Chemotherapy</i> , 2016, 71, 339-343.	1.3	24
824	Phylogeny and dating of divergences within the genus <i>Thymallus</i> (Salmonidae: Thymallinae) using complete mitochondrial genomes. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 3602-3611.	0.7	15



#	ARTICLE	IF	CITATIONS
825	The complete mitochondrial genome of the White-throated Tinamou, <i>Tinamus guttatus</i> (Tinamiformes.) <i>Tj ETQq0 0,0 rgBT /Overlock 10</i>	0.7	5
826	The complete mitochondrial genome of <i>Astatotilapia burtoni</i> . <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 2379-2380.	0.7	3
827	The complete mitochondrial genome of the American crow, <i>Corvus brachyrhynchos</i> (Passeriformes.) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5</i>	0.7	5
828	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
829	Evolutionary Dynamics of Pandemic Methicillin-Sensitive <i>Staphylococcus aureus</i> ST398 and Its International Spread via Routes of Human Migration. <i>MBio</i> , 2017, 8, .	1.8	56
830	Tracking the variability of phenotypic traits on a molecular phylogeny: an example from scolopendrid centipedes in peninsular India. <i>Organisms Diversity and Evolution</i> , 2017, 17, 393-408.	0.7	5
831	<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
832	Molecular phylogeny of the tribe Erotini with description of a new genus from China (Coleoptera:) <i>Tj ETQq1 1 0.784314 rgBT /Overlock 0,3 5</i>	0.3	5
833	Historical introgression drives pervasive mitochondrial admixture between two species of pelagic sharks. <i>Molecular Phylogenetics and Evolution</i> , 2017, 110, 122-126.	1.2	24
834	<i>Crepidotus lutescens</i> sp. nov. (Inocybaceae, Agaricales), an ochraceous salmon colored species from northeast of China. <i>Phytotaxa</i> , 2017, 297, 189.	0.1	10
835	Genome assembly with in vitro proximity ligation data and whole-genome triplication in lettuce. <i>Nature Communications</i> , 2017, 8, 14953.	5.8	330
836	High levels of endemism among Galapagos basidiolichens. <i>Fungal Diversity</i> , 2017, 85, 45-73.	4.7	26
837	Multi-locus phylogeny supports the placement of <i>Endocarpon pulvinatum</i> within <i>Staurothele</i> s. str. (lichenised ascomycetes, Eurotiomycetes, Verrucariaceae). <i>Phytotaxa</i> , 2017, 306, 37.	0.1	8
838	Phylogenetic structure of arbuscular mycorrhizal fungal communities along an elevation gradient. <i>Mycorrhiza</i> , 2017, 27, 273-282.	1.3	44
839	Comprehensive global genome dynamics of <i>Chlamydia trachomatis</i> show ancient diversification followed by contemporary mixing and recent lineage expansion. <i>Genome Research</i> , 2017, 27, 1220-1229.	2.4	106
840	Analysis of complete genome sequence and major surface antigens of <i>Neorickettsia helminthoeca</i> , causative agent of salmon poisoning disease. <i>Microbial Biotechnology</i> , 2017, 10, 933-957.	2.0	11
841	Rapid radiations of both kiwifruit hybrid lineages and their parents shed light on a two-layer mode of species diversification. <i>New Phytologist</i> , 2017, 215, 877-890.	3.5	52
842	Scallop genome provides insights into evolution of bilaterian karyotype and development. <i>Nature Ecology and Evolution</i> , 2017, 1, 120.	3.4	353



#	ARTICLE	IF	CITATIONS
843	Adaptation to deep-sea chemosynthetic environments as revealed by mussel genomes. <i>Nature Ecology and Evolution</i> , 2017, 1, 121.	3.4	250
844	Bacterial virulence phenotypes of <i>Escherichia coli</i> and host susceptibility determine risk for urinary tract infections. <i>Science Translational Medicine</i> , 2017, 9, .	5.8	139
845	The mitochondrial genome of <i>Gatzara jezoensis</i> (Neuroptera: Myrmeleontidae) and phylogenetic analysis of Neuroptera. <i>Biochemical Systematics and Ecology</i> , 2017, 71, 230-235.	0.6	7
846	Diversity in warning coloration is easily recognized by avian predators. <i>Journal of Evolutionary Biology</i> , 2017, 30, 1288-1302.	0.8	18
847	The least known European native crayfish <i>Astacus pachypus</i> (Rathke, 1837) revealed its phylogenetic position. <i>Zoologischer Anzeiger</i> , 2017, 267, 151-154.	0.4	12
848	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
849	Two new species of the <i>Fusarium fujikuroi</i> species complex isolated from the natural environment. <i>Antonie Van Leeuwenhoek</i> , 2017, 110, 819-832.	0.7	37
850	Ecological diversification associated with the benthic to pelagic transition by North American minnows. <i>Journal of Evolutionary Biology</i> , 2017, 30, 549-560.	0.8	23
851	Complete mitochondrial genome of <i>Neochauliodes parasparsus</i> (Megaloptera: Corydalidae) with phylogenetic consideration. <i>Biochemical Systematics and Ecology</i> , 2017, 70, 192-199.	0.6	9
852	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
853	Investigation of a Cluster of Sequence Type 22 Methicillin-Resistant <i>Staphylococcus aureus</i> Transmission in a Community Setting. <i>Clinical Infectious Diseases</i> , 2017, 65, 2069-2077.	2.9	11
854	<i>Six1</i> and <i>Eya1</i> both promote and arrest neuronal differentiation by activating multiple Notch pathway genes. <i>Developmental Biology</i> , 2017, 431, 152-167.	0.9	19
855	Wholly <i>Rickettsia</i> ! Reconstructed Metabolic Profile of the Quintessential Bacterial Parasite of Eukaryotic Cells. <i>MBio</i> , 2017, 8, .	1.8	121
856	Geographic variation in hybridization across a reinforcement contact zone of chorus frogs ( <i>Pseudacris</i> ). <i>Ecology and Evolution</i> , 2017, 7, 9485-9502.	0.8	18
857	Whole-Genome Sequencing of Bacterial Pathogens: the Future of Nosocomial Outbreak Analysis. <i>Clinical Microbiology Reviews</i> , 2017, 30, 1015-1063.	5.7	310
858	New circumscription of <i>Cryptanthus</i> and new <i>Cryptanthoid</i> genera and subgenera (Bromeliaceae: Tj ETQq1 1 0.784314 rgBT /Overl	0.1	36
859	Insect-bacteria parallel evolution in multiple-co-obligate-aphid association: a case in Lachninae (Hemiptera: Aphididae). <i>Scientific Reports</i> , 2017, 7, 10204.	1.6	23
860	A new species and two new records of <i>Strigula</i> (lichenized Ascomycota) from China. <i>Mycoscience</i> , 2017, 58, 391-397.	0.3	8

#	ARTICLE	IF	CITATIONS
861	Genomic surveillance reveals low prevalence of livestock-associated methicillin-resistant <i>Staphylococcus aureus</i> in the East of England. <i>Scientific Reports</i> , 2017, 7, 7406.	1.6	25
862	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
863	Influence of age and body condition on astrovirus infection of bats in Singapore: An evolutionary and epidemiological analysis. <i>One Health</i> , 2017, 4, 27-33.	1.5	18
864	Molecular analyses uncover the phylogenetic placement of the lichenized hyphomycetous genus <i>Cheiromycina</i> . <i>Mycologia</i> , 2017, 109, 1-13.	0.8	5
865	The East Asian origin of the giant lobelias. <i>American Journal of Botany</i> , 2017, 104, 924-938.	0.8	20
866	25 years of serving the community with ribosomal RNA gene reference databases and tools. <i>Journal of Biotechnology</i> , 2017, 261, 169-176.	1.9	679
867	Genome-wide identification of nuclear receptor (NR) genes and the evolutionary significance of the NR1O subfamily in the monogonont rotifer <i>Brachionus</i> spp.. <i>General and Comparative Endocrinology</i> , 2017, 252, 219-225.	0.8	15
868	Genome-wide analysis of gene expression and protein secretion of <i>Babesia canis</i> during virulent infection identifies potential pathogenicity factors. <i>Scientific Reports</i> , 2017, 7, 3357.	1.6	35
869	Non-Toxin-Producing <i>Bacillus cereus</i> Strains Belonging to the <i>B. anthracis</i> Clade Isolated from the International Space Station. <i>MSystems</i> , 2017, 2, .	1.7	28
870	Longamoebia is not monophyletic: Phylogenomic and cytoskeleton analyses provide novel and well-resolved relationships of amoebozoan subclades. <i>Molecular Phylogenetics and Evolution</i> , 2017, 114, 249-260.	1.2	21
871	The complete mitochondrial genome of Chakouyi horse ( <i>Equus caballus</i> ). <i>Conservation Genetics Resources</i> , 2017, 9, 173-175.	0.4	1
872	Evolutionary processes and environmental factors underlying the genetic diversity and lifestyles of <i>Bacillus cereus</i> group bacteria. <i>Research in Microbiology</i> , 2017, 168, 309-318.	1.0	43
873	The Evolutionary Dynamics of the Odorant Receptor Gene Family in Corbiculate Bees. <i>Genome Biology and Evolution</i> , 2017, 9, 2023-2036.	1.1	44
874	HEALTH ASSESSMENT OF CAPTIVE PSITTACINE SPECIES IN PRERELEASE PROGRAMS AT COSTA RICAN RESCUE CENTERS. <i>Journal of Zoo and Wildlife Medicine</i> , 2017, 48, 1135-1145.	0.3	4
875	<i>Tuber griseolivaceum</i> sp. nov., a new olive-gray truffle species from China based on morphological and DNA data. <i>Phytotaxa</i> , 2017, 309, 166.	0.1	1
876	Finding optimal finite biological sequences over finite alphabets: The OptiFin toolbox. , 2017, , .		0
877	Characterization of tree shrew ( <i>Tupaia belangeri</i> ) interleukin-6 and its expression pattern in response to exogenous challenge. <i>International Journal of Molecular Medicine</i> , 2017, 40, 1679-1690.	1.8	4
878	A new species of <i>Rhabdops</i> Boulenger, 1893 (Serpentes: Natricinae) from the northern Western Ghats region of India. <i>Zootaxa</i> , 2017, 4319, 27.	0.2	11

#	ARTICLE	IF	CITATIONS
879	Effects of Growth Media on the Diversity of Culturable Fungi from Lichens. <i>Molecules</i> , 2017, 22, 824.	1.7	47
880	Identification of Cyanobacteria in a Eutrophic Coastal Lagoon on the Southern Baltic Coast. <i>Frontiers in Microbiology</i> , 2017, 8, 923.	1.5	55
881	Adaptations to High Salt in a Halophilic Protist: Differential Expression and Gene Acquisitions through Duplications and Gene Transfers. <i>Frontiers in Microbiology</i> , 2017, 8, 944.	1.5	71
882	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
883	AmoA-Targeted Polymerase Chain Reaction Primers for the Specific Detection and Quantification of Comammox Nitrospira in the Environment. <i>Frontiers in Microbiology</i> , 2017, 8, 1508.	1.5	313
884	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
885	Phylogenetic placement within <i>Lecanoromycetes</i> of lichenicolous fungi associated with <i>Cladonia</i> and some other genera. <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2017, 39, 91-117.	1.6	40
886	Integrated pipeline for inferring the evolutionary history of a gene family embedded in the species tree: a case study on the STIMATE gene family. <i>BMC Bioinformatics</i> , 2017, 18, 439.	1.2	2
887	Phylogenetic characterisation of circulating, clinical influenza isolates from Bali, Indonesia: preliminary report from the BaliMEI project. <i>BMC Infectious Diseases</i> , 2017, 17, 583.	1.3	2
888	A new species of Gomphidius from Northeast China. <i>Phytotaxa</i> , 2017, 316, 181.	0.1	3
889	Phylogenetic relationships, taxonomic revision and new taxa of Termitomyces (Lyophyllaceae,) Tj ETQq0 0 0 rGBT /Overlock 10 Tf 50 342	0.1	12
890	Phylogenomic Insights into Mouse Evolution Using a Pseudoreference Approach. <i>Genome Biology and Evolution</i> , 2017, 9, 726-739.	1.1	47
891	Emergence of Different Recombinant Porcine Reproductive and Respiratory Syndrome Viruses, China. <i>Scientific Reports</i> , 2018, 8, 4118.	1.6	23
892	Multigene phylogeny and cell evolution of chromist infrakingdom Rhizaria: contrasting cell organisation of sister phyla Cercozoa and Retaria. <i>Protoplasma</i> , 2018, 255, 1517-1574.	1.0	66
893	The Draft Genome of the Invasive Walking Stick, <i>Medauroidea extradendata</i> , Reveals Extensive Lineage-Specific Gene Family Expansions of Cell Wall Degrading Enzymes in Phasmatodea. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 1403-1408.	0.8	24
894	Constraining uncertainty in the timescale of angiosperm evolution and the veracity of a Cretaceous Terrestrial Revolution. <i>New Phytologist</i> , 2018, 218, 819-834.	3.5	149
895	Circumscription and phylogeny of the Lepidostromatales ( <i>Lichenized Basidiomycota</i> ) following discovery of new species from China and Africa. <i>Mycologia</i> , 2017, 109, 730-748.	0.8	10
896	Production of the bioactive pigment elsinochrome A by a cultured mycobiont strain of the lichen <i>Graphis elongata</i> . <i>Mycological Progress</i> , 2018, 17, 479-487.	0.5	6

#	ARTICLE	IF	CITATIONS
897	The transmission dynamics and diversity of human metapneumovirus in Peru. <i>Influenza and Other Respiratory Viruses</i> , 2018, 12, 508-513.	1.5	6
898	Patterns of Genomic Variation in the Opportunistic Pathogen <i>Candida glabrata</i> Suggest the Existence of Mating and a Secondary Association with Humans. <i>Current Biology</i> , 2018, 28, 15-27.e7.	1.8	114
899	Evaluating Fast Maximum Likelihood-Based Phylogenetic Programs Using Empirical Phylogenomic Data Sets. <i>Molecular Biology and Evolution</i> , 2018, 35, 486-503.	3.5	147
900	Serological detection and molecular characterization of piroplasmids in equids in Brazil. <i>Acta Tropica</i> , 2018, 179, 81-87.	0.9	15
901	The global regulator of pathogenesis PnCon7 positively regulates <i>Tox3</i> effector gene expression through direct interaction in the wheat pathogen <i>Parastagonospora nodorum</i> . <i>Molecular Microbiology</i> , 2018, 109, 78-90.	1.2	13
902	<i>Passiflora kumandayi</i> (Passifloraceae), a new species from the Colombian Andes in a new section within subgenus <i>Decaloba</i> . <i>Phytotaxa</i> , 2018, 344, 13.	0.1	9
903	Taxonomic and functional diversity in <i>Calogaya</i> (lichenised Ascomycota) in dry continental Asia. <i>Mycological Progress</i> , 2018, 17, 897-916.	0.5	10
904	<i>Leucangium carthusianum</i> var. <i>purpureum</i> , a new purple truffle from China. <i>Phytotaxa</i> , 2018, 347, 165.	0.1	0
905	Clonal Emergence of Invasive Multidrug-Resistant <i>Staphylococcus epidermidis</i> Deconvoluted via a Combination of Whole-Genome Sequencing and Microbiome Analyses. <i>Clinical Infectious Diseases</i> , 2018, 67, 398-406.	2.9	27
906	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
907	Genome-Based Discovery of Polyketide-Derived Secondary Metabolism Pathways in the Barley Pathogen <i>Ramularia collo-cygni</i> . <i>Molecular Plant-Microbe Interactions</i> , 2018, 31, 962-975.	1.4	13
908	The complete mitochondrial genome of <i>Triplophysa brevibarba</i> with phylogenetic consideration. <i>Conservation Genetics Resources</i> , 2018, 10, 79-83.	0.4	0
909	The complete mitochondrial genomes of <i>Xyleutes mineus</i> and <i>Zeuzera multistrigata</i> (Cossidae: Zeuzerinae): genome characterisation and phylogenetic implications. <i>Oriental Insects</i> , 2018, 52, 31-48.	0.1	0
910	Weighted parsimony outperforms other methods of phylogenetic inference under models appropriate for morphology. <i>Cladistics</i> , 2018, 34, 407-437.	1.5	273
911	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
912	The complete mitochondrial genome of the mixtured pygmy frog <i>Microhyla mixtura</i> (Anura, Tj ETQq1 1 0.784314 ggBT /Overclock 10 Tj	0.4	3
913	The complete mitochondrial genome of <i>Nautilus pompilius</i> (Nautiloids: Nautilidae). <i>Conservation Genetics Resources</i> , 2018, 10, 437-440.	0.4	4
914	Aridification driven diversification of fan-throated lizards from the Indian subcontinent. <i>Molecular Phylogenetics and Evolution</i> , 2018, 120, 53-62.	1.2	38

#	ARTICLE	IF	CITATIONS
915	The Phylogenomic Diversity of Herbivore-Associated <i>Fibrobacter</i> spp. Is Correlated to Lignocellulose-Degrading Potential. <i>MSphere</i> , 2018, 3, .	1.3	38
916	Genome Sequencing and Pan-Genome Analysis of 23 <i>Coralloccoccus</i> spp. Strains Reveal Unexpected Diversity, With Particular Plasticity of Predatory Gene Sets. <i>Frontiers in Microbiology</i> , 2018, 9, 3187.	1.5	68
917	Identificación molecular y características fisiológicas de aislamientos de <i>Trichoderma</i> para el biocontrol de dos patógenos en la piña. <i>Ciencias Ambientales</i> , 2018, 53, 125.	0.1	0
918	A practical implementation of large transcriptomic data analysis to resolve cryptic species diversity problems in microbial eukaryotes. <i>BMC Evolutionary Biology</i> , 2018, 18, 170.	3.2	17
919	Global emergence and population dynamics of divergent serotype 3 CC180 pneumococci. <i>PLoS Pathogens</i> , 2018, 14, e1007438.	2.1	74
920	Multi-drug resistant <i>Enterobacter bugandensis</i> species isolated from the International Space Station and comparative genomic analyses with human pathogenic strains. <i>BMC Microbiology</i> , 2018, 18, 175.	1.3	81
921	A new species and a new record of <i>Xanthagaricus</i> (Agaricaceae, Agaricales) from China. <i>Phytotaxa</i> , 2018, 371, 241.	0.1	3
922	Phylogenetic analysis of <i>Rhizoclonium</i> (Cladophoraceae, Cladophorales), and the description of <i>Rhizoclonium subtile</i> sp. nov. from China. <i>Phytotaxa</i> , 2018, 383, 147.	0.1	4
923	Evolution of Oviposition Techniques in Stick and Leaf Insects (Phasmatodea). <i>Frontiers in Ecology and Evolution</i> , 2018, 6, .	1.1	85
924	The monotypic Brazilian genus <i>Diacrodon</i> is a synonym of <i>Borreria</i> (Spermacoceae, Rubiaceae): morphological and molecular evidences. <i>Anais Da Academia Brasileira De Ciencias</i> , 2018, 90, 1397-1415.	0.3	11
925	<i>Ortholinea concentrica</i> n. sp. (Cnidaria: Myxozoa) from the Patagonian seabass <i>Acanthistius patachonicus</i> (Jenyns, 1840) (Perciformes: Serranidae) off Patagonia, Argentina. <i>Parasitology Research</i> , 2018, 117, 3953-3963.	0.6	4
926	Advances in Bioinformatics and Computational Biology. <i>Lecture Notes in Computer Science</i> , 2018, , .	1.0	0
927	Chinese black truffles: <i>Tuber yigongense</i> sp. nov., taxonomic reassessment of <i>T. indicum</i> s.l., and re-examination of the <i>T. sinense</i> isotype. <i>Mycotaxon</i> , 2018, 133, 183-196.	0.1	1
928	Ecological Analyses of Mycobacteria in Showerhead Biofilms and Their Relevance to Human Health. <i>MBio</i> , 2018, 9, .	1.8	90
929	Identificación molecular y distribución potencial del anfípodo terrestre <i>Talitroides topitotum</i> (Crustacea: Amphipoda: Talitridae) en Costa Rica. <i>Acta Biológica Colombiana</i> , 2018, 23, 104-114.	0.1	3
930	DM-PhyClus: a Bayesian phylogenetic algorithm for infectious disease transmission cluster inference. <i>BMC Bioinformatics</i> , 2018, 19, 324.	1.2	6
931	HIV-1 Transmissions Among Recently Infected Individuals in Southwest China are Predominantly Derived from Circulating Local Strains. <i>Scientific Reports</i> , 2018, 8, 12831.	1.6	16
932	A systematic revision of <i>Calotes</i> Cuvier, 1817 (Squamata: Agamidae) from the Western Ghats adds two genera and reveals two new species. <i>Zootaxa</i> , 2018, 4482, 401-450.	0.2	22

#	ARTICLE	IF	CITATIONS
933	Four new <i>Tuber</i> species added to the <i>Rufum</i> group from China based on morphological and molecular evidence. <i>Mycologia</i> , 2018, 110, 771-779.	0.8	4
934	The Protean <i>Acremonium</i> . <i>A. sclerotigenum/egyptiacum</i> : Revision, Food Contaminant, and Human Disease. <i>Microorganisms</i> , 2018, 6, 88.	1.6	32
935	The impact of serotype-specific vaccination on phylodynamic parameters of <i>Streptococcus pneumoniae</i> and the pneumococcal pan-genome. <i>PLoS Pathogens</i> , 2018, 14, e1006966.	2.1	25
936	Flatfish monophyly refuted by the relationship of <i>Psettodes</i> in Carangimorphariae. <i>BMC Genomics</i> , 2018, 19, 400.	1.2	18
937	New species of <i>Mycena</i> (Mycenaceae, Agaricales) with colored lamellae and three new species records from China. <i>Phytotaxa</i> , 2018, 361, 266.	0.1	7
938	DNA sequence-based re-assessment of archived <i>Cronobacter sakazakii</i> strains isolated from dairy products imported into China between 2005 and 2006. <i>BMC Genomics</i> , 2018, 19, 506.	1.2	5
939	Grafting or pruning in the animal tree: lateral gene transfer and gene loss?. <i>BMC Genomics</i> , 2018, 19, 470.	1.2	21
940	DNA analysis reveals rich diversity of <i>Hydnotrya</i> with emphasis on the species found in China. <i>Mycological Progress</i> , 2018, 17, 1123-1137.	0.5	2
941	Descriptions of two new endemic and cryptic species of <i>Sitana</i> Cuvier, 1829 from peninsular India. <i>Zootaxa</i> , 2018, 4434, 327.	0.2	5
942	<i>Arabidopsis thaliana</i> and <i>Pseudomonas</i> Pathogens Exhibit Stable Associations over Evolutionary Timescales. <i>Cell Host and Microbe</i> , 2018, 24, 168-179.e4.	5.1	145
943	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
944	Whole genome sequencing data of 1110 <i>Mycobacterium tuberculosis</i> isolates identifies insertions and deletions associated with drug resistance. <i>BMC Genomics</i> , 2018, 19, 365.	1.2	14
945	Phylogenomic analysis on the exceptionally diverse fish clade Gobioidae (Actinopterygii: Gobiiformes) and data-filtering based on molecular clocklikeness. <i>Molecular Phylogenetics and Evolution</i> , 2018, 128, 192-202.	1.2	32
946	GATC: a genetic algorithm for gene tree construction under the Duplication-Transfer-Loss model of evolution. <i>BMC Genomics</i> , 2018, 19, 102.	1.2	1
947	Genome-wide protein phylogenies for four African cichlid species. <i>BMC Evolutionary Biology</i> , 2018, 18, 1.	3.2	116
948	Contrasting prevalence of selection and drift in the community structuring of bacteria and microbial eukaryotes. <i>Environmental Microbiology</i> , 2018, 20, 2231-2240.	1.8	153
949	Comparison of metaheuristics to measure gene effects on phylogenetic supports and topologies. <i>BMC Bioinformatics</i> , 2018, 19, 218.	1.2	1
950	Bioengineered Viral Platform for Intramuscular Passive Vaccine Delivery to Human Skeletal Muscle. <i>Molecular Therapy - Methods and Clinical Development</i> , 2018, 10, 144-155.	1.8	21



#	ARTICLE	IF	CITATIONS
951	Genome-wide identification of 99 autophagy-related (Atg) genes in the monogonont rotifer <i>Brachionus</i> spp. and transcriptional modulation in response to cadmium. <i>Aquatic Toxicology</i> , 2018, 201, 73-82.	1.9	10
952	Complete genomic characterization of two <i>Escherichia coli</i> lineages responsible for a cluster of carbapenem-resistant infections in a Chinese hospital. <i>Journal of Antimicrobial Chemotherapy</i> , 2018, 73, 2340-2346.	1.3	44
953	Repressed <i>Beauveria bassiana</i> infections in <i>Delia antiqua</i> due to associated microbiota. <i>Pest Management Science</i> , 2019, 75, 170-179.	1.7	36
954	Comparative genomics and evolution of trans-activating RNAs in Class 2 CRISPR-Cas systems. <i>RNA Biology</i> , 2019, 16, 435-448.	1.5	45
955	<i>Melanothamnus maniticolasp.</i> nov. (Ceramiales, Rhodophyta): an epizoic species evolved for living on the West Indian Manatee. <i>Journal of Phycology</i> , 2019, 55, 1239-1245.	1.0	7
956	Challenges in funding and developing genomic software: roots and remedies. <i>Genome Biology</i> , 2019, 20, 147.	3.8	21
957	Co-circulation and persistence of multiple A/H3N2 influenza variants in China. <i>Emerging Microbes and Infections</i> , 2019, 8, 1157-1167.	3.0	20
958	On the systematic status of the genus <i>Oriocalotes</i> Anther, 1864 (Squamata: Agamidae: Draconinae) with the description of a new species from Mizoram state, Northeast India. <i>Zootaxa</i> , 2019, 4638, zootaxa.4638.4.1.	0.2	16
959	Characterization of Aminoacyl-tRNA Synthetases in Chromerids. <i>Genes</i> , 2019, 10, 582.	1.0	5
960	Transcriptome Landscape Variation in the Genus <i>Thymus</i> . <i>Genes</i> , 2019, 10, 620.	1.0	11
961	A Global Survey of Mycobacterial Diversity in Soil. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	46
962	Tamdy Virus in <i>Ixodid</i> Ticks Infesting Bactrian Camels, Xinjiang, China, 2018. <i>Emerging Infectious Diseases</i> , 2019, 25, 2136-2138.	2.0	21
963	Classification of human Herpesviridae proteins using Domain-architecture Aware Inference of Orthologs (DAIO). <i>Virology</i> , 2019, 529, 29-42.	1.1	12
964	The composition and functional protein subsystems of the human nasal microbiome in granulomatosis with polyangiitis: a pilot study. <i>Microbiome</i> , 2019, 7, 137.	4.9	22
965	<i>Ganoderma shanxiense</i> , a new species from northern China based on morphological and molecular evidence. <i>Phytotaxa</i> , 2019, 406, 129-136.	0.1	9
966	Phylogenetic relationship in Actinidia (Actinidiaceae) based on four noncoding chloroplast DNA sequences. <i>Plant Systematics and Evolution</i> , 2019, 305, 787-796.	0.3	6
967	Insight into adaptation mechanisms of marine bacterioplankton from comparative genomic analysis of the genus <i>Pseudohongiella</i> . <i>Deep-Sea Research Part II: Topical Studies in Oceanography</i> , 2019, 167, 62-69.	0.6	5
968	Machine Learning Approaches for Epidemiological Investigations of Food-Borne Disease Outbreaks. <i>Frontiers in Microbiology</i> , 2019, 10, 1722.	1.5	22



#	ARTICLE	IF	CITATIONS
969	Improving Comprehension of Large Taxonomic Graphs. , 2019, , .		0
970	High-quality <i>Schistosoma haematobium</i> genome achieved by single-molecule and long-range sequencing. <i>GigaScience</i> , 2019, 8, .	3.3	41
971	A new species of <i>Tubaria</i> (Tubariaceae, Agaricales) from northeast China. <i>Phytotaxa</i> , 2019, 409, 93-100.	0.1	0
972	Two new species of <i>Pachyphlodes</i> from China. <i>Phytotaxa</i> , 2019, 411, 105-115.	0.1	1
973	A new <i>Gerronema</i> species with striking colours from China. <i>Phytotaxa</i> , 2019, 405, 74.	0.1	3
974	Characterization and Whole Genome Sequencing of AR23, a Highly Toxic <i>Bacillus thuringiensis</i> Strain Isolated from Lebanese Soil. <i>Current Microbiology</i> , 2019, 76, 1503-1511.	1.0	9
975	Comparative analysis reveals conservation in genome organization among intestinal <i>Cryptosporidium</i> species and sequence divergence in potential secreted pathogenesis determinants among major human-infecting species. <i>BMC Genomics</i> , 2019, 20, 406.	1.2	37
976	Genome Analysis of Coxsackievirus A4 Isolates From Hand, Foot, and Mouth Disease Cases in Shandong, China. <i>Frontiers in Microbiology</i> , 2019, 10, 1001.	1.5	12
977	Genomic analyses of aminoacyl tRNA synthetases from human-infecting helminths. <i>BMC Genomics</i> , 2019, 20, 333.	1.2	1
978	A new genus and species of natricine snake from northeast India. <i>Zootaxa</i> , 2019, 4603, zootaxa.4603.2.2.	0.2	19
979	Diversification of Colonization Factors in a Multidrug-Resistant <i>Escherichia coli</i> Lineage Evolving under Negative Frequency-Dependent Selection. <i>MBio</i> , 2019, 10, .	1.8	106
980	A new species of <i>Ahaetulla</i> Link, 1807 (Serpentes: Colubridae: Ahaetullinae) from India. <i>Journal of Natural History</i> , 2019, 53, 497-516.	0.2	6
981	Numerical Optimization Techniques in Maximum Likelihood Tree Inference. <i>Computational Biology</i> , 2019, , 21-38.	0.1	4
982	Two new rock-inhabiting species of <i>Cyphellophora</i> from karst habitats in China. <i>Phytotaxa</i> , 2019, 397, 23.	0.1	1
983	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
984	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
985	<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
986	Genome-based epidemiology and antimicrobial resistance determinants of <i>Neisseria gonorrhoeae</i> isolates with decreased susceptibility and resistance to extended-spectrum cephalosporins in Argentina in 2011–16. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 1551-1559.	1.3	33

#	ARTICLE	IF	CITATIONS
987	A latent class approach to identify multi-risk profiles associated with phylogenetic clustering of recent hepatitis C virus infection in Australia and New Zealand from 2004 to 2015. <i>Journal of the International AIDS Society</i> , 2019, 22, e25222.	1.2	6
988	Phylogenetic relationships of Cypriniformes and plasticity of pharyngeal teeth in the adaptive radiation of cyprinids. <i>Science China Life Sciences</i> , 2019, 62, 553-565.	2.3	29
989	Phylogenetic relationships of rock-inhabiting black fungi belonging to the widespread genera <i>Lichenothelia</i> and <i>Saxomyces</i> . <i>Mycologia</i> , 2019, 111, 127-160.	0.8	13
990	Genera <i>Acremonium</i> and <i>Sarocladium</i> Cause Brown Spot on Bagged Apple Fruit in China. <i>Plant Disease</i> , 2019, 103, 1889-1901.	0.7	21
991	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
992	Expansion of a single transposable element family is associated with genome-size increase and radiation in the genus <i>Hydra</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 22915-22917.	3.3	38
993	Ancestral Reconstruction and Investigations of Genomic Recombination on some Pentapetalae Chloroplasts. <i>Journal of Integrative Bioinformatics</i> , 2019, 16, .	1.0	1
994	Deciphering protein evolution and fitness landscapes with latent space models. <i>Nature Communications</i> , 2019, 10, 5644.	5.8	64
995	The complete mitochondrial genomes of three populations in <i>Luehdorfia chinensis</i> (Leech, 1893) (Lepidoptera: Papilionidae), with a phylogenetic analysis of Papilionidae. <i>Oriental Insects</i> , 2019, 53, 320-339.	0.1	0
996	Niche-directed evolution modulates genome architecture in freshwater Planctomycetes. <i>ISME Journal</i> , 2019, 13, 1056-1071.	4.4	67
997	First mitochondrial genome of the superfamily Choreutoidea and its phylogenetic implications. <i>Oriental Insects</i> , 2019, 53, 483-496.	0.1	3
998	Genomic, transcriptomic, and proteomic insights into the symbiosis of deep-sea tubeworm holobionts. <i>ISME Journal</i> , 2020, 14, 135-150.	4.4	41
999	Divergence and support among slightly suboptimal likelihood gene trees. <i>Cladistics</i> , 2020, 36, 322-340.	1.5	20
1000	A novel haplotype of <i>Candidatus Liberibacter solanacearum</i> ™ found in Apiaceae and Polygonaceae family plants. <i>European Journal of Plant Pathology</i> , 2020, 156, 413-423.	0.8	27
1001	Molecular Epidemiology of Escherichia coli Producing CTX-M and pAmpC $\beta$ -Lactamases from Dairy Farms Identifies a Dominant Plasmid Encoding CTX-M-32 but No Evidence for Transmission to Humans in the Same Geographical Region. <i>Applied and Environmental Microbiology</i> , 2020, 87, .	1.4	17
1002	Unveiling the Hidden Diversity of Rock-Inhabiting Fungi: Chaetothyriales from China. <i>Journal of Fungi</i> (Basel, Switzerland), 2020, 6, 187.	1.5	30
1003	High-quality nuclear genome for <i>Sarcoptes scabiei</i> —A critical resource for a neglected parasite. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008720.	1.3	25
1004	Dominant subtype switch in avian influenza viruses during 2016–2019 in China. <i>Nature Communications</i> , 2020, 11, 5909.	5.8	93

#	ARTICLE	IF	CITATIONS
1005	Expression and functional characterization of odorant-binding protein genes in the endoparasitic wasp <i>Cotesia vestalis</i> . <i>Insect Science</i> , 2021, 28, 1354-1368.	1.5	16
1006	The Effector Repertoire of the Hop Downy Mildew Pathogen <i>Pseudoperonospora humuli</i> . <i>Frontiers in Genetics</i> , 2020, 11, 910.	1.1	9
1007	An Evolving View of Phylogenetic Support. <i>Systematic Biology</i> , 2022, 71, 921-928.	2.7	19
1008	Marked mitochondrial genetic variation in individuals and populations of the carcinogenic liver fluke <i>Clonorchis sinensis</i> . <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008480.	1.3	6
1009	A new species of <i>Clavariadelphus</i> (Basidiomycota) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 587	0.1	1
1010	New Genomes from the Congo Basin Expand History of CRF01_AE Origin and Dissemination. <i>AIDS Research and Human Retroviruses</i> , 2020, 36, 574-582.	0.5	7
1011	A multilocus molecular perspective on the systematics of the poorly known Northeast Indian colubrid snakes <i>Blythia reticulata</i> (Blyth, 1854), <i>B. hmuifang</i> Vogel, Lalremsanga & Vanlalhrima, 2017, and <i>Hebius xenura</i> (Wall, 1907). <i>Zootaxa</i> , 2020, 4768, zootaxa.4768.2.2.	0.2	9
1012	Genetic and antigenic characterization of influenza A/H5N1 viruses isolated from patients in Indonesia, 2008–2015. <i>Virus Genes</i> , 2020, 56, 417-429.	0.7	4
1013	Gradients Do Grow on Trees: A Linear-Time $O(N)$ -Dimensional Gradient for Statistical Phylogenetics. <i>Molecular Biology and Evolution</i> , 2020, 37, 3047-3060.	3.5	22
1014	The strange case of <i>Ocellomma rediuntum</i> (Arthoniales: Roccellaceae) in Australia: a remarkably disjunct lichen. <i>Lichenologist</i> , 2020, 52, 187-195.	0.5	2
1015	Simultaneous Nasal Carriage by Methicillin-Resistant and Methicillin Susceptible <i>Staphylococcus aureus</i> of Lineage ST398 in a Live Pig Transporter. <i>Pathogens</i> , 2020, 9, 401.	1.2	4
1016	Characterization of AmpC-hyperproducing <i>Escherichia coli</i> from humans and dairy farms collected in parallel in the same geographical region. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 2471-2479.	1.3	22
1017	Evaluating the Performance of Probabilistic Algorithms for Phylogenetic Analysis of Big Morphological Datasets: A Simulation Study. <i>Systematic Biology</i> , 2020, 69, 1088-1105.	2.7	20
1018	<i>Cladonia subturgida</i> (Cladoniaceae, Lecanoromycetes), an overlooked, but common species in the Mediterranean region. <i>Symbiosis</i> , 2020, 82, 9-18.	1.2	7
1019	Anchialine adjustments: an updated phylogeny and classification for the family Barbouriidae Christoffersen, 1987 (Decapoda: Caridea). <i>Journal of Crustacean Biology</i> , 2020, 40, 401-411.	0.3	4
1020	Typing methods based on whole genome sequencing data. <i>One Health Outlook</i> , 2020, 2, 3.	1.4	90
1021	Phylogeography and demographic history of <i>Gyrodactylus konovalovi</i> (Monogenoidea) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 107 Td (Gyrodactylidae) and Evolution, 2020, 10, 1454-1468.	0.8	2
1022	Reporter Assays for Ebola Virus Nucleoprotein Oligomerization, Virion-Like Particle Budding, and Minigenome Activity Reveal the Importance of Nucleoprotein Amino Acid Position 111. <i>Viruses</i> , 2020, 12, 105.	1.5	9

#	ARTICLE	IF	CITATIONS
1023	Transfer of <i>Xanthomonas campestris</i> pv. <i>arecae</i> and <i>X. campestris</i> pv. <i>musacearum</i> to <i>X. vasicola</i> (Vauterin) as <i>X. vasicola</i> pv. <i>arecae</i> comb. nov. and <i>X. vasicola</i> pv. <i>musacearum</i> comb. nov. and Description of <i>X. vasicola</i> pv. <i>vasculorum</i> pv. nov.. <i>Phytopathology</i> , 2020, 110, 1153-1160.	1.1	23
1024	Evolutionary rates of and selective constraints on the mitochondrial genomes of Orthoptera insects with different wing types. <i>Molecular Phylogenetics and Evolution</i> , 2020, 145, 106734.	1.2	47
1025	The Scaly-foot Snail genome and implications for the origins of biomineralised armour. <i>Nature Communications</i> , 2020, 11, 1657.	5.8	64
1026	Extensive photobiont sharing in a rapidly radiating cyanolichen clade. <i>Molecular Ecology</i> , 2021, 30, 1755-1776.	2.0	19
1027	Phylogenetics of <i>Paepalanthus</i> (Eriocaulaceae), a diverse Neotropical monocot lineage. <i>Botanical Journal of the Linnean Society</i> , 2021, 195, 34-52.	0.8	12
1028	Biological computation and computational biology: survey, challenges, and discussion. <i>Artificial Intelligence Review</i> , 2021, 54, 4169-4235.	9.7	7
1030	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
1031	Diversity and Molecular Characterization of Marine Halophilic Bacteria from Southeast Coast of India. <i>Geomicrobiology Journal</i> , 2021, 38, 524-531.	1.0	3
1032	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
1033	Variable influences of soil and seed-associated bacterial communities on the assembly of seedling microbiomes. <i>ISME Journal</i> , 2021, 15, 2748-2762.	4.4	63
1034	The Draft Genome of a Flat Peach ( <i>Prunus persica</i> L. cv. '124 Pan'™) Provides Insights into Its Good Fruit Flavor Traits. <i>Plants</i> , 2021, 10, 538.	1.6	16
1035	Isolation, Identification, and Analysis of Potential Functions of Culturable Bacteria Associated with an Invasive Gall Wasp, <i>Leptocybe invasa</i> . <i>Microbial Ecology</i> , 2022, 83, 151-166.	1.4	7
1037	Conserved pleiotropy of an ancient plant homeobox gene uncovered by cis-regulatory dissection. <i>Cell</i> , 2021, 184, 1724-1739.e16.	13.5	103
1038	<strong>Diversity and phylogeny of the brown alga <i>Lobophora</i> (Dictyotales, Phaeophyceae) in Singapore</strong> . <i>Phytotaxa</i> , 2021, 496, 215-227.	0.1	3
1039	Evolution of brood-site mimicry in Madagascan Impatiens (Balsaminaceae). <i>Perspectives in Plant Ecology, Evolution and Systematics</i> , 2021, 49, 125590.	1.1	1
1042	Collapsing dubiously resolved gene-tree branches in phylogenomic coalescent analyses. <i>Molecular Phylogenetics and Evolution</i> , 2021, 158, 107092.	1.2	24
1043	<i>Dipylidium caninum</i> draft genome - a new resource for comparative genomic and genetic explorations of flatworms. <i>Genomics</i> , 2021, 113, 1272-1280.	1.3	8
1044	Genomic and anatomical comparisons of skin support independent adaptation to life in water by cetaceans and hippos. <i>Current Biology</i> , 2021, 31, 2124-2139.e3.	1.8	30

#	ARTICLE	IF	CITATIONS
1045	Nine <i>Micarea</i> species new to Canada including five species new to North America. <i>Herzogia</i> , 2021, 34, .	0.1	2
1046	Insights into the ancestry evolution of the <i>Mycobacterium tuberculosis</i> complex from analysis of <i>Mycobacterium riyadhense</i> . <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab070.	1.5	3
1047	<i>Plectania lutea</i> (Sarcosomataceae), a new species from southwestern karst areas of China. <i>Phytotaxa</i> , 2021, 509, .	0.1	1
1048	Genomic, karyological and morphological changes of South American garlics ( <i>Ipheion</i> ) provide insights into mechanisms of speciation in the Pampean region. <i>Molecular Ecology</i> , 2021, 30, 3716-3729.	2.0	3
1049	<i>Leucogaster solidus</i> sp. nov. (Albatrellaceae, Russulales) from China. <i>Phytotaxa</i> , 2021, 508, .	0.1	0
1050	Genomics accelerated isolation of a new stem rust avirulence gene—wheat resistance gene pair. <i>Nature Plants</i> , 2021, 7, 1220-1228.	4.7	67
1051	A Chromosome-level Genome Assembly of Wild Castor Provides New Insights into its Adaptive Evolution in Tropical Desert. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 42-59.	3.0	18
1052	Phylogenetic Position of <i>Shiraia</i> -Like Endophytes on Bamboos and the Diverse Biosynthesis of Hypocrellin and Hypocrellin Derivatives. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 563.	1.5	3
1054	Updated description of <i>Atheniella</i> (Mycenaceae, Agaricales), including three new species with brightly coloured pilei from Yunnan Province, southwest China. <i>MycKeys</i> , 2021, 81, 139-164.	0.8	13
1055	Strong host-specific selection and over-dominance characterize arbuscular mycorrhizal fungal root colonizers of coastal sand dune plants of the Mediterranean region. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	7
1056	Molecular identification of <i>Streptococcus</i> sp. and antibiotic resistance genes present in <i>Tilapia</i> farms ( <i>Oreochromis niloticus</i> ) from the Northern Pacific region, Costa Rica. <i>Aquaculture International</i> , 2021, 29, 2337-2355.	1.1	8
1057	Limited phylogenetic overlap between fluoroquinolone-resistant <i>Escherichia coli</i> isolated on dairy farms and those causing bacteriuria in humans living in the same geographical region. <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 76, 3144-3150.	1.3	13
1058	Two new species of <i>Amanita</i> section <i>Roanokenses</i> with a radicating basal bulb. <i>Mycological Progress</i> , 2021, 20, 967-979.	0.5	1
1059	<i>Stropharia populicola</i> (Strophariaceae, Agaricales), a new species from China. <i>Phytotaxa</i> , 2021, 518, 251-260.	0.1	0
1060	Felsenstein Phylogenetic Likelihood. <i>Journal of Molecular Evolution</i> , 2021, 89, 134-145.	0.8	9
1061	Phylogenomics of the <i>Maverick</i> Virus-Like Mobile Genetic Elements of Vertebrates. <i>Molecular Biology and Evolution</i> , 2021, 38, 1731-1743.	3.5	22
1063	Parallel Divide-and-Conquer Phylogeny Reconstruction by Maximum Likelihood. <i>Lecture Notes in Computer Science</i> , 2005, , 776-785.	1.0	7
1064	Using Treemaps to Visualize Phylogenetic Trees. <i>Lecture Notes in Computer Science</i> , 2005, , 283-293.	1.0	5

#	ARTICLE	IF	CITATIONS
1065	Seaview Version 5: A Multiplatform Software for Multiple Sequence Alignment, Molecular Phylogenetic Analyses, and Tree Reconciliation. <i>Methods in Molecular Biology</i> , 2021, 2231, 241-260.	0.4	79
1066	A Not-So-Long Introduction to Computational Molecular Evolution. <i>Methods in Molecular Biology</i> , 2019, 1910, 71-117.	0.4	5
1068	Hybrid Genetic Algorithm and Lasso Test Approach for Inferring Well Supported Phylogenetic Trees Based on Subsets of Chloroplastic Core Genes. <i>Lecture Notes in Computer Science</i> , 2015, , 83-96.	1.0	5
1069	An Enhanced Algorithm for Reconstructing a Phylogenetic Tree Based on the Tree Rearrangement and Maximum Likelihood Method. <i>Lecture Notes in Computer Science</i> , 2015, , 530-541.	1.0	1
1070	Applying the Stream-Based Computing Model to Design Hardware Accelerators: A Case Study. <i>Lecture Notes in Computer Science</i> , 2009, , 237-246.	1.0	11
1071	Workflows with Model Selection: A Multilocus Approach to Phylogenetic Analysis. <i>Advances in Intelligent and Soft Computing</i> , 2011, , 39-47.	0.2	2
1072	Genomic, phylogenetic, and cell biological insights into metazoan origins. , 2009, , 24-32.		16
1073	The mouth, the anus, and the blastopore“open questions about questionable openings. , 2009, , 33-40.		21
1074	Origins of metazoan body plans: the larval revolution. , 2009, , 43-51.		3
1075	Assembling the spiralian tree of life. , 2009, , 52-64.		32
1076	The origins and evolution of the Ecdysozoa. , 2009, , 71-79.		2
1077	Deciphering deuterostome phylogeny: molecular, morphological, and palaeontological perspectives. , 2009, , 80-92.		5
1078	Invertebrate Problematica: kinds, causes, and solutions. , 2009, , 107-126.		2
1079	Improvement of molecular phylogenetic inference and the phylogeny of Bilateria. , 2009, , 127-138.		1
1080	Beyond linear sequence comparisons: the use of genome-level characters for phylogenetic reconstruction. , 2009, , 139-147.		1
1081	The animal in the genome: comparative genomics and evolution. , 2009, , 148-156.		1
1082	MicroRNAs and metazoan phylogeny: big trees from little genes. , 2009, , 157-170.		29
1083	Reassembling animal evolution: a four-dimensional puzzle. , 2009, , 191-196.		2

#	ARTICLE	IF	CITATIONS
1085	Primate census and survey techniques. , 2013, , 10-26.		21
1086	Darting, anesthesia, and handling. , 2013, , 27-39.		8
1087	Health assessment and epidemiology. , 2013, , 40-57.		5
1088	Behavior within groups. , 2013, , 58-78.		2
1089	Habitat assessment and species niche modeling. , 2013, , 79-102.		8
1090	Characterization of primate environments through assessment of plant phenology. , 2013, , 103-127.		11
1091	Methods in ethnoprimateology: exploring the humanâ€“non-human primate interface. , 2013, , 128-150.		73
1092	Social and spatial relationships between primate groups. , 2013, , 151-176.		13
1093	Experiments in primatology: from the lab to the field and back again. , 2013, , 177-194.		8
1094	Diet and nutrition. , 2013, , 195-212.		3
1095	Physiology and energetics. , 2013, , 213-223.		1
1096	Primate behavioral endocrinology. , 2013, , 224-237.		3
1097	Captive breeding and ex situ conservation. , 2013, , 294-322.		1
1098	Primates in trade. , 2013, , 323-345.		46
1099	Halarchaeum grantii sp. nov., a moderately acidophilic haloarchaeon isolated from a commercial salt sample. International Journal of Systematic and Evolutionary Microbiology, 2015, 65, 3830-3835.	0.8	12
1100	Halorubrum halodurans sp. nov., an extremely halophilic archaeon isolated from a hypersaline lake. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 435-444.	0.8	16
1101	Phyllonema aviceniicola gen. nov., sp. nov. and Foliisarcina bertiogensis gen. nov., sp. nov., epiphyllic cyanobacteria associated with Avicennia schaueriana leaves. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 689-700.	0.8	43
1102	Halopiger thermotolerans sp. nov., a thermo-tolerant haloarchaeon isolated from commercial salt. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 4975-4980.	0.8	10



#	ARTICLE	IF	CITATIONS
1103	Haloparvum alkalitolerans sp. nov., alkali-tolerant haloarchaeon isolated from commercial salt. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 5314-5319.	0.8	6
1104	Natrinema soli sp. nov., a novel halophilic archaeon isolated from a hypersaline wetland. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 2142-2147.	0.8	15
1105	Salinarchaeum chitinilyticum sp. nov., a chitin-degrading haloarchaeon isolated from commercial salt. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 2274-2278.	0.8	25
1106	Natronoarchaeum persicum sp. nov., a haloarchaeon isolated from a hypersaline lake. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 3339-3344.	0.8	8
1107	Directional gene flow and ecological separation in Yersinia enterocolitica. Microbial Genomics, 2015, 1, e000030.	1.0	16
1108	Phylogeographic separation and formation of sexually discrete lineages in a global population of Yersinia pseudotuberculosis. Microbial Genomics, 2017, 3, e000133.	1.0	17
1109	Comparative genomic analysis of three intestinal species reveals reductions in secreted pathogenesis determinants in bovine-specific and non-pathogenic Cryptosporidium species. Microbial Genomics, 2020, 6, .	1.0	13
1125	Genomic epidemiology and antimicrobial resistance determinants of <i>Neisseria gonorrhoeae</i> isolates from Ukraine, 2013–2018. Apmis, 2020, 128, 465-475.	0.9	13
1127	Gene flow in environmental Legionella pneumophila leads to genetic and pathogenic heterogeneity within a Legionnaires' disease outbreak. Genome Biology, 2014, 15, 504.	13.9	37
1128	Genome sequencing and analysis of fungus Hirsutella sinensis isolated from Ophiocordyceps sinensis. AMB Express, 2020, 10, 105.	1.4	16
1130	One Tree to Link Them All: A Phylogenetic Dataset for the European Tetrapoda. PLOS Currents, 2014, 6, .	1.4	18
1131	Diversity and distribution of nuclease bacteriocins in bacterial genomes revealed using Hidden Markov Models. PLoS Computational Biology, 2017, 13, e1005652.	1.5	52
1132	The Genomic Aftermath of Hybridization in the Opportunistic Pathogen Candida metapsilosis. PLoS Genetics, 2015, 11, e1005626.	1.5	139
1133	Group II Introns Break New Boundaries: Presence in a Bilaterian's Genome. PLoS ONE, 2008, 3, e1488.	1.1	78
1134	PALM: A Paralleled and Integrated Framework for Phylogenetic Inference with Automatic Likelihood Model Selectors. PLoS ONE, 2009, 4, e8116.	1.1	36
1135	Comparative Genomics of Gardnerella vaginalis Strains Reveals Substantial Differences in Metabolic and Virulence Potential. PLoS ONE, 2010, 5, e12411.	1.1	124
1136	MPI-PHYLIP: Parallelizing Computationally Intensive Phylogenetic Analysis Routines for the Analysis of Large Protein Families. PLoS ONE, 2010, 5, e13999.	1.1	17
1137	Genomic Markers Reveal Introgressive Hybridization in the Indo-West Pacific Mangroves: A Case Study. PLoS ONE, 2011, 6, e19671.	1.1	26

#	ARTICLE	IF	CITATIONS
1138	Evolutionary History of the Cancer Immunity Antigen MAGE Gene Family. PLoS ONE, 2011, 6, e20365.	1.1	39
1139	Phylogenetic Diversity, Host-Specificity and Community Profiling of Sponge-Associated Bacteria in the Northern Gulf of Mexico. PLoS ONE, 2011, 6, e26806.	1.1	71
1140	Exploiting Gene Families for Phylogenomic Analysis of Myzostomid Transcriptome Data. PLoS ONE, 2012, 7, e29843.	1.1	24
1141	The SAR11 Group of Alpha-Proteobacteria Is Not Related to the Origin of Mitochondria. PLoS ONE, 2012, 7, e30520.	1.1	71
1142	Fatal Cases of Influenza A(H3N2) in Children: Insights from Whole Genome Sequence Analysis. PLoS ONE, 2012, 7, e33166.	1.1	17
1143	Novel Bacterial Taxa in the Human Microbiome. PLoS ONE, 2012, 7, e35294.	1.1	86
1144	Proteome-Wide Analysis of Functional Divergence in Bacteria: Exploring a Host of Ecological Adaptations. PLoS ONE, 2012, 7, e35659.	1.1	16
1145	A Phylogenetic Perspective on the Evolution of Mediterranean Teleost Fishes. PLoS ONE, 2012, 7, e36443.	1.1	50
1146	Detecting the Immune System Response of a 500 Year-Old Inca Mummy. PLoS ONE, 2012, 7, e41244.	1.1	57
1147	Recombination in Hepatitis C Virus: Identification of Four Novel Naturally Occurring Inter-Subtype Recombinants. PLoS ONE, 2012, 7, e41997.	1.1	27
1148	Upper Airways Microbiota in Antibiotic-Naïve Wheezing and Healthy Infants from the Tropics of Rural Ecuador. PLoS ONE, 2012, 7, e46803.	1.1	89
1149	Subgenotyping of Genotype C Hepatitis B Virus: Correcting Misclassifications and Identifying a Novel Subgenotype. PLoS ONE, 2012, 7, e47271.	1.1	26
1150	Habitat-Associated Phylogenetic Community Patterns of Microbial Ammonia Oxidizers. PLoS ONE, 2012, 7, e47330.	1.1	55
1151	A Case Study for Effects of Operational Taxonomic Units from Intracellular Endoparasites and Ciliates on the Eukaryotic Phylogeny: Phylogenetic Position of the Haptophyta in Analyses of Multiple Slowly Evolving Genes. PLoS ONE, 2012, 7, e50827.	1.1	3
1152	Phylogeography of Poorly Dispersing Net-Winged Beetles: A Role of Drifting India in the Origin of Afrotropical and Oriental Fauna. PLoS ONE, 2013, 8, e67957.	1.1	43
1153	Diverse Honeydew-Consuming Fungal Communities Associated with Scale Insects. PLoS ONE, 2013, 8, e70316.	1.1	31
1154	A New Method for Extracting Skin Microbes Allows Metagenomic Analysis of Whole-Deep Skin. PLoS ONE, 2013, 8, e74914.	1.1	19
1155	Brood Ball-Mediated Transmission of Microbiome Members in the Dung Beetle, <i>Onthophagus taurus</i> (Coleoptera: Scarabaeidae). PLoS ONE, 2013, 8, e79061.	1.1	82

#	ARTICLE	IF	CITATIONS
1156	Chikungunya as a Cause of Acute Febrile Illness in Southern Sri Lanka. PLoS ONE, 2013, 8, e82259.	1.1	27
1157	Multiple Co-Evolutionary Networks Are Supported by the Common Tertiary Scaffold of the LacI/GalR Proteins. PLoS ONE, 2013, 8, e84398.	1.1	26
1158	Two-Step Source Tracing Strategy of <i>Yersinia pestis</i> and Its Historical Epidemiology in a Specific Region. PLoS ONE, 2014, 9, e85374.	1.1	9
1159	Patterns of Variation at <i>Ustilago maydis</i> Virulence Clusters 2A and 19A Largely Reflect the Demographic History of Its Populations. PLoS ONE, 2014, 9, e98837.	1.1	8
1160	Determining the Phylogenetic and Phylogeographic Origin of Highly Pathogenic Avian Influenza (H7N3) in Mexico. PLoS ONE, 2014, 9, e107330.	1.1	25
1161	Phylogenetic Distribution of Extant Richness Suggests Metamorphosis Is a Key Innovation Driving Diversification in Insects. PLoS ONE, 2014, 9, e109085.	1.1	115
1162	Separate Introns Gained within Short and Long Soluble Peridinin-Chlorophyll a-Protein Genes during Radiation of Symbiodinium (Dinophyceae) Clade A and B Lineages. PLoS ONE, 2014, 9, e110608.	1.1	2
1163	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
1164	Phylogeographic Structure in Penguin Ticks across an Ocean Basin Indicates Allopatric Divergence and Rare Trans-Oceanic Dispersal. PLoS ONE, 2015, 10, e0128514.	1.1	8
1165	Genome Analysis of Planctomycetes Inhabiting Blades of the Red Alga <i>Porphyra umbilicalis</i> . PLoS ONE, 2016, 11, e0151883.	1.1	39
1166	Within-Host Evolution of the Dutch High-Prevalent <i>Pseudomonas aeruginosa</i> Clone ST406 during Chronic Colonization of a Patient with Cystic Fibrosis. PLoS ONE, 2016, 11, e0158106.	1.1	23
1167	Towards a DNA Barcode Reference Database for Spiders and Harvestmen of Germany. PLoS ONE, 2016, 11, e0162624.	1.1	81
1168	Genomic sequence of 'Candidatus <i>Liberibacter solanacearum</i> ' haplotype C and its comparison with haplotype A and B genomes. PLoS ONE, 2017, 12, e0171531.	1.1	39
1171	Identificación y caracterización molecular de cianobacterias tropicales de los géneros <i>Nostoc</i> , <i>Calothrix</i> , <i>Tolypothrix</i> y <i>Scytonema</i> (Nostocales: Nostocaceae), con posible potencial biotecnológico. Cuadernos De Investigación UNED, 2017, 9, .	0.1	3
1172	Remarkable Records of <i>Micarea</i> from the Russian Far East and Significant Extension of <i>Micarea Laeta</i> and <i>M. Microareolata</i> Range. <i>Botanica</i> , 2019, 25, 186-201.	0.2	12
1173	Prospective genomic surveillance of methicillin-resistant <i>Staphylococcus aureus</i> (MRSA) associated with bloodstream infection, England, 1 October 2012 to 30 September 2013. <i>Eurosurveillance</i> , 2019, 24, .	3.9	19
1174	Whole genome sequencing reveals potential spread of <i>Clostridium difficile</i> between humans and farm animals in the Netherlands, 2002 to 2011. <i>Eurosurveillance</i> , 2014, 19, 20954.	3.9	188
1175	Host-parasite relationship of <i>Ortholinea lauquen</i> sp. nov. (Cnidaria: Myxozoa) and the fish <i>Galaxias maculatus</i> in northwestern Patagonia, Argentina. <i>Diseases of Aquatic Organisms</i> , 2019, 136, 163-174.	0.5	4

#	ARTICLE	IF	CITATIONS
1177	A MOLECULAR GENETIC EVIDENCE OF THE OCCURRENCE OF THE FRESHWATER SNAIL RADIX LAGOTIS (SCHRANK, 1803) (GASTROPODA: LYMNÆIDAE) IN BULGARIA. <i>Ecologica Montenegrina</i> , 0, 3, 29-39.	0.5	7
1178	Phylogenetic assessment of global <i>Suillus</i> ITS sequences supports morphologically defined species and reveals synonymous and undescribed taxa. <i>Mycologia</i> , 2016, 108, 1216-1228.	0.8	22
1179	Two new species of <i>Strigula</i> (lichenised Dothideomycetes, Ascomycota) from China, with a key to the Chinese foliicolous species. <i>MycKeys</i> , 0, 19, 31-42.	0.8	10
1180	Recognition of <i>Mycena</i> sect. <i>Amparoina</i> sect. nov. (Mycenaceae, Agaricales), including four new species and revision of the limits of sect. <i>Sacchariferae</i> . <i>MycKeys</i> , 2019, 52, 103-124.	0.8	8
1181	A molecular phylogeny of Graphidaceae (Ascomycota, Lecanoromycetes, Ostropales) including 428 species. <i>MycKeys</i> , 0, 6, 55-94.	0.8	68
1182	Seasonal variation of planktonic chrysophytes with special focus on Dinobryon.. <i>Fottea</i> , 2014, 14, 179-190.	0.4	44
1184	The origin of the odorant receptor gene family in insects. <i>ELife</i> , 2018, 7, .	2.8	103
1185	Genus-level phylogeny of cephalopods using molecular markers: current status and problematic areas. <i>PeerJ</i> , 2018, 6, e4331.	0.9	39
1186	PTree: pattern-based, stochastic search for maximum parsimony phylogenies. <i>PeerJ</i> , 2013, 1, e89.	0.9	3
1187	First Report of Stalk Rot of Celery Caused by <i>Erwinia rhapontici</i> in China. <i>Plant Disease</i> , 2022, 106, 1513.	0.7	1
1188	Genomic Profiling of <i>Mycobacterium tuberculosis</i> Strains, Myanmar. <i>Emerging Infectious Diseases</i> , 2021, 27, 2847-2855.	2.0	8
1189	TULIP Software and Web Server: Automatic Classification of Protein Sequences Based on Pairwise Comparisons and Z-Value Statistics. <i>Open Bioinformatics Journal</i> , 2009, 3, 18-25.	1.0	0
1190	Conserved developmental processes and the evolution of novel traits: wounds, embryos, veins, and butterfly eyespots. , 2009, , 183-190.		0
1191	The Ediacaran emergence of bilaterians: congruence between the genetic and the geological fossil records. , 2009, , 15-23.		0
1192	The evolution of nervous system centralization. , 2009, , 65-70.		0
1193	The evolution of developmental gene networks: lessons from comparative studies on holometabolous insects. , 2009, , 171-182.		0
1194	The earliest fossil record of the animals and its significance. , 2009, , 3-14.		0
1195	Molecular genetic insights into deuterostome evolution from the direct-developing hemichordate <i>Saccoglossus kowalevskii</i> . , 2009, , 93-104.		0

#	ARTICLE	IF	CITATIONS
1196	Molecular Evolution. , 2012, , 441-470.		0
1197	Applications and Algorithms for Inference of Huge Phylogenetic Trees: a Review. American Journal of Bioinformatics Research, 2012, 2, 21-26.	0.3	7
1198	Heuristic Algorithms for the Protein Model Assignment Problem. Lecture Notes in Computer Science, 2013, , 137-148.	1.0	1
1199	Population genetics, molecular phylogenetics, and phylogeography. , 2013, , 238-256.		0
1200	Demography, life histories, and population dynamics. , 2013, , 257-277.		0
1201	Determining conservation status and contributing to in situ conservation action. , 2013, , 278-293.		3
1202	Conclusion: the future of studying primates in a changing world. , 2013, , 346-350.		1
1203	Introduction: why a new methods book on primate ecology and conservation?. , 2013, , 1-9.		0
1204	Fancy a gene? A surprisingly complex evolutionary history of peroxiredoxins.. Microbial Cell, 2015, 2, 33-37.	1.4	1
1213	PHENOTYPIC CHARACTERIZATION AND MOLECULAR IDENTIFICATION OF A LUMINESCENT MARINE BACTERIUM ISOLATED FROM THE NW SHELF OF CUBA. Biotecnia, 2017, 19, 3-10.	0.1	0
1215	Parallel Solution Based on Collective Communication Operations for Phylogenetic Bootstrapping in PhyML 3.0. Lecture Notes in Computer Science, 2018, , 133-145.	1.0	0
1216	An Ancient Integration in a Plant NLR is Maintained as a Trans-species Polymorphism. SSRN Electronic Journal, 0, , .	0.4	7
1220	Minimum-Width Drawings of Phylogenetic Trees. Lecture Notes in Computer Science, 2019, , 39-55.	1.0	2
1223	Reassessment of Tristan da Cunha <i>Gelidium</i> (Gelidiales, Rhodophyta) species. Botanica Marina, 2020, 63, 455-462.	0.6	1
1225	Haloarcula mannanilytica sp. nov., a galactomannan-degrading haloarchaeon isolated from commercial salt. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 6331-6337.	0.8	10
1226	A new species of bulbil-forming lichenicolous fungi represents an isolated clade in the Cantharellales. Bryologist, 2020, 123, 155.	0.1	5
1227	A New Algorithm for Reconstruction of Phylogenetic Tree. , 2008, , 472-477.		0
1228	ParBaum: Large-Scale Maximum Likelihood-Based Phylogenetic Analyses. , 2009, , 111-125.		0

#	ARTICLE	IF	CITATIONS
1231	Efficient tree searches with available algorithms. <i>Evolutionary Bioinformatics</i> , 2007, 3, 341-56.	0.6	11
1233	<i>Dlhawksworthia flavoparmeliae</i> sp. nov., a new endolichenic fungus in Phaeosphaeriaceae. <i>Phytotaxa</i> , 2021, 525, 51-58.	0.1	1
1234	<i>Fusarium Oxysporum</i> f. sp. <i>Cannabis</i> Isolated from <i>Cannabis Sativa</i> L.: In Vitro and In Planta Biocontrol by a Plant Growth Promoting-Bacteria Consortium. <i>Plants</i> , 2021, 10, 2436.	1.6	4
1235	Resurrecting Golgi proteins to grasp Golgi ribbon formation and self-association under stress. <i>International Journal of Biological Macromolecules</i> , 2022, 194, 264-275.	3.6	5
1236	Chromosome-level genome and population genomic analysis provide insights into the evolution and environmental adaptation of Jinjiang oyster <i>Crassostrea ariakensis</i> . <i>Molecular Ecology Resources</i> , 2022, 22, 1529-1544.	2.2	16
1237	<i>Crepidotus yuanchui</i> sp. nov. and <i>C. caspari</i> found in subalpine areas of China. <i>Mycoscience</i> , 2021, 63, .	0.3	5
1238	Pre- and postzygotic mechanisms preventing hybridization in co-occurring species of the <i>Impatiens purpureoviolacea</i> complex. <i>Ecology and Evolution</i> , 2021, 11, 17485-17495.	0.8	1
1239	Elevational Constraints on the Composition and Genomic Attributes of Microbial Communities in Antarctic Soils. <i>MSystems</i> , 2022, 7, e0133021.	1.7	9
1241	Evidence that faecal carriage of resistant <i>Escherichia coli</i> by 16-week-old dogs in the United Kingdom is associated with raw feeding. <i>One Health</i> , 2022, 14, 100370.	1.5	6
1242	Comparative Genomics of Novel <i>Agrobacterium</i> G3 Strains Isolated From the International Space Station and Description of <i>Agrobacterium tomkonis</i> sp. nov.. <i>Frontiers in Microbiology</i> , 2021, 12, 765943.	1.5	22
1243	Nuclear genome of <i>Bulinus truncatus</i> , an intermediate host of the carcinogenic human blood fluke <i>Schistosoma haematobium</i> . <i>Nature Communications</i> , 2022, 13, 977.	5.8	14
1245	Commensal <i>Pseudomonas</i> strains facilitate protective response against pathogens in the host plant. <i>Nature Ecology and Evolution</i> , 2022, 6, 383-396.	3.4	44
1246	High-throughput phenotyping reveals differential transpiration behaviour within the banana wild relatives highlighting diversity in drought tolerance. <i>Plant, Cell and Environment</i> , 2022, 45, 1647-1663.	2.8	10
1249	Chromosome-scale <i>Echinococcus granulosus</i> (genotype G1) genome reveals the Eg95 gene family and conservation of the EG95-vaccine molecule. <i>Communications Biology</i> , 2022, 5, 199.	2.0	7
1250	Whole-Genome Sequencing of <i>Acer catalpifolium</i> Reveals Evolutionary History of Endangered Species. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	7
1251	Systematics of <i>Hypnea</i> (Cystocloniaceae, Rhodophyta) from coastal North Carolina, with a first report of <i>Calliblepharis saidana</i> from the United States Atlantic Coast. <i>Botanica Marina</i> , 2022, 65, 23-33.	0.6	0
1252	Two new <i>Clitocella</i> species from North China revealed by phylogenetic analyses and morphological characters. <i>Mycology</i> , 2022, 88, 151-170.	0.8	3
1286	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

#	ARTICLE	IF	CITATIONS
1287	The phylogeographical pattern of the Amur minnow <i>Rhynchocypris lagowskii</i> (Cypriniformes: Tj ETQq0 0 0 rgBT /Overlock 10 Tf	0.8	2
1290	Species diversity, phylogeny, endemism and geography of the truffle genus <i>Tuber</i> in China based on morphological and molecular data. <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2022, 48, 175-202.	1.6	8
1291	Taxonomic studies of bluish <i>Mycena</i> (Mycenaceae, Agaricales) with two new species from northern China. <i>MycKeys</i> , 0, 90, 119-145.	0.8	1
1292	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
1293	Morphological and Genetic Variability in <i>Radix auricularia</i> (Mollusca: Gastropoda: Lymnaeidae) of Lake Baikal, Siberia: The Story of an Unfinished Invasion into the Ancient Deepest Lake. <i>Diversity</i> , 2022, 14, 527.	0.7	4
1294	New insights on the evolutionary relationships between the major lineages of Amoebozoa. <i>Scientific Reports</i> , 2022, 12, .	1.6	9
1295	<i>Impatiens smetsiana</i> , another example of convergent evolution of flower morphology in <i>Impatiens</i> . <i>Plant Ecology and Evolution</i> , 2022, 155, 248-260.	0.3	3
1296	Updated taxonomy of Chinese <i>Clavaria</i> subg. <i>Syncoryne</i> (Clavariaceae, Agaricales): description of two new species and one newly recorded species. <i>Mycological Progress</i> , 2022, 21, .	0.5	1
1301	Patterns and correlates of hepatitis C virus phylogenetic clustering among people living with HIV in Australia in the direct-acting antiviral era: A molecular epidemiology study among participants in the CEASE cohort. <i>Health Science Reports</i> , 2022, 5, .	0.6	0
1302	The "Infernaccio" Gorges: Microbial Diversity of Black Deposits and Isolation of Manganese-Solubilizing Bacteria. <i>Biology</i> , 2022, 11, 1204.	1.3	3
1303	Multiomc approaches reveal novel lineage-specific effectors in the potato and tomato early blight pathogen <i>Alternaria solani</i> . <i>Phytopathology Research</i> , 2022, 4, .	0.9	6
1304	<i>Neopestalotiopsis longiappendiculata</i> as the agent of grey blight disease of <i>Camellia</i> spp.. <i>Journal of Phytopathology</i> , 2022, 170, 770-777.	0.5	2
1305	Morphological and Molecular Identification of <i>Fusarium ipomoeae</i> as the Causative Agent of Leaf Spot Disease in Tobacco from China. <i>Microorganisms</i> , 2022, 10, 1890.	1.6	2
1306	A new study of <i>Nagrajomyces</i> : with two new species proposed and taxonomic status inferred by phylogenetic methods. <i>MycKeys</i> , 0, 93, 131-148.	0.8	0
1307	Screening of Spore-Forming Bacteria with Probiotic Potential in Pristine Algerian Caves. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	0
1308	<i>Mycena subpiligera</i> sp. nov., a Symbiotic Species from China Associated with the Seed Germination of <i>Gastrodia elata</i> . <i>Mycobiology</i> , 2022, 50, 294-301.	0.6	1
1309	Whole-genome scanning reveals environmental selection mechanisms that shape diversity in populations of the epipelagic diatom <i>Chaetoceros</i> . <i>PLoS Biology</i> , 2022, 20, e3001893.	2.6	7
1310	Chromosome-Level Genome Assembly of the Speckled Blue Grouper ( <i>Epinephelus cyanopodus</i> ) Provides Insight into Its Adaptive Evolution. <i>Biology</i> , 2022, 11, 1810.	1.3	1



#	ARTICLE	IF	CITATIONS
1311	Widespread, human-associated redondoviruses infect the commensal protozoan <i>Entamoeba gingivalis</i> . <i>Cell Host and Microbe</i> , 2023, 31, 58-68.e5.	5.1	7
1312	Similar adaptative mechanism but divergent demographic history of four sympatric desert rodents in Eurasian inland. <i>Communications Biology</i> , 2023, 6, .	2.0	2
1313	Above- and below-ground microbiome in the annual developmental cycle of two olive tree varieties. <i>FEMS Microbes</i> , 2023, 4, .	0.8	2
1314	The Early Microbial Colonizers of a Short-Lived Volcanic Island in the Kingdom of Tonga. <i>MBio</i> , 2023, 14, .	1.8	3
1316	Taxonomic and phylogenetic approach to some Antarctic lichenicolous fungi. <i>Mycological Progress</i> , 2023, 22, .	0.5	0
1319	First draft of an annotated genome for a lichenised strain of the green alga <i>Diplosphaera chodatii</i> (Prasiolales, Trebouxiophyceae). <i>European Journal of Phycology</i> , 2023, 58, 427-437.	0.9	0
1345	Circular Arc Length-Based Kernel Matrix For Protein Sequence Classification. , 2023, , .		0