

Modeling Site Heterogeneity with Posterior Mean Site F Accurate Phylogenomic Estimation

Systematic Biology

67, 216-235

DOI: [10.1093/sysbio/syx068](https://doi.org/10.1093/sysbio/syx068)

Citation Report

#	ARTICLE	IF	CITATIONS
1	Accelerated Estimation of Frequency Classes in Site-Heterogeneous Profile Mixture Models. <i>Molecular Biology and Evolution</i> , 2018, 35, 1266-1283.	3.5	22
2	Deep mitochondrial origin outside the sampled alphaproteobacteria. <i>Nature</i> , 2018, 557, 101-105.	13.7	278
3	Plastid phylogenomics with broad taxon sampling further elucidates the distinct evolutionary origins and timing of secondary green plastids. <i>Scientific Reports</i> , 2018, 8, 1523.	1.6	66
4	Phylogenomic Analysis of <i>Nassula variabilis</i> n. sp., <i>Furgasonia blochmanni</i> , and <i>Pseudomicrothorax dubius</i> Confirms a Nassophorean Clade. <i>Protist</i> , 2018, 169, 180-189.	0.6	22
5	Phylogenomics Places Orphan Protistan Lineages in a Novel Eukaryotic Super-Group. <i>Genome Biology and Evolution</i> , 2018, 10, 427-433.	1.1	112
6	The genome and microbiome of a dikaryotic fungus (<i>Inocybe terrigena</i> , Inocybaceae) revealed by metagenomics. <i>Environmental Microbiology Reports</i> , 2018, 10, 155-166.	1.0	17
7	Ancient balancing selection on heterocyst function in a cosmopolitan cyanobacterium. <i>Nature Ecology and Evolution</i> , 2018, 2, 510-519.	3.4	24
8	Phylogenomics offers resolution of major tunicate relationships. <i>Molecular Phylogenetics and Evolution</i> , 2018, 121, 166-173.	1.2	56
9	Comparative genomic analysis of the “pseudofungus” <i>Hyphochytrium catenoides</i> . <i>Open Biology</i> , 2018, 8, 170184.	1.5	31
10	A phylogenomic resolution of the sea urchin tree of life. <i>BMC Evolutionary Biology</i> , 2018, 18, 189.	3.2	42
11	Hemimastigophora is a novel supra-kingdom-level lineage of eukaryotes. <i>Nature</i> , 2018, 564, 410-414.	13.7	101
12	Nuclear genome sequence of the plastid-lacking cryptomonad <i>Goniomonas avonlea</i> provides insights into the evolution of secondary plastids. <i>BMC Biology</i> , 2018, 16, 137.	1.7	42
13	Conditional Approximate Bayesian Computation: A New Approach for Across-Site Dependency in High-Dimensional Mutation Selection Models. <i>Molecular Biology and Evolution</i> , 2018, 35, 2819-2834.	3.5	5
14	Inferring Ancient Relationships with Genomic Data: A Commentary on Current Practices. <i>Integrative and Comparative Biology</i> , 2018, 58, 623-639.	0.9	14
15	Reanalyzing the Palaeoptera problem – The origin of insect flight remains obscure. <i>Arthropod Structure and Development</i> , 2018, 47, 328-338.	0.8	51
16	Secondary Plastids of Euglenids and Chlorarachniophytes Function with a Mix of Genes of Red and Green Algal Ancestry. <i>Molecular Biology and Evolution</i> , 2018, 35, 2198-2204.	3.5	17
17	Multiple Independent Origins of Apicomplexan-Like Parasites. <i>Current Biology</i> , 2019, 29, 2936-2941.e5.	1.8	84
18	<i>Nephromyces</i> represents a diverse and novel lineage of the Apicomplexa that has retained apicoplasts. <i>Genome Biology and Evolution</i> , 2019, 11, 2727-2740.	1.1	19

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19	A Robust Phylogenomic Time Tree for Biotechnologically and Medically Important Fungi in the Genera <i>Aspergillus</i> and <i>Penicillium</i> . <i>MBio</i> , 2019, 10, .	1.8	106
20	OMA standalone: orthology inference among public and custom genomes and transcriptomes. <i>Genome Research</i> , 2019, 29, 1152-1163.	2.4	111
21	Transferrin Identification in Sterlet (<i>Acipenser ruthenus</i>) Reproductive System. <i>Animals</i> , 2019, 9, 753.	1.0	8
22	Diversification rates have no effect on the convergent evolution of foraging strategies in the most speciose genus of bats, <i>Myotis</i> *. <i>Evolution; International Journal of Organic Evolution</i> , 2019, 73, 2263-2280.	1.1	40
23	Diversification of giant and large eukaryotic dsDNA viruses predated the origin of modern eukaryotes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 19585-19592.	3.3	119
24	Targeted metagenomic recovery of four divergent viruses reveals shared and distinctive characteristics of giant viruses of marine eukaryotes. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20190086.	1.8	22
25	New Phylogenomic Analysis of the Enigmatic Phylum Telonemia Further Resolves the Eukaryote Tree of Life. <i>Molecular Biology and Evolution</i> , 2019, 36, 757-765.	3.5	93
26	In silico Identification of Novel Toxin Homologs and Associated Mobile Genetic Elements in <i>Clostridium perfringens</i> . <i>Pathogens</i> , 2019, 8, 16.	1.2	15
27	A natural toroidal microswimmer with a rotary eukaryotic flagellum. <i>Nature Microbiology</i> , 2019, 4, 1620-1626.	5.9	14
28	Phylogenomics of Aplacophora (Mollusca, Aculifera) and a solenogaster without a foot. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20190115.	1.2	22
29	Organelar DNA Polymerases in Complex Plastid-Bearing Algae. <i>Biomolecules</i> , 2019, 9, 140.	1.8	14
30	Asgard archaea capable of anaerobic hydrocarbon cycling. <i>Nature Communications</i> , 2019, 10, 1822.	5.8	165
31	The Relative Importance of Modeling Site Pattern Heterogeneity Versus Partition-Wise Heterotachy in Phylogenomic Inference. <i>Systematic Biology</i> , 2019, 68, 1003-1019.	2.7	45
32	Proposal of the reverse flow model for the origin of the eukaryotic cell based on comparative analyses of Asgard archaeal metabolism. <i>Nature Microbiology</i> , 2019, 4, 1138-1148.	5.9	143
33	Phylogenomics of the superfamily Dytiscoidea (Coleoptera: Adephaga) with an evaluation of phylogenetic conflict and systematic error. <i>Molecular Phylogenetics and Evolution</i> , 2019, 135, 270-285.	1.2	36
34	Physicochemical Amino Acid Properties Better Describe Substitution Rates in Large Populations. <i>Molecular Biology and Evolution</i> , 2019, 36, 679-690.	3.5	20
35	Phylogenomics and Morphological Reconstruction of Arcellinida Testate Amoebae Highlight Diversity of Microbial Eukaryotes in the Neoproterozoic. <i>Current Biology</i> , 2019, 29, 991-1001.e3.	1.8	49
36	A Critical Appraisal of the Placement of Xiphosura (Chelicerata) with Account of Known Sources of Phylogenetic Error. <i>Systematic Biology</i> , 2019, 68, 896-917.	2.7	138

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37	Characterization of the complete mitochondrial genome of <i>Homidia socia</i> (Collembola: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50,742 Td (E	0.2	2
38	Phylogenomics of 10,575 genomes reveals evolutionary proximity between domains Bacteria and Archaea. <i>Nature Communications</i> , 2019, 10, 5477.	5.8	197
39	Plastid Genomes and Proteins Illuminate the Evolution of Eustigmatophyte Algae and Their Bacterial Endosymbionts. <i>Genome Biology and Evolution</i> , 2019, 11, 362-379.	1.1	29
40	Phylogenomics supports the monophyly of the Cercozoa. <i>Molecular Phylogenetics and Evolution</i> , 2019, 130, 416-423.	1.2	16
41	Whole Genome Shotgun Phylogenomics Resolves the Pattern and Timing of Swallowtail Butterfly Evolution. <i>Systematic Biology</i> , 2020, 69, 38-60.	2.7	65
42	Serial horizontal transfer of vitamin-biosynthetic genes enables the establishment of new nutritional symbionts in aphidsâ€™ di-symbiotic systems. <i>ISME Journal</i> , 2020, 14, 259-273.	4.4	79
43	The New Tree of Eukaryotes. <i>Trends in Ecology and Evolution</i> , 2020, 35, 43-55.	4.2	537
44	Genetic and functional diversity of the multiple lungfish myoglobins. <i>FEBS Journal</i> , 2020, 287, 1598-1611.	2.2	6
45	Scalable Empirical Mixture Models That Account for Across-Site Compositional Heterogeneity. <i>Molecular Biology and Evolution</i> , 2020, 37, 3616-3631.	3.5	32
46	Arachnid monophyly: Morphological, palaeontological and molecular support for a single terrestrialization within Chelicerata. <i>Arthropod Structure and Development</i> , 2020, 59, 100997.	0.8	35
47	Selection for Reducing Energy Cost of Protein Production Drives the GC Content and Amino Acid Composition Bias in Gene Transfer Agents. <i>MBio</i> , 2020, 11, .	1.8	12
48	<i>Vickermania</i> gen. nov., trypanosomatids that use two joined flagella to resist midgut peristaltic flow within the fly host. <i>BMC Biology</i> , 2020, 18, 187.	1.7	17
49	Resolving the phylogenetic position of Hygrobiidae (Coleoptera: Adephaga) requires objective statistical tests and exhaustive phylogenetic methodology: a response to Cai et al. (2020). <i>Molecular Phylogenetics and Evolution</i> , 2021, 162, 106923.	1.2	9
50	Barthelonids represent a deep-branching metamonad clade with mitochondrion-related organelles predicted to generate no ATP. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20201538.	1.2	13
51	Chlamydial contribution to anaerobic metabolism during eukaryotic evolution. <i>Science Advances</i> , 2020, 6, eabb7258.	4.7	18
52	Topology-dependent asymmetry in systematic errors affects phylogenetic placement of Ctenophora and Xenacoelomorpha. <i>Science Advances</i> , 2020, 6, .	4.7	102
53	Four myriapod relatives â€œ but who are sisters? No end to debates on relationships among the four major myriapod subgroups. <i>BMC Evolutionary Biology</i> , 2020, 20, 144.	3.2	13
54	Genomics of New Ciliate Lineages Provides Insight into the Evolution of Obligate Anaerobiosis. <i>Current Biology</i> , 2020, 30, 2037-2050.e6.	1.8	48

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56	Catalase and Ascorbate Peroxidase in Euglenozoan Protists. <i>Pathogens</i> , 2020, 9, 317.	1.2	12
57	An integrative phylogenomic approach to elucidate the evolutionary history and divergence times of Neuropterida (Insecta: Holometabola). <i>BMC Evolutionary Biology</i> , 2020, 20, 64.	3.2	48
58	Marine Sediments Illuminate Chlamydiae Diversity and Evolution. <i>Current Biology</i> , 2020, 30, 1032-1048.e7.	1.8	52
59	The evolution of the Puf superfamily of proteins across the tree of eukaryotes. <i>BMC Biology</i> , 2020, 18, 77.	1.7	9
60	Streamlining universal single-copy orthologue and ultraconserved element design: A case study in Collembola. <i>Molecular Ecology Resources</i> , 2020, 20, 706-717.	2.2	10
61	Dinoflagellates with relic endosymbiont nuclei as models for elucidating organellogenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 5364-5375.	3.3	36
62	Phylogenomic analysis of novel Diaforarchaea is consistent with sulfite but not sulfate reduction in volcanic environments on early Earth. <i>ISME Journal</i> , 2020, 14, 1316-1331.	4.4	24
63	Unique Dynamics of Paramylon Storage in the Marine Euglenozoan <i>Diplonema papillatum</i> . <i>Protist</i> , 2020, 171, 125717.	0.6	8
64	New data from Monoplacophora and a carefully-curated dataset resolve molluscan relationships. <i>Scientific Reports</i> , 2020, 10, 101.	1.6	56
65	Genome-Wide Analysis of the Cryptochrome Gene Family in Plants. <i>Tropical Plant Biology</i> , 2020, 13, 117-126.	1.0	6
66	Continuous pre- and post-transplant exposure to a disease-associated gut microbiome promotes hyper-acute graft-versus-host disease in wild-type mice. <i>Gut Microbes</i> , 2020, 11, 754-770.	4.3	17
67	Mitochondrial genome to aid species delimitation and effective conservation of the Sharpnose Guitarfish (<i>Glaucostegus granulatus</i>). <i>Meta Gene</i> , 2020, 24, 100648.	0.3	13
68	Phylomitogenomic analyses on collembolan higher taxa with enhanced taxon sampling and discussion on method selection. <i>PLoS ONE</i> , 2020, 15, e0230827.	1.1	17
69	Phylogenomic analyses recover a clade of large-bodied decapodiform cephalopods. <i>Molecular Phylogenetics and Evolution</i> , 2021, 156, 107038.	1.2	29
70	Coevolving Plasmids Drive Gene Flow and Genome Plasticity in Host-Associated Intracellular Bacteria. <i>Current Biology</i> , 2021, 31, 346-357.e3.	1.8	21
71	A Total-Evidence Dated Phylogeny of Echinoidea Combining Phylogenomic and Paleontological Data. <i>Systematic Biology</i> , 2021, 70, 421-439.	2.7	33
72	Phage Origin of Mitochondrion-Localized Family A DNA Polymerases in Kinetoplastids and Diplonemids. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	7

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73	Evolutionary Trajectory of the Replication Mode of Bacterial Replicons. <i>MBio</i> , 2021, 12, .	1.8	10
75	Isolation and genotyping of novel T4 cyanophages associated with diverse coral reef invertebrates. <i>Coral Reefs</i> , 2021, 40, 485-504.	0.9	1
76	A Comprehensive Evolutionary Scenario of Cell Division and Associated Processes in the Firmicutes. <i>Molecular Biology and Evolution</i> , 2021, 38, 2396-2412.	3.5	4
77	Characterization of the complete mitochondrial genome of <i>Sogatella kolophon</i> (Hemiptera: Tj ETQq1 1 0.784314 $\frac{0.92}{0.2}$ /Overlock 10	0.2	10
78	Long Branch Attraction Biases in Phylogenetics. <i>Systematic Biology</i> , 2021, 70, 838-843.	2.7	26
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80	Inferring the Deep Past from Molecular Data. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	19
81	The Roles of Protein Structure, Taxon Sampling, and Model Complexity in Phylogenomics: A Case Study Focused on Early Animal Divergences. <i>Biophysica</i> , 2021, 1, 87-105.	0.6	2
82	A molecular timescale for eukaryote evolution with implications for the origin of red algal-derived plastids. <i>Nature Communications</i> , 2021, 12, 1879.	5.8	124
83	Signal, bias, and the role of transcriptome assembly quality in phylogenomic inference. <i>Bmc Ecology and Evolution</i> , 2021, 21, 43.	0.7	8
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90	And Then There Were Three: Extreme Regeneration Ability of the Solitary Chordate <i>Polycarpa mytiligera</i> . <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 652466.	1.8	15
92	Smelling in the dark: Phylogenomic insights into the chemosensory system of a subterranean beetle. <i>Molecular Ecology</i> , 2021, 30, 2573-2590.	2.0	9
93	A rooted phylogeny resolves early bacterial evolution. <i>Science</i> , 2021, 372, .	6.0	128

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94	A human respiratory tract-associated bacterium with an extremely small genome. <i>Communications Biology</i> , 2021, 4, 628.	2.0	3
95	Phylogenomic Insights into the Origin of Primary Plastids. <i>Systematic Biology</i> , 2021, 71, 105-120.	2.7	22
96	St. Louis Encephalitis Virus in the Southwestern United States: A Phylogeographic Case for a Multi-Variant Introduction Event. <i>Frontiers in Genetics</i> , 2021, 12, 667895.	1.1	5
97	Pangenomics reveals alternative environmental lifestyles among chlamydiae. <i>Nature Communications</i> , 2021, 12, 4021.	5.8	29
98	A standardized archaeal taxonomy for the Genome Taxonomy Database. <i>Nature Microbiology</i> , 2021, 6, 946-959.	5.9	198
99	Multigene phylogenetics of euglenids based on single-cell transcriptomics of diverse phagotrophs. <i>Molecular Phylogenetics and Evolution</i> , 2021, 159, 107088.	1.2	15
100	Advances and Discoveries in Myxozoan Genomics. <i>Trends in Parasitology</i> , 2021, 37, 552-568.	1.5	18
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104	Phylogeny of the Varidnaviria Morphogenesis Module: Congruence and Incongruence With the Tree of Life and Viral Taxonomy. <i>Frontiers in Microbiology</i> , 2021, 12, 704052.	1.5	18
105	Phylogenetic Signal, Congruence, and Uncertainty across Bacteria and Archaea. <i>Molecular Biology and Evolution</i> , 2021, 38, 5514-5527.	3.5	42
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112	Phylogenomics of a new fungal phylum reveals multiple waves of reductive evolution across Holomycota. <i>Nature Communications</i> , 2021, 12, 4973.	5.8	48
113	Expanding Archaeal Diversity and Phylogeny: Past, Present, and Future. <i>Annual Review of Microbiology</i> , 2021, 75, 359-381.	2.9	34
114	Signs of the plastid: Enzymes involved in plastid-localized metabolic pathways in a eugregarine species. <i>Parasitology International</i> , 2021, 83, 102364.	0.6	4
116	Questioning the source of identified non-foodborne pathogens from food-contact wooden surfaces used in Hong Kong's urban wet markets. <i>One Health</i> , 2021, 13, 100300.	1.5	4
117	Pervasive duplication of tumor suppressors in Afrotherians during the evolution of large bodies and reduced cancer risk. <i>ELife</i> , 2021, 10, .	2.8	38
118	Predatory colponemids are the sister group to all other alveolates. <i>Molecular Phylogenetics and Evolution</i> , 2020, 149, 106839.	1.2	16
119	The Iron-Responsive Genome of the Chiton <i>Acanthopleura granulata</i> . <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	42

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120	IQ-TREE 2: New Models and Efficient Methods for Phylogenetic Inference in the Genomic Era. <i>Molecular Biology and Evolution</i> , 2020, 37, 1530-1534.	3.5	5,960
138	Reduced Genome of the Gut Symbiotic Bacterium <i>Candidatus Benitsuchiphilus tojoi</i> Provides Insight Into Its Possible Roles in Ecology and Adaptation of the Host Insect. <i>Frontiers in Microbiology</i> , 2020, 11, 840.	1.5	7
139	The complete mitogenome of <i>Helix pomatia</i> and the basal phylogeny of Helicinae (Gastropoda). <i>Open Access Journal of Biology</i> , 2020, 10, 15066.	0.5	1
140	Microbial eukaryotes have adapted to hypoxia by horizontal acquisitions of a gene involved in rhodoquinone biosynthesis. <i>ELife</i> , 2018, 7, .	2.8	51
141	Support for a clade of Placozoa and Cnidaria in genes with minimal compositional bias. <i>ELife</i> , 2018, 7, .	2.8	82
142	An updated phylogeny of the Alphaproteobacteria reveals that the parasitic Rickettsiales and Holosporales have independent origins. <i>ELife</i> , 2019, 8, .	2.8	91
146	The Transcriptome of <i>Paraphelidium Tribonemae</i> Illuminates the Ancestry of Fungi and Opisthosporidia. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
158	Anaeramoebae are a divergent lineage of eukaryotes that shed light on the transition from anaerobic mitochondria to hydrogenosomes. <i>Current Biology</i> , 2021, 31, 5605-5612.e5.	1.8	29
159	Genomic Insights Into the Archaea Inhabiting an Australian Radioactive Legacy Site. <i>Frontiers in Microbiology</i> , 2021, 12, 732575.	1.5	5
161	Role of Plasma Gelsolin Protein in the Final Stage of Erythropoiesis and in Correction of Erythroid Dysplasia In Vitro. <i>International Journal of Molecular Sciences</i> , 2020, 21, 7132.	1.8	3
167	Single cell genomics reveals plastid-lacking Picozoa are close relatives of red algae. <i>Nature Communications</i> , 2021, 12, 6651.	5.8	40
168	Leave no stone unturned: individually adapted xerotolerant Thaumarchaeota sheltered below the boulders of the Atacama Desert hyperarid core. <i>Microbiome</i> , 2021, 9, 234.	4.9	18
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171	Phylogenomic Analysis of the Phylum Nematoda: Conflicts and Congruences With Morphology, 18S rRNA, and Mitogenomes. <i>Frontiers in Ecology and Evolution</i> , 2022, 9, .	1.1	28
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173	Host Adaptation in <i>Legionellales</i> Is 1.9 Ga, Coincident with Eukaryogenesis. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	15
174	Chromosome-level genome assembly, annotation, and phylogenomics of the gooseneck barnacle <i>Pollicipes pollicipes</i> . <i>GigaScience</i> , 2022, 11, .	3.3	8
175	An estimate of the deepest branches of the tree of life from ancient vertically evolving genes. <i>ELife</i> , 2022, 11, .	2.8	43

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177	Anaerobic derivatives of mitochondria and peroxisomes in the free-living amoeba <i>Pelomyxa schiedti</i> revealed by single-cell genomics. <i>BMC Biology</i> , 2022, 20, 56.	1.7	13
178	Testing the systematic status of <i>Homalictus</i> and <i>Rostrohalictus</i> with weakened crossâ€vein groups within Halictini (Hymenoptera: Halictidae) using lowâ€coverage wholeâ€genome sequencing. <i>Insect Science</i> , 2022, 29, 1819-1833.	1.5	7
179	Independent Size Expansions and Intron Proliferation in Red Algal Plastid and Mitochondrial Genomes. <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	5
180	Phylogenomics of Elongate-Bodied Springtails Reveals Independent Transitions from Aboveground to Belowground Habitats in Deep Time. <i>Systematic Biology</i> , 2022, 71, 1023-1031.	2.7	10
181	Phylogenomic analyses of echinoid diversification prompt a re-evaluation of their fossil record. <i>ELife</i> , 2022, 11, .	2.8	22
182	Phylotranscriptomic insights into a Mesoproterozoicâ€Neoproterozoic origin and early radiation of green seaweeds (Ulvophyceae). <i>Nature Communications</i> , 2022, 13, 1610.	5.8	21
183	An Enigmatic Stramenopile Sheds Light on Early Evolution in Ochrophyta Plastid Organellenogenesis. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	8
184	Phylogenomic resolution of the root of Panpulmonata, a hyperdiverse radiation of gastropods: new insight into the evolution of air breathing. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2022, 289, 20211855.	1.2	9
186	Monophyly of diverse Bigyromonadea and their impact on phylogenomic relationships within stramenopiles. <i>Molecular Phylogenetics and Evolution</i> , 2022, 171, 107468.	1.2	7
191	Functional Differentiation among the <i>Arabidopsis</i> Phosphatidylinositol 4-Phosphate 5-Kinase Genes <i>PIP5K1</i> , <i>PIP5K2</i> and <i>PIP5K3</i> . <i>Plant and Cell Physiology</i> , 2022, 63, 635-648.	1.5	7
192	The closest lineage of Archaeplastida is revealed by phylogenomics analyses that include <i>Microheliella maris</i> . <i>Open Biology</i> , 2022, 12, 210376.	1.5	13
194	Conflict over the Eukaryote Root Resides in Strong Outliers, Mosaics and Missing Data Sensitivity of Site-Specific (CAT) Mixture Models. <i>Systematic Biology</i> , 2023, 72, 1-16.	2.7	11
195	The SITE-100 Project: Site-Based Biodiversity Genomics for Species Discovery, Community Ecology, and a Global Tree-of-Life. <i>Frontiers in Ecology and Evolution</i> , 2022, 10, .	1.1	6
196	Phylogenomic approaches untangle early divergences and complex diversifications of the olive plant family. <i>BMC Biology</i> , 2022, 20, 92.	1.7	30
197	AliSim: A Fast and Versatile Phylogenetic Sequence Simulator for the Genomic Era. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	28
198	Context-Aware Phylogenetic Trees for Phylogeny-Based Taxonomy Visualization. <i>Frontiers in Genetics</i> , 2022, 13, .	1.1	1
199	Evidence for an Independent Hydrogenosome-to-Mitosome Transition in the CL3 Lineage of Fornicates. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	3
200	Ant phylogenomics reveals a natural selection hotspot preceding the origin of complex eusociality. <i>Current Biology</i> , 2022, 32, 2942-2947.e4.	1.8	20

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201	CT295 Is <i>Chlamydia trachomatis</i> ™ Phosphoglucomutase and a Type 3 Secretion Substrate. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	1
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