

# Alexandros Stamatakis

## List of Publications by Year in descending order

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Version: 2024-02-01

165  
papers

79,423  
citations

30047

54  
h-index

12933

131  
g-index

212  
all docs

212  
docs citations

212  
times ranked

71908  
citing authors

#	ARTICLE	IF	CITATIONS
1	RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. <i>Bioinformatics</i> , 2014, 30, 1312-1313.	1.8	26,744
2	RAxML-VI-HPC: maximum likelihood-based phylogenetic analyses with thousands of taxa and mixed models. <i>Bioinformatics</i> , 2006, 22, 2688-2690.	1.8	14,675
3	A Rapid Bootstrap Algorithm for the RAxML Web Servers. <i>Systematic Biology</i> , 2008, 57, 758-771.	2.7	6,439
4	ARB: a software environment for sequence data. <i>Nucleic Acids Research</i> , 2004, 32, 1363-1371.	6.5	5,816
5	PEAR: a fast and accurate Illumina Paired-End reAd mergeR. <i>Bioinformatics</i> , 2014, 30, 614-620.	1.8	3,776
6	RAxML-NG: a fast, scalable and user-friendly tool for maximum likelihood phylogenetic inference. <i>Bioinformatics</i> , 2019, 35, 4453-4455.	1.8	2,287
7	Phylogenomics resolves the timing and pattern of insect evolution. <i>Science</i> , 2014, 346, 763-767.	6.0	2,096
8	A general species delimitation method with applications to phylogenetic placements. <i>Bioinformatics</i> , 2013, 29, 2869-2876.	1.8	2,059
9	Whole-genome analyses resolve early branches in the tree of life of modern birds. <i>Science</i> , 2014, 346, 1320-1331.	6.0	1,583
10	ModelTest-NG: A New and Scalable Tool for the Selection of DNA and Protein Evolutionary Models. <i>Molecular Biology and Evolution</i> , 2020, 37, 291-294.	3.5	1,021
11	How Many Bootstrap Replicates Are Necessary?. <i>Journal of Computational Biology</i> , 2010, 17, 337-354.	0.8	800
12	Eleven grand challenges in single-cell data science. <i>Genome Biology</i> , 2020, 21, 31.	3.8	742
13	Assessing the root of bilaterian animals with scalable phylogenomic methods. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2009, 276, 4261-4270.	1.2	645
14	Selecting optimal partitioning schemes for phylogenomic datasets. <i>BMC Evolutionary Biology</i> , 2014, 14, 82.	3.2	575
15	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
16	Metagenomic species profiling using universal phylogenetic marker genes. <i>Nature Methods</i> , 2013, 10, 1196-1199.	9.0	442
17	ExaBayes: Massively Parallel Bayesian Tree Inference for the Whole-Genome Era. <i>Molecular Biology and Evolution</i> , 2014, 31, 2553-2556.	3.5	423
18	EPA-ng: Massively Parallel Evolutionary Placement of Genetic Sequences. <i>Systematic Biology</i> , 2019, 68, 365-369.	2.7	400

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19	The iPlant Collaborative: Cyberinfrastructure for Plant Biology. <i>Frontiers in Plant Science</i> , 2011, 2, 34.	1.7	396
20	SweeD: Likelihood-Based Detection of Selective Sweeps in Thousands of Genomes. <i>Molecular Biology and Evolution</i> , 2013, 30, 2224-2234.	3.5	395
21	Pruning Rogue Taxa Improves Phylogenetic Accuracy: An Efficient Algorithm and Webservice. <i>Systematic Biology</i> , 2013, 62, 162-166.	2.7	327
22	SATĀ©-II: Very Fast and Accurate Simultaneous Estimation of Multiple Sequence Alignments and Phylogenetic Trees. <i>Systematic Biology</i> , 2012, 61, 90.	2.7	310
23	Short Tree, Long Tree, Right Tree, Wrong Tree: New Acquisition Bias Corrections for Inferring SNP Phylogenies. <i>Systematic Biology</i> , 2015, 64, 1032-1047.	2.7	286
24	How Many Bootstrap Replicates Are Necessary?. <i>Lecture Notes in Computer Science</i> , 2009, , 184-200.	1.0	263
25	Parasites dominate hyperdiverse soil protist communities in Neotropical rainforests. <i>Nature Ecology and Evolution</i> , 2017, 1, 91.	3.4	262
26	Novel Information Theory-Based Measures for Quantifying Incongruence among Phylogenetic Trees. <i>Molecular Biology and Evolution</i> , 2014, 31, 1261-1271.	3.5	259
27	Pancrustacean Phylogeny in the Light of New Phylogenomic Data: Support for Remipedia as the Possible Sister Group of Hexapoda. <i>Molecular Biology and Evolution</i> , 2012, 29, 1031-1045.	3.5	223
28	A Critical Assessment of Storytelling: Gene Ontology Categories and the Importance of Validating Genomic Scans. <i>Molecular Biology and Evolution</i> , 2012, 29, 3237-3248.	3.5	220
29	Using RAxML to Infer Phylogenies. <i>Current Protocols in Bioinformatics</i> , 2015, 51, 6.14.1-6.14.14.	25.8	215
30	ExaML version 3: a tool for phylogenomic analyses on supercomputers. <i>Bioinformatics</i> , 2015, 31, 2577-2579.	1.8	209
31	Aligning short reads to reference alignments and trees. <i>Bioinformatics</i> , 2011, 27, 2068-2075.	1.8	184
32	Genesis and Gappa: processing, analyzing and visualizing phylogenetic (placement) data. <i>Bioinformatics</i> , 2020, 36, 3263-3265.	1.8	171
33	Understanding angiosperm diversification using small and large phylogenetic trees. <i>American Journal of Botany</i> , 2011, 98, 404-414.	0.8	161
34	The evolutionary history of holometabolous insects inferred from transcriptome-based phylogeny and comprehensive morphological data. <i>BMC Evolutionary Biology</i> , 2014, 14, 52.	3.2	147
35	A Functional Phylogenomic View of the Seed Plants. <i>PLoS Genetics</i> , 2011, 7, e1002411.	1.5	134
36	MPBoot: fast phylogenetic maximum parsimony tree inference and bootstrap approximation. <i>BMC Evolutionary Biology</i> , 2018, 18, 11.	3.2	129

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37	Decisive Data Sets in Phylogenomics: Lessons from Studies on the Phylogenetic Relationships of Primarily Wingless Insects. <i>Molecular Biology and Evolution</i> , 2014, 31, 239-249.	3.5	127
38	Phylogenetic Analysis of SARS-CoV-2 Data Is Difficult. <i>Molecular Biology and Evolution</i> , 2021, 38, 1777-1791.	3.5	119
39	The Phylogenetic Likelihood Library. <i>Systematic Biology</i> , 2015, 64, 356-362.	2.7	118
40	BrassiBase: Introduction to a Novel Knowledge Database on Brassicaceae Evolution. <i>Plant and Cell Physiology</i> , 2014, 55, e3-e3.	1.5	117
41	Quantifying the Phylodynamic Forces Driving Papillomavirus Evolution. <i>Molecular Biology and Evolution</i> , 2011, 28, 2101-2113.	3.5	114
42	Use of a Monte Carlo-based probability matrix for 3-D iterative reconstruction of MADPET-II data. <i>IEEE Transactions on Nuclear Science</i> , 2004, 51, 2597-2605.	1.2	110
43	Multiple Evolutionary Mechanisms Drive Papillomavirus Diversification. <i>Molecular Biology and Evolution</i> , 2007, 24, 1242-1258.	3.5	101
44	MLTreeMap - accurate Maximum Likelihood placement of environmental DNA sequences into taxonomic and functional reference phylogenies. <i>BMC Genomics</i> , 2010, 11, 461.	1.2	100
45	Placing Environmental Next-Generation Sequencing Amplicons from Microbial Eukaryotes into a Phylogenetic Context. <i>Molecular Biology and Evolution</i> , 2014, 31, 993-1009.	3.5	97
46	Phylogeny-aware identification and correction of taxonomically mislabeled sequences. <i>Nucleic Acids Research</i> , 2016, 44, 5022-5033.	6.5	97
47	Time and memory efficient likelihood-based tree searches on phylogenomic alignments with missing data. <i>Bioinformatics</i> , 2010, 26, i132-i139.	1.8	96
48	Want to track pandemic variants faster? Fix the bioinformatics bottleneck. <i>Nature</i> , 2021, 591, 30-33.	13.7	92
49	GeneRax: A Tool for Species-Tree-Aware Maximum Likelihood-Based Gene Family Tree Inference under Gene Duplication, Transfer, and Loss. <i>Molecular Biology and Evolution</i> , 2020, 37, 2763-2774.	3.5	87
50	Large-scale maximum likelihood-based phylogenetic analysis on the IBM BlueGene/L. , 2007, , .		84
51	Efficient computation of the phylogenetic likelihood function on multi-gene alignments and multi-core architectures. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2008, 363, 3977-3984.	1.8	81
52	RAxML-OMP: An Efficient Program for Phylogenetic Inference on SMPs. <i>Lecture Notes in Computer Science</i> , 2005, , 288-302.	1.0	80
53	<i>UniEuk</i>: Time to Speak a Common Language in Protistology!. <i>Journal of Eukaryotic Microbiology</i> , 2017, 64, 407-411.	0.8	74
54	Computing the Internode Certainty and Related Measures from Partial Gene Trees. <i>Molecular Biology and Evolution</i> , 2016, 33, 1606-1617.	3.5	73

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55	Phylogenomic analyses data of the avian phylogenomics project. <i>GigaScience</i> , 2015, 4, 4.	3.3	72
56	Long-read metabarcoding of the eukaryotic rDNA operon to phylogenetically and taxonomically resolve environmental diversity. <i>Molecular Ecology Resources</i> , 2020, 20, 429-443.	2.2	68
57	Sampling bias and incorrect rooting make phylogenetic network tracing of SARS-COV-2 infections unreliable. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 12522-12523.	3.3	68
58	Scalable methods for analyzing and visualizing phylogenetic placement of metagenomic samples. <i>PLoS ONE</i> , 2019, 14, e0217050.	1.1	65
59	The Trichoptera barcode initiative: a strategy for generating a species-level Tree of Life. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2016, 371, 20160025.	1.8	62
60	A Format for Phylogenetic Placements. <i>PLoS ONE</i> , 2012, 7, e31009.	1.1	60
61	A Nuclear Ribosomal DNA Phylogeny of <i>Acer</i> Inferred with Maximum Likelihood, Splits Graphs, and Motif Analysis of 606 Sequences. <i>Evolutionary Bioinformatics</i> , 2006, 2, 117693430600200.	0.6	51
62	ParGenes: a tool for massively parallel model selection and phylogenetic tree inference on thousands of genes. <i>Bioinformatics</i> , 2019, 35, 1771-1773.	1.8	51
63	RAxML-II: a program for sequential, parallel and distributed inference of large phylogenetic trees. <i>Concurrency Computation Practice and Experience</i> , 2005, 17, 1705-1723.	1.4	50
64	Algorithms, data structures, and numerics for likelihood-based phylogenetic inference of huge trees. <i>BMC Bioinformatics</i> , 2011, 12, 470.	1.2	50
65	A daily-updated tree of (sequenced) life as a reference for genome research. <i>Scientific Reports</i> , 2013, 3, 2015.	1.6	47
66	Dynamic multigrain parallelization on the cell broadband engine. , 2007, , .		46
67	Impacts of Terraces on Phylogenetic Inference. <i>Systematic Biology</i> , 2015, 64, 709-726.	2.7	46
68	Swarm v3: towards tera-scale amplicon clustering. <i>Bioinformatics</i> , 2021, 38, 267-269.	1.8	40
69	AxPcoords & parallel AxParafit: statistical co-phylogenetic analyses on thousands of taxa. <i>BMC Bioinformatics</i> , 2007, 8, 405.	1.2	39
70	Hybrid MPI/Pthreads parallelization of the RAxML phylogenetics code. , 2010, , .		39
71	A roadmap for global synthesis of the plant tree of life. <i>American Journal of Botany</i> , 2018, 105, 614-622.	0.8	38
72	Quartet-Based Computations of Internode Certainty Provide Robust Measures of Phylogenetic Incongruence. <i>Systematic Biology</i> , 2020, 69, 308-324.	2.7	38

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73	Fine-grain Parallelism Using Multi-core, Cell/BE, and GPU Systems: Accelerating the Phylogenetic Likelihood Function. , 2009, , .		37
74	The State of Software for Evolutionary Biology. Molecular Biology and Evolution, 2018, 35, 1037-1046.	3.5	36
75	Efficient PC-FPGA Communication over Gigabit Ethernet. , 2010, , .		34
76	Methods for automatic reference trees and multilevel phylogenetic placement. Bioinformatics, 2019, 35, 1151-1158.	1.8	33
77	Uncovering Hidden Phylogenetic Consensus in Large Data Sets. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 902-911.	1.9	32
78	Does the choice of nucleotide substitution models matter topologically?. BMC Bioinformatics, 2016, 17, 143.	1.2	32
79	RAxML-Cell: Parallel Phylogenetic Tree Inference on the Cell Broadband Engine. , 2007, , .		30
80	A Simple and Accurate Method for Rogue Taxon Identification. , 2011, , .		29
81	Novel Parallelization Schemes for Large-Scale Likelihood-based Phylogenetic Inference. , 2013, , .		29
82	Resolving complex phylogeographic patterns in the Balkan Peninsula using closely related wall-lizard species as a model system. Molecular Phylogenetics and Evolution, 2018, 125, 100-115.	1.2	29
83	SpeciesRax: A Tool for Maximum Likelihood Species Tree Inference from Gene Family Trees under Duplication, Transfer, and Loss. Molecular Biology and Evolution, 2022, 39, .	3.5	29
84	A Critical Review on the Use of Support Values in Tree Viewers and Bioinformatics Toolkits. Molecular Biology and Evolution, 2017, 34, 1535-1542.	3.5	28
85	CellPhy: accurate and fast probabilistic inference of single-cell phylogenies from scDNA-seq data. Genome Biology, 2022, 23, 37.	3.8	28
86	Exploiting Fine-Grained Parallelism in the Phylogenetic Likelihood Function with MPI, Pthreads, and OpenMP: A Performance Study. Lecture Notes in Computer Science, 2008, , 424-435.	1.0	26
87	PICS-Ord: unlimited coding of ambiguous regions by pairwise identity and cost scores ordination. BMC Bioinformatics, 2011, 12, 10.	1.2	24
88	Optimization strategies for fast detection of positive selection on phylogenetic trees. Bioinformatics, 2014, 30, 1129-1137.	1.8	24
89	Runtime scheduling of dynamic parallelism on accelerator-based multi-core systems. Parallel Computing, 2007, 33, 700-719.	1.3	23
90	Prediction of missing sequences and branch lengths in phylogenomic data. Bioinformatics, 2016, 32, 1331-1337.	1.8	23

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91	Morphology-based phylogenetic binning of the lichen genera <i>Graphis</i> and <i>Allographa</i> (Ascomycota: Graphidaceae) using molecular site weight calibration. <i>Taxon</i> , 2011, 60, 1450-1457.	0.4	22
92	A nuclear ribosomal DNA phylogeny of acer inferred with maximum likelihood, splits graphs, and motif analysis of 606 sequences. <i>Evolutionary Bioinformatics</i> , 2007, 2, 7-22.	0.6	22
93	Fine-grain parallelism using multi-core, Cell/BE, and GPU Systems. <i>Parallel Computing</i> , 2012, 38, 365-390.	1.3	20
94	Treerecs: an integrated phylogenetic tool, from sequences to reconciliations. <i>Bioinformatics</i> , 2020, 36, 4822-4824.	1.8	20
95	Root Digger: a root placement program for phylogenetic trees. <i>BMC Bioinformatics</i> , 2021, 22, 225.	1.2	20
96	Photoreceptor Diversification Accompanies the Evolution of Anthozoa. <i>Molecular Biology and Evolution</i> , 2021, 38, 1744-1760.	3.5	20
97	PUmPER: phylogenies updated perpetually. <i>Bioinformatics</i> , 2014, 30, 1476-1477.	1.8	19
98	Computational Grand Challenges in Assembling the Tree of Life: Problems and Solutions. <i>Advances in Computers</i> , 2006, , 127-176.	1.2	18
99	HIV-1 Full-Genome Phylogenetics of Generalized Epidemics in Sub-Saharan Africa: Impact of Missing Nucleotide Characters in Next-Generation Sequences. <i>AIDS Research and Human Retroviruses</i> , 2017, 33, 1083-1098.	0.5	18
100	Metagenomic Analysis Using Phylogenetic Placement—A Review of the First Decade. <i>Frontiers in Bioinformatics</i> , 2022, 2, .	1.0	17
101	Efficient floating-point logarithm unit for FPGAs. , 2010, , .		16
102	A fast and memory-efficient implementation of the transfer bootstrap. <i>Bioinformatics</i> , 2020, 36, 2280-2281.	1.8	15
103	The Divisible Load Balance Problem and Its Application to Phylogenetic Inference. <i>Lecture Notes in Computer Science</i> , 2014, , 204-216.	1.0	15
104	Large-Scale Phylogenetic Analysis on Current HPC Architectures. <i>Scientific Programming</i> , 2008, 16, 255-270.	0.5	14
105	Accuracy of morphology-based phylogenetic fossil placement under Maximum Likelihood. , 2010, , .		14
106	FPGA Acceleration of the Phylogenetic Parsimony Kernel?. , 2011, , .		14
107	A reconfigurable architecture for the Phylogenetic Likelihood Function. , 2009, , .		13
108	Rapid forward-in-time simulation at the chromosome and genome level. <i>BMC Bioinformatics</i> , 2013, 14, 216.	1.2	13

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109	NetRAX: accurate and fast maximum likelihood phylogenetic network inference. <i>Bioinformatics</i> , 2022, 38, 3725-3733.	1.8	13
110	SlimCodeML: An Optimized Version of CodeML for the Branch-Site Model. , 2012, , .		12
111	Coupling SIMD and SIMT architectures to boost performance of a phylogeny-aware alignment kernel. <i>BMC Bioinformatics</i> , 2012, 13, 196.	1.2	12
112	Parallelized phylogenetic post-analysis on multi-core architectures. <i>Journal of Computational Science</i> , 2010, 1, 107-114.	1.5	11
113	The Multi-Processor Scheduling Problem in Phylogenetics. , 2012, , .		11
114	An Efficient Independence Sampler for Updating Branches in Bayesian Markov chain Monte Carlo Sampling of Phylogenetic Trees. <i>Systematic Biology</i> , 2016, 65, 161-176.	2.7	11
115	RAxML Grove: an empirical phylogenetic tree database. <i>Bioinformatics</i> , 2022, 38, 1741-1742.	1.8	11
116	A Generic Vectorization Scheme and a GPU Kernel for the Phylogenetic Likelihood Library. , 2013, , .		10
117	Modeling Structural Constraints on Protein Evolution via Side-Chain Conformational States. <i>Molecular Biology and Evolution</i> , 2019, 36, 2086-2103.	3.5	10
118	Load Balance in the Phylogenetic Likelihood Kernel. , 2009, , .		9
119	CHROMATO GATE: A TOOL FOR DETECTING BASE MIS-CALLS IN MULTIPLE SEQUENCE ALIGNMENTS BY SEMI-AUTOMATIC CHROMATOGRAM INSPECTION. <i>Computational and Structural Biotechnology Journal</i> , 2013, 6, e201303001.	1.9	9
120	MoTeX. , 2013, , .		9
121	libgapmis: extending short-read alignments. <i>BMC Bioinformatics</i> , 2013, 14, S4.	1.2	8
122	Parallel computation of phylogenetic consensus trees. <i>Procedia Computer Science</i> , 2010, 1, 1065-1073.	1.2	7
123	Accelerating Phylogeny-Aware Short DNA Read Alignment with FPGAs. , 2011, , .		7
124	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
125	Boosting the Performance of Bayesian Divergence Time Estimation with the Phylogenetic Likelihood Library. , 2013, , .		6
126	The SoftWipe tool and benchmark for assessing coding standards adherence of scientific software. <i>Scientific Reports</i> , 2021, 11, 10015.	1.6	6



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127	The wall lizards of the Balkan peninsula: Tackling questions at the interface of phylogenomics and population genomics. <i>Molecular Phylogenetics and Evolution</i> , 2021, 159, 107121.	1.2	6
128	Accuracy and Performance of Single versus Double Precision Arithmetics for Maximum Likelihood Phylogeny Reconstruction. <i>Lecture Notes in Computer Science</i> , 2010, , 270-279.	1.0	6
129	Exploiting Multi-grain Parallelism for Efficient Selective Sweep Detection. <i>Lecture Notes in Computer Science</i> , 2012, , 56-68.	1.0	6
130	An Optimal Algorithm for Computing All Subtree Repeats in Trees. <i>Lecture Notes in Computer Science</i> , 2013, , 269-282.	1.0	6
131	Orchestrating the Phylogenetic Likelihood Function on Emerging Parallel Architectures. <i>Embedded Multi-core Systems</i> , 2010, , 85-115.	0.1	5
132	A generic and versatile architecture for inference of evolutionary trees under maximum likelihood. , 2010, , .		5
133	Result verification, code verification and computation of support values in phylogenetics. <i>Briefings in Bioinformatics</i> , 2011, 12, 270-279.	3.2	5
134	The Divisible Load Balance Problem with Shared Cost and Its Application to Phylogenetic Inference. , 2016, , .		5
135	<scp>SCRAPP</scp>: A tool to assess the diversity of microbial samples from phylogenetic placements. <i>Molecular Ecology Resources</i> , 2021, 21, 340-349.	2.2	5
136	Using Treemaps to Visualize Phylogenetic Trees. <i>Lecture Notes in Computer Science</i> , 2005, , 283-293.	1.0	5
137	Evolutionary placement of short sequence reads on multi-core architectures. , 2010, , .		4
138	Evolutionary Relationships among <i>Chlamydomonas reinhardtii</i> Variant Strains Inferred by rRNA Secondary Structure-Based Phylogeny. <i>PLoS ONE</i> , 2011, 6, e19813.	1.1	4
139	An Optimized Reconfigurable System for Computing the Phylogenetic Likelihood Function on DNA Data. , 2012, , .		4
140	Efficient Computation of the Phylogenetic Likelihood Function&#x00A0;&#x00A0;on the Intel MIC Architecture. , 2014, , .		4
141	A Review of Approaches for Optimizing Phylogenetic Likelihood Calculations. <i>Computational Biology</i> , 2019, , 1-19.	0.1	4
142	Exploring parallel MPI fault tolerance mechanisms for phylogenetic inference with RAxML-NG. <i>Bioinformatics</i> , 2021, 37, 4056-4063.	1.8	4
143	Parallel Structural Graph Clustering. <i>Lecture Notes in Computer Science</i> , 2011, , 256-272.	1.0	4
144	Accelerating String Matching on MIC Architecture for Motif Extraction. <i>Lecture Notes in Computer Science</i> , 2014, , 258-267.	1.0	4

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145	Computing the Phylogenetic Likelihood Function Out-of-Core. , 2011, , .		3
146	A Novel Heuristic for Data Distribution in Massively Parallel Phylogenetic Inference Using Site Repeats. , 2017, , .		3
147	SPART: A versatile and standardized data exchange format for species partition information. Molecular Ecology Resources, 2022, 22, 430-438.	2.2	3
148	Automated, phylogeny-based genotype delimitation of the Hepatitis Viruses HBV and HCV. PeerJ, 2019, 7, e7754.	0.9	3
149	Large-Scale Co-Phylogenetic Analysis on the Grid. International Journal of Grid and High Performance Computing, 2009, 1, 39-54.	0.7	2
150	Assessment of barrier implementations for fine-grain parallel regions on current multi-core architectures. , 2010, , .		2
151	FPGA Optimizations for a Pipelined Floating-Point Exponential Unit. Lecture Notes in Computer Science, 2011, , 316-327.	1.0	2
152	A Vector-Like Reconfigurable Floating-Point Unit for the Logarithm. International Journal of Reconfigurable Computing, 2011, 2011, 1-12.	0.2	2
153	A new phylogenetic tree sampling method for maximum parsimony bootstrapping and proof-of-concept implementation. , 2016, , .		2
154	Preparing RAxML for the SPEC MPI Benchmark Suite. , 2010, , 757-768.		2
155	Is the Protein Model Assignment problem under linked branch lengths NP-hard?. Theoretical Computer Science, 2014, 524, 48-58.	0.5	1
156	Heuristic Algorithms for the Protein Model Assignment Problem. Lecture Notes in Computer Science, 2013, , 137-148.	1.0	1
157	A LASSO-based approach to sample sites for phylogenetic tree search. Bioinformatics, 2022, 38, i118-i124.	1.8	1
158	Inference of Huge Trees under Maximum Likelihood. , 2012, , .		0
159	An Efficient Approach to Merging Paired-End Reads and Incorporation of Uncertainties. , 2017, , 299-325.		0
160	Population and Evolutionary Genetic Inferences in the Whole-Genome Era: Software Challenges. Population Genomics, 2018, , 161-175.	0.2	0
161	Data Distribution for Phylogenetic Inference with Site Repeats via Judicious Hypergraph Partitioning. , 2019, , .		0
162	Efficient Memory Management in Likelihood-based Phylogenetic Placement. , 2021, , .		0

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163	Large-Scale Co-Phylogenetic Analysis on the Grid. , 2009, , 731-745.		0
164	Large-Scale Co-Phylogenetic Analysis on the Grid. , 0, , 222-237.		0
165	ParBaum: Large-Scale Maximum Likelihood-Based Phylogenetic Analyses. , 2009, , 111-125.		0