

Alexandros Stamatakis

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

181
papers

57,103
citations

52
h-index

212
g-index

212
ext. papers

71,466
ext. citations

6.4
avg, IF

9.15
L-index

#	Paper	IF	Citations
181	RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. <i>Bioinformatics</i> , 2014 , 30, 1312-3	7.2	17427
180	RAxML-VI-HPC: maximum likelihood-based phylogenetic analyses with thousands of taxa and mixed models. <i>Bioinformatics</i> , 2006 , 22, 2688-90	7.2	12661
179	A rapid bootstrap algorithm for the RAxML Web servers. <i>Systematic Biology</i> , 2008 , 57, 758-71	8.4	5512
178	ARB: a software environment for sequence data. <i>Nucleic Acids Research</i> , 2004 , 32, 1363-71	20.1	5075
177	PEAR: a fast and accurate Illumina Paired-End read mergeR. <i>Bioinformatics</i> , 2014 , 30, 614-20	7.2	2340
176	Phylogenomics resolves the timing and pattern of insect evolution. <i>Science</i> , 2014 , 346, 763-7	33.3	1489
175	A general species delimitation method with applications to phylogenetic placements. <i>Bioinformatics</i> , 2013 , 29, 2869-76	7.2	1376
174	Whole-genome analyses resolve early branches in the tree of life of modern birds. <i>Science</i> , 2014 , 346, 1320-31	33.3	1182
173	RAxML-NG: a fast, scalable and user-friendly tool for maximum likelihood phylogenetic inference. <i>Bioinformatics</i> , 2019 , 35, 4453-4455	7.2	863
172	How many bootstrap replicates are necessary?. <i>Journal of Computational Biology</i> , 2010 , 17, 337-54	1.7	601
171	Assessing the root of bilaterian animals with scalable phylogenomic methods. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2009 , 276, 4261-70	4.4	564
170	Selecting optimal partitioning schemes for phylogenomic datasets. <i>BMC Evolutionary Biology</i> , 2014 , 14, 82	3	426
169	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	8.3	372
168	Metagenomic species profiling using universal phylogenetic marker genes. <i>Nature Methods</i> , 2013 , 10, 1196-9	21.6	340
167	Performance, accuracy, and Web server for evolutionary placement of short sequence reads under maximum likelihood. <i>Systematic Biology</i> , 2011 , 60, 291-302	8.4	335
166	The iPlant Collaborative: Cyberinfrastructure for Plant Biology. <i>Frontiers in Plant Science</i> , 2011 , 2, 34	6.2	306
165	ExaBayes: massively parallel bayesian tree inference for the whole-genome era. <i>Molecular Biology and Evolution</i> , 2014 , 31, 2553-6	8.3	289

164	Eleven grand challenges in single-cell data science. <i>Genome Biology</i> , 2020 , 21, 31	18.3	274
163	SATe-II: very fast and accurate simultaneous estimation of multiple sequence alignments and phylogenetic trees. <i>Systematic Biology</i> , 2012 , 61, 90-106	8.4	257
162	Pruning rogue taxa improves phylogenetic accuracy: an efficient algorithm and webservice. <i>Systematic Biology</i> , 2013 , 62, 162-6	8.4	249
161	SweeD: likelihood-based detection of selective sweeps in thousands of genomes. <i>Molecular Biology and Evolution</i> , 2013 , 30, 2224-34	8.3	236
160	How Many Bootstrap Replicates Are Necessary?. <i>Lecture Notes in Computer Science</i> , 2009 , 184-200	0.9	216
159	Novel information theory-based measures for quantifying incongruence among phylogenetic trees. <i>Molecular Biology and Evolution</i> , 2014 , 31, 1261-71	8.3	199
158	Short Tree, Long Tree, Right Tree, Wrong Tree: New Acquisition Bias Corrections for Inferring SNP Phylogenies. <i>Systematic Biology</i> , 2015 , 64, 1032-47	8.4	191
157	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, 1031-45	8.3	184
156	EPA-ng: Massively Parallel Evolutionary Placement of Genetic Sequences. <i>Systematic Biology</i> , 2019 , 68, 365-369	8.4	172
155	A critical assessment of storytelling: gene ontology categories and the importance of validating genomic scans. <i>Molecular Biology and Evolution</i> , 2012 , 29, 3237-48	8.3	164
154	ExaML version 3: a tool for phylogenomic analyses on supercomputers. <i>Bioinformatics</i> , 2015 , 31, 2577-9	7.2	161
153	Parasites dominate hyperdiverse soil protist communities in Neotropical rainforests. <i>Nature Ecology and Evolution</i> , 2017 , 1, 91	12.3	147
152	Understanding angiosperm diversification using small and large phylogenetic trees. <i>American Journal of Botany</i> , 2011 , 98, 404-14	2.7	143
151	Aligning short reads to reference alignments and trees. <i>Bioinformatics</i> , 2011 , 27, 2068-75	7.2	134
150	Using RAxML to Infer Phylogenies. <i>Current Protocols in Bioinformatics</i> , 2015 , 51, 6.14.1-6.14.14	24.2	127
149	The evolutionary history of holometabolous insects inferred from transcriptome-based phylogeny and comprehensive morphological data. <i>BMC Evolutionary Biology</i> , 2014 , 14, 52	3	120
148	A functional phylogenomic view of the seed plants. <i>PLoS Genetics</i> , 2011 , 7, e1002411	6	117
147	Decisive data sets in phylogenomics: lessons from studies on the phylogenetic relationships of primarily wingless insects. <i>Molecular Biology and Evolution</i> , 2014 , 31, 239-49	8.3	100

146	Quantifying the phylodynamic forces driving papillomavirus evolution. <i>Molecular Biology and Evolution</i> , 2011 , 28, 2101-13	8.3	99
145	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	1.7	95
144	MLTreeMap--accurate Maximum Likelihood placement of environmental DNA sequences into taxonomic and functional reference phylogenies. <i>BMC Genomics</i> , 2010 , 11, 461	4.5	93
143	Multiple evolutionary mechanisms drive papillomavirus diversification. <i>Molecular Biology and Evolution</i> , 2007 , 24, 1242-58	8.3	91
142	BrassiBase: introduction to a novel knowledge database on Brassicaceae evolution. <i>Plant and Cell Physiology</i> , 2014 , 55, e3	4.9	83
141	Time and memory efficient likelihood-based tree searches on phylogenomic alignments with missing data. <i>Bioinformatics</i> , 2010 , 26, i132-9	7.2	77
140	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, 3977-84	5.8	76
139	Placing environmental next-generation sequencing amplicons from microbial eukaryotes into a phylogenetic context. <i>Molecular Biology and Evolution</i> , 2014 , 31, 993-1009	8.3	73
138	Genesis and Gappa: processing, analyzing and visualizing phylogenetic (placement) data. <i>Bioinformatics</i> , 2020 , 36, 3263-3265	7.2	69
137	Phylogeny-aware identification and correction of taxonomically mislabeled sequences. <i>Nucleic Acids Research</i> , 2016 , 44, 5022-33	20.1	67
136	MPBoot: fast phylogenetic maximum parsimony tree inference and bootstrap approximation. <i>BMC Evolutionary Biology</i> , 2018 , 18, 11	3	65
135	The phylogenetic likelihood library. <i>Systematic Biology</i> , 2015 , 64, 356-62	8.4	64
134	Large-scale maximum likelihood-based phylogenetic analysis on the IBM BlueGene/L 2007 ,		64
133	RAXML-OMP: An Efficient Program for Phylogenetic Inference on SMPs. <i>Lecture Notes in Computer Science</i> , 2005 , 288-302	0.9	62
132	Computing the Internode Certainty and Related Measures from Partial Gene Trees. <i>Molecular Biology and Evolution</i> , 2016 , 33, 1606-17	8.3	56
131	Phylogenomic analyses data of the avian phylogenomics project. <i>GigaScience</i> , 2015 , 4, 4	7.6	54
130	Phylogenetic Analysis of SARS-CoV-2 Data Is Difficult. <i>Molecular Biology and Evolution</i> , 2021 , 38, 1777-1791	7.9	52
129	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,	5.8	49

128	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	11.5	46
127	RAxML-NG: A fast, scalable, and user-friendly tool for maximum likelihood phylogenetic inference		44
126	A Nuclear Ribosomal DNA Phylogeny of Acer Inferred with Maximum Likelihood, Splits Graphs, and Motif Analysis of 606 Sequences. <i>Evolutionary Bioinformatics</i> , 2006 , 2, 117693430600200	1.9	42
125	Scalable methods for analyzing and visualizing phylogenetic placement of metagenomic samples. <i>PLoS ONE</i> , 2019 , 14, e0217050	3.7	41
124	Algorithms, data structures, and numerics for likelihood-based phylogenetic inference of huge trees. <i>BMC Bioinformatics</i> , 2011 , 12, 470	3.6	40
123	UniEuk: Time to Speak a Common Language in Protistology!. <i>Journal of Eukaryotic Microbiology</i> , 2017 , 64, 407-411	3.6	39
122	A daily-updated tree of (sequenced) life as a reference for genome research. <i>Scientific Reports</i> , 2013 , 3, 2015	4.9	39
121	AxPcoords & parallel AxParafit: statistical co-phylogenetic analyses on thousands of taxa. <i>BMC Bioinformatics</i> , 2007 , 8, 405	3.6	37
120	A format for phylogenetic placements. <i>PLoS ONE</i> , 2012 , 7, e31009	3.7	36
119	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	36
118	Long-read metabarcoding of the eukaryotic rDNA operon to phylogenetically and taxonomically resolve environmental diversity. <i>Molecular Ecology Resources</i> , 2020 , 20, 429-443	8.4	33
117	Hybrid MPI/Pthreads parallelization of the RAxML phylogenetics code 2010 ,		30
116	A roadmap for global synthesis of the plant tree of life. <i>American Journal of Botany</i> , 2018 , 105, 614-622	2.7	29
115	Uncovering hidden phylogenetic consensus in large data sets. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011 , 8, 902-11	3	29
114	Impacts of Terraces on Phylogenetic Inference. <i>Systematic Biology</i> , 2015 , 64, 709-26	8.4	28
113	Fine-grain Parallelism Using Multi-core, Cell/BE, and GPU Systems: Accelerating the Phylogenetic Likelihood Function 2009 ,		28
112	Initial Experiences Porting a Bioinformatics Application to a Graphics Processor. <i>Lecture Notes in Computer Science</i> , 2005 , 415-425	0.9	27
111	Want to track pandemic variants faster? Fix the bioinformatics bottleneck. <i>Nature</i> , 2021 , 591, 30-33	50.4	27

110	Novel Parallelization Schemes for Large-Scale Likelihood-based Phylogenetic Inference 2013 ,		25
109	The State of Software for Evolutionary Biology. <i>Molecular Biology and Evolution</i> , 2018 , 35, 1037-1046	8.3	23
108	Efficient PC-FPGA Communication over Gigabit Ethernet 2010 ,		22
107	Dynamic multigrain parallelization on the cell broadband engine 2007 ,		22
106	RAXML-Cell: Parallel Phylogenetic Tree Inference on the Cell Broadband Engine 2007 ,		21
105	Exploiting Fine-Grained Parallelism in the Phylogenetic Likelihood Function with MPI, Pthreads, and OpenMP: A Performance Study. <i>Lecture Notes in Computer Science</i> , 2008 , 424-435	0.9	21
104	Methods for automatic reference trees and multilevel phylogenetic placement. <i>Bioinformatics</i> , 2019 , 35, 1151-1158	7.2	21
103	ParGenes: a tool for massively parallel model selection and phylogenetic tree inference on thousands of genes. <i>Bioinformatics</i> , 2019 , 35, 1771-1773	7.2	21
102	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	8.3	20
101	Does the choice of nucleotide substitution models matter topologically?. <i>BMC Bioinformatics</i> , 2016 , 17, 143	3.6	20
100	Runtime scheduling of dynamic parallelism on accelerator-based multi-core systems. <i>Parallel Computing</i> , 2007 , 33, 700-719	1	20
99	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	1.9	20
98	Morphology-based phylogenetic binning of the lichen genera Graphis and Allographa (Ascomycota: Graphidaceae) using molecular site weight calibration. <i>Taxon</i> , 2011 , 60, 1450-1457	0.8	19
97	A Simple and Accurate Method for Rogue Taxon Identification 2011 ,		19
96	Optimization strategies for fast detection of positive selection on phylogenetic trees. <i>Bioinformatics</i> , 2014 , 30, 1129-1137	7.2	18
95	Fine-grain parallelism using multi-core, Cell/BE, and GPU Systems. <i>Parallel Computing</i> , 2012 , 38, 365-390	1	18
94	Resolving complex phylogeographic patterns in the Balkan Peninsula using closely related wall-lizard species as a model system. <i>Molecular Phylogenetics and Evolution</i> , 2018 , 125, 100-115	4.1	17
93	Quartet-Based Computations of Internode Certainty Provide Robust Measures of Phylogenetic Incongruence. <i>Systematic Biology</i> , 2020 , 69, 308-324	8.4	17

92	Prediction of missing sequences and branch lengths in phylogenomic data. <i>Bioinformatics</i> , 2016 , 32, 1331-7	1.7	15
91	ModelTest-NG: a new and scalable tool for the selection of DNA and protein evolutionary models		15
90	PUMPER: phylogenies updated perpetually. <i>Bioinformatics</i> , 2014 , 30, 1476-7	7.2	14
89	PICS-Ord: unlimited coding of ambiguous regions by pairwise identity and cost scores ordination. <i>BMC Bioinformatics</i> , 2011 , 12, 10	3.6	14
88	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	1.6	13
87	Rapid forward-in-time simulation at the chromosome and genome level. <i>BMC Bioinformatics</i> , 2013 , 14, 216	3.6	13
86	A Critical Review on the Use of Support Values in Tree Viewers and Bioinformatics Toolkits. <i>Molecular Biology and Evolution</i> , 2017 , 34, 1535-1542	8.3	13
85	Large-Scale Phylogenetic Analysis on Current HPC Architectures. <i>Scientific Programming</i> , 2008 , 16, 255-270	1.0	13
84	Parallel Inference of a 10.000-Taxon Phylogeny with Maximum Likelihood. <i>Lecture Notes in Computer Science</i> , 2004 , 997-1004	0.9	13
83	Phylogenetic analysis of SARS-CoV-2 data is difficult		12
82	The Multi-Processor Scheduling Problem in Phylogenetics 2012 ,		10
81	Coupling SIMD and SIMT architectures to boost performance of a phylogeny-aware alignment kernel. <i>BMC Bioinformatics</i> , 2012 , 13, 196	3.6	10
80	Efficient floating-point logarithm unit for FPGAs 2010 ,		10
79	FPGA Acceleration of the Phylogenetic Parsimony Kernel? 2011 ,		10
78	A reconfigurable architecture for the Phylogenetic Likelihood Function 2009 ,		10
77	Parallelized phylogenetic post-analysis on multi-core architectures. <i>Journal of Computational Science</i> , 2010 , 1, 107-114	3.4	10
76	Computational Grand Challenges in Assembling the Tree of Life: Problems and Solutions. <i>Advances in Computers</i> , 2006 , 127-176	2.9	10
75	The Divisible Load Balance Problem and Its Application to Phylogenetic Inference. <i>Lecture Notes in Computer Science</i> , 2014 , 204-216	0.9	10

74	A fast and memory-efficient implementation of the transfer bootstrap. <i>Bioinformatics</i> , 2020 , 36, 2280-2281	10
73	Accuracy of morphology-based phylogenetic fossil placement under Maximum Likelihood 2010 ,	9
72	Load Balance in the Phylogenetic Likelihood Kernel 2009 ,	9
71	An Efficient Independence Sampler for Updating Branches in Bayesian Markov chain Monte Carlo Sampling of Phylogenetic Trees. <i>Systematic Biology</i> , 2016 , 65, 161-76	8.4 8
70	A Generic Vectorization Scheme and a GPU Kernel for the Phylogenetic Likelihood Library 2013 ,	8
69	Quartet-based computations of internode certainty provide accurate and robust measures of phylogenetic incongruence	8
68	Swarm v3: towards tera-scale amplicon clustering. <i>Bioinformatics</i> , 2021 ,	7.2 8
67	SlimCodeML: An Optimized Version of CodeML for the Branch-Site Model 2012 ,	7
66	MoTeX 2013 ,	7
65	Treerecs: an integrated phylogenetic tool, from sequences to reconciliations. <i>Bioinformatics</i> , 2020 , 36, 4822-4824	7.2 7
64	Accelerating Phylogeny-Aware Short DNA Read Alignment with FPGAs 2011 ,	6
63	Exploiting Multi-grain Parallelism for Efficient Selective Sweep Detection. <i>Lecture Notes in Computer Science</i> , 2012 , 56-68	0.9 6
62	EPA-ng: Massively Parallel Evolutionary Placement of Genetic Sequences	6
61	Modeling Structural Constraints on Protein Evolution via Side-Chain Conformational States. <i>Molecular Biology and Evolution</i> , 2019 , 36, 2086-2103	8.3 5
60	libgapmis: extending short-read alignments. <i>BMC Bioinformatics</i> , 2013 , 14 Suppl 11, S4	3.6 5
59	Maximum Likelihood Analyses of 3,490 rbcL Sequences: Scalability of Comprehensive Inference versus Group-Specific Taxon Sampling. <i>Evolutionary Bioinformatics</i> , 2010 , 6, 73-90	1.9 5
58	Orchestrating the Phylogenetic Likelihood Function on Emerging Parallel Architectures. <i>Embedded Multi-core Systems</i> , 2010 , 85-115	5
57	Parallel computation of phylogenetic consensus trees. <i>Procedia Computer Science</i> , 2010 , 1, 1065-1073	1.6 5

56	An Optimal Algorithm for Computing All Subtree Repeats in Trees. <i>Lecture Notes in Computer Science</i> , 2013 , 269-282	0.9	5
55	Genesis and Gappa: Processing, Analyzing and Visualizing Phylogenetic (Placement) Data		5
54	SpeciesRax: A tool for maximum likelihood species tree inference from gene family trees under duplication, transfer, and loss		5
53	Using Treemaps to Visualize Phylogenetic Trees. <i>Lecture Notes in Computer Science</i> , 2005 , 283-293	0.9	5
52	An Optimized Reconfigurable System for Computing the Phylogenetic Likelihood Function on DNA Data 2012 ,		4
51	2013 ,		4
50	Evolutionary relationships among <i>Chlamydomonas</i> abortus variant strains inferred by rRNA secondary structure-based phylogeny. <i>PLoS ONE</i> , 2011 , 6, e19813	3.7	4
49	Result verification, code verification and computation of support values in phylogenetics. <i>Briefings in Bioinformatics</i> , 2011 , 12, 270-9	13.4	4
48	CellPhy: accurate and fast probabilistic inference of single-cell phylogenies from scDNA-seq data		4
47	ChromatoGate: A Tool for Detecting Base Mis-Calls in Multiple Sequence Alignments by Semi-Automatic Chromatogram Inspection. <i>Computational and Structural Biotechnology Journal</i> , 2013 , 6, e201303001	6.8	3
46	Inferring and Postprocessing Huge Phylogenies 2013 , 1049-1072		3
45	A generic and versatile architecture for inference of evolutionary trees under maximum likelihood 2010 ,		3
44	Phylogenetic Search Algorithms for Maximum Likelihood 2010 , 547-577		3
43	Automated, phylogeny-based genotype delimitation of the Hepatitis Viruses HBV and HCV. <i>PeerJ</i> , 2019 , 7, e7754	3.1	3
42	Accuracy and Performance of Single versus Double Precision Arithmetics for Maximum Likelihood Phylogeny Reconstruction. <i>Lecture Notes in Computer Science</i> , 2010 , 270-279	0.9	3
41	Parallel Structural Graph Clustering. <i>Lecture Notes in Computer Science</i> , 2011 , 256-272	0.9	3
40	Photoreceptor Diversification Accompanies the Evolution of Anthozoa. <i>Molecular Biology and Evolution</i> , 2021 , 38, 1744-1760	8.3	3
39	ParGenes: a tool for massively parallel model selection and phylogenetic tree inference on thousands of genes		3

38	Long metabarcoding of the eukaryotic rDNA operon to phylogenetically and taxonomically resolve environmental diversity		3
37	GeneRax: A tool for species tree-aware maximum likelihood based gene family tree inference under gene duplication, transfer, and loss		3
36	Root Digger: a root placement program for phylogenetic trees. <i>BMC Bioinformatics</i> , 2021 , 22, 225	3.6	3
35	The Divisible Load Balance Problem with Shared Cost and Its Application to Phylogenetic Inference 2016 ,		3
34	NetRAX: Accurate and Fast Maximum Likelihood Phylogenetic Network Inference?		3
33	A Review of Approaches for Optimizing Phylogenetic Likelihood Calculations. <i>Computational Biology</i> , 2019 , 1-19	0.7	2
32	2014 ,		2
31	Evolutionary placement of short sequence reads on multi-core architectures 2010 ,		2
30	Assessment of barrier implementations for fine-grain parallel regions on current multi-core architectures 2010 ,		2
29	Computing the Phylogenetic Likelihood Function Out-of-Core 2011 ,		2
28	Large-Scale Co-Phylogenetic Analysis on the Grid. <i>International Journal of Grid and High Performance Computing</i> , 2009 , 1, 39-54	0.7	2
27	SpeciesRax: A tool for maximum likelihood species tree inference from gene family trees under duplication, transfer, and loss.. <i>Molecular Biology and Evolution</i> , 2022 ,	8.3	2
26	12 Grand Challenges in Single-Cell Data Science		2
25	Preparing RAXML for the SPEC MPI Benchmark Suite 2010 , 757-768		2
24	Accelerating String Matching on MIC Architecture for Motif Extraction. <i>Lecture Notes in Computer Science</i> , 2014 , 258-267	0.9	2
23	Scalable methods for analyzing and visualizing phylogenetic placement of metagenomic samples		2
22	Computing the Internode Certainty and related measures from partial gene trees		2
21	SCRAPP: A tool to assess the diversity of microbial samples from phylogenetic placements. <i>Molecular Ecology Resources</i> , 2021 , 21, 340-349	8.4	2

20	Metagenomic Analysis Using Phylogenetic Placement: A Review of the First Decade. <i>Frontiers in Bioinformatics</i> , 2022 , 2,		2
19	2017 ,		1
18	Is the Protein Model Assignment problem under linked branch lengths NP-hard?. <i>Theoretical Computer Science</i> , 2014 , 524, 48-58	1.1	1
17	A Vector-Like Reconfigurable Floating-Point Unit for the Logarithm. <i>International Journal of Reconfigurable Computing</i> , 2011 , 2011, 1-12	2.1	1
16	CellPhy: accurate and fast probabilistic inference of single-cell phylogenies from scDNA-seq data.. <i>Genome Biology</i> , 2022 , 23, 37	18.3	1
15	The divisible load balance problem with shared cost and its application to phylogenetic inference		1
14	RootDigger: a root placement program for phylogenetic trees		1
13	Treerecs: an integrated phylogenetic tool, from sequences to reconciliations		1
12	Soil Protists in Three Neotropical Rainforests are Hyperdiverse and Dominated by Parasites		1
11	The SoftWipe tool and benchmark for assessing coding standards adherence of scientific software. <i>Scientific Reports</i> , 2021 , 11, 10015	4.9	1
10	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	4.1	1
9	FPGA Optimizations for a Pipelined Floating-Point Exponential Unit. <i>Lecture Notes in Computer Science</i> , 2011 , 316-327	0.9	0
8	An Efficient Approach to Merging Paired-End Reads and Incorporation of Uncertainties 2017 , 299-325		
7	Automated Plausibility Analysis of Large Phylogenies 2015 , 457-482		
6	Large-Scale Co-Phylogenetic Analysis on the Grid 2009 , 731-745		
5	ParBaum: Large-Scale Maximum Likelihood-Based Phylogenetic Analyses 2009 , 111-125		
4	Tool Environments in CORBA-Based Medical High Performance Computing. <i>Lecture Notes in Computer Science</i> , 2001 , 447-455	0.9	
3	Large-Scale Co-Phylogenetic Analysis on the Grid 2009 , 731-745		

- 2 Heuristic Algorithms for the Protein Model Assignment Problem. *Lecture Notes in Computer Science*, **2013**, 137-148 0.9
- 1 Population and Evolutionary Genetic Inferences in the Whole-Genome Era: Software Challenges. *Population Genomics*, **2018**, 161-175 1.4