Alexandros Stamatakis

List of Publications by Year in Descending Order

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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	CellPhy: accurate and fast probabilistic inference of single-cell phylogenies from scDNA-seq data.. *Genome Biology*, **2022**, 23, 37	18.3	1
180	SpeciesRax: A tool for maximum likelihood species tree inference from gene family trees under duplication, transfer, and loss.. *Molecular Biology and Evolution*, **2022**,	8.3	2
179	Metagenomic Analysis Using Phylogenetic Placement A Review of the First Decade. *Frontiers in Bioinformatics*, **2022**, 2,		2
178	Photoreceptor Diversification Accompanies the Evolution of Anthozoa. *Molecular Biology and Evolution*, **2021**, 38, 1744-1760	8.3	3
177	Want to track pandemic variants faster? Fix the bioinformatics bottleneck. *Nature*, **2021**, 591, 30-33	50.4	27
176	Root Digger: a root placement program for phylogenetic trees. *BMC Bioinformatics*, **2021**, 22, 225	3.6	3
175	The SoftWipe tool and benchmark for assessing coding standards adherence of scientific software. *Scientific Reports*, **2021**, 11, 10015	4.9	1
174	The wall lizards of the Balkan peninsula: Tackling questions at the interface of phylogenomics and population genomics. *Molecular Phylogenetics and Evolution*, **2021**, 159, 107121	4.1	1
173	Swarm v3: towards tera-scale amplicon clustering. *Bioinformatics*, **2021**,	7.2	8
172	SCRAPP: A tool to assess the diversity of microbial samples from phylogenetic placements. *Molecular Ecology Resources*, **2021**, 21, 340-349	8.4	2
171	Phylogenetic Analysis of SARS-CoV-2 Data Is Difficult. *Molecular Biology and Evolution*, **2021**, 38, 1777-1791	8.3	52
170	Sampling bias and incorrect rooting make phylogenetic network tracing of SARS-COV-2 infections unreliable. *Proceedings of the National Academy of Sciences of the United States of America*, **2020**, 117, 12522-12523	11.5	46
169	GeneRax: A Tool for Species-Tree-Aware Maximum Likelihood-Based Gene Family Tree Inference under Gene Duplication, Transfer, and Loss. *Molecular Biology and Evolution*, **2020**, 37, 2763-2774	8.3	20
168	Eleven grand challenges in single-cell data science. *Genome Biology*, **2020**, 21, 31	18.3	274
167	Genesis and Gappa: processing, analyzing and visualizing phylogenetic (placement) data. *Bioinformatics*, **2020**, 36, 3263-3265	7.2	69
166	Long-read metabarcoding of the eukaryotic rDNA operon to phylogenetically and taxonomically resolve environmental diversity. *Molecular Ecology Resources*, **2020**, 20, 429-443	8.4	33
165	A fast and memory-efficient implementation of the transfer bootstrap. *Bioinformatics*, **2020**, 36, 2280-2281	7.2	10

164	Treerecs: an integrated phylogenetic tool, from sequences to reconciliations. *Bioinformatics*, **2020**, 36, 4822-4824	7.2	7
163	Quartet-Based Computations of Internode Certainty Provide Robust Measures of Phylogenetic Incongruence. *Systematic Biology*, **2020**, 69, 308-324	8.4	17
162	ModelTest-NG: A New and Scalable Tool for the Selection of DNA and Protein Evolutionary Models. *Molecular Biology and Evolution*, **2020**, 37, 291-294	8.3	372
161	RAxML-NG: a fast, scalable and user-friendly tool for maximum likelihood phylogenetic inference. *Bioinformatics*, **2019**, 35, 4453-4455	7.2	863
160	A Review of Approaches for Optimizing Phylogenetic Likelihood Calculations. *Computational Biology*, **2019**, 1-19	0.7	2
159	EPA-ng: Massively Parallel Evolutionary Placement of Genetic Sequences. *Systematic Biology*, **2019**, 68, 365-369	8.4	172
158	Scalable methods for analyzing and visualizing phylogenetic placement of metagenomic samples. *PLoS ONE*, **2019**, 14, e0217050	3.7	41
157	Modeling Structural Constraints on Protein Evolution via Side-Chain Conformational States. *Molecular Biology and Evolution*, **2019**, 36, 2086-2103	8.3	5
156	Automated, phylogeny-based genotype delimitation of the Hepatitis Viruses HBV and HCV. *PeerJ*, **2019**, 7, e7754	3.1	3
155	Methods for automatic reference trees and multilevel phylogenetic placement. *Bioinformatics*, **2019**, 35, 1151-1158	7.2	21
154	ParGenes: a tool for massively parallel model selection and phylogenetic tree inference on thousands of genes. *Bioinformatics*, **2019**, 35, 1771-1773	7.2	21
153	A roadmap for global synthesis of the plant tree of life. *American Journal of Botany*, **2018**, 105, 614-622	2.7	29
152	The State of Software for Evolutionary Biology. *Molecular Biology and Evolution*, **2018**, 35, 1037-1046	8.3	23
151	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	4.1	17
150	MPBoot: fast phylogenetic maximum parsimony tree inference and bootstrap approximation. *BMC Evolutionary Biology*, **2018**, 18, 11	3	65
149	Population and Evolutionary Genetic Inferences in the Whole-Genome Era: Software Challenges. *Population Genomics*, **2018**, 161-175	1.4	
148	HIV-1 full-genome phylogenetics of generalized epidemics in sub-Saharan Africa: impact of missing nucleotide characters in next-generation sequences. *AIDS Research and Human Retroviruses*, **2017**, 33, 1083-1098	1.6	13
147	UniEuk: Time to Speak a Common Language in Protistology!. *Journal of Eukaryotic Microbiology*, **2017**, 64, 407-411	3.6	39

146	Parasites dominate hyperdiverse soil protist communities in Neotropical rainforests. *Nature Ecology and Evolution*, **2017**, 1, 91	12.3	147
145	**2017**,		1
144	An Efficient Approach to Merging Paired-End Reads and Incorporation of Uncertainties **2017**, 299-325		
143	A Critical Review on the Use of Support Values in Tree Viewers and Bioinformatics Toolkits. *Molecular Biology and Evolution*, **2017**, 34, 1535-1542	8.3	13
142	The Trichoptera barcode initiative: a strategy for generating a species-level Tree of Life. *Philosophical Transactions of the Royal Society B: Biological Sciences*, **2016**, 371,	5.8	49
141	Does the choice of nucleotide substitution models matter topologically?. *BMC Bioinformatics*, **2016**, 17, 143	3.6	20
140	An Efficient Independence Sampler for Updating Branches in Bayesian Markov chain Monte Carlo Sampling of Phylogenetic Trees. *Systematic Biology*, **2016**, 65, 161-76	8.4	8
139	Computing the Internode Certainty and Related Measures from Partial Gene Trees. *Molecular Biology and Evolution*, **2016**, 33, 1606-17	8.3	56
138	Prediction of missing sequences and branch lengths in phylogenomic data. *Bioinformatics*, **2016**, 32, 1331-7	7.2	15
137	The Divisible Load Balance Problem with Shared Cost and Its Application to Phylogenetic Inference **2016**,		3
136	Phylogeny-aware identification and correction of taxonomically mislabeled sequences. *Nucleic Acids Research*, **2016**, 44, 5022-33	20.1	67
135	ExaML version 3: a tool for phylogenomic analyses on supercomputers. *Bioinformatics*, **2015**, 31, 2577-9	7.2	161
134	Phylogenomic analyses data of the avian phylogenomics project. *GigaScience*, **2015**, 4, 4	7.6	54
133	Short Tree, Long Tree, Right Tree, Wrong Tree: New Acquisition Bias Corrections for Inferring SNP Phylogenies. *Systematic Biology*, **2015**, 64, 1032-47	8.4	191
132	The phylogenetic likelihood library. *Systematic Biology*, **2015**, 64, 356-62	8.4	64
131	Using RAxML to Infer Phylogenies. *Current Protocols in Bioinformatics*, **2015**, 51, 6.14.1-6.14.14	24.2	127
130	Automated Plausibility Analysis of Large Phylogenies **2015**, 457-482		
129	Impacts of Terraces on Phylogenetic Inference. *Systematic Biology*, **2015**, 64, 709-26	8.4	28

128	RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. *Bioinformatics*, **2014**, 30, 1312-3	7.2	17427
127	Phylogenomics resolves the timing and pattern of insect evolution. *Science*, **2014**, 346, 763-7	33.3	1489
126	Decisive data sets in phylogenomics: lessons from studies on the phylogenetic relationships of primarily wingless insects. *Molecular Biology and Evolution*, **2014**, 31, 239-49	8.3	100
125	Placing environmental next-generation sequencing amplicons from microbial eukaryotes into a phylogenetic context. *Molecular Biology and Evolution*, **2014**, 31, 993-1009	8.3	73
124	Novel information theory-based measures for quantifying incongruence among phylogenetic trees. *Molecular Biology and Evolution*, **2014**, 31, 1261-71	8.3	199
123	The evolutionary history of holometabolous insects inferred from transcriptome-based phylogeny and comprehensive morphological data. *BMC Evolutionary Biology*, **2014**, 14, 52	3	120
122	Selecting optimal partitioning schemes for phylogenomic datasets. *BMC Evolutionary Biology*, **2014**, 14, 82	3	426
121	Is the Protein Model Assignment problem under linked branch lengths NP-hard?. *Theoretical Computer Science*, **2014**, 524, 48-58	1.1	1
120	**2014**,		2
119	BrassiBase: introduction to a novel knowledge database on Brassicaceae evolution. *Plant and Cell Physiology*, **2014**, 55, e3	4.9	83
118	PUmPER: phylogenies updated perpetually. *Bioinformatics*, **2014**, 30, 1476-7	7.2	14
117	ExaBayes: massively parallel bayesian tree inference for the whole-genome era. *Molecular Biology and Evolution*, **2014**, 31, 2553-6	8.3	289
116	Whole-genome analyses resolve early branches in the tree of life of modern birds. *Science*, **2014**, 346, 1320-31	33.3	1182
115	PEAR: a fast and accurate Illumina Paired-End reAd mergeR. *Bioinformatics*, **2014**, 30, 614-20	7.2	2340
114	Optimization strategies for fast detection of positive selection on phylogenetic trees. *Bioinformatics*, **2014**, 30, 1129-1137	7.2	18
113	Accelerating String Matching on MIC Architecture for Motif Extraction. *Lecture Notes in Computer Science*, **2014**, 258-267	0.9	2
112	The Divisible Load Balance Problem and Its Application to Phylogenetic Inference. *Lecture Notes in Computer Science*, **2014**, 204-216	0.9	10
111	Rapid forward-in-time simulation at the chromosome and genome level. *BMC Bioinformatics*, **2013**, 14, 216	3.6	13

110	A general species delimitation method with applications to phylogenetic placements. *Bioinformatics*, **2013**, 29, 2869-76	7.2	1376
109	Metagenomic species profiling using universal phylogenetic marker genes. *Nature Methods*, **2013**, 10, 1196-9	21.6	340
108	libgapmis: extending short-read alignments. *BMC Bioinformatics*, **2013**, 14 Suppl 11, S4	3.6	5
107	A Generic Vectorization Scheme and a GPU Kernel for the Phylogenetic Likelihood Library **2013**,		8
106	A daily-updated tree of (sequenced) life as a reference for genome research. *Scientific Reports*, **2013**, 3, 2015	4.9	39
105	**2013**,		4
104	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	6.8	3
103	SweeD: likelihood-based detection of selective sweeps in thousands of genomes. *Molecular Biology and Evolution*, **2013**, 30, 2224-34	8.3	236
102	Novel Parallelization Schemes for Large-Scale Likelihood-based Phylogenetic Inference **2013**,		25
101	Inferring and Postprocessing Huge Phylogenies **2013**, 1049-1072		3
100	Pruning rogue taxa improves phylogenetic accuracy: an efficient algorithm and webservice. *Systematic Biology*, **2013**, 62, 162-6	8.4	249
99	MoTeX **2013**,		7
98	An Optimal Algorithm for Computing All Subtree Repeats in Trees. *Lecture Notes in Computer Science*, **2013**, 269-282	0.9	5
97	Heuristic Algorithms for the Protein Model Assignment Problem. *Lecture Notes in Computer Science*, **2013**, 137-148	0.9	
96	Pancrustacean phylogeny in the light of new phylogenomic data: support for Remipedia as the possible sister group of Hexapoda. *Molecular Biology and Evolution*, **2012**, 29, 1031-45	8.3	184
95	SlimCodeML: An Optimized Version of CodeML for the Branch-Site Model **2012**,		7
94	The Multi-Processor Scheduling Problem in Phylogenetics **2012**,		10
93	Fine-grain parallelism using multi-core, Cell/BE, and GPU Systems. *Parallel Computing*, **2012**, 38, 365-390	1	18

92	SATe-II: very fast and accurate simultaneous estimation of multiple sequence alignments and phylogenetic trees. *Systematic Biology*, **2012**, 61, 90-106	8.4	257
91	Coupling SIMD and SIMT architectures to boost performance of a phylogeny-aware alignment kernel. *BMC Bioinformatics*, **2012**, 13, 196	3.6	10
90	An Optimized Reconfigurable System for Computing the Phylogenetic Likelihood Function on DNA Data **2012**,		4
89	A format for phylogenetic placements. *PLoS ONE*, **2012**, 7, e31009	3.7	36
88	A critical assessment of storytelling: gene ontology categories and the importance of validating genomic scans. *Molecular Biology and Evolution*, **2012**, 29, 3237-48	8.3	164
87	Exploiting Multi-grain Parallelism for Efficient Selective Sweep Detection. *Lecture Notes in Computer Science*, **2012**, 56-68	0.9	6
86	FPGA Optimizations for a Pipelined Floating-Point Exponential Unit. *Lecture Notes in Computer Science*, **2011**, 316-327	0.9	0
85	Morphology-based phylogenetic binning of the lichen genera Graphis and Allographa (Ascomycota: Graphidaceae) using molecular site weight calibration. *Taxon*, **2011**, 60, 1450-1457	0.8	19
84	A Vector-Like Reconfigurable Floating-Point Unit for the Logarithm. *International Journal of Reconfigurable Computing*, **2011**, 2011, 1-12	2.1	1
83	The iPlant Collaborative: Cyberinfrastructure for Plant Biology. *Frontiers in Plant Science*, **2011**, 2, 34	6.2	306
82	Evolutionary relationships among Chlamydophila abortus variant strains inferred by rRNA secondary structure-based phylogeny. *PLoS ONE*, **2011**, 6, e19813	3.7	4
81	PICS-Ord: unlimited coding of ambiguous regions by pairwise identity and cost scores ordination. *BMC Bioinformatics*, **2011**, 12, 10	3.6	14
80	Algorithms, data structures, and numerics for likelihood-based phylogenetic inference of huge trees. *BMC Bioinformatics*, **2011**, 12, 470	3.6	40
79	A Simple and Accurate Method for Rogue Taxon Identification **2011**,		19
78	Uncovering hidden phylogenetic consensus in large data sets. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2011**, 8, 902-11	3	29
77	Computing the Phylogenetic Likelihood Function Out-of-Core **2011**,		2
76	Understanding angiosperm diversification using small and large phylogenetic trees. *American Journal of Botany*, **2011**, 98, 404-14	2.7	143
75	FPGA Acceleration of the Phylogenetic Parsimony Kernel? **2011**,		10

74	Accelerating Phylogeny-Aware Short DNA Read Alignment with FPGAs **2011**,		6
73	Quantifying the phylodynamic forces driving papillomavirus evolution. *Molecular Biology and Evolution*, **2011**, 28, 2101-13	8.3	99
72	Result verification, code verification and computation of support values in phylogenetics. *Briefings in Bioinformatics*, **2011**, 12, 270-9	13.4	4
71	Aligning short reads to reference alignments and trees. *Bioinformatics*, **2011**, 27, 2068-75	7.2	134
70	Performance, accuracy, and Web server for evolutionary placement of short sequence reads under maximum likelihood. *Systematic Biology*, **2011**, 60, 291-302	8.4	335
69	A functional phylogenomic view of the seed plants. *PLoS Genetics*, **2011**, 7, e1002411	6	117
68	Parallel Structural Graph Clustering. *Lecture Notes in Computer Science*, **2011**, 256-272	0.9	3
67	Maximum Likelihood Analyses of 3,490 rbcL Sequences: Scalability of Comprehensive Inference versus Group-Specific Taxon Sampling. *Evolutionary Bioinformatics*, **2010**, 6, 73-90	1.9	5
66	Time and memory efficient likelihood-based tree searches on phylogenomic alignments with missing data. *Bioinformatics*, **2010**, 26, i132-9	7.2	77
65	Efficient floating-point logarithm unit for FPGAs **2010**,		10
64	A generic and versatile architecture for inference of evolutionary trees under maximum likelihood **2010**,		3
63	How many bootstrap replicates are necessary?. *Journal of Computational Biology*, **2010**, 17, 337-54	1.7	601
62	Accuracy of morphology-based phylogenetic fossil placement under Maximum Likelihood **2010**,		9
61	Evolutionary placement of short sequence reads on multi-core architectures **2010**,		2
60	Hybrid MPI/Pthreads parallelization of the RAxML phylogenetics code **2010**,		30
59	Assessment of barrier implementations for fine-grain parallel regions on current multi-core architectures **2010**,		2
58	Phylogenetic Search Algorithms for Maximum Likelihood **2010**, 547-577		3
57	Orchestrating the Phylogenetic Likelihood Function on Emerging Parallel Architectures. *Embedded Multi-core Systems*, **2010**, 85-115		5

56	Efficient PC-FPGA Communication over Gigabit Ethernet **2010**,		22
55	MLTreeMap--accurate Maximum Likelihood placement of environmental DNA sequences into taxonomic and functional reference phylogenies. *BMC Genomics*, **2010**, 11, 461	4.5	93
54	Parallel computation of phylogenetic consensus trees. *Procedia Computer Science*, **2010**, 1, 1065-1073	1.6	5
53	Parallelized phylogenetic post-analysis on multi-core architectures. *Journal of Computational Science*, **2010**, 1, 107-114	3.4	10
52	Preparing RAxML for the SPEC MPI Benchmark Suite **2010**, 757-768		2
51	Accuracy and Performance of Single versus Double Precision Arithmetics for Maximum Likelihood Phylogeny Reconstruction. *Lecture Notes in Computer Science*, **2010**, 270-279	0.9	3
50	Large-Scale Co-Phylogenetic Analysis on the Grid. *International Journal of Grid and High Performance Computing*, **2009**, 1, 39-54	0.7	2
49	Load Balance in the Phylogenetic Likelihood Kernel **2009**,		9
48	Fine-grain Parallelism Using Multi-core, Cell/BE, and GPU Systems: Accelerating the Phylogenetic Likelihood Function **2009**,		28
47	Assessing the root of bilaterian animals with scalable phylogenomic methods. *Proceedings of the Royal Society B: Biological Sciences*, **2009**, 276, 4261-70	4.4	564
46	How Many Bootstrap Replicates Are Necessary?. *Lecture Notes in Computer Science*, **2009**, 184-200	0.9	216
45	A reconfigurable architecture for the Phylogenetic Likelihood Function **2009**,		10
44	ParBaum: Large-Scale Maximum Likelihood-Based Phylogenetic Analyses **2009**, 111-125		
43	Large-Scale Co-Phylogenetic Analysis on the Grid **2009**, 731-745		
42	A rapid bootstrap algorithm for the RAxML Web servers. *Systematic Biology*, **2008**, 57, 758-71	8.4	5512
41	Efficient computation of the phylogenetic likelihood function on multi-gene alignments and multi-core architectures. *Philosophical Transactions of the Royal Society B: Biological Sciences*, **2008**, 363, 3977-84	5.8	76
40	Large-Scale Phylogenetic Analysis on Current HPC Architectures. *Scientific Programming*, **2008**, 16, 255-270	1.4	13
39	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	0.9	21

38	Runtime scheduling of dynamic parallelism on accelerator-based multi-core systems. *Parallel Computing*, **2007**, 33, 700-719	1	20
37	AxPcoords & parallel AxParafit: statistical co-phylogenetic analyses on thousands of taxa. *BMC Bioinformatics*, **2007**, 8, 405	3.6	37
36	Large-scale maximum likelihood-based phylogenetic analysis on the IBM BlueGene/L **2007**,		64
35	Dynamic multigrain parallelization on the cell broadband engine **2007**,		22
34	Multiple evolutionary mechanisms drive papillomavirus diversification. *Molecular Biology and Evolution*, **2007**, 24, 1242-58	8.3	91
33	RAxML-Cell: Parallel Phylogenetic Tree Inference on the Cell Broadband Engine **2007**,		21
32	A nuclear ribosomal DNA phylogeny of acer inferred with maximum likelihood, splits graphs, and motif analysis of 606 sequences. *Evolutionary Bioinformatics*, **2007**, 2, 7-22	1.9	20
31	Computational Grand Challenges in Assembling the Tree of Life: Problems and Solutions. *Advances in Computers*, **2006**, 127-176	2.9	10
30	RAxML-VI-HPC: maximum likelihood-based phylogenetic analyses with thousands of taxa and mixed models. *Bioinformatics*, **2006**, 22, 2688-90	7.2	12661
29	A Nuclear Ribosomal DNA Phylogeny of Acer Inferred with Maximum Likelihood, Splits Graphs, and Motif Analysis of 606 Sequences. *Evolutionary Bioinformatics*, **2006**, 2, 117693430600200	1.9	42
28	RAxML-OMP: An Efficient Program for Phylogenetic Inference on SMPs. *Lecture Notes in Computer Science*, **2005**, 288-302	0.9	62
27	Initial Experiences Porting a Bioinformatics Application to a Graphics Processor. *Lecture Notes in Computer Science*, **2005**, 415-425	0.9	27
26	RAxML-II: a program for sequential, parallel and distributed inference of large phylogenetic trees. *Concurrency Computation Practice and Experience*, **2005**, 17, 1705-1723	1.4	36
25	Using Treemaps to Visualize Phylogenetic Trees. *Lecture Notes in Computer Science*, **2005**, 283-293	0.9	5
24	ARB: a software environment for sequence data. *Nucleic Acids Research*, **2004**, 32, 1363-71	20.1	5075
23	Use of a Monte Carlo-based probability matrix for 3-D iterative reconstruction of MADPET-II data. *IEEE Transactions on Nuclear Science*, **2004**, 51, 2597-2605	1.7	95
22	Parallel Inference of a 10.000-Taxon Phylogeny with Maximum Likelihood. *Lecture Notes in Computer Science*, **2004**, 997-1004	0.9	13
21	Tool Environments in CORBA-Based Medical High Performance Computing. *Lecture Notes in Computer Science*, **2001**, 447-455	0.9	

20	Large-Scale Co-Phylogenetic Analysis on the Grid222-237	
19	12 Grand Challenges in Single-Cell Data Science	2
18	The divisible load balance problem with shared cost and its application to phylogenetic inference	1
17	Quartet-based computations of internode certainty provide accurate and robust measures of phylogenetic incongruence	8
16	RootDigger: a root placement program for phylogenetic trees	1
15	CellPhy: accurate and fast probabilistic inference of single-cell phylogenies from scDNA-seq data	4
14	Phylogenetic analysis of SARS-CoV-2 data is difficult	12
13	EPA-ng: Massively Parallel Evolutionary Placement of Genetic Sequences	6
12	Scalable methods for analyzing and visualizing phylogenetic placement of metagenomic samples	2
11	ParGenes: a tool for massively parallel model selection and phylogenetic tree inference on thousands of genes	3
10	RAxML-NG: A fast, scalable, and user-friendly tool for maximum likelihood phylogenetic inference	44
9	ModelTest-NG: a new and scalable tool for the selection of DNA and protein evolutionary models	15
8	Long metabarcoding of the eukaryotic rDNA operon to phylogenetically and taxonomically resolve environmental diversity	3
7	Genesis and Gappa: Processing, Analyzing and Visualizing Phylogenetic (Placement) Data	5
6	GeneRax: A tool for species tree-aware maximum likelihood based gene family tree inference under gene duplication, transfer, and loss	3
5	Treerecs: an integrated phylogenetic tool, from sequences to reconciliations	1
4	Computing the Internode Certainty and related measures from partial gene trees	2
3	Soil Protists in Three Neotropical Rainforests are Hyperdiverse and Dominated by Parasites	1