

Alexandros Stamatakis

List of Publications by Year in descending order

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Version: 2024-02-01

165
papers

79,423
citations

29994

54
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12910

131
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212
all docs

212
docs citations

212
times ranked

71908
citing authors

#	ARTICLE	IF	CITATIONS
1	SPART: A versatile and standardized data exchange format for species partition information. <i>Molecular Ecology Resources</i> , 2022, 22, 430-438.	2.2	3
2	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, 39, .	3.5	29
3	CellPhy: accurate and fast probabilistic inference of single-cell phylogenies from scDNA-seq data. <i>Genome Biology</i> , 2022, 23, 37.	3.8	28
4	RAxML Grove: an empirical phylogenetic tree database. <i>Bioinformatics</i> , 2022, 38, 1741-1742.	1.8	11
5	A LASSO-based approach to sample sites for phylogenetic tree search. <i>Bioinformatics</i> , 2022, 38, i118-i124.	1.8	1
6	Metagenomic Analysis Using Phylogenetic Placementâ€”A Review of the First Decade. <i>Frontiers in Bioinformatics</i> , 2022, 2, .	1.0	17
7	NetRAX: accurate and fast maximum likelihood phylogenetic network inference. <i>Bioinformatics</i> , 2022, 38, 3725-3733.	1.8	13
8	<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
9	Phylogenetic Analysis of SARS-CoV-2 Data Is Difficult. <i>Molecular Biology and Evolution</i> , 2021, 38, 1777-1791.	3.5	119
10	Want to track pandemic variants faster? Fix the bioinformatics bottleneck. <i>Nature</i> , 2021, 591, 30-33.	13.7	92
11	Exploring parallel MPI fault tolerance mechanisms for phylogenetic inference with RAxML-NG. <i>Bioinformatics</i> , 2021, 37, 4056-4063.	1.8	4
12	Root Digger: a root placement program for phylogenetic trees. <i>BMC Bioinformatics</i> , 2021, 22, 225.	1.2	20
13	The SoftWipe tool and benchmark for assessing coding standards adherence of scientific software. <i>Scientific Reports</i> , 2021, 11, 10015.	1.6	6
14	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
15	Efficient Memory Management in Likelihood-based Phylogenetic Placement. , 2021, , .		0
16	Swarm v3: towards tera-scale amplicon clustering. <i>Bioinformatics</i> , 2021, 38, 267-269.	1.8	40
17	Photoreceptor Diversification Accompanies the Evolution of Anthozoa. <i>Molecular Biology and Evolution</i> , 2021, 38, 1744-1760.	3.5	20
18	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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19	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
20	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
21	A fast and memory-efficient implementation of the transfer bootstrap. <i>Bioinformatics</i> , 2020, 36, 2280-2281.	1.8	15
22	Treerecs: an integrated phylogenetic tool, from sequences to reconciliations. <i>Bioinformatics</i> , 2020, 36, 4822-4824.	1.8	20
23	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
24	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
25	Eleven grand challenges in single-cell data science. <i>Genome Biology</i> , 2020, 21, 31.	3.8	742
26	Genesis and Gappa: processing, analyzing and visualizing phylogenetic (placement) data. <i>Bioinformatics</i> , 2020, 36, 3263-3265.	1.8	171
27	EPA-ng: Massively Parallel Evolutionary Placement of Genetic Sequences. <i>Systematic Biology</i> , 2019, 68, 365-369.	2.7	400
28	Scalable methods for analyzing and visualizing phylogenetic placement of metagenomic samples. <i>PLoS ONE</i> , 2019, 14, e0217050.	1.1	65
29	Modeling Structural Constraints on Protein Evolution via Side-Chain Conformational States. <i>Molecular Biology and Evolution</i> , 2019, 36, 2086-2103.	3.5	10
30	Data Distribution for Phylogenetic Inference with Site Repeats via Judicious Hypergraph Partitioning. , 2019, , .		0
31	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
32	A Review of Approaches for Optimizing Phylogenetic Likelihood Calculations. <i>Computational Biology</i> , 2019, , 1-19.	0.1	4
33	Methods for automatic reference trees and multilevel phylogenetic placement. <i>Bioinformatics</i> , 2019, 35, 1151-1158.	1.8	33
34	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
35	Automated, phylogeny-based genotype delimitation of the Hepatitis Viruses HBV and HCV. <i>PeerJ</i> , 2019, 7, e7754.	0.9	3
36	A roadmap for global synthesis of the plant tree of life. <i>American Journal of Botany</i> , 2018, 105, 614-622.	0.8	38

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37	The State of Software for Evolutionary Biology. <i>Molecular Biology and Evolution</i> , 2018, 35, 1037-1046.	3.5	36
38	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.	1.2	29
39	Population and Evolutionary Genetic Inferences in the Whole-Genome Era: Software Challenges. <i>Population Genomics</i> , 2018, , 161-175.	0.2	0
40	MPBoot: fast phylogenetic maximum parsimony tree inference and bootstrap approximation. <i>BMC Evolutionary Biology</i> , 2018, 18, 11.	3.2	129
41	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
42	<i>UniEuk</i>: Time to Speak a Common Language in Protistology!. <i>Journal of Eukaryotic Microbiology</i> , 2017, 64, 407-411.	0.8	74
43	Parasites dominate hyperdiverse soil protist communities in Neotropical rainforests. <i>Nature Ecology and Evolution</i> , 2017, 1, 91.	3.4	262
44	An Efficient Approach to Merging Paired-End Reads and Incorporation of Uncertainties. , 2017, , 299-325.		0
45	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.	3.5	28
46	A Novel Heuristic for Data Distribution in Massively Parallel Phylogenetic Inference Using Site Repeats. , 2017, , .		3
47	A new phylogenetic tree sampling method for maximum parsimony bootstrapping and proof-of-concept implementation. , 2016, , .		2
48	The Divisible Load Balance Problem with Shared Cost and Its Application to Phylogenetic Inference. , 2016, , .		5
49	Phylogeny-aware identification and correction of taxonomically mislabeled sequences. <i>Nucleic Acids Research</i> , 2016, 44, 5022-5033.	6.5	97
50	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
51	Does the choice of nucleotide substitution models matter topologically?. <i>BMC Bioinformatics</i> , 2016, 17, 143.	1.2	32
52	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
53	Computing the Internode Certainty and Related Measures from Partial Gene Trees. <i>Molecular Biology and Evolution</i> , 2016, 33, 1606-1617.	3.5	73
54	Prediction of missing sequences and branch lengths in phylogenomic data. <i>Bioinformatics</i> , 2016, 32, 1331-1337.	1.8	23

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55	Using RAxML to Infer Phylogenies. <i>Current Protocols in Bioinformatics</i> , 2015, 51, 6.14.1-6.14.14.	25.8	215
56	Impacts of Terraces on Phylogenetic Inference. <i>Systematic Biology</i> , 2015, 64, 709-726.	2.7	46
57	ExaML version 3: a tool for phylogenomic analyses on supercomputers. <i>Bioinformatics</i> , 2015, 31, 2577-2579.	1.8	209
58	Phylogenomic analyses data of the avian phylogenomics project. <i>GigaScience</i> , 2015, 4, 4.	3.3	72
59	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
60	The Phylogenetic Likelihood Library. <i>Systematic Biology</i> , 2015, 64, 356-362.	2.7	118
61	BrassiBase: Introduction to a Novel Knowledge Database on Brassicaceae Evolution. <i>Plant and Cell Physiology</i> , 2014, 55, e3-e3.	1.5	117
62	PUMPER: phylogenies updated perpetually. <i>Bioinformatics</i> , 2014, 30, 1476-1477.	1.8	19
63	ExaBayes: Massively Parallel Bayesian Tree Inference for the Whole-Genome Era. <i>Molecular Biology and Evolution</i> , 2014, 31, 2553-2556.	3.5	423
64	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
65	PEAR: a fast and accurate Illumina Paired-End reAd mergeR. <i>Bioinformatics</i> , 2014, 30, 614-620.	1.8	3,776
66	Optimization strategies for fast detection of positive selection on phylogenetic trees. <i>Bioinformatics</i> , 2014, 30, 1129-1137.	1.8	24
67	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
68	Phylogenomics resolves the timing and pattern of insect evolution. <i>Science</i> , 2014, 346, 763-767.	6.0	2,096
69	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
70	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
71	Novel Information Theory-Based Measures for Quantifying Incongruence among Phylogenetic Trees. <i>Molecular Biology and Evolution</i> , 2014, 31, 1261-1271.	3.5	259
72	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

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73	Selecting optimal partitioning schemes for phylogenomic datasets. BMC Evolutionary Biology, 2014, 14, 82.	3.2	575
74	Is the Protein Model Assignment problem under linked branch lengths NP-hard?. Theoretical Computer Science, 2014, 524, 48-58.	0.5	1
75	Efficient Computation of the Phylogenetic Likelihood Function on the Intel MIC Architecture. , 2014, , .		4
76	Accelerating String Matching on MIC Architecture for Motif Extraction. Lecture Notes in Computer Science, 2014, , 258-267.	1.0	4
77	The Divisible Load Balance Problem and Its Application to Phylogenetic Inference. Lecture Notes in Computer Science, 2014, , 204-216.	1.0	15
78	Rapid forward-in-time simulation at the chromosome and genome level. BMC Bioinformatics, 2013, 14, 216.	1.2	13
79	A general species delimitation method with applications to phylogenetic placements. Bioinformatics, 2013, 29, 2869-2876.	1.8	2,059
80	Metagenomic species profiling using universal phylogenetic marker genes. Nature Methods, 2013, 10, 1196-1199.	9.0	442
81	libgampis: extending short-read alignments. BMC Bioinformatics, 2013, 14, S4.	1.2	8
82	A Generic Vectorization Scheme and a GPU Kernel for the Phylogenetic Likelihood Library. , 2013, , .		10
83	A daily-updated tree of (sequenced) life as a reference for genome research. Scientific Reports, 2013, 3, 2015.	1.6	47
84	Boosting the Performance of Bayesian Divergence Time Estimation with the Phylogenetic Likelihood Library. , 2013, , .		6
85	CHROMATO GATE: A TOOL FOR DETECTING BASE MIS-CALLS IN MULTIPLE SEQUENCE ALIGNMENTS BY SEMI-AUTOMATIC CHROMATOGRAM INSPECTION. Computational and Structural Biotechnology Journal, 2013, 6, e201303001.	1.9	9
86	SweeD: Likelihood-Based Detection of Selective Sweeps in Thousands of Genomes. Molecular Biology and Evolution, 2013, 30, 2224-2234.	3.5	395
87	Novel Parallelization Schemes for Large-Scale Likelihood-based Phylogenetic Inference. , 2013, , .		29
88	Pruning Rogue Taxa Improves Phylogenetic Accuracy: An Efficient Algorithm and Webservice. Systematic Biology, 2013, 62, 162-166.	2.7	327
89	MoTeX. , 2013, , .		9
90	An Optimal Algorithm for Computing All Subtree Repeats in Trees. Lecture Notes in Computer Science, 2013, , 269-282.	1.0	6

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91	Heuristic Algorithms for the Protein Model Assignment Problem. Lecture Notes in Computer Science, 2013, , 137-148.	1.0	1
92	Inference of Huge Trees under Maximum Likelihood. , 2012, , .		0
93	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, 1031-1045.	3.5	223
94	SlimCodeML: An Optimized Version of CodeML for the Branch-Site Model. , 2012, , .		12
95	The Multi-Processor Scheduling Problem in Phylogenetics. , 2012, , .		11
96	Fine-grain parallelism using multi-core, Cell/BE, and GPU Systems. Parallel Computing, 2012, 38, 365-390.	1.3	20
97	SAT@-II: Very Fast and Accurate Simultaneous Estimation of Multiple Sequence Alignments and Phylogenetic Trees. Systematic Biology, 2012, 61, 90.	2.7	310
98	Coupling SIMD and SIMT architectures to boost performance of a phylogeny-aware alignment kernel. BMC Bioinformatics, 2012, 13, 196.	1.2	12
99	An Optimized Reconfigurable System for Computing the Phylogenetic Likelihood Function on DNA Data. , 2012, , .		4
100	A Format for Phylogenetic Placements. PLoS ONE, 2012, 7, e31009.	1.1	60
101	A Critical Assessment of Storytelling: Gene Ontology Categories and the Importance of Validating Genomic Scans. Molecular Biology and Evolution, 2012, 29, 3237-3248.	3.5	220
102	Exploiting Multi-grain Parallelism for Efficient Selective Sweep Detection. Lecture Notes in Computer Science, 2012, , 56-68.	1.0	6
103	A Simple and Accurate Method for Rogue Taxon Identification. , 2011, , .		29
104	Uncovering Hidden Phylogenetic Consensus in Large Data Sets. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 902-911.	1.9	32
105	Computing the Phylogenetic Likelihood Function Out-of-Core. , 2011, , .		3
106	FPGA Optimizations for a Pipelined Floating-Point Exponential Unit. Lecture Notes in Computer Science, 2011, , 316-327.	1.0	2
107	Morphology-based phylogenetic binning of the lichen genera <i>Graphis</i> and <i>Allographa</i> (Ascomycota: Graphidaceae) using molecular site weight calibration. Taxon, 2011, 60, 1450-1457.	0.4	22
108	A Vector-Like Reconfigurable Floating-Point Unit for the Logarithm. International Journal of Reconfigurable Computing, 2011, 2011, 1-12.	0.2	2

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109	The iPlant Collaborative: Cyberinfrastructure for Plant Biology. <i>Frontiers in Plant Science</i> , 2011, 2, 34.	1.7	396
110	Evolutionary Relationships among <i>Chlamydomonas</i> abortus Variant Strains Inferred by rRNA Secondary Structure-Based Phylogeny. <i>PLoS ONE</i> , 2011, 6, e19813.	1.1	4
111	PICS-Ord: unlimited coding of ambiguous regions by pairwise identity and cost scores ordination. <i>BMC Bioinformatics</i> , 2011, 12, 10.	1.2	24
112	Algorithms, data structures, and numerics for likelihood-based phylogenetic inference of huge trees. <i>BMC Bioinformatics</i> , 2011, 12, 470.	1.2	50
113	Understanding angiosperm diversification using small and large phylogenetic trees. <i>American Journal of Botany</i> , 2011, 98, 404-414.	0.8	161
114	FPGA Acceleration of the Phylogenetic Parsimony Kernel?. , 2011, , .		14
115	Accelerating Phylogeny-Aware Short DNA Read Alignment with FPGAs. , 2011, , .		7
116	Quantifying the Phylodynamic Forces Driving Papillomavirus Evolution. <i>Molecular Biology and Evolution</i> , 2011, 28, 2101-2113.	3.5	114
117	Result verification, code verification and computation of support values in phylogenetics. <i>Briefings in Bioinformatics</i> , 2011, 12, 270-279.	3.2	5
118	Aligning short reads to reference alignments and trees. <i>Bioinformatics</i> , 2011, 27, 2068-2075.	1.8	184
119	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
120	A Functional Phylogenomic View of the Seed Plants. <i>PLoS Genetics</i> , 2011, 7, e1002411.	1.5	134
121	Parallel Structural Graph Clustering. <i>Lecture Notes in Computer Science</i> , 2011, , 256-272.	1.0	4
122	Orchestrating the Phylogenetic Likelihood Function on Emerging Parallel Architectures. <i>Embedded Multi-core Systems</i> , 2010, , 85-115.	0.1	5
123	Efficient PC-FPGA Communication over Gigabit Ethernet. , 2010, , .		34
124	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
125	Parallel computation of phylogenetic consensus trees. <i>Procedia Computer Science</i> , 2010, 1, 1065-1073.	1.2	7
126	Parallelized phylogenetic post-analysis on multi-core architectures. <i>Journal of Computational Science</i> , 2010, 1, 107-114.	1.5	11

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127	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
128	Time and memory efficient likelihood-based tree searches on phylogenomic alignments with missing data. <i>Bioinformatics</i> , 2010, 26, i132-i139.	1.8	96
129	Efficient floating-point logarithm unit for FPGAs. , 2010, , .		16
130	A generic and versatile architecture for inference of evolutionary trees under maximum likelihood. , 2010, , .		5
131	How Many Bootstrap Replicates Are Necessary?. <i>Journal of Computational Biology</i> , 2010, 17, 337-354.	0.8	800
132	Accuracy of morphology-based phylogenetic fossil placement under Maximum Likelihood. , 2010, , .		14
133	Evolutionary placement of short sequence reads on multi-core architectures. , 2010, , .		4
134	Hybrid MPI/Pthreads parallelization of the RAxML phylogenetics code. , 2010, , .		39
135	Assessment of barrier implementations for fine-grain parallel regions on current multi-core architectures. , 2010, , .		2
136	Preparing RAxML for the SPEC MPI Benchmark Suite. , 2010, , 757-768.		2
137	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
138	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
139	Load Balance in the Phylogenetic Likelihood Kernel. , 2009, , .		9
140	Fine-grain Parallelism Using Multi-core, Cell/BE, and GPU Systems: Accelerating the Phylogenetic Likelihood Function. , 2009, , .		37
141	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
142	How Many Bootstrap Replicates Are Necessary?. <i>Lecture Notes in Computer Science</i> , 2009, , 184-200.	1.0	263
143	A reconfigurable architecture for the Phylogenetic Likelihood Function. , 2009, , .		13
144	Large-Scale Co-Phylogenetic Analysis on the Grid. , 2009, , 731-745.		0

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145	ParBaum: Large-Scale Maximum Likelihood-Based Phylogenetic Analyses. , 2009, , 111-125.		0
146	A Rapid Bootstrap Algorithm for the RAxML Web Servers. Systematic Biology, 2008, 57, 758-771.	2.7	6,439
147	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, 3977-3984.	1.8	81
148	Large-Scale Phylogenetic Analysis on Current HPC Architectures. Scientific Programming, 2008, 16, 255-270.	0.5	14
149	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
150	Large-scale maximum likelihood-based phylogenetic analysis on the IBM BlueGene/L. , 2007, , .		84
151	Dynamic multigrain parallelization on the cell broadband engine. , 2007, , .		46
152	Multiple Evolutionary Mechanisms Drive Papillomavirus Diversification. Molecular Biology and Evolution, 2007, 24, 1242-1258.	3.5	101
153	RAxML-Cell: Parallel Phylogenetic Tree Inference on the Cell Broadband Engine. , 2007, , .		30
154	Runtime scheduling of dynamic parallelism on accelerator-based multi-core systems. Parallel Computing, 2007, 33, 700-719.	1.3	23
155	AxPcoords & parallel AxParafit: statistical co-phylogenetic analyses on thousands of taxa. BMC Bioinformatics, 2007, 8, 405.	1.2	39
156	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.	0.6	22
157	RAxML-VI-HPC: maximum likelihood-based phylogenetic analyses with thousands of taxa and mixed models. Bioinformatics, 2006, 22, 2688-2690.	1.8	14,675
158	A Nuclear Ribosomal DNA Phylogeny of <i>Acer</i> Inferred with Maximum Likelihood, Splits Graphs, and Motif Analysis of 606 Sequences. Evolutionary Bioinformatics, 2006, 2, 117693430600200.	0.6	51
159	Computational Grand Challenges in Assembling the Tree of Life: Problems and Solutions. Advances in Computers, 2006, , 127-176.	1.2	18
160	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	50
161	RAxML-OMP: An Efficient Program for Phylogenetic Inference on SMPs. Lecture Notes in Computer Science, 2005, , 288-302.	1.0	80
162	Using Treemaps to Visualize Phylogenetic Trees. Lecture Notes in Computer Science, 2005, , 283-293.	1.0	5

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163	ARB: a software environment for sequence data. Nucleic Acids Research, 2004, 32, 1363-1371.	6.5	5,816
164	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.	1.2	110
165	Large-Scale Co-Phylogenetic Analysis on the Grid. , 0, , 222-237.		0