## Alexandros Stamatakis

List of Publications by Year in descending order

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ALEXANDROS STAMATAKIS

#	Article	IF	CITATIONS
1	SPART: A versatile and standardized data exchange format for species partition information. Molecular Ecology Resources, 2022, 22, 430-438.	4.8	3
2	SpeciesRax: A Tool for Maximum Likelihood Species Tree Inference from Gene Family Trees under Duplication, Transfer, and Loss. Molecular Biology and Evolution, 2022, 39, .	8.9	29
3	CellPhy: accurate and fast probabilistic inference of single-cell phylogenies from scDNA-seq data. Genome Biology, 2022, 23, 37.	8.8	28
4	RAxML Grove: an empirical phylogenetic tree database. Bioinformatics, 2022, 38, 1741-1742.	4.1	11
5	A LASSO-based approach to sample sites for phylogenetic tree search. Bioinformatics, 2022, 38, i118-i124.	4.1	1
6	Metagenomic Analysis Using Phylogenetic Placement—A Review of the First Decade. Frontiers in Bioinformatics, 2022, 2, .	2.1	17
7	NetRAX: accurate and fast maximum likelihood phylogenetic network inference. Bioinformatics, 2022, 38, 3725-3733.	4.1	13
8	<scp>SCRAPP</scp> : A tool to assess the diversity of microbial samples from phylogenetic placements. Molecular Ecology Resources, 2021, 21, 340-349.	4.8	5
9	Phylogenetic Analysis of SARS-CoV-2 Data Is Difficult. Molecular Biology and Evolution, 2021, 38, 1777-1791.	8.9	119
10	Want to track pandemic variants faster? Fix the bioinformatics bottleneck. Nature, 2021, 591, 30-33.	27.8	92
11	Exploring parallel MPI fault tolerance mechanisms for phylogenetic inference with RAxML-NG. Bioinformatics, 2021, 37, 4056-4063.	4.1	4
12	Root Digger: a root placement program for phylogenetic trees. BMC Bioinformatics, 2021, 22, 225.	2.6	20
13	The SoftWipe tool and benchmark for assessing coding standards adherence of scientific software. Scientific Reports, 2021, 11, 10015.	3.3	6
14	The wall lizards of the Balkan peninsula: Tackling questions at the interface of phylogenomics and population genomics. Molecular Phylogenetics and Evolution, 2021, 159, 107121.	2.7	6
15	Efficient Memory Management in Likelihood-based Phylogenetic Placement. , 2021, , .		0
16	Swarm v3: towards tera-scale amplicon clustering. Bioinformatics, 2021, 38, 267-269.	4.1	40
17	Photoreceptor Diversification Accompanies the Evolution of Anthozoa. Molecular Biology and Evolution, 2021, 38, 1744-1760.	8.9	20
18	Quartet-Based Computations of Internode Certainty Provide Robust Measures of Phylogenetic Incongruence. Systematic Biology, 2020, 69, 308-324.	5.6	38

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19	ModelTest-NG: A New and Scalable Tool for the Selection of DNA and Protein Evolutionary Models. Molecular Biology and Evolution, 2020, 37, 291-294.	8.9	1,021
20	Longâ€read metabarcoding of the eukaryotic rDNA operon to phylogenetically and taxonomically resolve environmental diversity. Molecular Ecology Resources, 2020, 20, 429-443.	4.8	68
21	A fast and memory-efficient implementation of the transfer bootstrap. Bioinformatics, 2020, 36, 2280-2281.	4.1	15
22	Treerecs: an integrated phylogenetic tool, from sequences to reconciliations. Bioinformatics, 2020, 36, 4822-4824.	4.1	20
23	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.	7.1	68
24	GeneRax: A Tool for Species-Tree-Aware Maximum Likelihood-Based Gene ÂFamily Tree Inference under Gene Duplication, Transfer, and Loss. Molecular Biology and Evolution, 2020, 37, 2763-2774.	8.9	87
25	Eleven grand challenges in single-cell data science. Genome Biology, 2020, 21, 31.	8.8	742
26	Genesis and Gappa: processing, analyzing and visualizing phylogenetic (placement) data. Bioinformatics, 2020, 36, 3263-3265.	4.1	171
27	EPA-ng: Massively Parallel Evolutionary Placement of Genetic Sequences. Systematic Biology, 2019, 68, 365-369.	5.6	400
28	Scalable methods for analyzing and visualizing phylogenetic placement of metagenomic samples. PLoS ONE, 2019, 14, e0217050.	2.5	65
29	Modeling Structural Constraints on Protein Evolution via Side-Chain Conformational States. Molecular Biology and Evolution, 2019, 36, 2086-2103.	8.9	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. Bioinformatics, 2019, 35, 4453-4455.	4.1	2,287
32	A Review of Approaches for Optimizing Phylogenetic Likelihood Calculations. Computational Biology, 2019, , 1-19.	0.2	4
33	Methods for automatic reference trees and multilevel phylogenetic placement. Bioinformatics, 2019, 35, 1151-1158.	4.1	33
34	ParGenes: a tool for massively parallel model selection and phylogenetic tree inference on thousands of genes. Bioinformatics, 2019, 35, 1771-1773.	4.1	51
35	Automated, phylogeny-based genotype delimitation of the Hepatitis Viruses HBV and HCV. PeerJ, 2019, 7, e7754.	2.0	3
36	A roadmap for global synthesis of the plant tree of life. American Journal of Botany, 2018, 105, 614-622.	1.7	38

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37	The State of Software for Evolutionary Biology. Molecular Biology and Evolution, 2018, 35, 1037-1046.	8.9	36
38	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.	2.7	29
39	Population and Evolutionary Genetic Inferences in the Whole-Genome Era: Software Challenges. Population Genomics, 2018, , 161-175.	0.5	0
40	MPBoot: fast phylogenetic maximum parsimony tree inference and bootstrap approximation. BMC Evolutionary Biology, 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. AIDS Research and Human Retroviruses, 2017, 33, 1083-1098.	1.1	18
42	<i>UniEuk</i> : Time to Speak a Common Language in Protistology!. Journal of Eukaryotic Microbiology, 2017, 64, 407-411.	1.7	74
43	Parasites dominate hyperdiverse soil protist communities in Neotropical rainforests. Nature Ecology and Evolution, 2017, 1, 91.	7.8	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. Molecular Biology and Evolution, 2017, 34, 1535-1542.	8.9	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. Nucleic Acids Research, 2016, 44, 5022-5033.	14.5	97
50	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, 20160025.	4.0	62
51	Does the choice of nucleotide substitution models matter topologically?. BMC Bioinformatics, 2016, 17, 143.	2.6	32
52	An Efficient Independence Sampler for Updating Branches in Bayesian Markov chain Monte Carlo Sampling of Phylogenetic Trees. Systematic Biology, 2016, 65, 161-176.	5.6	11
53	Computing the Internode Certainty and Related Measures from Partial Gene Trees. Molecular Biology and Evolution, 2016, 33, 1606-1617.	8.9	73
54	Prediction of missing sequences and branch lengths in phylogenomic data. Bioinformatics, 2016, 32, 1331-1337.	4.1	23

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55	Using RAxML to Infer Phylogenies. Current Protocols in Bioinformatics, 2015, 51, 6.14.1-6.14.14.	25.8	215
56	Impacts of Terraces on Phylogenetic Inference. Systematic Biology, 2015, 64, 709-726.	5.6	46
57	ExaML version 3: a tool for phylogenomic analyses on supercomputers. Bioinformatics, 2015, 31, 2577-2579.	4.1	209
58	Phylogenomic analyses data of the avian phylogenomics project. GigaScience, 2015, 4, 4.	6.4	72
59	Short Tree, Long Tree, Right Tree, Wrong Tree: New Acquisition Bias Corrections for Inferring SNP Phylogenies. Systematic Biology, 2015, 64, 1032-1047.	5.6	286
60	The Phylogenetic Likelihood Library. Systematic Biology, 2015, 64, 356-362.	5.6	118
61	BrassiBase: Introduction to a Novel Knowledge Database on Brassicaceae Evolution. Plant and Cell Physiology, 2014, 55, e3-e3.	3.1	117
62	PUmPER: phylogenies updated perpetually. Bioinformatics, 2014, 30, 1476-1477.	4.1	19
63	ExaBayes: Massively Parallel Bayesian Tree Inference for the Whole-Genome Era. Molecular Biology and Evolution, 2014, 31, 2553-2556.	8.9	423
64	Whole-genome analyses resolve early branches in the tree of life of modern birds. Science, 2014, 346, 1320-1331.	12.6	1,583
65	PEAR: a fast and accurate Illumina Paired-End reAd mergeR. Bioinformatics, 2014, 30, 614-620.	4.1	3,776
66	Optimization strategies for fast detection of positive selection on phylogenetic trees. Bioinformatics, 2014, 30, 1129-1137.	4.1	24
67	RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. Bioinformatics, 2014, 30, 1312-1313.	4.1	26,744
68	Phylogenomics resolves the timing and pattern of insect evolution. Science, 2014, 346, 763-767.	12.6	2,096
69	Decisive Data Sets in Phylogenomics: Lessons from Studies on the Phylogenetic Relationships of Primarily Wingless Insects. Molecular Biology and Evolution, 2014, 31, 239-249.	8.9	127
70	Placing Environmental Next-Generation Sequencing Amplicons from Microbial Eukaryotes into a Phylogenetic Context. Molecular Biology and Evolution, 2014, 31, 993-1009.	8.9	97
71	Novel Information Theory-Based Measures for Quantifying Incongruence among Phylogenetic Trees. Molecular Biology and Evolution, 2014, 31, 1261-1271.	8.9	259
72	The evolutionary history of holometabolous insects inferred from transcriptome-based phylogeny and comprehensive morphological data. BMC Evolutionary Biology, 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.	0.9	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.	1.3	4
77	The Divisible Load Balance Problem and Its Application to Phylogenetic Inference. Lecture Notes in Computer Science, 2014, , 204-216.	1.3	15
78	Rapid forward-in-time simulation at the chromosome and genome level. BMC Bioinformatics, 2013, 14, 216.	2.6	13
79	A general species delimitation method with applications to phylogenetic placements. Bioinformatics, 2013, 29, 2869-2876.	4.1	2,059
80	Metagenomic species profiling using universal phylogenetic marker genes. Nature Methods, 2013, 10, 1196-1199.	19.0	442
81	libgapmis: extending short-read alignments. BMC Bioinformatics, 2013, 14, S4.	2.6	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.	3.3	47
84	Boosting the Performance of Bayesian Divergence Time Estimation with the Phylogenetic Likelihood Library. , 2013, , .		6
85	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.	4.1	9
86	SweeD: Likelihood-Based Detection of Selective Sweeps in Thousands of Genomes. Molecular Biology and Evolution, 2013, 30, 2224-2234.	8.9	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.	5.6	327
89	MoTeX. , 2013, , .		9
90	An Optimal Algorithm for Computing All Subtree Repeats in Trees. Lecture Notes in Computer Science, 2013, , 269-282.	1.3	6

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91	Heuristic Algorithms for the Protein Model Assignment Problem. Lecture Notes in Computer Science, 2013, , 137-148.	1.3	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.	8.9	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 CPU Systems. Parallel Computing, 2012, 38, 365-390.	2.1	20
97	SATé-II: Very Fast and Accurate Simultaneous Estimation of Multiple Sequence Alignments and Phylogenetic Trees. Systematic Biology, 2012, 61, 90.	5.6	310
98	Coupling SIMD and SIMT architectures to boost performance of a phylogeny-aware alignment kernel. BMC Bioinformatics, 2012, 13, 196.	2.6	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.	2.5	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.	8.9	220
102	Exploiting Multi-grain Parallelism for Efficient Selective Sweep Detection. Lecture Notes in Computer Science, 2012, , 56-68.	1.3	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.	3.0	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.	1.3	2
107	Morphologyâ€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.	0.7	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. Frontiers in Plant Science, 2011, 2, 34.	3.6	396
110	Evolutionary Relationships among Chlamydophila abortus Variant Strains Inferred by rRNA Secondary Structure-Based Phylogeny. PLoS ONE, 2011, 6, e19813.	2.5	4
111	PICS-Ord: unlimited coding of ambiguous regions by pairwise identity and cost scores ordination. BMC Bioinformatics, 2011, 12, 10.	2.6	24
112	Algorithms, data structures, and numerics for likelihood-based phylogenetic inference of huge trees. BMC Bioinformatics, 2011, 12, 470.	2.6	50
113	Understanding angiosperm diversification using small and large phylogenetic trees. American Journal of Botany, 2011, 98, 404-414.	1.7	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. Molecular Biology and Evolution, 2011, 28, 2101-2113.	8.9	114
117	Result verification, code verification and computation of support values in phylogenetics. Briefings in Bioinformatics, 2011, 12, 270-279.	6.5	5
118	Aligning short reads to reference alignments and trees. Bioinformatics, 2011, 27, 2068-2075.	4.1	184
119	Performance, Accuracy, and Web Server for Evolutionary Placement of Short Sequence Reads under Maximum Likelihood. Systematic Biology, 2011, 60, 291-302.	5.6	476
120	A Functional Phylogenomic View of the Seed Plants. PLoS Genetics, 2011, 7, e1002411.	3.5	134
121	Parallel Structural Graph Clustering. Lecture Notes in Computer Science, 2011, , 256-272.	1.3	4
122	Orchestrating the Phylogenetic Likelihood Function on Emerging Parallel Architectures. Embedded Multi-core Systems, 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. BMC Genomics, 2010, 11, 461.	2.8	100
125	Parallel computation of phylogenetic consensus trees. Procedia Computer Science, 2010, 1, 1065-1073.	2.0	7
126	Parallelized phylogenetic post-analysis on multi-core architectures. Journal of Computational Science, 2010, 1, 107-114.	2.9	11

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127	Maximum Likelihood Analyses of 3,490 rbcL Sequences: Scalability of Comprehensive Inference versus Group-Specific Taxon Sampling. Evolutionary Bioinformatics, 2010, 6, EBO.S4528.	1.2	6
128	Time and memory efficient likelihood-based tree searches on phylogenomic alignments with missing data. Bioinformatics, 2010, 26, i132-i139.	4.1	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?. Journal of Computational Biology, 2010, 17, 337-354.	1.6	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. Lecture Notes in Computer Science, 2010, , 270-279.	1.3	6
138	Large-Scale Co-Phylogenetic Analysis on the Grid. International Journal of Grid and High Performance Computing, 2009, 1, 39-54.	0.9	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. Proceedings of the Royal Society B: Biological Sciences, 2009, 276, 4261-4270.	2.6	645
142	How Many Bootstrap Replicates Are Necessary?. Lecture Notes in Computer Science, 2009, , 184-200.	1.3	263
143	A reconfigurable architecture for the Phylogenetic Likelihood Function. , 2009, , .		13

Large-Scale Co-Phylogenetic Analysis on the Grid. , 2009, , 731-745.

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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.	5.6	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.	4.0	81
148	Large-Scale Phylogenetic Analysis on Current HPC Architectures. Scientific Programming, 2008, 16, 255-270.	0.7	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.	1.3	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.	8.9	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.	2.1	23
155	AxPcoords & parallel AxParafit: statistical co-phylogenetic analyses on thousands of taxa. BMC Bioinformatics, 2007, 8, 405.	2.6	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.	1.2	22
157	RAxML-VI-HPC: maximum likelihood-based phylogenetic analyses with thousands of taxa and mixed models. Bioinformatics, 2006, 22, 2688-2690.	4.1	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.	1.2	51
159	Computational Grand Challenges in Assembling the Tree of Life: Problems and Solutions. Advances in Computers, 2006, , 127-176.	1.6	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.	2.2	50
161	RAxML-OMP: An Efficient Program for Phylogenetic Inference on SMPs. Lecture Notes in Computer Science, 2005, , 288-302.	1.3	80
162	Using Treemaps to Visualize Phylogenetic Trees. Lecture Notes in Computer Science, 2005, , 283-293.	1.3	5

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163	ARB: a software environment for sequence data. Nucleic Acids Research, 2004, 32, 1363-1371.	14.5	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.	2.0	110
165	Large-Scale Co-Phylogenetic Analysis on the Grid. , 0, , 222-237.		0