

Michael J Sanderson

List of Publications by Year in descending order

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87
papers

15,154
citations

44069

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49909

87
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94
docs citations

94
times ranked

13994
citing authors

#	ARTICLE	IF	CITATIONS
1	Accuracy in Near-Perfect Virus Phylogenies. <i>Systematic Biology</i> , 2022, 71, 426-438.	5.6	8
2	Origin and Diversification of the Saguaro Cactus (<i>Carnegiea gigantea</i>): A Within-Species Phylogenomic Analysis. <i>Systematic Biology</i> , 2022, 71, 1178-1194.	5.6	3
3	Plastome Structural Evolution and Homoplastic Inversions in Neo-Astragalus (Fabaceae). <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	13
4	Evolution of 4,5-dioxygenase activity allows for recurrent specialisation to betalain pigmentation in Caryophyllales. <i>New Phytologist</i> , 2020, 227, 914-929.	7.3	48
5	The Implications of Lineage-Specific Rates for Divergence Time Estimation. <i>Systematic Biology</i> , 2020, 69, 660-670.	5.6	16
6	Genomes of 13 domesticated and wild rice relatives highlight genetic conservation, turnover and innovation across the genus <i>Oryza</i> . <i>Nature Genetics</i> , 2018, 50, 285-296.	21.4	413
7	The prevalence of terraced treescapes in analyses of phylogenetic data sets. <i>BMC Evolutionary Biology</i> , 2018, 18, 46.	3.2	13
8	Toward a Self-Updating Platform for Estimating Rates of Speciation and Migration, Ages, and Relationships of Taxa. <i>Systematic Biology</i> , 2017, 66, syw066.	5.6	42
9	A new subfamily classification of the Leguminosae based on a taxonomically comprehensive phylogeny: The Legume Phylogeny Working Group (LPWG). <i>Taxon</i> , 2017, 66, 44-77.	0.7	803
10	Extensive gene tree discordance and hemiplasy shaped the genomes of North American columnar cacti. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 12003-12008.	7.1	90
11	Back to the past: a new take on the timing of flowering plant diversification. <i>New Phytologist</i> , 2015, 207, 257-259.	7.3	7
12	Confluence, synnovation, and depauperons in plant diversification. <i>New Phytologist</i> , 2015, 207, 260-274.	7.3	202
13	Tradeoff between robustness and elaboration in carotenoid networks produces cycles of avian color diversification. <i>Biology Direct</i> , 2015, 10, 45.	4.6	18
14	STBase: One Million Species Trees for Comparative Biology. <i>PLoS ONE</i> , 2015, 10, e0117987.	2.5	8
15	Impacts of Terraces on Phylogenetic Inference. <i>Systematic Biology</i> , 2015, 64, 709-726.	5.6	46
16	Exceptional reduction of the plastid genome of saguaro cactus (<i>Carnegiea gigantea</i>): Loss of the <i>ndh</i> gene suite and inverted repeat. <i>American Journal of Botany</i> , 2015, 102, 1115-1127.	1.7	137
17	Evolutionary dynamics of leucine-rich repeat receptor-like kinases and related genes in plants: A phylogenomic approach. <i>Journal of Integrative Plant Biology</i> , 2014, 56, 648-662.	8.5	12
18	EvoMiner: frequent subtree mining in phylogenetic databases. <i>Knowledge and Information Systems</i> , 2014, 41, 559-590.	3.2	13

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19	Ceiba: scalable visualization of phylogenies and 2D/3D image collections. <i>Bioinformatics</i> , 2014, 30, 2506-2507.	4.1	2
20	Disentangling Methodological and Biological Sources of Gene Tree Discordance on <i>Oryza</i> (Poaceae) Chromosome 3. <i>Systematic Biology</i> , 2014, 63, 645-659.	5.6	43
21	Diversity and evolution of a trait mediating ant-plant interactions: insights from extrafloral nectaries in <i>Senna</i> (Leguminosae). <i>Annals of Botany</i> , 2013, 111, 1263-1275.	2.9	26
22	Identifying a species tree subject to random lateral gene transfer. <i>Journal of Theoretical Biology</i> , 2013, 322, 81-93.	1.7	16
23	Legume phylogeny and classification in the 21st century: Progress, prospects and lessons for other species-rich clades. <i>Taxon</i> , 2013, 62, 217-248.	0.7	305
24	LOCATING EVOLUTIONARY PRECURSORS ON A PHYLOGENETIC TREE. <i>Evolution; International Journal of Organic Evolution</i> , 2012, 66, 3918-3930.	2.3	77
25	Angiosperm phylogeny: 17 genes, 640 taxa. <i>American Journal of Botany</i> , 2011, 98, 704-730.	1.7	590
26	The iPlant Collaborative: Cyberinfrastructure for Plant Biology. <i>Frontiers in Plant Science</i> , 2011, 2, 34.	3.6	396
27	Terraces in Phylogenetic Tree Space. <i>Science</i> , 2011, 333, 448-450.	12.6	115
28	Phylogenomic Analysis of BAC-end Sequence Libraries in <i>Oryza</i> (Poaceae). <i>Systematic Botany</i> , 2010, 35, 512-523.	0.5	8
29	Phylogenomics with incomplete taxon coverage: the limits to inference. <i>BMC Evolutionary Biology</i> , 2010, 10, 155.	3.2	116
30	Characterizing phylogenetically decisive taxon coverage. <i>Applied Mathematics Letters</i> , 2010, 23, 82-86.	2.7	33
31	Relaxed Molecular Clocks, the Bias-Variance Trade-off, and the Quality of Phylogenetic Inference. <i>Systematic Biology</i> , 2010, 59, 1-8.	5.6	71
32	Groves of Phylogenetic Trees. <i>Annals of Combinatorics</i> , 2009, 13, 139-167.	0.6	8
33	Phylogeny, biogeography, and rates of diversification of New World <i>Astragalus</i> (Leguminosae) with an emphasis on South American radiations. <i>American Journal of Botany</i> , 2008, 95, 1030-1039.	1.7	114
34	Phylogenetic Signal in the Eukaryotic Tree of Life. <i>Science</i> , 2008, 321, 121-123.	12.6	42
35	The PhyLoTA Browser: Processing GenBank for Molecular Phylogenetics Research. <i>Systematic Biology</i> , 2008, 57, 335-346.	5.6	110
36	Penalized Likelihood Phylogenetic Inference: Bridging the Parsimony-Likelihood Gap. <i>Systematic Biology</i> , 2008, 57, 665-674.	5.6	55

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37	Construction and annotation of large phylogenetic trees. <i>Australian Systematic Botany</i> , 2007, 20, 287.	0.9	19
38	Inferring angiosperm phylogeny from EST data with widespread gene duplication. <i>BMC Evolutionary Biology</i> , 2007, 7, S3.	3.2	89
39	Minimum-Flip Supertrees: Complexity and Algorithms. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2006, 3, 165-173.	3.0	39
40	Nematode Small Subunit Phylogeny Correlates with Alignment Parameters. <i>Systematic Biology</i> , 2006, 55, 972-992.	5.6	69
41	TESTING FOR DIFFERENT RATES OF CONTINUOUS TRAIT EVOLUTION USING LIKELIHOOD. <i>Evolution; International Journal of Organic Evolution</i> , 2006, 60, 922-933.	2.3	516
42	Phylogenetic Supermatrix Analysis of GenBank Sequences from 2228 Papilionoid Legumes. <i>Systematic Biology</i> , 2006, 55, 818-836.	5.6	148
43	Supertree Bootstrapping Methods for Assessing Phylogenetic Variation among Genes in Genome-Scale Data Sets. <i>Systematic Biology</i> , 2006, 55, 426-440.	5.6	48
44	Cenozoic insect-plant diversification in the tropics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 10827-10828.	7.1	1
45	Paloverde: an OpenGL 3D phylogeny browser. <i>Bioinformatics</i> , 2006, 22, 1004-1006.	4.1	22
46	Phylogenetics of New World Astragalus: Screening of novel nuclear loci for the reconstruction of phylogenies at low taxonomic levels. <i>Brittonia</i> , 2005, 57, 354-366.	0.2	18
47	ANGIOSPERM DIVERGENCE TIMES: THE EFFECT OF GENES, CODON POSITIONS, AND TIME CONSTRAINTS. <i>Evolution; International Journal of Organic Evolution</i> , 2005, 59, 1653-1670.	2.3	134
48	Advances in Legume Systematics. Part 10. Higher Level Systematics. B. B. Klitgaard and A. Bruneau (eds.). 2003. Royal Botanic Gardens, Kew. 422 pp. ISBN 1-84246-054-4. \$116.05 (paperback).. <i>Systematic Biology</i> , 2005, 54, 510-511.	5.6	0
49	Covariation Structure in Plastid Genome Evolution: A New Statistical Test. <i>Molecular Biology and Evolution</i> , 2005, 22, 914-924.	8.9	66
50	Missing the Forest for the Trees: Phylogenetic Compression and Its Implications for Inferring Complex Evolutionary Histories. <i>Systematic Biology</i> , 2005, 54, 146-157.	5.6	47
51	Performance of Flip Supertree Construction with a Heuristic Algorithm. <i>Systematic Biology</i> , 2004, 53, 299-308.	5.6	57
52	The Significance of Few Versus Many in the Tree of Life. <i>Science</i> , 2004, 303, 643-643.	12.6	57
53	Prospects for Building the Tree of Life from Large Sequence Databases. <i>Science</i> , 2004, 306, 1172-1174.	12.6	233
54	A phylogeny of legumes (Leguminosae) based on analysis of the plastid <i>matK</i> gene resolves many well-supported subclades within the family. <i>American Journal of Botany</i> , 2004, 91, 1846-1862.	1.7	699

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55	Molecular evidence on plant divergence times. <i>American Journal of Botany</i> , 2004, 91, 1656-1665.	1.7	256
56	The challenge of constructing large phylogenetic trees. <i>Trends in Plant Science</i> , 2003, 8, 374-379.	8.8	80
57	Molecular data from 27 proteins do not support a Precambrian origin of land plants. <i>American Journal of Botany</i> , 2003, 90, 954-956.	1.7	118
58	r8s: inferring absolute rates of molecular evolution and divergence times in the absence of a molecular clock. <i>Bioinformatics</i> , 2003, 19, 301-302.	4.1	1,622
59	Obtaining Maximal Concatenated Phylogenetic Data Sets from Large Sequence Databases. <i>Molecular Biology and Evolution</i> , 2003, 20, 1036-1042.	8.9	96
60	Relationships among seed plants inferred from highly conserved genes: sorting conflicting phylogenetic signals among ancient lineages. <i>American Journal of Botany</i> , 2002, 89, 1991-2006.	1.7	107
61	Estimating Absolute Rates of Molecular Evolution and Divergence Times: A Penalized Likelihood Approach. <i>Molecular Biology and Evolution</i> , 2002, 19, 101-109.	8.9	1,854
62	Troubleshooting Molecular Phylogenetic Analyses. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2002, 33, 49-72.	6.7	270
63	ABSOLUTE DIVERSIFICATION RATES IN ANGIOSPERM CLADES. <i>Evolution; International Journal of Organic Evolution</i> , 2001, 55, 1762-1780.	2.3	780
64	Sources of error and confidence intervals in estimating the age of angiosperms from rbcL and 18S rDNA data. <i>American Journal of Botany</i> , 2001, 88, 1499-1516.	1.7	235
65	Identifying Tertiary Radiations of Fabaceae in the Greater Antilles: Alternatives to Cladistic Vicariance Analysis. <i>International Journal of Plant Sciences</i> , 2001, 162, S53-S76.	1.3	46
66	Improved Bootstrap Confidence Limits in Large-Scale Phylogenies, with an Example from Neo-Astragalus (Leguminosae). <i>Systematic Biology</i> , 2000, 49, 671-685.	5.6	129
67	Phylogenetic systematics of the tribe Millettieae (Leguminosae) based on chloroplast trn K / mat K sequences and its implications for evolutionary patterns in Papilionoideae. <i>American Journal of Botany</i> , 2000, 87, 418-430.	1.7	165
68	Parametric Phylogenetics?. <i>Systematic Biology</i> , 2000, 49, 817-829.	5.6	151
69	Classification, origins, and patterns of diversification in New Zealand Carmichaelinae (Fabaceae). <i>American Journal of Botany</i> , 1999, 86, 1346-1356.	1.7	54
70	Phylogenetic supertrees: Assembling the trees of life. <i>Trends in Ecology and Evolution</i> , 1998, 13, 105-109.	8.7	401
71	Age and rate of diversification of the Hawaiian silversword alliance (Compositae). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1998, 95, 9402-9406.	7.1	619
72	Diversification Rates in a Temperate Legume Clade: Are there "So Many Species" of Astragalus (Fabaceae). <i>American Journal of Botany</i> , 1996, 83, 1488.	1.7	92

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73	Reconstructing shifts in diversification rates on phylogenetic trees. <i>Trends in Ecology and Evolution</i> , 1996, 11, 15-20.	8.7	177
74	Diversification rates in a temperate legume clade: Are there "so many species" of <i>Astragalus</i> (Fabaceae)?. <i>American Journal of Botany</i> , 1996, 83, 1488-1502.	1.7	119
75	How Many Taxa Must Be Sampled to Identify the Root Node of a Large Clade?. <i>Systematic Biology</i> , 1996, 45, 168-173.	5.6	39
76	Objections to Bootstrapping Phylogenies: A Critique. <i>Systematic Biology</i> , 1995, 44, 299-320.	5.6	185
77	MacClade, Version 3.0.. <i>Systematic Biology</i> , 1993, 42, 218.	5.6	26
78	Does Cladistic Information Affect Inferences About Branching Rates?. <i>Systematic Biology</i> , 1993, 42, 1.	5.6	4
79	MONOPHYLY OF ANEUPLOID ASTRAGALUS (FABACEAE): EVIDENCE FROM NUCLEAR RIBOSOMAL DNA INTERNAL TRANSCRIBED SPACER SEQUENCES. <i>American Journal of Botany</i> , 1993, 80, 711-722.	1.7	158
80	Reconstruction of Organismal and Gene Phylogenies from Data on Multigene Families: Concerted Evolution, Homoplasy, and Confidence. <i>Systematic Biology</i> , 1992, 41, 4.	5.6	26
81	ESTIMATING RATES OF SPECIATION AND EVOLUTION: A BIAS DUE TO HOMOPLASY. <i>Cladistics</i> , 1990, 6, 387-391.	3.3	46
82	Flexible Phylogeny Reconstruction: A Review of Phylogenetic Inference Packages Using Parsimony. <i>Systematic Zoology</i> , 1990, 39, 414.	1.6	19
83	CONFIDENCE LIMITS ON PHYLOGENIES: THE BOOTSTRAP REVISITED. <i>Cladistics</i> , 1989, 5, 113-129.	3.3	293
84	PATTERNS OF VARIATION IN LEVELS OF HOMOPLASY. <i>Evolution; International Journal of Organic Evolution</i> , 1989, 43, 1781-1795.	2.3	572
85	The effect of the reproductive system on mutation load. <i>Theoretical Population Biology</i> , 1988, 33, 243-265.	1.1	18
86	Evolution of social behavior by reciprocation. <i>Journal of Theoretical Biology</i> , 1982, 99, 319-339.	1.7	65
87	Perspective: Challenges in assembling the "next generation" Tree of Life. , 0, , 13-27.		0