

# Mark P Simmons

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9046529/publications.pdf>

Version: 2024-02-01

114  
papers

7,997  
citations

81900

39  
h-index

49909

87  
g-index

114  
all docs

114  
docs citations

114  
times ranked

7896  
citing authors

#	ARTICLE	IF	CITATIONS
1	Gaps as Characters in Sequence-Based Phylogenetic Analyses. <i>Systematic Biology</i> , 2000, 49, 369-381.	5.6	2,312
2	Functional trait niches of North American lotic insects: traits-based ecological applications in light of phylogenetic relationships. <i>Journal of the North American Benthological Society</i> , 2006, 25, 730-755.	3.1	704
3	How Meaningful Are Bayesian Support Values?. <i>Molecular Biology and Evolution</i> , 2004, 21, 188-199.	8.9	326
4	Independence of alignment and tree search. <i>Molecular Phylogenetics and Evolution</i> , 2004, 31, 874-879.	2.7	272
5	A Phylogeny of the Monocots, as Inferred from <i>rbcl</i> and <i>atpA</i> Sequence Variation, and a Comparison of Methods for Calculating Jackknife and Bootstrap Values. <i>Systematic Botany</i> , 2004, 29, 467-510.	0.5	173
6	Incorporation, Relative Homoplasy, and Effect of Gap Characters in Sequence-Based Phylogenetic Analyses. <i>Systematic Biology</i> , 2001, 50, 454-462.	5.6	166
7	Narrow thermal tolerance and low dispersal drive higher speciation in tropical mountains. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 12471-12476.	7.1	161
8	Data Decisiveness, Data Quality, and Incongruence in Phylogenetic Analysis: An Example From the Monocotyledons Using Mitochondrial <i>atp A</i> Sequences. <i>Systematic Biology</i> , 1998, 47, 282-310.	5.6	157
9	Incorporation, Relative Homoplasy, and Effect of Gap Characters in Sequence-Based Phylogenetic Analyses. <i>Systematic Biology</i> , 2001, 50, 454-462.	5.6	138
10	Whole-Genome Comparison of Leucine-Rich Repeat Extensins in Arabidopsis and Rice. A Conserved Family of Cell Wall Proteins Form a Vegetative and a Reproductive Clade. <i>Plant Physiology</i> , 2003, 131, 1313-1326.	4.8	128
11	Phylogeny of the Cucurbitales based on DNA sequences of nine loci from three genomes: Implications for morphological and sexual system evolution. <i>Molecular Phylogenetics and Evolution</i> , 2006, 39, 305-322.	2.7	121
12	New Guinea has the world's richest island flora. <i>Nature</i> , 2020, 584, 579-583.	27.8	108
13	Comprehensive comparative analysis of kinesins in photosynthetic eukaryotes. <i>BMC Genomics</i> , 2006, 7, 18.	2.8	102
14	Phylogeny and Delimitation of the Celastrales Inferred from Nuclear and Plastid Genes. <i>Systematic Botany</i> , 2006, 31, 122-137.	0.5	99
15	Misleading results of likelihood-based phylogenetic analyses in the presence of missing data. <i>Cladistics</i> , 2012, 28, 208-222.	3.3	90
16	Phylogeny of the Celastraceae Inferred from 26S Nuclear Ribosomal DNA, Phytochrome B, <i>rbcl</i> , <i>atpB</i> , and Morphology. <i>Molecular Phylogenetics and Evolution</i> , 2001, 19, 353-366.	2.7	89
17	The relative performance of indel-coding methods in simulations. <i>Molecular Phylogenetics and Evolution</i> , 2007, 44, 724-740.	2.7	88
18	Miocene Dispersal Drives Island Radiations in the Palm Tribe Trachycarpeae (Arecaceae). <i>Systematic Biology</i> , 2012, 61, 426-442.	5.6	77

#	ARTICLE	IF	CITATIONS
19	Coalescence vs. concatenation: Sophisticated analyses vs. first principles applied to rooting the angiosperms. <i>Molecular Phylogenetics and Evolution</i> , 2015, 91, 98-122.	2.7	77
20	Spurious 99% bootstrap and jackknife support for unsupported clades. <i>Molecular Phylogenetics and Evolution</i> , 2011, 61, 177-191.	2.7	76
21	Phylogeny of the Celastraceae inferred from phytochrome B gene sequence and morphology. <i>American Journal of Botany</i> , 2001, 88, 313-325.	1.7	75
22	Radical instability and spurious branch support by likelihood when applied to matrices with non-random distributions of missing data. <i>Molecular Phylogenetics and Evolution</i> , 2012, 62, 472-484.	2.7	75
23	Molecular analyses of the Chinese herb Leigongteng ( <i>Tripterygium wilfordii</i> Hook.f.). <i>Phytochemistry</i> , 2011, 72, 21-26.	2.9	74
24	Resolution of a concatenation/coalescence kerfuffle: partitioned coalescence support and a robust family-level tree for Mammalia. <i>Cladistics</i> , 2017, 33, 295-332.	3.3	70
25	Transcriptome-wide comparison of selenium hyperaccumulator and nonaccumulator <i>Stanleya</i> species provides new insight into key processes mediating the hyperaccumulation syndrome. <i>Plant Biotechnology Journal</i> , 2018, 16, 1582-1594.	8.3	67
26	Phylogeny of the Celastreae (Celastraceae) and the relationships of <i>Catha edulis</i> (qat) inferred from morphological characters and nuclear and plastid genes. <i>Molecular Phylogenetics and Evolution</i> , 2008, 48, 745-757.	2.7	59
27	Amino acid vs. nucleotide characters: challenging preconceived notions. <i>Molecular Phylogenetics and Evolution</i> , 2002, 24, 78-90.	2.7	55
28	A Thorny Dilemma: Testing Alternative Intrageneric Classifications within <i>Ziziphus</i> (Rhamnaceae). <i>Systematic Botany</i> , 2006, 31, 826-842.	0.5	55
29	Characterization of selenium and sulfur accumulation across the genus <i>Stanleya</i> (Brassicaceae): A field survey and common-garden experiment. <i>American Journal of Botany</i> , 2014, 101, 830-839.	1.7	55
30	A confounding effect of missing data on character conflict in maximum likelihood and Bayesian MCMC phylogenetic analyses. <i>Molecular Phylogenetics and Evolution</i> , 2014, 80, 267-280.	2.7	53
31	Rapid Intraspecific Evolution of miRNA and siRNA Genes in the Mosquito <i>Aedes aegypti</i> . <i>PLoS ONE</i> , 2012, 7, e44198.	2.5	52
32	The Complete Plastid Genome of <i>Lagerstroemia fauriei</i> and Loss of rpl2 Intron from <i>Lagerstroemia</i> (Lythraceae). <i>PLoS ONE</i> , 2016, 11, e0150752.	2.5	52
33	A penalty of using anonymous dominant markers (AFLPs, ISSRs, and RAPDs) for phylogenetic inference. <i>Molecular Phylogenetics and Evolution</i> , 2007, 42, 528-542.	2.7	51
34	Relationships and Morphological Character Change among Genera of Celastraceae Sensu Lato (Including Hippocrateaceae). <i>Annals of the Missouri Botanical Garden</i> , 1999, 86, 723.	1.3	50
35	Efficiently resolving the basal clades of a phylogenetic tree using Bayesian and parsimony approaches: a case study using mitogenomic data from 100 higher teleost fishes. <i>Molecular Phylogenetics and Evolution</i> , 2004, 31, 351-362.	2.7	49
36	Divergent maximum-likelihood-branch-support values for polytomies. <i>Molecular Phylogenetics and Evolution</i> , 2014, 73, 87-96.	2.7	49

#	ARTICLE	IF	CITATIONS
37	The effects of subsampling gene trees on coalescent methods applied to ancient divergences. <i>Molecular Phylogenetics and Evolution</i> , 2016, 97, 76-89.	2.7	45
38	Congruence of Molecular, Morphological, and Biochemical Profiles in Rutaceae: a Cladistic Analysis of the Subfamilies Rutoideae and Toddalioideae. <i>Systematic Botany</i> , 2007, 32, 837-846.	0.5	43
39	The effects of increasing genetic distance on alignment of, and tree construction from, rDNA internal transcribed spacer sequences. <i>Molecular Phylogenetics and Evolution</i> , 2003, 26, 444-451.	2.7	42
40	Evaluating multiple criteria for species delimitation: an empirical example using Hawaiian palms (Arecaceae: Pritchardia). <i>BMC Evolutionary Biology</i> , 2012, 12, 23.	3.2	42
41	Phylogeny of the Asian Hedyotis–Oldenlandia complex (Spermacoceae, Rubiaceae): Evidence for high levels of polyphyly and the parallel evolution of diplophragmous capsules. <i>Molecular Phylogenetics and Evolution</i> , 2013, 67, 110-122.	2.7	42
42	GEOGRAPHIC AND TAXONOMIC DISPARITIES IN SPECIES DIVERSITY: DISPERSAL AND DIVERSIFICATION RATES ACROSS WALLACE'S LINE. <i>Evolution; International Journal of Organic Evolution</i> , 2013, 67, 2058-2071.	2.3	42
43	Artifacts of Coding Amino Acids and Other Composite Characters for Phylogenetic Analysis. <i>Cladistics</i> , 2002, 18, 354-365.	3.3	40
44	Uninode coding vs gene tree parsimony for phylogenetic reconstruction using duplicate genes. <i>Molecular Phylogenetics and Evolution</i> , 2002, 23, 481-498.	2.7	39
45	Relative character-state space, amount of potential phylogenetic information, and heterogeneity of nucleotide and amino acid characters. <i>Molecular Phylogenetics and Evolution</i> , 2004, 32, 913-926.	2.7	39
46	From basepairs to birdsongs: phylogenetic data in the age of genomics. <i>Cladistics</i> , 2003, 19, 333-347.	3.3	38
47	Delimitation of the Segregate Genera of <i>Maytenus</i> s. l. (Celastraceae) Based on Morphological and Molecular Characters. <i>Systematic Botany</i> , 2011, 36, 922-932.	0.5	38
48	Are mitochondrial genes useful for the analysis of monocot relationships?. <i>Taxon</i> , 2006, 55, 857-870.	0.7	37
49	Evolution of selenium hyperaccumulation in <i>Stanleya</i> (Brassicaceae) as inferred from phylogeny, physiology and X-ray microprobe analysis. <i>New Phytologist</i> , 2015, 205, 583-595.	7.3	37
50	Origin and Evolution of Kinesin-Like Calmodulin-Binding Protein. <i>Plant Physiology</i> , 2005, 138, 1711-1722.	4.8	34
51	A Fundamental Problem with Amino-Acid-Sequence Characters for Phylogenetic Analyses. <i>Cladistics</i> , 2000, 16, 274-282.	3.3	33
52	Character-state space versus rate of evolution in phylogenetic inference. <i>Cladistics</i> , 2004, 20, 191-204.	3.3	33
53	Phylogeny of Celastraceae tribe Euonymieae inferred from morphological characters and nuclear and plastid genes. <i>Molecular Phylogenetics and Evolution</i> , 2012, 62, 9-20.	2.7	33
54	Gene-wise resampling outperforms site-wise resampling in phylogenetic coalescence analyses. <i>Molecular Phylogenetics and Evolution</i> , 2019, 131, 80-92.	2.7	33

#	ARTICLE	IF	CITATIONS
55	How Can Third Codon Positions Outperform First and Second Codon Positions in Phylogenetic Inference? An Empirical Example from the Seed Plants. <i>Systematic Biology</i> , 2006, 55, 245-258.	5.6	32
56	Application of DNA barcodes in <i>Hedyotis</i> L. (Spermacoceae, Rubiaceae). <i>Journal of Systematics and Evolution</i> , 2011, 49, 203-212.	3.1	31
57	Partitioned coalescence support reveals biases in species-tree methods and detects gene trees that determine phylogenomic conflicts. <i>Molecular Phylogenetics and Evolution</i> , 2019, 139, 106539.	2.7	31
58	Phylogeny Reconstruction Using Duplicate Genes. <i>Molecular Biology and Evolution</i> , 2000, 17, 469-473.	8.9	30
59	ILS-Aware Analysis of Low-Homoplasy Retroelement Insertions: Inference of Species Trees and Introgression Using Quartets. <i>Journal of Heredity</i> , 2020, 111, 147-168.	2.4	30
60	Linear Plasmids and the Rate of Sequence Evolution in Plant Mitochondrial Genomes. <i>Genome Biology and Evolution</i> , 2016, 8, 364-374.	2.5	29
61	Conflict between Amino Acid and Nucleotide Characters. <i>Cladistics</i> , 2002, 18, 200-206.	3.3	27
62	Quantification and relative severity of inflated branch-support values generated by alternative methods: An empirical example. <i>Molecular Phylogenetics and Evolution</i> , 2013, 67, 277-296.	2.7	27
63	Biogeography of the Malagasy Celastraceae: Multiple independent origins followed by widespread dispersal of genera from Madagascar. <i>Molecular Phylogenetics and Evolution</i> , 2016, 94, 365-382.	2.7	27
64	Quantification of the success of phylogenetic inference in simulations. <i>Cladistics</i> , 2006, 22, 249-255.	3.3	26
65	An artifact caused by undersampling optimal trees in supermatrix analyses of locally sampled characters. <i>Molecular Phylogenetics and Evolution</i> , 2013, 69, 265-275.	2.7	26
66	Dubious resolution and support from published sparse supermatrices: The importance of thorough tree searches. <i>Molecular Phylogenetics and Evolution</i> , 2014, 78, 334-348.	2.7	26
67	Phylogeny of Celastraceae Subfamily Salacioideae and Tribe Lophopetaleae Inferred from Morphological Characters and Nuclear and Plastid Genes. <i>Systematic Botany</i> , 2010, 35, 358-367.	0.5	25
68	Mitochondrial fatty acid $\beta$ -oxidation is required for storage lipid catabolism in a marine diatom. <i>New Phytologist</i> , 2020, 228, 946-958.	7.3	25
69	Relative benefits of amino acid, codon, degeneracy, DNA, and purine-pyrimidine character coding for phylogenetic analyses of exons. <i>Journal of Systematics and Evolution</i> , 2017, 55, 85-109.	3.1	24
70	Collapsing dubiously resolved gene-tree branches in phylogenomic coalescent analyses. <i>Molecular Phylogenetics and Evolution</i> , 2021, 158, 107092.	2.7	24
71	Phylogeny of Celastraceae subfamily Hippocrateoideae inferred from morphological characters and nuclear and plastid loci. <i>Molecular Phylogenetics and Evolution</i> , 2011, 59, 320-330.	2.7	23
72	Systematics of New World <i>Maytenus</i> (Celastraceae) and a New Delimitation of the Genus. <i>Systematic Botany</i> , 2017, 42, 680-693.	0.5	23

#	ARTICLE	IF	CITATIONS
73	Co-variation in methanotroph community composition and activity in three temperate grassland soils. <i>Soil Biology and Biochemistry</i> , 2016, 95, 78-86.	8.8	22
74	A phylogeny of Anisophylleaceae based on six nuclear and plastid loci: Ancient disjunctions and recent dispersal between South America, Africa, and Asia. <i>Molecular Phylogenetics and Evolution</i> , 2007, 44, 1057-1067.	2.7	21
75	Alignment of, and phylogenetic inference from, random sequences: The susceptibility of alternative alignment methods to creating artifactual resolution and support. <i>Molecular Phylogenetics and Evolution</i> , 2010, 57, 1004-1016.	2.7	21
76	Phylogeny of Celastraceae Subfamilies Cassinoideae and Tripterygioidae Inferred from Morphological Characters and Nuclear and Plastid Loci. <i>Systematic Botany</i> , 2012, 37, .	0.5	21
77	Limitations of Relative Apparent Synapomorphy Analysis (RASA) for Measuring Phylogenetic Signal. <i>Molecular Biology and Evolution</i> , 2002, 19, 14-23.	8.9	20
78	Phylogeny of the <i>Elaeodendron</i> Group (Celastraceae) Inferred from Morphological Characters and Nuclear and Plastid Genes. <i>Systematic Botany</i> , 2006, 31, 512-524.	0.5	20
79	Divergence and support among slightly suboptimal likelihood gene trees. <i>Cladistics</i> , 2020, 36, 322-340.	3.3	20
80	Disparate parametric branch-support values from ambiguous characters. <i>Molecular Phylogenetics and Evolution</i> , 2014, 78, 66-86.	2.7	18
81	The relative performance of Bayesian and parsimony approaches when sampling characters evolving under homogeneous and heterogeneous sets of parameters. <i>Cladistics</i> , 2006, 22, 171-185.	3.3	17
82	Evaluation of microsatellites of <i>Catha edulis</i> (qat; Celastraceae) identified using pyrosequencing. <i>Biochemical Systematics and Ecology</i> , 2013, 49, 1-9.	1.3	17
83	Mutually exclusive phylogenomic inferences at the root of the angiosperms: <i>Amborella</i> is supported as sister and Observed Variability is biased. <i>Cladistics</i> , 2017, 33, 488-512.	3.3	16
84	Gene-tree misrooting drives conflicts in phylogenomic coalescent analyses of palaeognath birds. <i>Molecular Phylogenetics and Evolution</i> , 2022, 167, 107344.	2.7	16
85	Limitations of locally sampled characters in phylogenetic analyses of sparse supermatrices. <i>Molecular Phylogenetics and Evolution</i> , 2014, 74, 1-14.	2.7	15
86	Molecular phylogeny and revised classification of <i>Eucosma</i> and related genera (Lepidoptera: Tortricidae: Eucosmini). <i>Systematic Entomology</i> , 2014, 39, 49-67.	3.9	14
87	Biases of tree-independent-character-subsampling methods. <i>Molecular Phylogenetics and Evolution</i> , 2016, 100, 424-443.	2.7	11
88	Artifacts of Coding Amino Acids and Other Composite Characters for Phylogenetic Analysis. <i>Cladistics</i> , 2002, 18, 354-365.	3.3	11
89	The deterministic effects of alignment bias in phylogenetic inference. <i>Cladistics</i> , 2011, 27, 402-416.	3.3	10
90	A New Species of <i>Maytenus</i> (Celastraceae) with Fleshy Fruits from Eastern Brazil, with Notes on the Delimitation of <i>Maytenus</i> . <i>Systematic Botany</i> , 2014, 39, 478-484.	0.5	10

#	ARTICLE	IF	CITATIONS
91	Thistle be a mess: Untangling the taxonomy of <i>Cirsium</i> (Cardueae: Compositae) in North America. <i>Journal of Systematics and Evolution</i> , 2020, 58, 881-912.	3.1	10
92	Bias in Tree Searches and its Consequences for Measuring Group Supports. <i>Systematic Biology</i> , 2014, 63, 851-861.	5.6	9
93	Phylogeography of the wild and cultivated stimulant plant qat ( <i>Catha edulis</i> , Celastraceae) in areas of historical cultivation. <i>American Journal of Botany</i> , 2017, 104, 538-549.	1.7	9
94	Alternative analyses of compensatory base changes in an ITS2 phylogeny of <i>Corydalis</i> (Papaveraceae). <i>Annals of Botany</i> , 2019, 124, 233-243.	2.9	9
95	A Fundamental Problem with Amino-Acid-Sequence Characters for Phylogenetic Analyses. <i>Cladistics</i> , 2000, 16, 274-282.	3.3	9
96	Potential use of host-derived genome signatures to root virus phylogenies. <i>Molecular Phylogenetics and Evolution</i> , 2008, 49, 969-978.	2.7	8
97	Incorporation of gap characters and lineage-specific regions into phylogenetic analyses of gene families from divergent clades: an example from the kinesin superfamily across eukaryotes. <i>Cladistics</i> , 2008, 24, 372-384.	3.3	7
98	The relative sensitivity of different alignment methods and character codings in sensitivity analysis. <i>Cladistics</i> , 2008, 24, 1039-1050.	3.3	7
99	Employing Two-Stage Derivatisation and GC-MS to Assay for Cathine and Related Stimulant Alkaloids across the Celastraceae. <i>Phytochemical Analysis</i> , 2017, 28, 257-266.	2.4	7
100	Adenine-cytosine substitutions are an alternative pathway of compensatory mutation in angiosperm ITS2. <i>Rna</i> , 2020, 26, 209-217.	3.5	7
101	Revision of the Cerrado Hemicryptophytic Chamaesyce of Boissier's "Pleiadeniae" (Euphorbiaceae). <i>Brittonia</i> , 1997, 49, 155.	0.2	6
102	<i>Wilczekra</i> , a New Genus of Celastraceae for a Disjunct Lineage of <i>Euonymus</i> . <i>Systematic Botany</i> , 2013, 38, 148-153.	0.5	6
103	Contribution of molecular cladistics to the taxonomy of Rutaceae in China*. <i>Journal of Systematics and Evolution</i> , 2009, 47, 144-150.	3.1	5
104	Wood Anatomy of <i>Amanoa</i> (Euphorbiaceae). <i>IAWA Journal</i> , 1993, 14, 205-213.	2.7	3
105	Development of microsatellites in the Hawaiian endemic palm <i>Pritchardia martii</i> (Arecaceae) and their utility in congeners. <i>American Journal of Botany</i> , 2011, 98, e139-e140.	1.7	3
106	From basepairs to birdsongs: phylogenetic data in the age of genomics. <i>Cladistics</i> , 2003, 19, 333-347.	3.3	3
107	Phylogenetic inference using non-redundant coding of dependent characters versus alternative approaches for protein-coding genes. <i>Cladistics</i> , 2011, 27, 186-196.	3.3	2
108	Haydenoxylon, a Replacement Name for <i>Haydenia</i> (Celastraceae). <i>Novon</i> , 2014, 23, 224-225.	0.3	2

#	ARTICLE	IF	CITATIONS
109	Pleurostylia serrulata and Two Allied New Species from Africa are Actually Members of the New World Crossopetalum (Celastraceae). Systematic Botany, 2016, 41, 851-864.	0.5	2
110	Ten Simple Rules for Writing a Reply Paper. PLoS Computational Biology, 2015, 11, e1004536.	3.2	1
111	Benefits of alignment quality control processing steps and an Angiosperms353 phylogenomics pipeline applied to the Celastrales. Cladistics, 2022, 38, 595-611.	3.3	1
112	Relative character-state space, amount of potential phylogenetic information, and heterogeneity of nucleotide and amino acid characters*1. Molecular Phylogenetics and Evolution, 2004, 32, 913-913.	2.7	0
113	Ten Rules for Associate Editors. Botanical Review, The, 2018, 84, 99-107.	3.9	0
114	Clonal Diversity, Cultivar Traits, Geographic Dispersal, and the Ethnotaxonomy of Cultivated Qat (Catha edulis, Celastraceae). Economic Botany, 2020, 74, 273-291.	1.7	0