

# Sean W Graham

## List of Publications by Year in descending order

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104  
papers

15,083  
citations

39113

52  
h-index

37326

100  
g-index

107  
all docs

107  
docs citations

107  
times ranked

14130  
citing authors

#	ARTICLE	IF	CITATIONS
1	Macroevolutionary dynamics in the transition of angiosperms to aquatic environments. <i>New Phytologist</i> , 2022, 235, 344-355.	3.5	3
2	Incomplete lineage sorting and local extinction shaped the complex evolutionary history of the Paleogene relict conifer genus, <i>Chamaecyparis</i> (Cupressaceae). <i>Molecular Phylogenetics and Evolution</i> , 2022, 172, 107485.	1.2	4
3	Mitochondrial genomic data are effective at placing mycoheterotrophic lineages in plant phylogeny. <i>New Phytologist</i> , 2022, 236, 1908-1921.	3.5	14
4	Discordant Phylogenomic Placement of Hydnoraceae and Lactoridaceae Within Piperales Using Data From All Three Genomes. <i>Frontiers in Plant Science</i> , 2021, 12, 642598.	1.7	19
5	Genomic Rearrangements and Sequence Evolution across Brown Algal Organelles. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	12
6	Exploring Angiosperms353: Developing and applying a universal toolkit for flowering plant phylogenomics. <i>Applications in Plant Sciences</i> , 2021, 9, .	0.8	13
7	Exploring Angiosperms353: An open, community toolkit for collaborative phylogenomic research on flowering plants. <i>American Journal of Botany</i> , 2021, 108, 1059-1065.	0.8	36
8	A new carnivorous plant lineage ( <i>Triantha</i> ) with a unique sticky-inflorescence trap. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	26
9	Sequencing and Analyzing the Transcriptomes of a Thousand Species Across the Tree of Life for Green Plants. <i>Annual Review of Plant Biology</i> , 2020, 71, 741-765.	8.6	41
10	Organellomic data sets confirm a cryptic consensus on (unrooted) landâ€plant relationships and provide new insights into bryophyte molecular evolution. <i>American Journal of Botany</i> , 2020, 107, 91-115.	0.8	38
11	A biâ€organellar phylogenomic study of Pandanales: inference of higherâ€order relationships and unusual rateâ€variation patterns. <i>Cladistics</i> , 2020, 36, 481-504.	1.5	17
12	A transcriptome-based resolution for a key taxonomic controversy in Cupressaceae. <i>Annals of Botany</i> , 2019, 123, 153-167.	1.4	18
13	A Target Capture-Based Method to Estimate Ploidy From Herbarium Specimens. <i>Frontiers in Plant Science</i> , 2019, 10, 937.	1.7	53
14	A customized nuclear target enrichment approach for developing a phylogenomic baseline for <i>Dioscorea</i> yams (Dioscoreaceae). <i>Applications in Plant Sciences</i> , 2019, 7, e11254.	0.8	49
15	Mycoheterotrophic <i>Epirixanthes</i> (Polygalaceae) has a typical angiosperm mitogenome but unorthodox plastid genomes. <i>Annals of Botany</i> , 2019, 124, 791-807.	1.4	14
16	A comprehensive kelp phylogeny sheds light on the evolution of an ecosystem. <i>Molecular Phylogenetics and Evolution</i> , 2019, 136, 138-150.	1.2	62
17	Cryptic species in an ancient floweringâ€plant lineage (Hydatellaceae, Nymphaeales) revealed by molecular and micromorphological data. <i>Taxon</i> , 2019, 68, 1-19.	0.4	13
18	One thousand plant transcriptomes and theâ€phylogenomics of green plants. <i>Nature</i> , 2019, 574, 679-685.	13.7	1,162

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19	10KP: A phylodiverse genome sequencing plan. <i>GigaScience</i> , 2018, 7, 1-9.	3.3	169
20	The <i>Physcomitrella patens</i> chromosome-scale assembly reveals moss genome structure and evolution. <i>Plant Journal</i> , 2018, 93, 515-533.	2.8	406
21	Evolution of <i>Geosiris</i> (Iridaceae): historical biogeography and plastid-genome evolution in a genus of non-photosynthetic tropical rainforest herbs disjunct across the Indian Ocean. <i>Australian Systematic Botany</i> , 2018, , .	0.3	8
22	Monocot plastid phylogenomics, timeline, net rates of species diversification, the power of multi-gene analyses, and a functional model for the origin of monocots. <i>American Journal of Botany</i> , 2018, 105, 1888-1910.	0.8	161
23	Comprehensive cross-genome survey and phylogeny of glycoside hydrolase family 16 members reveals the evolutionary origin of <i>EG</i> and <i>XTH</i> proteins in plant lineages. <i>Plant Journal</i> , 2018, 95, 1114-1128.	2.8	41
24	Phylogenomic inference <i>in extremis</i> : A case study with mycoheterotroph plastomes. <i>American Journal of Botany</i> , 2018, 105, 480-494.	0.8	40
25	Plastomes on the edge: the evolutionary breakdown of mycoheterotroph plastid genomes. <i>New Phytologist</i> , 2017, 214, 48-55.	3.5	148
26	Insights into the Evolution of Hydroxyproline-Rich Glycoproteins from 1000 Plant Transcriptomes. <i>Plant Physiology</i> , 2017, 174, 904-921.	2.3	62
27	Morphological and phylogenetic relationships of the threatened geophyte <i>Wurmbea novae-zelandiae</i> (Colchicaceae) from New Zealand, with notes on typification. <i>Phytotaxa</i> , 2017, 307, 123.	0.1	0
28	Evolution of strigolactone receptors by gradual neo-functionalization of KAI2 paralogues. <i>BMC Biology</i> , 2017, 15, 52.	1.7	99
29	Using Herbarium-derived DNAs to Assemble a Large-scale DNA Barcode Library for the Vascular Plants of Canada. <i>Applications in Plant Sciences</i> , 2017, 5, 1700079.	0.8	64
30	The Unique Role of the ECERIFERUM2-LIKE Clade of the BAHD Acyltransferase Superfamily in Cuticular Wax Metabolism. <i>Plants</i> , 2017, 6, 23.	1.6	31
31	Mitochondrial genome evolution in Alismatales: Size reduction and extensive loss of ribosomal protein genes. <i>PLoS ONE</i> , 2017, 12, e0177606.	1.1	36
32	Diversity of ABC transporter genes across the plant kingdom and their potential utility in biotechnology. <i>BMC Biotechnology</i> , 2016, 16, 47.	1.7	91
33	A few-gene plastid phylogenetic framework for mycoheterotrophic monocots. <i>American Journal of Botany</i> , 2016, 103, 692-708.	0.8	35
34	Microbial-type terpene synthase genes occur widely in nonseed land plants, but not in seed plants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 12328-12333.	3.3	70
35	Challenging the paradigms of leaf evolution: Class III HD-Zips in ferns and lycophytes. <i>New Phytologist</i> , 2016, 212, 745-758.	3.5	55
36	Self-pollination, style length development and seed set in self-compatible Asteraceae: evidence from <i>Senecio vulgaris</i> L.. <i>Plant Ecology and Diversity</i> , 2016, 9, 371-379.	1.0	9

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37	The Evolution of HD2 Proteins in Green Plants. <i>Trends in Plant Science</i> , 2016, 21, 1008-1016.	4.3	40
38	Localized Retroprocessing as a Model of Intron Loss in the Plant Mitochondrial Genome. <i>Genome Biology and Evolution</i> , 2016, 8, 2176-2189.	1.1	26
39	Plastid phylogenomics and molecular evolution of Alismatales. <i>Cladistics</i> , 2016, 32, 160-178.	1.5	98
40	Phylogenomics and historical biogeography of the monocot order Liliales: out of Australia and through Antarctica. <i>Cladistics</i> , 2016, 32, 581-605.	1.5	61
41	Transcriptome-derived evidence supports recent polyploidization and a major phylogeographic division in <i>Trituraria submersa</i> (Hydatellaceae, Nymphaeales). <i>New Phytologist</i> , 2016, 210, 310-323.	3.5	10
42	Phylogeny of the Alismatales (Monocotyledons) and the relationship of <i>Acorus</i> ( <i>Acorales</i> ?). <i>Cladistics</i> , 2016, 32, 141-159.	1.5	28
43	The origin and evolution of phototropins. <i>Frontiers in Plant Science</i> , 2015, 6, 637.	1.7	68
44	Ancient Gondwana breakup explains the distribution of the mycoheterotrophic family Corsiaceae (Liliales). <i>Journal of Biogeography</i> , 2015, 42, 1123-1136.	1.4	39
45	Monocot fossils suitable for molecular dating analyses. <i>Botanical Journal of the Linnean Society</i> , 2015, 178, 346-374.	0.8	102
46	Phytochrome diversity in green plants and the origin of canonical plant phytochromes. <i>Nature Communications</i> , 2015, 6, 7852.	5.8	139
47	The evolutionary history of ferns inferred from 25 low-copy nuclear genes. <i>American Journal of Botany</i> , 2015, 102, 1089-1107.	0.8	157
48	Does complete plastid genome sequencing improve species discrimination and phylogenetic resolution in <i>Araucaria</i> ?. <i>Molecular Ecology Resources</i> , 2015, 15, 1067-1078.	2.2	100
49	The Highly Reduced Plastome of Mycoheterotrophic <i>Sciaphila</i> (Triuridaceae) Is Colinear with Its Green Relatives and Is under Strong Purifying Selection. <i>Genome Biology and Evolution</i> , 2015, 7, 2220-2236.	1.1	60
50	Early genome duplications in conifers and other seed plants. <i>Science Advances</i> , 2015, 1, e1501084.	4.7	236
51	Paralogous Radiations of PIN Proteins with Multiple Origins of Noncanonical PIN Structure. <i>Molecular Biology and Evolution</i> , 2014, 31, 2042-2060.	3.5	111
52	Origin of a novel regulatory module by duplication and degeneration of an ancient plant transcription factor. <i>Molecular Phylogenetics and Evolution</i> , 2014, 81, 159-173.	1.2	14
53	Between Two Fern Genomes. <i>GigaScience</i> , 2014, 3, 15.	3.3	69
54	Data access for the 1,000 Plants (1KP) project. <i>GigaScience</i> , 2014, 3, 17.	3.3	582

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55	Phylotranscriptomic analysis of the origin and early diversification of land plants. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E4859-68.	3.3	1,123
56	Understanding the spectacular failure of <sc>DNA</sc> barcoding in willows (<i>Salix</i>): Does this result from a transâ€specific selective sweep?. Molecular Ecology, 2014, 23, 4737-4756.	2.0	109
57	Patterns of clade support across the major lineages of moss phylogeny. Cladistics, 2014, 30, 590-606.	1.5	16
58	Reconstructing the age and historical biogeography of the ancient flowering-plant family Hydatellaceae (Nymphaeales). BMC Evolutionary Biology, 2014, 14, 102.	3.2	17
59	Horizontal transfer of an adaptive chimeric photoreceptor from bryophytes to ferns. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 6672-6677.	3.3	146
60	A well-supported phylogenetic framework for the monocot order Alismatales reveals multiple losses of the plastid NADH dehydrogenase complex and a strong long-branch effect. , 2013, , .		28
61	Transcriptome-Mining for Single-Copy Nuclear Markers in Ferns. PLoS ONE, 2013, 8, e76957.	1.1	69
62	Molecular phylogenetics of Hydatellaceae (Nymphaeales): Sexualâ€system homoplasmy and a new sectional classification. American Journal of Botany, 2012, 99, 663-676.	0.8	24
63	Evaluating Methods for Isolating Total RNA and Predicting the Success of Sequencing Phylogenetically Diverse Plant Transcriptomes. PLoS ONE, 2012, 7, e50226.	1.1	172
64	Inferring the higherâ€order phylogeny of mosses (Bryophyta) and relatives using a large, multigene plastid data set. American Journal of Botany, 2011, 98, 839-849.	0.8	97
65	Discriminating plant species in a local temperate flora using the <i>rbcL</i>+<i>matK</i> DNA barcode. Methods in Ecology and Evolution, 2011, 2, 333-340.	2.2	154
66	Spatial patterns of plant diversity belowâ€ground as revealed by DNA barcoding. Molecular Ecology, 2011, 20, 1289-1302.	2.0	96
67	Choosing and Using a Plant DNA Barcode. PLoS ONE, 2011, 6, e19254.	1.1	946
68	Bryophyte-specific primers for retrieving plastid genes suitable for phylogenetic inference. American Journal of Botany, 2011, 98, e109-e113.	0.8	5
69	Reconciling Gene and Genome Duplication Events: Using Multiple Nuclear Gene Families to Infer the Phylogeny of the Aquatic Plant Family Pontederiaceae. Molecular Biology and Evolution, 2011, 28, 3009-3018.	3.5	48
70	Utility of a large, multigene plastid data set in inferring higherâ€order relationships in ferns and relatives (monilophytes). American Journal of Botany, 2010, 97, 1444-1456.	0.8	73
71	Assembling the Tree of the Monocotyledons: Plastome Sequence Phylogeny and Evolution of Poales<sup>1</sup>. Annals of the Missouri Botanical Garden, 2010, 97, 584-616.	1.3	202
72	Inference of phylogenetic relationships among the subfamilies of grasses (Poaceae: Poales) using meso-scale exemplar-based sampling of the plastid genome. Botany, 2010, 88, 65-84.	0.5	27

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73	Introduction to the Darwin special issue: The abominable mystery <sup>1</sup> . American Journal of Botany, 2009, 96, 3-4.	0.8	6
74	A DNA barcode for land plants. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 12794-12797.	3.3	2,120
75	Different gymnosperm outgroups have (mostly) congruent signal regarding the root of flowering plant phylogeny. American Journal of Botany, 2009, 96, 216-227.	0.8	60
76	Are plant species inherently harder to discriminate than animal species using DNA barcoding markers?. Molecular Ecology Resources, 2009, 9, 130-139.	2.2	234
77	How well do we understand the overall backbone of cycad phylogeny? New insights from a large, multigene plastid data set. Molecular Phylogenetics and Evolution, 2008, 47, 1232-1237.	1.2	45
78	Phylogenetic relationships in the monocot order Commelinales, with a focus on Philydraceae This paper is one of a selection of papers published in the Special Issue on Systematics Research.. Botany, 2008, 86, 719-731.	0.5	22
79	Inference of higher-order conifer relationships from a multi-locus plastid data set This paper is one of a selection of papers published in the Special Issue on Systematics Research.. Botany, 2008, 86, 658-669.	0.5	116
80	Introduction to "Plant systematics at the species level" / Introduction pour "La systématique des plantes au niveau de l'espèce". Botany, 2008, 86, vii-x.	0.5	0
81	Introduction to "The state of plant systematics research" / Introduction pour "L'état de la systématique des plantes". Botany, 2008, 86, vii-x.	0.5	0
82	A Phylogenetic Study of Evolutionary Transitions in Sexual Systems in Australasian <i>Wurmbea</i> (Colchicaceae). International Journal of Plant Sciences, 2008, 169, 141-156.	0.6	38
83	Multiple Multilocus DNA Barcodes from the Plastid Genome Discriminate Plant Species Equally Well. PLoS ONE, 2008, 3, e2802.	1.1	526
84	Towards a phylogenetic nomenclature of <i>Tracheophyta</i> . Taxon, 2007, 56, 822-846.	0.4	101
85	Towards a phylogenetic nomenclature of <i>Tracheophyta</i> . Taxon, 2007, 56, E1.	0.4	71
86	Hydatellaceae identified as a new branch near the base of the angiosperm phylogenetic tree. Nature, 2007, 446, 312-315.	13.7	208
87	Molecular evidence for the systematic positions of two enigmatic mosses: <i>Pterogonidium pulchellum</i> (Sematophyllaceae, Musci) and <i>Piloecium pseudorufescens</i> (Myuriaceae, Musci). Canadian Journal of Botany, 2006, 84, 501-507.	1.2	5
88	Repeated evolution of net venation and fleshy fruits among monocots in shaded habitats confirms a priori predictions: evidence from an ndhF phylogeny. Proceedings of the Royal Society B: Biological Sciences, 2005, 272, 1481-1490.	1.2	100
89	Phylogenetic reconstruction of the evolution of stylar polymorphisms in <i>Narcissus</i> (Amaryllidaceae). American Journal of Botany, 2004, 91, 1007-1021.	0.8	83
90	Patterns of genetic variation in <i>Phialocephala fortinii</i> across a broad latitudinal transect in Canada. Mycological Research, 2004, 108, 955-964.	2.5	40

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91	The imbalanced supertree of flowering-plant phylogeny. <i>Genome Biology</i> , 2004, 5, 236.	13.9	0
92	Parallel Loss of a Slowly Evolving Intron from Two Closely Related Families in Asparagales. <i>Systematic Botany</i> , 2004, 29, 296-307.	0.2	19
93	Inference of higher-order relationships in the cycads from a large chloroplast data set. <i>Molecular Phylogenetics and Evolution</i> , 2003, 29, 350-359.	1.2	77
94	The Population Structure and Floral Biology of <i>Amborella Trichopoda</i> (Amborellaceae). <i>Annals of the Missouri Botanical Garden</i> , 2003, 90, 466.	1.3	77
95	Rooting Phylogenetic Trees with Distant Outgroups: A Case Study from the Commelinoid Monocots. <i>Molecular Biology and Evolution</i> , 2002, 19, 1769-1781.	3.5	129
96	Characterization of the adenosine deaminase-related growth factor (ADGF) gene family in <i>Drosophila</i> . <i>Gene</i> , 2001, 280, 27-36.	1.0	32
97	Evolutionary significance of an unusual chloroplast DNA inversion found in two basal angiosperm lineages. <i>Current Genetics</i> , 2000, 37, 183-188.	0.8	38
98	Utility of 17 chloroplast genes for inferring the phylogeny of the basal angiosperms. <i>American Journal of Botany</i> , 2000, 87, 1712-1730.	0.8	305
99	Microstructural Changes in Noncoding Chloroplast DNA: Interpretation, Evolution, and Utility of Indels and Inversions in Basal Angiosperm Phylogenetic Inference. <i>International Journal of Plant Sciences</i> , 2000, 161, S83-S96.	0.6	225
100	Phylogenetic Congruence and Discordance Among One Morphological and Three Molecular Data Sets from Pontederiaceae. <i>Systematic Biology</i> , 1998, 47, 545-567.	2.7	104
101	RECONSTRUCTION OF THE EVOLUTION OF REPRODUCTIVE CHARACTERS IN PONTEDERIACEAE USING PHYLOGENETIC EVIDENCE FROM CHLOROPLAST DNA RESTRICTION-SITE VARIATION. <i>Evolution; International Journal of Organic Evolution</i> , 1996, 50, 1454-1469.	1.1	119
102	Reconstruction of the Evolution of Reproductive Characters in Pontederiaceae Using Phylogenetic Evidence from Chloroplast DNA Restriction-Site Variation. <i>Evolution; International Journal of Organic Evolution</i> , 1996, 50, 1454.	1.1	45
103	Phylogenetics of Seed Plants: An Analysis of Nucleotide Sequences from the Plastid Gene <i>rbcl</i> . <i>Annals of the Missouri Botanical Garden</i> , 1993, 80, 528.	1.3	1,708
104	Contrasting patterns of support among plastid genes and genomes for major clades of the monocotyledons. , 0, , 315-349.		10