

Michael S Barker

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

90
papers

7,516
citations

35
h-index

86
g-index

101
ext. papers

10,229
ext. citations

8.4
avg, IF

6.91
L-index

#	Paper	IF	Citations
90	The frequency of polyploid speciation in vascular plants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 13875-9	11.5	847
89	Phylotranscriptomic analysis of the origin and early diversification of land plants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, E4859-68	11.5	835
88	The Selaginella genome identifies genetic changes associated with the evolution of vascular plants. <i>Science</i> , 2011 , 332, 960-3	33.3	622
87	A community-derived classification for extant lycophytes and ferns. <i>Journal of Systematics and Evolution</i> , 2016 , 54, 563-603	2.9	562
86	One thousand plant transcriptomes and the phylogenomics of green plants. <i>Nature</i> , 2019 , 574, 679-685	50.4	529
85	Data access for the 1,000 Plants (1KP) project. <i>GigaScience</i> , 2014 , 3, 17	7.6	403
84	Recently formed polyploid plants diversify at lower rates. <i>Science</i> , 2011 , 333, 1257	33.3	308
83	The butterfly plant arms-race escalated by gene and genome duplications. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 8362-6	11.5	307
82	Multiple paleopolyploidizations during the evolution of the Compositae reveal parallel patterns of duplicate gene retention after millions of years. <i>Molecular Biology and Evolution</i> , 2008 , 25, 2445-55	8.3	264
81	On the relative abundance of autopolyploids and allopolyploids. <i>New Phytologist</i> , 2016 , 210, 391-8	9.8	194
80	Fern genomes elucidate land plant evolution and cyanobacterial symbioses. <i>Nature Plants</i> , 2018 , 4, 460-472	17.5	176
79	Early genome duplications in conifers and other seed plants. <i>Science Advances</i> , 2015 , 1, e1501084	14.3	167
78	Paleopolyploidy in the Brassicales: analyses of the Cleome transcriptome elucidate the history of genome duplications in Arabidopsis and other Brassicales. <i>Genome Biology and Evolution</i> , 2009 , 1, 391-9	3.9	167
77	Rarely successful polyploids and their legacy in plant genomes. <i>Current Opinion in Plant Biology</i> , 2012 , 15, 140-6	9.9	160
76	Probabilistic models of chromosome number evolution and the inference of polyploidy. <i>Systematic Biology</i> , 2010 , 59, 132-44	8.4	148
75	Impact of whole-genome duplication events on diversification rates in angiosperms. <i>American Journal of Botany</i> , 2018 , 105, 348-363	2.7	134
74	De novo characterization of the gametophyte transcriptome in bracken fern, <i>Pteridium aquilinum</i> . <i>BMC Genomics</i> , 2011 , 12, 99	4.5	96

73	Comparative genomic and population genetic analyses indicate highly porous genomes and high levels of gene flow between divergent helianthus species. <i>Evolution; International Journal of Organic Evolution</i> , 2009 , 63, 2061-75	3.8	96
72	Multiple large-scale gene and genome duplications during the evolution of hexapods. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 4713-4718	11.5	80
71	Anthoceros genomes illuminate the origin of land plants and the unique biology of hornworts. <i>Nature Plants</i> , 2020 , 6, 259-272	11.5	77
70	Unfurling Fern Biology in the Genomics Age. <i>BioScience</i> , 2010 , 60, 177-185	5.7	69
69	EvoPipes.net: Bioinformatic Tools for Ecological and Evolutionary Genomics. <i>Evolutionary Bioinformatics</i> , 2010 , 6, 143-9	1.9	68
68	Genomics of Compositae weeds: EST libraries, microarrays, and evidence of introgression. <i>American Journal of Botany</i> , 2012 , 99, 209-18	2.7	66
67	Most Compositae (Asteraceae) are descendants of a paleohexaploid and all share a paleotetraploid ancestor with the Calyceraceae. <i>American Journal of Botany</i> , 2016 , 103, 1203-11	2.7	63
66	Ancient genome duplications during the evolution of kiwifruit (Actinidia) and related Ericales. <i>Annals of Botany</i> , 2010 , 106, 497-504	4.1	60
65	Spreading Winge and flying high: The evolutionary importance of polyploidy after a century of study. <i>American Journal of Botany</i> , 2016 , 103, 1139-45	2.7	58
64	Between two fern genomes. <i>GigaScience</i> , 2014 , 3, 15	7.6	56
63	Methods for studying polyploid diversification and the dead end hypothesis: a reply to Soltis et al. (2014). <i>New Phytologist</i> , 2015 , 206, 27-35	9.8	55
62	Diverse genome organization following 13 independent mesopolyploid events in Brassicaceae contrasts with convergent patterns of gene retention. <i>Plant Journal</i> , 2017 , 91, 3-21	6.9	53
61	Access to RNA-sequencing data from 1,173 plant species: The 1000 Plant transcriptomes initiative (1KP). <i>GigaScience</i> , 2019 , 8,	7.6	52
60	Polyploid plants have faster rates of multivariate niche differentiation than their diploid relatives. <i>Ecology Letters</i> , 2020 , 23, 68-78	10	46
59	Maternal expression relaxes constraint on innovation of the anterior determinant, bicoid. <i>PLoS Genetics</i> , 2005 , 1, e57	6	45
58	Establishing genomic tools and resources for <i>Guizotia abyssinica</i> (L.f.) Cass.-the development of a library of expressed sequence tags, microsatellite loci, and the sequencing of its chloroplast genome. <i>Molecular Ecology Resources</i> , 2010 , 10, 1048-58	8.4	42
57	Genomic inferences of domestication events are corroborated by written records in <i>Brassica rapa</i> . <i>Molecular Ecology</i> , 2017 , 26, 3373-3388	5.7	38
56	Genomics of Compositae crops: reference transcriptome assemblies and evidence of hybridization with wild relatives. <i>Molecular Ecology Resources</i> , 2014 , 14, 166-77	8.4	38

55	The Compositae Tree of Life in the age of phylogenomics. <i>Journal of Systematics and Evolution</i> , 2017 , 55, 405-410	2.9	35
54	Transcriptome and organellar sequencing highlights the complex origin and diversification of allotetraploid <i>Brassica napus</i> . <i>Nature Communications</i> , 2019 , 10, 2878	17.4	34
53	A total evidence approach to understanding phylogenetic relationships and ecological diversity in <i>Selaginella</i> subg. <i>Tetragonostachys</i> . <i>American Journal of Botany</i> , 2013 , 100, 1672-82	2.7	30
52	Assessing the Performance of Ks Plots for Detecting Ancient Whole Genome Duplications. <i>Genome Biology and Evolution</i> , 2018 , 10, 2882-2898	3.9	29
51	The Small Nuclear Genomes of <i>Selaginella</i> Are Associated with a Low Rate of Genome Size Evolution. <i>Genome Biology and Evolution</i> , 2016 , 8, 1516-25	3.9	26
50	Duplications and Turnover in Plant Genomes 2012 , 155-169		24
49	Evolution of the nuclear genome of ferns and lycophytes 175-198		23
48	Karyotype and Genome Evolution in Pteridophytes 2013 , 245-253		22
47	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	30.7	22
46	Is hybridization driving the evolution of climatic niche in <i>Alyssum montanum</i> . <i>American Journal of Botany</i> , 2016 , 103, 1348-57	2.7	19
45	Inferring putative ancient whole-genome duplications in the 1000 Plants (1KP) initiative: access to gene family phylogenies and age distributions. <i>GigaScience</i> , 2020 , 9,	7.6	18
44	Molecular evolution across the Asteraceae: micro- and macroevolutionary processes. <i>Molecular Biology and Evolution</i> , 2011 , 28, 3225-35	8.3	18
43	Gene co-inheritance and gene transfer. <i>Science</i> , 2007 , 315, 1685	33.3	18
42	The <i>Chimonanthus salicifolius</i> genome provides insight into magnoliid evolution and flavonoid biosynthesis. <i>Plant Journal</i> , 2020 , 103, 1910-1923	6.9	17
41	An Evaluation of <i>Sceptridium dissectum</i> (Ophioglossaceae) with ISSR Markers: Implications for <i>Sceptridium</i> Systematics. <i>American Fern Journal</i> , 2003 , 93, 1-19	0.6	15
40	Development of an ultra-dense genetic map of the sunflower genome based on single-feature polymorphisms. <i>PLoS ONE</i> , 2012 , 7, e51360	3.7	12
39	SCARF: maximizing next-generation EST assemblies for evolutionary and population genomic analyses. <i>Bioinformatics</i> , 2009 , 25, 535-6	7.2	12
38	Analysis of the <i>Coptis chinensis</i> genome reveals the diversification of protoberberine-type alkaloids. <i>Nature Communications</i> , 2021 , 12, 3276	17.4	12

37	Patterns and Processes of Diploidization in Land Plants. <i>Annual Review of Plant Biology</i> , 2021 , 72, 387-410.	10.7	10
36	Lepidopteran Soral Crystis on Caribbean Ferns ¹ . <i>Biotropica</i> , 2005 , 37, 314-316	2.3	9
35	Nuclear Genome Size is Positively Correlated with Median LTR-RT Insertion Time in Fern and Lycoplyte Genomes. <i>American Fern Journal</i> , 2019 , 109, 248	0.6	9
34	Phylogeny and multiple independent whole-genome duplication events in the Brassicales. <i>American Journal of Botany</i> , 2020 , 107, 1148-1164	2.7	9
33	Reply to Nakatani and McLysaght: Analyzing deep duplication events. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 1819-1820	11.5	8
32	Transcriptome-derived evidence supports recent polyploidization and a major phylogeographic division in <i>Trithuria submersa</i> (Hydatellaceae, Nymphaeales). <i>New Phytologist</i> , 2016 , 210, 310-23	9.8	8
31	Genes derived from ancient polyploidy have higher genetic diversity and are associated with domestication in <i>Brassica rapa</i> . <i>New Phytologist</i> , 2021 , 230, 372-386	9.8	7
30	Modelling of gene loss propensity in the pangenomes of three Brassica species suggests different mechanisms between polyploids and diploids. <i>Plant Biotechnology Journal</i> , 2021 , 19, 2488-2500	11.6	7
29	A TAXONOMIC REVISION OF CARIBBEAN ADIANTOPSIS (PTERIDACEAE) ^{1,2} . <i>Annals of the Missouri Botanical Garden</i> , 2006 , 93, 371-401	1.8	6
28	Inferring the Demographic History of Inbred Species from Genome-Wide SNP Frequency Data. <i>Molecular Biology and Evolution</i> , 2020 , 37, 2124-2136	8.3	6
27	Polyploids increase overall diversity despite higher turnover than diploids in the Brassicaceae. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020 , 287, 20200962	4.4	6
26	Chromosome-scale inference of hybrid speciation and admixture with convolutional neural networks. <i>Molecular Ecology Resources</i> , 2021 , 21, 2676-2688	8.4	6
25	Multilocus phylogenetic reconstruction informing polyploid relationships of <i>Aconitum</i> subgenus <i>Lycocotnum</i> (Ranunculaceae) in China. <i>Plant Systematics and Evolution</i> , 2017 , 303, 727-744	1.3	5
24	Inferring putative ancient whole genome duplications in the 1000 Plants (1KP) initiative: access to gene family phylogenies and age distributions		4
23	Phylogeny and Multiple Independent Whole-Genome Duplication Events in the Brassicales		4
22	The contributions from the progenitor genomes of the mesopolyploid Brassicaceae are evolutionarily distinct but functionally compatible. <i>Genome Research</i> , 2021 , 31, 799-810	9.7	4
21	Genome size evolution in the diverse insect order Trichoptera.. <i>GigaScience</i> , 2022 , 11,	7.6	4
20	Quantitative visualization of biological data in Google Earth using R2G2, an R CRAN package. <i>Molecular Ecology Resources</i> , 2012 , 12, 1177-9	8.4	3

19	An Adiantopsis Hybrid from Northeastern Argentina and Vicinity. <i>American Fern Journal</i> , 2003 , 93, 42-44	0.6	3
18	Underwater CAM photosynthesis elucidated by Isoetes genome. <i>Nature Communications</i> , 2021 , 12, 6348	17.4	3
17	Chromosome-scale inference of hybrid speciation and admixture with convolutional neural networks		3
16	Polyploidy increases overall diversity despite higher turnover than diploids in the Brassicaceae		3
15	TagSeq for gene expression in non-model plants: A pilot study at the Santa Rita Experimental Range NEON core site. <i>Applications in Plant Sciences</i> , 2020 , 8, e11398	2.3	2
14	A Successful <i>in vitro</i> Propagation Technique for Resurrection Plants of the Selaginellaceae. <i>American Fern Journal</i> , 2017 , 107, 96-104	0.6	2
13	Diverse genome organization following 13 independent mesopolyploid events in Brassicaceae contrasts with convergent patterns of gene retention		2
12	Progress Towards Plant Community Transcriptomics: Pilot RNA-Seq Data from 24 Species of Vascular Plants at Harvard Forest		2
11	Animal chromosome counts reveal a similar range of chromosome numbers but with less polyploidy in animals compared to flowering plants. <i>Journal of Evolutionary Biology</i> , 2021 , 34, 1333-1339	2.3	2
10	A Gneato nuclear genome. <i>Nature Plants</i> , 2018 , 4, 63-64	11.5	1
9	NU-IN: Nucleotide evolution and input module for the EvolSimulator genome simulation platform. <i>BMC Research Notes</i> , 2010 , 3, 217	2.3	1
8	Polyploid plants have faster rates of multivariate climatic niche evolution than their diploid relatives		1
7	Current Status and Future Prospects for Fern and Lycophyte Genomics: Introduction to an American Fern Journal Special Issue. <i>American Fern Journal</i> , 2019 , 109, 177	0.6	1
6	Most Compositae (Asteraceae) are descendants of a paleohexaploid and all share a paleotetraploid ancestor with the Calyceraceae		1
5	TagSeq for gene expression in non-model plants: a pilot study at the Santa Rita Experimental Range NEON core site		1
4	Animal chromosome counts reveal similar range of chromosome numbers but with less polyploidy in animals compared to flowering plants		1
3	Multiple large-scale gene and genome duplications during the evolution of hexapods		1
2	Genome size evolution in the diverse insect order Trichoptera		1

1 Pilot RNA-seq data from 24 species of vascular plants at Harvard Forest. *Applications in Plant Sciences*, **2021**, 9, e11409 2.3 1