Michael S Barker

List of Publications by Year
in descending order

81 papers	11,907 citations	71102 41 h-index	71685 76 g-index
101 all docs	101 docs citations	101 times ranked	10875 citing authors

#	Article	IF	Citations
1	One thousand plant transcriptomes and theÂphylogenomics of green plants. Nature, 2019, 574, 679-685.	27.8	1,162
2	The frequency of polyploid speciation in vascular plants. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 13875-13879.	7.1	1,136
3	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.	7.1	1,123
4	A communityâ€derived classification for extant lycophytes and ferns. Journal of Systematics and Evolution, 2016, 54, 563-603.	3.1	1,040
5	The Selaginella Genome Identifies Genetic Changes Associated with the Evolution of Vascular Plants. Science, 2011, 332, 960-963.	12.6	794
6	Data access for the 1,000 Plants (1KP) project. GigaScience, 2014, 3, 17.	6.4	582
7	The butterfly plant arms-race escalated by gene and genome duplications. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 8362-8366.	7.1	458
8	Recently Formed Polyploid Plants Diversify at Lower Rates. Science, 2011, 333, 1257-1257.	12.6	424
9	Fern genomes elucidate land plant evolution and cyanobacterial symbioses. Nature Plants, 2018, 4, 460-472.	9.3	391
10	On the relative abundance of autopolyploids and allopolyploids. New Phytologist, 2016, 210, 391-398.	7.3	340
11	Multiple Paleopolyploidizations during the Evolution of the Compositae Reveal Parallel Patterns of Duplicate Gene Retention after Millions of Years. Molecular Biology and Evolution, 2008, 25, 2445-2455.	8.9	322
12	Impact of wholeâ€genome duplication events on diversification rates in angiosperms. American Journal of Botany, 2018, 105, 348-363.	1.7	270
13	Early genome duplications in conifers and other seed plants. Science Advances, 2015, 1, e1501084.	10.3	236
14	Paleopolyploidy in the Brassicales: Analyses of the Cleome Transcriptome Elucidate the History of Genome Duplications in Arabidopsis and Other Brassicales. Genome Biology and Evolution, 2009, 1, 391-399.	2.5	226
15	Anthoceros genomes illuminate the origin of land plants and the unique biology of hornworts. Nature Plants, 2020, 6, 259-272.	9.3	225
16	Rarely successful polyploids and their legacy in plant genomes. Current Opinion in Plant Biology, 2012, 15, 140-146.	7.1	209
17	Probabilistic Models of Chromosome Number Evolution and the Inference of Polyploidy. Systematic Biology, 2010, 59, 132-144.	5.6	190
18	Multiple large-scale gene and genome duplications during the evolution of hexapods. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 4713-4718.	7.1	151

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19	Access to RNA-sequencing data from 1,173 plant species: The 1000 Plant transcriptomes initiative (1KP). GigaScience, 2019, 8, .	6.4	118
20	De novo characterization of the gametophyte transcriptome in bracken fern, Pteridium aquilinum. BMC Genomics, 2011, 12, 99.	2.8	113
21	COMPARATIVE GENOMIC AND POPULATION GENETIC ANALYSES INDICATE HIGHLY POROUS GENOMES AND HIGH LEVELS OF GENE FLOW BETWEEN DIVERGENT<i>HELIANTHUS</i>SPECIES. Evolution; International Journal of Organic Evolution, 2009, 63, 2061-2075.	2.3	107
22	Polyploid plants have faster rates of multivariate niche differentiation than their diploid relatives. Ecology Letters, 2020, 23, 68-78.	6.4	106
23	Most Compositae (Asteraceae) are descendants of a paleohexaploid and all share a paleotetraploid ancestor with the Calyceraceae. American Journal of Botany, 2016, 103, 1203-1211.	1.7	98
24	Diverse genome organization following 13 independent mesopolyploid events in Brassicaceae contrasts with convergent patterns of gene retention. Plant Journal, 2017, 91, 3-21.	5.7	95
25	Unfurling Fern Biology in the Genomics Age. BioScience, 2010, 60, 177-185.	4.9	90
26	Ancient genome duplications during the evolution of kiwifruit (Actinidia) and related Ericales. Annals of Botany, 2010, 106, 497-504.	2.9	87
27	EvoPipes.net: Bioinformatic Tools for Ecological and Evolutionary Genomics. Evolutionary Bioinformatics, 2010, 6, EBO.S5861.	1.2	83
28	Methods for studying polyploid diversification and the dead end hypothesis: a reply to Soltis <i>etÂal</i>. (2014). New Phytologist, 2015, 206, 27-35.	7.3	82
29	Spreading Winge and flying high: The evolutionary importance of polyploidy after a century of study. American Journal of Botany, 2016, 103, 1139-1145.	1.7	81
30	Genomics of Compositae weeds: EST libraries, microarrays, and evidence of introgression. American Journal of Botany, 2012, 99, 209-218.	1.7	80
31	Transcriptome and organellar sequencing highlights the complex origin and diversification of allotetraploid Brassica napus. Nature Communications, 2019, 10, 2878.	12.8	78
32	Patterns and Processes of Diploidization in Land Plants. Annual Review of Plant Biology, 2021, 72, 387-410.	18.7	76
33	Between Two Fern Genomes. GigaScience, 2014, 3, 15.	6.4	69
34	Analysis of the Coptis chinensis genome reveals the diversification of protoberberine-type alkaloids. Nature Communications, 2021, 12, 3276.	12.8	68
35	Genomic inferences of domestication events are corroborated by written records in <i>Brassica rapa</i>. Molecular Ecology, 2017, 26, 3373-3388.	3.9	66
36	The Compositae Tree of Life in the age of phylogenomics. Journal of Systematics and Evolution, 2017, 55, 405-410.	3.1	61

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37	Assessing the performance of Ks plots for detecting ancient whole genome duplications. Genome Biology and Evolution, 2018, 10, 2882-2898.	2.5	60
38	Underwater CAM photosynthesis elucidated by Isoetes genome. Nature Communications, 2021, 12, 6348.	12.8	56
39	Maternal Expression Relaxes Constraint on Innovation of the Anterior Determinant, bicoid. PLoS Genetics, 2005, 1, e57.	3.5	55
40	Establishing genomic tools and resources for <i>Guizotia abyssinica</i> (L.f.) Cass.â€"the development of a library of expressed sequence tags, microsatellite loci, and the sequencing of its chloroplast genome. Molecular Ecology Resources, 2010, 10, 1048-1058.	4.8	52
41	A total evidence approach to understanding phylogenetic relationships and ecological diversity in <i>Selaginella</i> subg. <i>Tetragonostachys</i>. American Journal of Botany, 2013, 100, 1672-1682.	1.7	50
42	Inferring putative ancient whole-genome duplications in the 1000 Plants (1KP) initiative: access to gene family phylogenies and age distributions. GigaScience, 2020, 9, .	6.4	49
43	Genomics of <scp>C</scp>ompositae crops: reference transcriptome assemblies and evidence of hybridization with wild relatives. Molecular Ecology Resources, 2014, 14, 166-177.	4.8	45
44	Modelling of gene loss propensity in the pangenomes of three <i>Brassica</i> species suggests different mechanisms between polyploids and diploids. Plant Biotechnology Journal, 2021, 19, 2488-2500.	8.3	44
45	Is hybridization driving the evolution of climatic niche in <i>Alyssum montanum</i>. American Journal of Botany, 2016, 103, 1348-1357.	1.7	43
46	Sequencing and Analyzing the Transcriptomes of a Thousand Species Across the Tree of Life for Green Plants. Annual Review of Plant Biology, 2020, 71, 741-765.	18.7	41
47	The <i>Chimonanthus salicifolius</i> genome provides insight into magnoliid evolution and flavonoid biosynthesis. Plant Journal, 2020, 103, 1910-1923.	5.7	41
48	Duplications and Turnover in Plant Genomes. , 2012, , 155-169.		34
49	Evolution of the nuclear genome of ferns and lycophytes. , 2008, , 175-198.		32
50	Phylogeny and multiple independent wholeâ€genome duplication events in the Brassicales. American Journal of Botany, 2020, 107, 1148-1164.	1.7	32
51	Karyotype and Genome Evolution in Pteridophytes. , 2013, , 245-253.		31
52	The Small Nuclear Genomes of<i>Selaginella</i>Are Associated with a Low Rate of Genome Size Evolution. Genome Biology and Evolution, 2016, 8, 1516-1525.	2.5	29
53	Genes derived from ancient polyploidy have higher genetic diversity and are associated with domestication in <i>Brassica rapa</i>. New Phytologist, 2021, 230, 372-386.	7.3	26
54	Inferring the Demographic History of Inbred Species from Genome-Wide SNP Frequency Data. Molecular Biology and Evolution, 2020, 37, 2124-2136.	8.9	24

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55	Genome size evolution in the diverse insect order Trichoptera. GigaScience, 2022, 11, .	6.4	24
56	Gene Co-Inheritance and Gene Transfer. Science, 2007, 315, 1685-1685.	12.6	22
57	The contributions from the progenitor genomes of the mesopolyploid Brassiceae are evolutionarily distinct but functionally compatible. Genome Research, 2021, 31, 799-810.	5.5	21
58	Molecular Evolution across the Asteraceae: Micro- and Macroevolutionary Processes. Molecular Biology and Evolution, 2011, 28, 3225-3235.	8.9	19
59	Reply to Nakatani and McLysaght: Analyzing deep duplication events. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 1819-1820.	7.1	17
60	An Evaluation of Sceptridium dissectum (Ophioglossaceae) with ISSR Markers: Implications for Sceptridium Systematics. American Fern Journal, 2003, 93, 1-19.	0.3	16
61	Nuclear Genome Size is Positively Correlated with Median LTR-RT Insertion Time in Fern and Lycophyte Genomes. American Fern Journal, 2019, 109, 248.	0.3	16
62	Animal chromosome counts reveal a similar range of chromosome numbers but with less polyploidy in animals compared to flowering plants. Journal of Evolutionary Biology, 2021, 34, 1333-1339.	1.7	14
63	SCARF: maximizing next-generation EST assemblies for evolutionary and population genomic analyses. Bioinformatics, 2009, 25, 535-536.	4.1	13
64	Polyploids increase overall diversity despite higher turnover than diploids in the Brassicaceae. Proceedings of the Royal Society B: Biological Sciences, 2020, 287, 20200962.	2.6	13
65	Chromosomeâ€scale inference of hybrid speciation and admixture with convolutional neural networks. Molecular Ecology Resources, 2021, 21, 2676-2688.	4.8	13
66	Development of an Ultra-Dense Genetic Map of the Sunflower Genome Based on Single-Feature Polymorphisms. PLoS ONE, 2012, 7, e51360.	2.5	12
67	Lepidopteran Soral Crypsis on Caribbean Ferns1. Biotropica, 2005, 37, 314-316.	1.6	11
68	Transcriptomeâ€derived evidence supports recent polyploidization and a major phylogeographic division in T rithuria submersa (H ydatellaceae, N ymphaeales). New Phytologist, 2016, 210, 310-323.	7.3	10
69	A TAXONOMIC REVISION OF CARIBBEAN ADIANTOPSIS (PTERIDACEAE)^{1,}². Annals of the Missouri Botanical Garden, 2006, 93, 371-401.	1.3	8
70	Multilocus phylogenetic reconstruction informing polyploid relationships of Aconitum subgenus Lycoctonum (Ranunculaceae) in China. Plant Systematics and Evolution, 2017, 303, 727-744.	0.9	8
71	A Successful<i>in vitro</i>Propagation Technique for Resurrection Plants of the Selaginellaceae. American Fern Journal, 2017, 107, 96-104.	0.3	6
72	An Adiantopsis Hybrid from Northeastern Argentina and Vicinity. American Fern Journal, 2003, 93, 42-44.	0.3	5

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73	Quantitative visualization of biological data in G oogle E arth using R 2 G 2, an R CRAN package. Molecular Ecology Resources, 2012, 12, 1177-1179.	4.8	4
74	TagSeq for gene expression in nonâ€model plants: A pilot study at the Santa Rita Experimental Range NEON core site. Applications in Plant Sciences, 2020, 8, e11398.	2.1	4
75	Chromosome-Scale Genome Assembly of <i>Gilia yorkii</i> Enables Genetic Mapping of Floral Traits in an Interspecies Cross. Genome Biology and Evolution, 2022, 14, .	2.5	4
76	Pilot RNAâ€seq data from 24 species of vascular plants at Harvard Forest. Applications in Plant Sciences, 2021, 9, e11409.	2.1	3
77	NU-IN: Nucleotide evolution and input module for the EvolSimulator genome simulation platform. BMC Research Notes, 2010, 3, 217.	1.4	1
78	A Gneato nuclear genome. Nature Plants, 2018, 4, 63-64.	9.3	1
79	Current Status and Future Prospects for Fern and Lycophyte Genomics: Introduction to an American Fern Journal Special Issue. American Fern Journal, 2019, 109, 177.	0.3	1
80	Botrychium lanceolatum subsp. angustisegmentum in Ohio. American Fern Journal, 2003, 93, 93-94.	0.3	0
81	Contribution to The Pteridophyte Flora of Puerto Rico. American Fern Journal, 2008, 98, 107-111.	0.3	0