

Michael S Barker

List of Publications by Year in descending order

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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	Chromosome-Scale Genome Assembly of <i>Gilia yorkii</i> Enables Genetic Mapping of Floral Traits in an Interspecies Cross. <i>Genome Biology and Evolution</i> , 2022, 14, .	2.5	4
2	Genome size evolution in the diverse insect order Trichoptera. <i>GigaScience</i> , 2022, 11, .	6.4	24
3	Pilot RNA-seq data from 24 species of vascular plants at Harvard Forest. <i>Applications in Plant Sciences</i> , 2021, 9, e11409.	2.1	3
4	Chromosome-scale inference of hybrid speciation and admixture with convolutional neural networks. <i>Molecular Ecology Resources</i> , 2021, 21, 2676-2688.	4.8	13
5	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.	7.3	26
6	The contributions from the progenitor genomes of the mesopolyploid Brassiceae are evolutionarily distinct but functionally compatible. <i>Genome Research</i> , 2021, 31, 799-810.	5.5	21
7	Analysis of the <i>Coptis chinensis</i> genome reveals the diversification of protoberberine-type alkaloids. <i>Nature Communications</i> , 2021, 12, 3276.	12.8	68
8	Patterns and Processes of Diploidization in Land Plants. <i>Annual Review of Plant Biology</i> , 2021, 72, 387-410.	18.7	76
9	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.	1.7	14
10	Modelling of gene loss propensity in the pangenomes of three <i>Brassica</i> species suggests different mechanisms between polyploids and diploids. <i>Plant Biotechnology Journal</i> , 2021, 19, 2488-2500.	8.3	44
11	Underwater CAM photosynthesis elucidated by <i>Isoetes</i> genome. <i>Nature Communications</i> , 2021, 12, 6348.	12.8	56
12	Polyploid plants have faster rates of multivariate niche differentiation than their diploid relatives. <i>Ecology Letters</i> , 2020, 23, 68-78.	6.4	106
13	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.	18.7	41
14	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.	2.6	13
15	Phylogeny and multiple independent whole-genome duplication events in the Brassicales. <i>American Journal of Botany</i> , 2020, 107, 1148-1164.	1.7	32
16	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.	2.1	4
17	The <i>Chimonanthus salicifolius</i> genome provides insight into magnoliid evolution and flavonoid biosynthesis. <i>Plant Journal</i> , 2020, 103, 1910-1923.	5.7	41
18	Anthoceros genomes illuminate the origin of land plants and the unique biology of hornworts. <i>Nature Plants</i> , 2020, 6, 259-272.	9.3	225

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19	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, .	6.4	49
20	Inferring the Demographic History of Inbred Species from Genome-Wide SNP Frequency Data. <i>Molecular Biology and Evolution</i> , 2020, 37, 2124-2136.	8.9	24
21	Transcriptome and organellar sequencing highlights the complex origin and diversification of allotetraploid <i>Brassica napus</i> . <i>Nature Communications</i> , 2019, 10, 2878.	12.8	78
22	Access to RNA-sequencing data from 1,173 plant species: The 1000 Plant transcriptomes initiative (1KP). <i>GigaScience</i> , 2019, 8, .	6.4	118
23	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.	7.1	17
24	One thousand plant transcriptomes and the phylogenomics of green plants. <i>Nature</i> , 2019, 574, 679-685.	27.8	1,162
25	Nuclear Genome Size is Positively Correlated with Median LTR-RT Insertion Time in Fern and Lycophyte Genomes. <i>American Fern Journal</i> , 2019, 109, 248.	0.3	16
26	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.	0.3	1
27	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.	7.1	151
28	A Gneato nuclear genome. <i>Nature Plants</i> , 2018, 4, 63-64.	9.3	1
29	Impact of whole-genome duplication events on diversification rates in angiosperms. <i>American Journal of Botany</i> , 2018, 105, 348-363.	1.7	270
30	Assessing the performance of Ks plots for detecting ancient whole genome duplications. <i>Genome Biology and Evolution</i> , 2018, 10, 2882-2898.	2.5	60
31	Fern genomes elucidate land plant evolution and cyanobacterial symbioses. <i>Nature Plants</i> , 2018, 4, 460-472.	9.3	391
32	Genomic inferences of domestication events are corroborated by written records in <i>Brassica rapa</i> . <i>Molecular Ecology</i> , 2017, 26, 3373-3388.	3.9	66
33	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.	5.7	95
34	Multilocus phylogenetic reconstruction informing polyploid relationships of <i>Aconitum</i> subgenus <i>Lycoctonum</i> (Ranunculaceae) in China. <i>Plant Systematics and Evolution</i> , 2017, 303, 727-744.	0.9	8
35	A Successful <i>in vitro</i> Propagation Technique for Resurrection Plants of the Selaginellaceae. <i>American Fern Journal</i> , 2017, 107, 96-104.	0.3	6
36	The Compositae Tree of Life in the age of phylogenomics. <i>Journal of Systematics and Evolution</i> , 2017, 55, 405-410.	3.1	61

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37	A community-derived classification for extant lycophytes and ferns. <i>Journal of Systematics and Evolution</i> , 2016, 54, 563-603.	3.1	1,040
38	On the relative abundance of autopolyploids and allopolyploids. <i>New Phytologist</i> , 2016, 210, 391-398.	7.3	340
39	Is hybridization driving the evolution of climatic niche in <i>Alyssum montanum</i> . <i>American Journal of Botany</i> , 2016, 103, 1348-1357.	1.7	43
40	Spreading Wings and flying high: The evolutionary importance of polyploidy after a century of study. <i>American Journal of Botany</i> , 2016, 103, 1139-1145.	1.7	81
41	Transcriptome-derived evidence supports recent polyploidization and a major phylogeographic division in <i>Trituraria submersa</i> (Hydrocharitaceae, Nymphaeales). <i>New Phytologist</i> , 2016, 210, 310-323.	7.3	10
42	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, 1516-1525.	2.5	29
43	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, 1203-1211.	1.7	98
44	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.	7.3	82
45	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, 8362-8366.	7.1	458
46	Early genome duplications in conifers and other seed plants. <i>Science Advances</i> , 2015, 1, e1501084.	10.3	236
47	Between Two Fern Genomes. <i>GigaScience</i> , 2014, 3, 15.	6.4	69
48	Data access for the 1,000 Plants (1KP) project. <i>GigaScience</i> , 2014, 3, 17.	6.4	582
49	Genomics of Compositae crops: reference transcriptome assemblies and evidence of hybridization with wild relatives. <i>Molecular Ecology Resources</i> , 2014, 14, 166-177.	4.8	45
50	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.	7.1	1,123
51	Karyotype and Genome Evolution in Pteridophytes. , 2013, , 245-253.		31
52	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, 1672-1682.	1.7	50
53	Quantitative visualization of biological data in Google Earth using R2G2, an R CRAN package. <i>Molecular Ecology Resources</i> , 2012, 12, 1177-1179.	4.8	4
54	Genomics of Compositae weeds: EST libraries, microarrays, and evidence of introgression. <i>American Journal of Botany</i> , 2012, 99, 209-218.	1.7	80

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55	Development of an Ultra-Dense Genetic Map of the Sunflower Genome Based on Single-Feature Polymorphisms. <i>PLoS ONE</i> , 2012, 7, e51360.	2.5	12
56	Duplications and Turnover in Plant Genomes. , 2012, , 155-169.		34
57	Rarely successful polyploids and their legacy in plant genomes. <i>Current Opinion in Plant Biology</i> , 2012, 15, 140-146.	7.1	209
58	The <i>Selaginella</i> Genome Identifies Genetic Changes Associated with the Evolution of Vascular Plants. <i>Science</i> , 2011, 332, 960-963.	12.6	794
59	Recently Formed Polyploid Plants Diversify at Lower Rates. <i>Science</i> , 2011, 333, 1257-1257.	12.6	424
60	De novo characterization of the gametophyte transcriptome in bracken fern, <i>Pteridium aquilinum</i> . <i>BMC Genomics</i> , 2011, 12, 99.	2.8	113
61	Molecular Evolution across the Asteraceae: Micro- and Macroevolutionary Processes. <i>Molecular Biology and Evolution</i> , 2011, 28, 3225-3235.	8.9	19
62	NU-IN: Nucleotide evolution and input module for the EvolSimulator genome simulation platform. <i>BMC Research Notes</i> , 2010, 3, 217.	1.4	1
63	Ancient genome duplications during the evolution of kiwifruit (<i>Actinidia</i>) and related Ericales. <i>Annals of Botany</i> , 2010, 106, 497-504.	2.9	87
64	EvoPipes.net: Bioinformatic Tools for Ecological and Evolutionary Genomics. <i>Evolutionary Bioinformatics</i> , 2010, 6, EBO.S5861.	1.2	83
65	Unfurling Fern Biology in the Genomics Age. <i>BioScience</i> , 2010, 60, 177-185.	4.9	90
66	Probabilistic Models of Chromosome Number Evolution and the Inference of Polyploidy. <i>Systematic Biology</i> , 2010, 59, 132-144.	5.6	190
67	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. <i>Molecular Ecology Resources</i> , 2010, 10, 1048-1058.	4.8	52
68	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, 13875-13879.	7.1	1,136
69	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, 391-399.	2.5	226
70	SCARF: maximizing next-generation EST assemblies for evolutionary and population genomic analyses. <i>Bioinformatics</i> , 2009, 25, 535-536.	4.1	13
71	COMPARATIVE GENOMIC AND POPULATION GENETIC ANALYSES INDICATE HIGHLY POROUS GENOMES AND HIGH LEVELS OF GENE FLOW BETWEEN DIVERGENT <i>HELIANTHUS</i> SPECIES. <i>Evolution; International Journal of Organic Evolution</i> , 2009, 63, 2061-2075.	2.3	107
72	Contribution to The Pteridophyte Flora of Puerto Rico. <i>American Fern Journal</i> , 2008, 98, 107-111.	0.3	0

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73	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, 2445-2455.	8.9	322
74	Evolution of the nuclear genome of ferns and lycophytes. , 2008, , 175-198.		32
75	Gene Co-Inheritance and Gene Transfer. <i>Science</i> , 2007, 315, 1685-1685.	12.6	22
76	A TAXONOMIC REVISION OF CARIBBEAN ADIANTOPSIS (PTERIDACEAE) ^{1,}². <i>Annals of the Missouri Botanical Garden</i> , 2006, 93, 371-401.	1.3	8
77	Lepidopteran Soral Crpsis on Caribbean Ferns1. <i>Biotropica</i> , 2005, 37, 314-316.	1.6	11
78	Maternal Expression Relaxes Constraint on Innovation of the Anterior Determinant, bicoid. <i>PLoS Genetics</i> , 2005, 1, e57.	3.5	55
79	An Adiantopsis Hybrid from Northeastern Argentina and Vicinity. <i>American Fern Journal</i> , 2003, 93, 42-44.	0.3	5
80	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.	0.3	16
81	<i>Botrychium lanceolatum</i> subsp. <i>angustisegmentum</i> in Ohio. <i>American Fern Journal</i> , 2003, 93, 93-94.	0.3	0