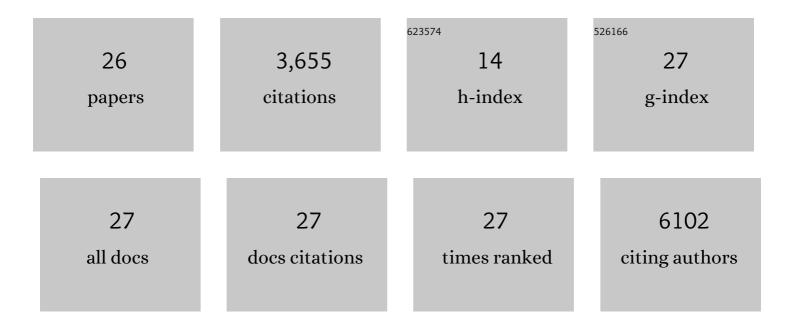
Chunfang Zheng

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/10186150/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Two divergent haplotypes from a highly heterozygous lychee genome suggest independent domestication events for early and late-maturing cultivars. Nature Genetics, 2022, 54, 73-83.	9.4	88
2	Genome sequence and evolution of <i>Betula platyphylla</i> . Horticulture Research, 2021, 8, 37.	2.9	53
3	The contributions from the progenitor genomes of the mesopolyploid Brassiceae are evolutionarily distinct but functionally compatible. Genome Research, 2021, 31, 799-810.	2.4	21
4	Integrated synteny- and similarity-based inference on the polyploidization–fractionation cycle. Interface Focus, 2021, 11, 20200059.	1.5	5
5	RACCROCHE: Ancestral Flowering Plant Chromosomes and Gene Orders Based on Generalized Adjacencies and Chromosomal Gene Co-occurrences. Lecture Notes in Computer Science, 2021, , 97-115.	1.0	4
6	The monoploid chromosome complement of reconstructed ancestral genomes in a phylogeny. Journal of Bioinformatics and Computational Biology, 2021, 19, 2140008.	0.3	1
7	Ancestral Flowering Plant Chromosomes and Gene Orders Based on Generalized Adjacencies and Chromosomal Gene Co-Occurrences. Journal of Computational Biology, 2021, 28, 1156-1179.	0.8	6
8	A high-contiguity Brassica nigra genome localizes active centromeres and defines the ancestral Brassica genome. Nature Plants, 2020, 6, 929-941.	4.7	94
9	Excision Dominates Pseudogenization During Fractionation After Whole Genome Duplication and in Gene Loss After Speciation in Plants. Frontiers in Genetics, 2020, 11, 603056.	1.1	5
10	A branching process for homology distribution-based inference of polyploidy, speciation and loss. Algorithms for Molecular Biology, 2019, 14, 18.	0.3	4
11	The avocado genome informs deep angiosperm phylogeny, highlights introgressive hybridization, and reveals pathogen-influenced gene space adaptation. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 17081-17089.	3.3	134
12	Distinguishing successive ancient polyploidy levels based on genome-internal syntenic alignment. BMC Bioinformatics, 2019, 20, 635.	1.2	3
13	Whole Genome Duplication in Plants: Implications for Evolutionary Analysis. Methods in Molecular Biology, 2018, 1704, 291-315.	0.4	15
14	Allele-defined genome of the autopolyploid sugarcane Saccharum spontaneum L Nature Genetics, 2018, 50, 1565-1573.	9.4	463
15	Resolution effects in reconstructing ancestral genomes. BMC Genomics, 2018, 19, 100.	1.2	2
16	Pinning down ploidy in paleopolyploid plants. BMC Genomics, 2018, 19, 287.	1.2	10
17	Genome of the pitcher plant Cephalotus reveals genetic changes associated with carnivory. Nature Ecology and Evolution, 2017, 1, 59.	3.4	99
18	Long-read sequencing uncovers the adaptive topography of a carnivorous plant genome. Proceedings of the United States of America, 2017, 114, F4435-F4441	3.3	95

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19	The nuclear genome of Rhazya stricta and the evolution of alkaloid diversity in a medically relevant clade of Apocynaceae. Scientific Reports, 2016, 6, 33782.	1.6	26
20	Locating rearrangement events in a phylogeny based on highly fragmented assemblies. BMC Genomics, 2016, 17, 1.	1.2	740
21	The pineapple genome and the evolution of CAM photosynthesis. Nature Genetics, 2015, 47, 1435-1442.	9.4	472
22	Practical halving; the Nelumbo nucifera evidence on early eudicot evolution. Computational Biology and Chemistry, 2014, 50, 75-81.	1.1	6
23	The coffee genome provides insight into the convergent evolution of caffeine biosynthesis. Science, 2014, 345, 1181-1184.	6.0	520
24	The <i>Amborella</i> Genome and the Evolution of Flowering Plants. Science, 2013, 342, 1241089.	6.0	743
25	Ancient eudicot hexaploidy meets ancestral eurosid gene order. BMC Genomics, 2013, 14, S3.	1.2	29
26	Gene order in rosid phylogeny, inferred from pairwise syntenies among extant genomes. BMC Bioinformatics, 2012, 13, S9.	1.2	7