

# Chunfang Zheng

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/10186150/publications.pdf>

Version: 2024-02-01

26  
papers

3,655  
citations

623574

14  
h-index

526166

27  
g-index

27  
all docs

27  
docs citations

27  
times ranked

6102  
citing authors

#	ARTICLE	IF	CITATIONS
1	The <i>Amborella</i> Genome and the Evolution of Flowering Plants. <i>Science</i> , 2013, 342, 1241089.	6.0	743
2	Locating rearrangement events in a phylogeny based on highly fragmented assemblies. <i>BMC Genomics</i> , 2016, 17, 1.	1.2	740
3	The coffee genome provides insight into the convergent evolution of caffeine biosynthesis. <i>Science</i> , 2014, 345, 1181-1184.	6.0	520
4	The pineapple genome and the evolution of CAM photosynthesis. <i>Nature Genetics</i> , 2015, 47, 1435-1442.	9.4	472
5	Allele-defined genome of the autopolyploid sugarcane <i>Saccharum spontaneum</i> L.. <i>Nature Genetics</i> , 2018, 50, 1565-1573.	9.4	463
6	The avocado genome informs deep angiosperm phylogeny, highlights introgressive hybridization, and reveals pathogen-influenced gene space adaptation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 17081-17089.	3.3	134
7	Genome of the pitcher plant <i>Cephalotus</i> reveals genetic changes associated with carnivory. <i>Nature Ecology and Evolution</i> , 2017, 1, 59.	3.4	99
8	Long-read sequencing uncovers the adaptive topography of a carnivorous plant genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E4435-E4441.	3.3	95
9	A high-contiguity <i>Brassica nigra</i> genome localizes active centromeres and defines the ancestral <i>Brassica</i> genome. <i>Nature Plants</i> , 2020, 6, 929-941.	4.7	94
10	Two divergent haplotypes from a highly heterozygous lychee genome suggest independent domestication events for early and late-maturing cultivars. <i>Nature Genetics</i> , 2022, 54, 73-83.	9.4	88
11	Genome sequence and evolution of <i>Betula platyphylla</i> . <i>Horticulture Research</i> , 2021, 8, 37.	2.9	53
12	Ancient eudicot hexaploidy meets ancestral eurosoid gene order. <i>BMC Genomics</i> , 2013, 14, S3.	1.2	29
13	The nuclear genome of <i>Rhazya stricta</i> and the evolution of alkaloid diversity in a medically relevant clade of Apocynaceae. <i>Scientific Reports</i> , 2016, 6, 33782.	1.6	26
14	The contributions from the progenitor genomes of the mesopolyploid Brassiceae are evolutionarily distinct but functionally compatible. <i>Genome Research</i> , 2021, 31, 799-810.	2.4	21
15	Whole Genome Duplication in Plants: Implications for Evolutionary Analysis. <i>Methods in Molecular Biology</i> , 2018, 1704, 291-315.	0.4	15
16	Pinning down ploidy in paleopolyploid plants. <i>BMC Genomics</i> , 2018, 19, 287.	1.2	10
17	Gene order in rosoid phylogeny, inferred from pairwise syntenies among extant genomes. <i>BMC Bioinformatics</i> , 2012, 13, S9.	1.2	7
18	Practical halving; the <i>Nelumbo nucifera</i> evidence on early eudicot evolution. <i>Computational Biology and Chemistry</i> , 2014, 50, 75-81.	1.1	6

#	ARTICLE	IF	CITATIONS
19	Ancestral Flowering Plant Chromosomes and Gene Orders Based on Generalized Adjacencies and Chromosomal Gene Co-Occurrences. <i>Journal of Computational Biology</i> , 2021, 28, 1156-1179.	0.8	6
20	Excision Dominates Pseudogenization During Fractionation After Whole Genome Duplication and in Gene Loss After Speciation in Plants. <i>Frontiers in Genetics</i> , 2020, 11, 603056.	1.1	5
21	Integrated synteny- and similarity-based inference on the polyploidization–fractionation cycle. <i>Interface Focus</i> , 2021, 11, 20200059.	1.5	5
22	A branching process for homology distribution-based inference of polyploidy, speciation and loss. <i>Algorithms for Molecular Biology</i> , 2019, 14, 18.	0.3	4
23	RACCROCHE: Ancestral Flowering Plant Chromosomes and Gene Orders Based on Generalized Adjacencies and Chromosomal Gene Co-occurrences. <i>Lecture Notes in Computer Science</i> , 2021, , 97-115.	1.0	4
24	Distinguishing successive ancient polyploidy levels based on genome-internal syntenic alignment. <i>BMC Bioinformatics</i> , 2019, 20, 635.	1.2	3
25	Resolution effects in reconstructing ancestral genomes. <i>BMC Genomics</i> , 2018, 19, 100.	1.2	2
26	The monoploid chromosome complement of reconstructed ancestral genomes in a phylogeny. <i>Journal of Bioinformatics and Computational Biology</i> , 2021, 19, 2140008.	0.3	1