

Zhen-Xiang Xi

List of Publications by Year in descending order

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Version: 2024-02-01

45
papers

2,905
citations

236912
25
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223791
46
g-index

51
all docs

51
docs citations

51
times ranked

3667
citing authors

#	ARTICLE	IF	CITATIONS
1	Diversity patterns and conservation gaps of Magnoliaceae species in China. <i>Science of the Total Environment</i> , 2022, 813, 152665.	8.0	11
2	Species Tree Estimation and the Impact of Gene Loss Following Whole-Genome Duplication. <i>Systematic Biology</i> , 2022, 71, 1348-1361.	5.6	10
3	Warming-induced increase in carbon uptake is linked to earlier spring phenology in temperate and boreal forests. <i>Nature Communications</i> , 2022, 13, .	12.8	27
4	Phylotranscriptomics reveals extensive gene duplication in the subtribe Gentianinae (Gentianaceae). <i>Journal of Systematics and Evolution</i> , 2021, 59, 1198-1208.	3.1	21
5	The Perfect Storm: Gene Tree Estimation Error, Incomplete Lineage Sorting, and Ancient Gene Flow Explain the Most Recalcitrant Ancient Angiosperm Clade, Malpighiales. <i>Systematic Biology</i> , 2021, 70, 491-507.	5.6	61
6	A chromosome-level genome assembly for the tertiary relict plant <i>Tetracentron sinense</i> Oliv. (Trochodendraceae). <i>Molecular Ecology Resources</i> , 2021, 21, 1186-1199.	4.8	12
7	Population Transcriptomics Reveals Gene Flow and Introgression Between Two Non-sister Alpine Gentians. <i>Frontiers in Ecology and Evolution</i> , 2021, 9, .	2.2	2
8	Deeply Altered Genome Architecture in the Endoparasitic Flowering Plant <i>Sapria himalayana</i> Griff. (Rafflesiaceae). <i>Current Biology</i> , 2021, 31, 1002-1011.e9.	3.9	63
9	Genome-wide (ChIP-seq) identification of target genes regulated by WRKY33 during submergence stress in <i>Arabidopsis</i> . <i>BMC Genomic Data</i> , 2021, 22, 16.	1.7	5
10	A chromosome-level <i>Camptotheca acuminata</i> genome assembly provides insights into the evolutionary origin of camptothecin biosynthesis. <i>Nature Communications</i> , 2021, 12, 3531.	12.8	66
11	Chromosome-level genome assembly of Sichuan pepper provides insights into apomixis, drought tolerance, and alkaloid biosynthesis. <i>Molecular Ecology Resources</i> , 2021, 21, 2533-2545.	4.8	30
12	Contrasting temporal variations in responses of leaf unfolding to daytime and nighttime warming. <i>Global Change Biology</i> , 2021, 27, 5084-5093.	9.5	20
13	The Conservation of Chloroplast Genome Structure and Improved Resolution of Intrafamilial Relationships of Crassulaceae. <i>Frontiers in Plant Science</i> , 2021, 12, 631884.	3.6	16
14	Genome evolution of the psammophyte <i>Pugionium</i> for desert adaptation and further speciation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	22
15	Phylogenomics of the genus <i>Populus</i> reveals extensive interspecific gene flow and balancing selection. <i>New Phytologist</i> , 2020, 225, 1370-1382.	7.3	93
16	A chromosome-scale reference genome of <i>Lobularia maritima</i> , an ornamental plant with high stress tolerance. <i>Horticulture Research</i> , 2020, 7, 197.	6.3	6
17	Water lily (<i>Nymphaea thermarum</i>) genome reveals variable genomic signatures of ancient vascular cambium losses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 8649-8656.	7.1	33
18	Prickly waterlily and rigid hornwort genomes shed light on early angiosperm evolution. <i>Nature Plants</i> , 2020, 6, 215-222.	9.3	88

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19	Machine learning predicts large scale declines in native plant phylogenetic diversity. <i>New Phytologist</i> , 2020, 227, 1544-1556.	7.3	19
20	Widespread ancient whole-genome duplications in Malpighiales coincide with Eocene global climatic upheaval. <i>New Phytologist</i> , 2019, 221, 565-576.	7.3	86
21	Intergeneric Relationships within the Family Salicaceae s.l. based on Plastid Phylogenomics. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3788.	4.1	18
22	The complete chloroplast genome of the endangered species <i>Oyama sinensis</i> (Magnoliaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 830-831.	0.4	1
23	A chromosome-level genome assembly of the Chinese tupelo <i>Nyssa sinensis</i> . <i>Scientific Data</i> , 2019, 6, 282.	5.3	10
24	The complete plastome of <i>Nyssa yunnanensis</i> , a critically endangered tree species. <i>Conservation Genetics Resources</i> , 2019, 11, 313-315.	0.8	1
25	Shifts in plant distributions in response to climate warming in a biodiversity hotspot, the Hengduan Mountains. <i>Journal of Biogeography</i> , 2018, 45, 1334-1344.	3.0	115
26	Taxon sampling effects on the quantification and comparison of community phylogenetic diversity. <i>Molecular Ecology</i> , 2018, 27, 1296-1308.	3.9	34
27	Ancient polymorphisms and divergence hitchhiking contribute to genomic islands of divergence within a poplar species complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E236-E243.	7.1	126
28	Plastome phylogeny and lineage diversification of Salicaceae with focus on poplars and willows. <i>Ecology and Evolution</i> , 2018, 8, 7817-7823.	1.9	47
29	Unraveling the biogeographical history of Chrysobalanaceae from plastid genomes. <i>American Journal of Botany</i> , 2016, 103, 1089-1102.	1.7	20
30	The Impact of Missing Data on Species Tree Estimation. <i>Molecular Biology and Evolution</i> , 2016, 33, 838-860.	8.9	134
31	Implementing and testing the multispecies coalescent model: A valuable paradigm for phylogenomics. <i>Molecular Phylogenetics and Evolution</i> , 2016, 94, 447-462.	2.7	321
32	Phylogeny of Elatinaceae and the Tropical Gondwanan Origin of the Centroplacaceae (Malpighiaceae). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf</i>	2.5	22
33	Estimating phylogenetic trees from genome-scale data. <i>Annals of the New York Academy of Sciences</i> , 2015, 1360, 36-53.	3.8	165
34	Horizontal gene transfer in parasitic plants. <i>Current Opinion in Plant Biology</i> , 2015, 26, 14-19.	7.1	78
35	Phylogeny of Gracilariaceae (Rhodophyta): evidence from plastid and mitochondrial nucleotide sequences. <i>Journal of Phycology</i> , 2015, 51, 356-366.	2.3	38
36	Genes with minimal phylogenetic information are problematic for coalescent analyses when gene tree estimation is biased. <i>Molecular Phylogenetics and Evolution</i> , 2015, 92, 63-71.	2.7	104

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37	Coalescent Methods Are Robust to the Simultaneous Effects of Long Branches and Incomplete Lineage Sorting. <i>Molecular Biology and Evolution</i> , 2015, 32, 791-805.	8.9	69
38	The establishment of Central American migratory corridors and the biogeographic origins of seasonally dry tropical forests in Mexico. <i>Frontiers in Genetics</i> , 2014, 5, 433.	2.3	32
39	Coalescent versus Concatenation Methods and the Placement of Amborella as Sister to Water Lilies. <i>Systematic Biology</i> , 2014, 63, 919-932.	5.6	166
40	Massive Mitochondrial Gene Transfer in a Parasitic Flowering Plant Clade. <i>PLoS Genetics</i> , 2013, 9, e1003265.	3.5	115
41	Phylogenomics and Coalescent Analyses Resolve Extant Seed Plant Relationships. <i>PLoS ONE</i> , 2013, 8, e80870.	2.5	69
42	Horizontal transfer of expressed genes in a parasitic flowering plant. <i>BMC Genomics</i> , 2012, 13, 227.	2.8	90
43	Phylogenomics and a posteriori data partitioning resolve the Cretaceous angiosperm radiation Malpighiales. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 17519-17524.	7.1	305
44	Phylogenetic Analysis of the Plastid Inverted Repeat for 244 Species: Insights into Deeper-Level Angiosperm Relationships from a Long, Slowly Evolving Sequence Region. <i>International Journal of Plant Sciences</i> , 2011, 172, 541-558.	1.3	80
45	Species delimitation of North American <i>Nyssa</i> species. <i>Journal of Systematics and Evolution</i> , 0, , .	3.1	2