

Ning Zhang

List of Publications by Year in descending order

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29
papers

1,838
citations

471509

17
h-index

642732

23
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29
all docs

29
docs citations

29
times ranked

2717
citing authors

#	ARTICLE	IF	CITATIONS
1	Resolution of deep angiosperm phylogeny using conserved nuclear genes and estimates of early divergence times. <i>Nature Communications</i> , 2014, 5, 4956.	12.8	330
2	Resolution of Brassicaceae Phylogeny Using Nuclear Genes Uncovers Nested Radiations and Supports Convergent Morphological Evolution. <i>Molecular Biology and Evolution</i> , 2016, 33, 394-412.	8.9	259
3	Widespread Whole Genome Duplications Contribute to Genome Complexity and Species Diversity in Angiosperms. <i>Molecular Plant</i> , 2018, 11, 414-428.	8.3	251
4	Highly conserved low-copy nuclear genes as effective markers for phylogenetic analyses in angiosperms. <i>New Phytologist</i> , 2012, 195, 923-937.	7.3	192
5	Resolution of deep eudicot phylogeny and their temporal diversification using nuclear genes from transcriptomic and genomic datasets. <i>New Phytologist</i> , 2017, 214, 1338-1354.	7.3	134
6	Patterns of gene duplication and functional diversification during the evolution of the AP1/SQUA subfamily of plant MADS-box genes. <i>Molecular Phylogenetics and Evolution</i> , 2007, 44, 26-41.	2.7	104
7	Congruent Deep Relationships in the Grape Family (Vitaceae) Based on Sequences of Chloroplast Genomes and Mitochondrial Genes via Genome Skimming. <i>PLoS ONE</i> , 2015, 10, e0144701.	2.5	81
8	Interactions among Proteins of Floral MADS-Box Genes in Basal Eudicots: Implications for Evolution of the Regulatory Network for Flower Development. <i>Molecular Biology and Evolution</i> , 2010, 27, 1598-1611.	8.9	72
9	Chloroplast phylogenomics resolves key relationships in ferns. <i>Journal of Systematics and Evolution</i> , 2015, 53, 448-457.	3.1	64
10	Another look at the phylogenetic position of the grape order Vitales: Chloroplast phylogenomics with an expanded sampling of key lineages. <i>Molecular Phylogenetics and Evolution</i> , 2016, 101, 216-223.	2.7	44
11	Expression patterns of <i>AP1</i> , <i>FUL</i> , <i>FT</i> and <i>LEAFY</i> orthologs in Vitaceae support the homology of tendrils and inflorescences throughout the grape family. <i>Journal of Systematics and Evolution</i> , 2015, 53, 469-476.	3.1	39
12	Phylogenomic analyses of large-scale nuclear genes provide new insights into the evolutionary relationships within the rosids. <i>Molecular Phylogenetics and Evolution</i> , 2016, 105, 166-176.	2.7	38
13	The ubiquitin-interacting motif-type ubiquitin receptor HDR3 interacts with and stabilizes the histone acetyltransferase GW6a to control the grain size in rice. <i>Plant Cell</i> , 2021, 33, 3331-3347.	6.6	38
14	Phylogenomic Analyses of Nuclear Genes Reveal the Evolutionary Relationships within the BEP Clade and the Evidence of Positive Selection in Poaceae. <i>PLoS ONE</i> , 2013, 8, e64642.	2.5	37
15	Cell permeability and nuclear DNA staining by propidium iodide in basidiomycetous yeasts. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 4183-4191.	3.6	35
16	A Novel Return-to-Zero FSK Format for 40-Gb/s Transmission System Applications. <i>Journal of Lightwave Technology</i> , 2010, 28, 1770-1782.	4.6	31
17	Differential evolution of members of the <i>rhomboid</i> gene family with conservative and divergent patterns. <i>New Phytologist</i> , 2015, 206, 368-380.	7.3	23
18	Mapping and validation of the quantitative trait loci for leaf stay-green associated parameters in maize. <i>Plant Breeding</i> , 2017, 136, 188-196.	1.9	19

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19	Evolutionary divergence of the APETALA1 and CAULIFLOWER proteins. <i>Journal of Systematics and Evolution</i> , 2012, 50, 502-511.	3.1	14
20	Selectable marker recycling in the nonconventional yeast <i>Xanthophyllomyces dendrorhous</i> by transient expression of Cre on a genetically unstable vector. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 963-971.	3.6	14
21	Joint utilization of genetic analysis and semi-cloning technology reveals a digenic etiology of MÄ4llerian anomalies. <i>Cell Research</i> , 2020, 30, 91-94.	12.0	10
22	Mapping quantitative trait loci and predicting candidate genes for leaf angle in maize. <i>PLoS ONE</i> , 2021, 16, e0245129.	2.5	7
23	Comprehensive Analysis of CRISPR-Cas9 Editing Outcomes in Yeast <i>Xanthophyllomyces dendrorhous</i> . <i>CRISPR Journal</i> , 2022, 5, 558-570.	2.9	2
24	Mapping quantitative trait loci and predicting candidate genes for leaf angle in maize. , 2021, 16, e0245129.		0
25	Mapping quantitative trait loci and predicting candidate genes for leaf angle in maize. , 2021, 16, e0245129.		0
26	Mapping quantitative trait loci and predicting candidate genes for leaf angle in maize. , 2021, 16, e0245129.		0
27	Mapping quantitative trait loci and predicting candidate genes for leaf angle in maize. , 2021, 16, e0245129.		0
28	Mapping quantitative trait loci and predicting candidate genes for leaf angle in maize. , 2021, 16, e0245129.		0
29	Mapping quantitative trait loci and predicting candidate genes for leaf angle in maize. , 2021, 16, e0245129.		0