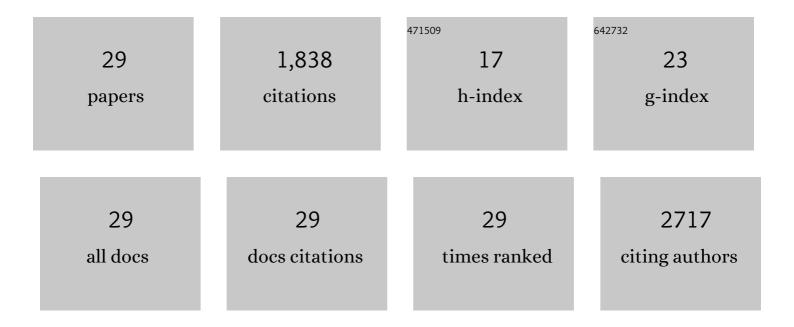
Ning Zhang

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Comprehensive Analysis of CRISPR-Cas9 Editing Outcomes in Yeast <i>Xanthophyllomyces dendrorhous</i> . CRISPR Journal, 2022, 5, 558-570.	2.9	2
2	Mapping quantitative trait loci and predicting candidate genes for leaf angle in maize. PLoS ONE, 2021, 16, e0245129.	2.5	7
3	The ubiquitin-interacting motif-type ubiquitin receptor HDR3 interacts with and stabilizes the histone acetyltransferase GW6a to control the grain size in rice. Plant Cell, 2021, 33, 3331-3347.	6.6	38
4	Mapping quantitative trait loci and predicting candidate genes for leaf angle in maize. , 2021, 16, e0245129.		0
5	Mapping quantitative trait loci and predicting candidate genes for leaf angle in maize. , 2021, 16, e0245129.		0
6	Mapping quantitative trait loci and predicting candidate genes for leaf angle in maize. , 2021, 16, e0245129.		0
7	Mapping quantitative trait loci and predicting candidate genes for leaf angle in maize. , 2021, 16, e0245129.		0
8	Mapping quantitative trait loci and predicting candidate genes for leaf angle in maize. , 2021, 16, e0245129.		0
9	Mapping quantitative trait loci and predicting candidate genes for leaf angle in maize. , 2021, 16, e0245129.		0
10	Joint utilization of genetic analysis and semi-cloning technology reveals a digenic etiology of Müllerian anomalies. Cell Research, 2020, 30, 91-94.	12.0	10
11	Selectable marker recycling in the nonconventional yeast Xanthophyllomyces dendrorhous by transient expression of Cre on a genetically unstable vector. Applied Microbiology and Biotechnology, 2019, 103, 963-971.	3.6	14
12	Widespread Whole Genome Duplications Contribute to Genome Complexity and Species Diversity in Angiosperms. Molecular Plant, 2018, 11, 414-428.	8.3	251
13	Cell permeability and nuclear DNA staining by propidium iodide in basidiomycetous yeasts. Applied Microbiology and Biotechnology, 2018, 102, 4183-4191.	3.6	35
14	Mapping and validation of the quantitative trait loci for leaf stayâ€greenâ€associated parameters in maize. Plant Breeding, 2017, 136, 188-196.	1.9	19
15	Resolution of deep eudicot phylogeny and their temporal diversification using nuclear genes from transcriptomic and genomic datasets. New Phytologist, 2017, 214, 1338-1354.	7.3	134
16	Another look at the phylogenetic position of the grape order Vitales: Chloroplast phylogenomics with an expanded sampling of key lineages. Molecular Phylogenetics and Evolution, 2016, 101, 216-223.	2.7	44
17	Phylogenomic analyses of large-scale nuclear genes provide new insights into the evolutionary relationships within the rosids. Molecular Phylogenetics and Evolution, 2016, 105, 166-176.	2.7	38
18	Resolution of Brassicaceae Phylogeny Using Nuclear Genes Uncovers Nested Radiations and Supports Convergent Morphological Evolution. Molecular Biology and Evolution, 2016, 33, 394-412.	8.9	259

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#	Article	IF	CITATIONS
19	Chloroplast phylogenomics resolves key relationships in ferns. Journal of Systematics and Evolution, 2015, 53, 448-457.	3.1	64
20	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. Journal of Systematics and Evolution, 2015, 53, 469-476.	3.1	39
21	Differential evolution of members of the <i>rhomboid</i> gene family with conservative and divergent patterns. New Phytologist, 2015, 206, 368-380.	7.3	23
22	Congruent Deep Relationships in the Grape Family (Vitaceae) Based on Sequences of Chloroplast Genomes and Mitochondrial Genes via Genome Skimming. PLoS ONE, 2015, 10, e0144701.	2.5	81
23	Resolution of deep angiosperm phylogeny using conserved nuclear genes and estimates of early divergence times. Nature Communications, 2014, 5, 4956.	12.8	330
24	Phylogenomic Analyses of Nuclear Genes Reveal the Evolutionary Relationships within the BEP Clade and the Evidence of Positive Selection in Poaceae. PLoS ONE, 2013, 8, e64642.	2.5	37
25	Highly conserved lowâ€copy nuclear genes as effective markers for phylogenetic analyses in angiosperms. New Phytologist, 2012, 195, 923-937.	7.3	192
26	Evolutionary divergence of the APETALA1 and CAULIFLOWER proteins. Journal of Systematics and Evolution, 2012, 50, 502-511.	3.1	14
27	Interactions among Proteins of Floral MADS-Box Genes in Basal Eudicots: Implications for Evolution of the Regulatory Network for Flower Development. Molecular Biology and Evolution, 2010, 27, 1598-1611.	8.9	72
28	A Novel Return-to-Zero FSK Format for 40-Gb/s Transmission System Applications. Journal of Lightwave Technology, 2010, 28, 1770-1782.	4.6	31
29	Patterns of gene duplication and functional diversification during the evolution of the AP1/SQUA subfamily of plant MADS-box genes. Molecular Phylogenetics and Evolution, 2007, 44, 26-41.	2.7	104