Ti-Cao Zhang

List of Publications by Year
in descending order

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23 papers	748 citations	687363 13 h-index	677142 22 g-index
23 all docs	23 docs citations	23 times ranked	1018 citing authors

#	Article	IF	Citations
1	Genome of Crucihimalaya himalaica , a close relative of Arabidopsis , shows ecological adaptation to high altitude. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 7137-7146.	7.1	108
2	Chloroplast phylogeography of Terminalia franchetii (Combretaceae) from the eastern Sino-Himalayan region and its correlation with historical river capture events. Molecular Phylogenetics and Evolution, 2011, 60, 1-12.	2.7	94
3	Complete Chloroplast Genome Sequence of Holoparasite Cistanche deserticola (Orobanchaceae) Reveals Gene Loss and Horizontal Gene Transfer from Its Host Haloxylon ammodendron (Chenopodiaceae). PLoS ONE, 2013, 8, e58747.	2.5	90
4	Proteasome-Mediated Degradation of FRIGIDA Modulates Flowering Time in Arabidopsis during Vernalization. Plant Cell, 2014, 26, 4763-4781.	6.6	71
5	Transcriptome sequencing of Crucihimalaya himalaica (Brassicaceae) reveals how Arabidopsis close relative adapt to the Qinghai-Tibet Plateau. Scientific Reports, 2016, 6, 21729.	3.3	47
6	Reply to: Revisiting the origin of octoploid strawberry. Nature Genetics, 2020, 52, 5-7.	21.4	44
7	Evolutionary history and pan-genome dynamics of strawberry (Fragaria spp.). Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	43
8	Phylogeographic structure of Terminalia franchetii (Combretaceae) in southwest China and its implications for drainage geological history. Journal of Plant Research, 2011, 124, 63-73.	2.4	38
9	Comparative Transcriptomics of Strawberries (Fragaria spp.) Provides Insights into Evolutionary Patterns. Frontiers in Plant Science, 2016, 7, 1839.	3.6	33
10	The genome and transcriptome of Trichormus sp. NMC-1: insights into adaptation to extreme environments on the Qinghai-Tibet Plateau. Scientific Reports, 2016, 6, 29404.	3.3	33
11	Genome-wide and molecular evolution analysis of the subtilase gene family in Vitis vinifera. BMC Genomics, 2014, 15, 1116.	2.8	28
12	Genomic analysis of field pennycress (Thlaspi arvense) provides insights into mechanisms of adaptation to high elevation. BMC Biology, 2021, 19, 143.	3.8	23
13	Molecular Analysis of Evolution and Origins of Cultivated Hawthorn (Crataegus spp.) and Related Species in China. Frontiers in Plant Science, 2019, 10, 443.	3.6	21
14	Investigation and taxonomy of wild Fragaria resources in Tibet, China. Genetic Resources and Crop Evolution, 2018, 65, 405-415.	1.6	16
15	Phylogeography of Thlaspi arvense (Brassicaceae) in China Inferred from Chloroplast and Nuclear DNA Sequences and Ecological Niche Modeling. International Journal of Molecular Sciences, 2015, 16, 13339-13355.	4.1	13
16	Detecting adaptive evolution and functional divergence in aminocyclopropane-1-carboxylate synthase (ACS) gene family. Computational Biology and Chemistry, 2012, 38, 10-16.	2.3	11
17	Effects of drainage reorganization on phytogeographic pattern in Sino-Himalaya. Alpine Botany, 2022, 132, 141-151.	2.4	10
18	Evaluation of genetic diversity and population structure of Fragaria nilgerrensis using EST-SSR markers. Gene, 2021, 796-797, 145791.	2.2	9

#	Article	IF	Citations
19	Increased epigenetic diversity and transient epigenetic memory in response to salinity stress in Thlaspi arvense. Ecology and Evolution, 2020, 10, 11622-11630.	1.9	6
20	Dynamic Changes of DNA Methylation During Wild Strawberry (Fragaria nilgerrensis) Tissue Culture. Frontiers in Plant Science, 2021, 12, 765383.	3.6	5
21	Spatial genetic and epigenetic structure of <i>Thlaspi arvense</i> (field pennycress) in China. Genes and Genetic Systems, 2020, 95, 225-234.	0.7	4
22	Phylogeography of Excoecaria acerifolia (Euphorbiaceae) suggests combined effects of historical drainage reorganization events and climatic changes on riparian plants in the Sinoâ€“Himalayan region. Botanical Journal of the Linnean Society, 2019, , .	1.6	1
23	The complete chloroplast genome and phylogenetic analysis of Saussurea wettsteiniana (Compositae). Mitochondrial DNA Part B: Resources, 2021, 6, 2001-2003.	0.4	0