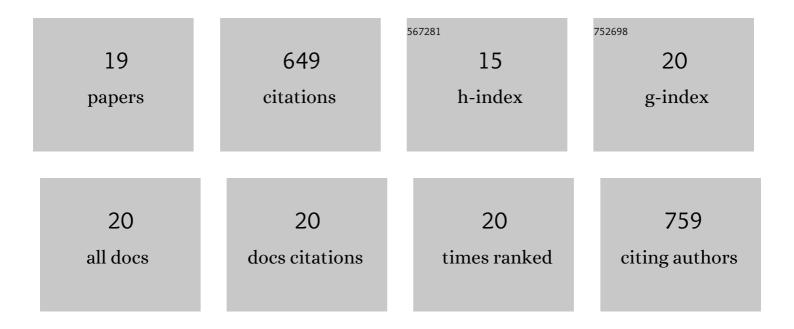
Jian Huang

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Genome-Wide Identification of WRKY Transcription Factors in Chinese jujube (Ziziphus jujuba Mill.) and Their Involvement in Fruit Developing, Ripening, and Abiotic Stress. Genes, 2019, 10, 360.	2.4	26
2	Genetic diversity of Ziziphus mauritiana germplasm based on SSR markers and ploidy level estimation. Planta, 2019, 249, 1875-1887.	3.2	16
3	Transcript analyses of ethylene pathway genes during ripening of Chinese jujube fruit. Journal of Plant Physiology, 2018, 224-225, 1-10.	3.5	26
4	Soil propagule bank of ectomycorrhizal fungi associated with Masson pine (Pinus massoniana) grown in a manganese mine wasteland. PLoS ONE, 2018, 13, e0198628.	2.5	7
5	The ectomycorrhizal fungal communities associated with Quercus liaotungensis in different habitats across northern China. Mycorrhiza, 2017, 27, 441-449.	2.8	16
6	Diversity and community structure of ectomycorrhizal fungi associated with Larix chinensis across the alpine treeline ecotone of Taibai Mountain. Mycorrhiza, 2017, 27, 487-497.	2.8	22
7	Comparative Analysis of the Complete Chloroplast Genome of Four Known Ziziphus Species. Genes, 2017, 8, 340.	2.4	35
8	The Jujube Genome Provides Insights into Genome Evolution and the Domestication of Sweetness/Acidity Taste in Fruit Trees. PLoS Genetics, 2016, 12, e1006433.	3.5	136
9	Transcriptomic Analysis Reveals the Metabolic Mechanism of L-Ascorbic Acid in Ziziphus jujuba Mill Frontiers in Plant Science, 2016, 7, 122.	3.6	19
10	Biochemical Responses of Ten Ectomycorrhizal Fungal Isolates to Manganese. Water, Air, and Soil Pollution, 2016, 227, 1.	2.4	8
11	Construction of a high-density genetic map of Ziziphus jujuba Mill. using genotyping by sequencing technology. Tree Genetics and Genomes, 2016, 12, 1.	1.6	42
12	Ectomycorrhizal fungal communities associated with Populus simonii and Pinus tabuliformis in the hilly-gully region of the Loess Plateau, China. Scientific Reports, 2016, 6, 24336.	3.3	33
13	Soil Propagule Banks of Ectomycorrhizal Fungi Along Forest Development Stages After Mining. Microbial Ecology, 2015, 69, 768-777.	2.8	21
14	Genetic diversity and population structure of sour jujube, Ziziphus acidojujuba. Tree Genetics and Genomes, 2015, 11, 1.	1.6	24
15	Inoculation of ectomycorrhizal fungi contributes to the survival of tree seedlings in a copper mine tailing. Journal of Forest Research, 2015, 20, 493-500.	1.4	35
16	Identification of appropriate reference genes for RT-qPCR analysis in Ziziphus jujuba Mill Scientia Horticulturae, 2015, 197, 166-169.	3.6	29
17	Development of Chloroplast Microsatellite Markers and Analysis of Chloroplast Diversity in Chinese Jujube (Ziziphus jujuba Mill.) and Wild Jujube (Ziziphus acidojujuba Mill.). PLoS ONE, 2015, 10, e0134519.	2.5	57
18	Ectomycorrhizal fungal communities associated with Masson pine (Pinus massoniana) and white oak (Quercus fabri) in a manganese mining region in Hunan Province, China. Fungal Ecology, 2014, 9, 1-10.	1.6	48

#	Article	IF	CITATIONS
19	Ectomycorrhizal fungal communities associated with Masson pine (Pinus massoniana Lamb.) in Pb–Zn mine sites of central south China. Mycorrhiza, 2012, 22, 589-602.	2.8	48