

# Jian Huang

## List of Publications by Year in descending order

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Version: 2024-02-01

19  
papers

649  
citations

567281

15  
h-index

752698

20  
g-index

20  
all docs

20  
docs citations

20  
times ranked

759  
citing authors

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

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