

Jian Huang

List of Publications by Year in descending order

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19
papers

649
citations

567281

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20
docs citations

20
times ranked

759
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	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
3	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
4	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
5	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
6	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
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	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
9	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
10	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
11	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
12	Genetic diversity and population structure of sour jujube, <i>Ziziphus acidojujuba</i> . <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	1.6	24
13	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
14	Soil Propagule Banks of Ectomycorrhizal Fungi Along Forest Development Stages After Mining. <i>Microbial Ecology</i> , 2015, 69, 768-777.	2.8	21
15	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
16	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
17	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
18	Biochemical Responses of Ten Ectomycorrhizal Fungal Isolates to Manganese. <i>Water, Air, and Soil Pollution</i> , 2016, 227, 1.	2.4	8

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19	Soil propagule bank of ectomycorrhizal fungi associated with Masson pine (<i>Pinus massoniana</i>) grown in a manganese mine wasteland. PLoS ONE, 2018, 13, e0198628.	2.5	7