

Xingang Li

List of Publications by Year in descending order

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papers

979
citations

430874

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docs citations

40
times ranked

934
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	Genome-wide identification of AP2/ERF superfamily genes and their expression during fruit ripening of Chinese jujube. <i>Scientific Reports</i> , 2018, 8, 15612.	3.3	67
3	Metabolomic and Transcriptomic Analyses of Anthocyanin Biosynthesis Mechanisms in the Color Mutant <i>Ziziphus jujuba</i> cv. Tailihong. <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 15186-15198.	5.2	62
4	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
5	Comparative Analysis of Pigments, Phenolics, and Antioxidant Activity of Chinese Jujube (<i>Ziziphus</i>) Tj ETQq1 1 0.784314 rgBT /Overlook	3.8	55
6	Sugar transport played a more important role than sugar biosynthesis in fruit sugar accumulation during Chinese jujube domestication. <i>Planta</i> , 2018, 248, 1187-1199.	3.2	53
7	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
8	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
9	Comparative Analysis of the Complete Chloroplast Genome of Four Known <i>Ziziphus</i> Species. <i>Genes</i> , 2017, 8, 340.	2.4	35
10	Ectomycorrhizal fungal communities associated with <i>Populus simonii</i> and <i>Pinus tabulaeformis</i> in the hilly-gully region of the Loess Plateau, China. <i>Scientific Reports</i> , 2016, 6, 24336.	3.3	33
11	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
12	Nutrient composition and quality traits of dried jujube fruits in seven producing areas based on metabolomics analysis. <i>Food Chemistry</i> , 2022, 385, 132627.	8.2	27
13	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
14	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
15	Jujube metabolome selection determined the edible properties acquired during domestication. <i>Plant Journal</i> , 2022, 109, 1116-1133.	5.7	25
16	Genetic diversity and population structure of sour jujube, <i>Ziziphus acidojujuba</i> . <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	1.6	24
17	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
18	Soil Propagule Banks of Ectomycorrhizal Fungi Along Forest Development Stages After Mining. <i>Microbial Ecology</i> , 2015, 69, 768-777.	2.8	21

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19	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
20	Anthocyanin Synthesis and the Expression Patterns of bHLH Transcription Factor Family during Development of the Chinese Jujube Fruit (<i>Ziziphus jujuba</i> Mill.). <i>Forests</i> , 2019, 10, 346.	2.1	19
21	Influences of Environmental Factors on Leaf Morphology of Chinese Jujubes. <i>PLoS ONE</i> , 2015, 10, e0127825.	2.5	16
22	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
23	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
24	Genetic variation in leaf characters of F1 hybrids of Chinese Jujube. <i>Scientia Horticulturae</i> , 2019, 244, 372-378.	3.6	14
25	High-Density Genetic Map Construction and QTL Mapping of Leaf and Needling Traits in <i>Ziziphus jujuba</i> Mill. <i>Frontiers in Plant Science</i> , 2019, 10, 1424.	3.6	13
26	Integrative Morphological, Physiological, Proteomics Analyses of Jujube Fruit Development Provide Insights Into Fruit Quality Domestication From Wild Jujube to Cultivated Jujube. <i>Frontiers in Plant Science</i> , 2021, 12, 773825.	3.6	12
27	Mycorrhizal symbiosis reprograms ion fluxes and fatty acid metabolism in wild jujube during salt stress. <i>Plant Physiology</i> , 2022, 189, 2481-2499.	4.8	12
28	Transcript analyses reveal a comprehensive role of abscisic acid in modulating fruit ripening in Chinese jujube. <i>BMC Plant Biology</i> , 2019, 19, 189.	3.6	10
29	Biochemical Responses of Ten Ectomycorrhizal Fungal Isolates to Manganese. <i>Water, Air, and Soil Pollution</i> , 2016, 227, 1.	2.4	8
30	Shot-gun proteome and transcriptome mapping of the jujube floral organ and identification of a pollen-specific S-locus F-box gene. <i>PeerJ</i> , 2017, 5, e3588.	2.0	8
31	Metabolite and Gene Expression Analysis Underlying Temporal and Spatial Accumulation of Pentacyclic Triterpenoids in Jujube. <i>Genes</i> , 2022, 13, 823.	2.4	8
32	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
33	Comprehensive analysis of antibacterial and anti-hepatoma activity of metabolites from jujube fruit. <i>Food Bioscience</i> , 2022, 47, 101511.	4.4	7
34	Development and characterization of microsatellite markers for sour jujube (<i>Ziziphus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 142 Td (0.5	6
35	The complete chloroplast genome of <i>Acer truncatum</i> Bunge (Aceraceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 607-608.	0.4	4
36	Bioactive properties of streptomycetes may affect the dominance of <i>Tricholoma matsutake</i> in shiro. <i>Symbiosis</i> , 2020, 81, 1-13.	2.3	4

#	ARTICLE	IF	CITATIONS
37	Association of Bitter Metabolites and Flavonoid Synthesis Pathway in Jujube Fruit. <i>Frontiers in Nutrition</i> , 2022, 9, .	3.7	3
38	The complete chloroplast genome sequence of <i>Juniperus saltuaria</i> (Cupressaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2565-2567.	0.4	1
39	The complete chloroplast genome of the endangered species <i>Cephalotaxus hainanensis</i> (Cephalotaxaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 1280-1281.	0.4	0