

Yingyue Li

List of Publications by Year in descending order

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#	ARTICLE	IF	CITATIONS
1	Comparative Transcriptomic Analyses of Different Jujube Cultivars Reveal the Co-Regulation of Multiple Pathways during Fruit Cracking. <i>Genes</i> , 2022, 13, 105.	1.0	8
2	Genome-Wide Identification of Direct Targets of ZjVND7 Reveals the Putative Roles of Whole-Genome Duplication in Sour Jujube in Regulating Xylem Vessel Differentiation and Drought Tolerance. <i>Frontiers in Plant Science</i> , 2022, 13, 829765.	1.7	1
3	Hybrid Triploid Induced by Megaspore Chromosome Doubling in Jujube (<i>Ziziphus jujuba</i> Mill.) "Maya" and Its Characteristics. <i>Forests</i> , 2021, 12, 112.	0.9	3
4	Multiple responses contribute to the enhanced drought tolerance of the autotetraploid <i>Ziziphus jujuba</i> Mill. var. <i>spinosa</i> . <i>Cell and Bioscience</i> , 2021, 11, 119.	2.1	20
5	Genome-wide identification and expression analysis of NAC transcription factors in <i>Ziziphus jujuba</i> Mill. reveal their putative regulatory effects on tissue senescence and abiotic stress responses. <i>Industrial Crops and Products</i> , 2021, 173, 114093.	2.5	18
6	Genome-wide association studies of fruit quality traits in jujube germplasm collections using genotyping-by-sequencing. <i>Plant Genome</i> , 2020, 13, e20036.	1.6	14
7	Comparative transcriptome profiling reveals cold stress responsiveness in two contrasting Chinese jujube cultivars. <i>BMC Plant Biology</i> , 2020, 20, 240.	1.6	23
8	Megasporogenesis, microsporogenesis, and female and male gametophyte development in <i>Ziziphus jujuba</i> Mill. <i>Protoplasma</i> , 2019, 256, 1519-1530.	1.0	5
9	Autotetraploidization in <i>Ziziphus jujuba</i> Mill. var. <i>spinosa</i> enhances salt tolerance conferred by active, diverse stress responses. <i>Environmental and Experimental Botany</i> , 2019, 165, 92-107.	2.0	20
10	Genome-wide identification, characterization, and expression analysis of the expansin gene family in Chinese jujube (<i>Ziziphus jujuba</i> Mill.). <i>Planta</i> , 2019, 249, 815-829.	1.6	32
11	Genome-wide identification and analysis of the DREB genes and their expression profiles under abiotic stresses in Chinese jujube (<i>Ziziphus jujuba</i> Mill.). <i>Journal of Forestry Research</i> , 2019, 30, 1277-1287.	1.7	7
12	Optimisation of a highly efficient shoot regeneration system using leaf explants of Chinese jujube (<i>Ziziphus jujuba</i> Mill.) by response surface methodology. <i>Journal of Horticultural Science and Biotechnology</i> , 2018, 93, 289-295.	0.9	0
13	Genetic Evaluation of Natural Populations of the Endangered Conifer <i>Thuja koraiensis</i> Using Microsatellite Markers by Restriction-Associated DNA Sequencing. <i>Genes</i> , 2018, 9, 218.	1.0	10
14	De Novo Transcriptome Assembly and Population Genetic Analyses for an Endangered Chinese Endemic <i>Acer miaotaiense</i> (Aceraceae). <i>Genes</i> , 2018, 9, 378.	1.0	44
15	In vitro induction of tetraploid <i>Ziziphus jujuba</i> Mill. var. <i>spinosa</i> plants from leaf explants. <i>Plant Cell, Tissue and Organ Culture</i> , 2017, 131, 175-182.	1.2	36
16	Genetic Diversity, Population Structure, and Linkage Disequilibrium of a Core Collection of <i>Ziziphus jujuba</i> Assessed with Genome-wide SNPs Developed by Genotyping-by-sequencing and SSR Markers. <i>Frontiers in Plant Science</i> , 2017, 8, 575.	1.7	54
17	Genome-Wide Organization and Expression Profiling of the SBP-Box Gene Family in Chinese Jujube (<i>Ziziphus jujuba</i> Mill.). <i>International Journal of Molecular Sciences</i> , 2017, 18, 1734.	1.8	25
18	Identifying the genetic diversity, genetic structure and a core collection of <i>Ziziphus jujuba</i> Mill. var. <i>jujuba</i> accessions using microsatellite markers. <i>Scientific Reports</i> , 2016, 6, 31503.	1.6	54

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19	A Chinese jujube (<i>Ziziphus jujuba</i> Mill.) fruit-expressed sequence tag (EST) library: Annotation and EST-SSR characterization. <i>Scientia Horticulturae</i> , 2014, 165, 99-105.	1.7	23
20	High-Level Genetic Diversity and Complex Population Structure of Siberian Apricot (<i>Prunus sibirica</i> L.) in China as Revealed by Nuclear SSR Markers. <i>PLoS ONE</i> , 2014, 9, e87381.	1.1	46
21	Isolation and Characterization of Microsatellite Markers and Analysis of Genetic Diversity in Chinese Jujube (<i>Ziziphus jujuba</i> Mill.). <i>PLoS ONE</i> , 2014, 9, e99842.	1.1	46
22	De Novo Assembly and Characterization of the Fruit Transcriptome of Chinese Jujube (<i>Ziziphus jujuba</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T 2014, 9, e106438.	1.1	27
23	Identification of genes associated with fruit ripening in <i>Ziziphus jujuba</i> using suppression subtractive hybridization approach. <i>Acta Physiologiae Plantarum</i> , 2013, 35, 1997-2008.	1.0	2