

Qianqian Shi

List of Publications by Year in descending order

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#	ARTICLE	IF	CITATIONS
1	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
2	Pollination promotes ABA synthesis but not sexual reproduction in the apomictic species <i>Zanthoxylum bungeanum</i> Maxim.. <i>Tree Physiology</i> , 2021, 41, 1497-1509.	3.1	1
3	ZbAGL11, a class D MADS-box transcription factor of <i>Zanthoxylum bungeanum</i> , is involved in sporophytic apomixis. <i>Horticulture Research</i> , 2021, 8, 23.	6.3	14
4	Genome-wide identification and functional characterization of the PheE2F/DP gene family in Moso bamboo. <i>BMC Plant Biology</i> , 2021, 21, 158.	3.6	6
5	Transcriptome and volatile compounds profiling analyses provide insights into the molecular mechanism underlying the floral fragrance of tree peony. <i>Industrial Crops and Products</i> , 2021, 162, 113286.	5.2	21
6	Transcriptome and anatomical comparisons reveal the specific characteristics and genes involved in distinct types of growing culms. <i>Industrial Crops and Products</i> , 2021, 171, 113865.	5.2	3
7	Integrating full-length transcriptomics and metabolomics reveals the regulatory mechanisms underlying yellow pigmentation in tree peony (<i>Paeonia suffruticosa</i> Andr.) flowers. <i>Horticulture Research</i> , 2021, 8, 235.	6.3	26
8	Genome-Wide Identification and Comparative Profiling of MicroRNAs Reveal Flavonoid Biosynthesis in Two Contrasting Flower Color Cultivars of Tree Peony. <i>Frontiers in Plant Science</i> , 2021, 12, 797799.	3.6	9
9	RNA sequencing and functional analyses reveal regulation of novel drought-responsive, long-non-coding RNA in <i>Zanthoxylum bungeanum</i> Maxim. <i>Plant Growth Regulation</i> , 2020, 90, 425-440.	3.4	7
10	Variation of floral volatiles and fragrance reveals the phylogenetic relationship among nine wild tree peony species. <i>Flavour and Fragrance Journal</i> , 2020, 35, 227-241.	2.6	14
11	Characterization of Metabolites and Transcripts Involved in Flower Pigmentation in <i>Primula vulgaris</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 572517.	3.6	18
12	Dynamic Changes in Metabolite Accumulation and the Transcriptome during Leaf Growth and Development in <i>Eucommia ulmoides</i> . <i>International Journal of Molecular Sciences</i> , 2019, 20, 4030.	4.1	23
13	Comparative transcriptome analyses reveal genes related to pigmentation in the petals of red and white <i>Primula vulgaris</i> cultivars. <i>Physiology and Molecular Biology of Plants</i> , 2019, 25, 1029-1041.	3.1	16
14	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
15	Identification of MicroRNAs and Their Targets Involved in <i>Paeonia rockii</i> Petal Variegation Using High-throughput Sequencing. <i>Journal of the American Society for Horticultural Science</i> , 2019, 144, 118-129.	1.0	5
16	Transcriptomic Analysis of Leaf in Tree Peony Reveals Differentially Expressed Pigments Genes. <i>Molecules</i> , 2017, 22, 324.	3.8	32
17	Biochemical and Comparative Transcriptomic Analyses Identify Candidate Genes Related to Variegation Formation in <i>Paeonia rockii</i> . <i>Molecules</i> , 2017, 22, 1364.	3.8	18
18	Transcriptomic Analysis Reveals Transcription Factors Related to Leaf Anthocyanin Biosynthesis in <i>Paeonia qiui</i> . <i>Molecules</i> , 2017, 22, 2186.	3.8	31

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19	Transcriptomic Analysis of <i>Paeonia delavayi</i> Wild Population Flowers to Identify Differentially Expressed Genes Involved in Purple-Red and Yellow Petal Pigmentation. PLoS ONE, 2015, 10, e0135038.	2.5	36
20	Overexpression of Ps-CHI1, a homologue of the chalcone isomerase gene from tree peony (<i>Paeonia</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 and Organ Culture, 2014, 116, 285-295.	2.3	43