

Qianqian Shi

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3950494/publications.pdf>

Version: 2024-02-01

20
papers

369
citations

687363

13
h-index

839539

18
g-index

23
all docs

23
docs citations

23
times ranked

293
citing authors

#	ARTICLE	IF	CITATIONS
1	Overexpression of Ps-CHI1, a homologue of the chalcone isomerase gene from tree peony (<i>Paeonia</i>) Tj ETQq1 1 and Organ Culture, 2014, 116, 285-295.	0.784314	43
2	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
3	Transcriptomic Analysis of Leaf in Tree Peony Reveals Differentially Expressed Pigments Genes. Molecules, 2017, 22, 324.	3.8	32
4	Transcriptomic Analysis Reveals Transcription Factors Related to Leaf Anthocyanin Biosynthesis in <i>Paeonia qiui</i> . Molecules, 2017, 22, 2186.	3.8	31
5	Nutrient composition and quality traits of dried jujube fruits in seven producing areas based on metabolomics analysis. Food Chemistry, 2022, 385, 132627.	8.2	27
6	Integrating full-length transcriptomics and metabolomics reveals the regulatory mechanisms underlying yellow pigmentation in tree peony (<i>Paeonia suffruticosa</i> Andr.) flowers. Horticulture Research, 2021, 8, 235.	6.3	26
7	Dynamic Changes in Metabolite Accumulation and the Transcriptome during Leaf Growth and Development in <i>Eucommia ulmoides</i> . International Journal of Molecular Sciences, 2019, 20, 4030.	4.1	23
8	Transcriptome and volatile compounds profiling analyses provide insights into the molecular mechanism underlying the floral fragrance of tree peony. Industrial Crops and Products, 2021, 162, 113286.	5.2	21
9	Anthocyanin Synthesis and the Expression Patterns of bHLH Transcription Factor Family during Development of the Chinese Jujube Fruit (<i>Ziziphus jujuba</i> Mill.). Forests, 2019, 10, 346.	2.1	19
10	Biochemical and Comparative Transcriptomic Analyses Identify Candidate Genes Related to Variegation Formation in <i>Paeonia rockii</i> . Molecules, 2017, 22, 1364.	3.8	18
11	Characterization of Metabolites and Transcripts Involved in Flower Pigmentation in <i>Primula vulgaris</i> . Frontiers in Plant Science, 2020, 11, 572517.	3.6	18
12	Comparative transcriptome analyses reveal genes related to pigmentation in the petals of red and white <i>Primula vulgaris</i> cultivars. Physiology and Molecular Biology of Plants, 2019, 25, 1029-1041.	3.1	16
13	Variation of floral volatiles and fragrance reveals the phylogenetic relationship among nine wild tree peony species. Flavour and Fragrance Journal, 2020, 35, 227-241.	2.6	14
14	ZbAGL11, a class D MADS-box transcription factor of <i>Zanthoxylum bungeanum</i> , is involved in sporophytic apomixis. Horticulture Research, 2021, 8, 23.	6.3	14
15	Genome-Wide Identification and Comparative Profiling of MicroRNAs Reveal Flavonoid Biosynthesis in Two Contrasting Flower Color Cultivars of Tree Peony. Frontiers in Plant Science, 2021, 12, 797799.	3.6	9
16	RNA sequencing and functional analyses reveal regulation of novel drought-responsive, long-non-coding RNA in <i>Zanthoxylum bungeanum</i> Maxim. Plant Growth Regulation, 2020, 90, 425-440.	3.4	7
17	Genome-wide identification and functional characterization of the PheE2F/DP gene family in Moso bamboo. BMC Plant Biology, 2021, 21, 158.	3.6	6
18	Identification of MicroRNAs and Their Targets Involved in <i>Paeonia rockii</i> Petal Variegation Using High-throughput Sequencing. Journal of the American Society for Horticultural Science, 2019, 144, 118-129.	1.0	5

#	ARTICLE	IF	CITATIONS
19	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
20	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