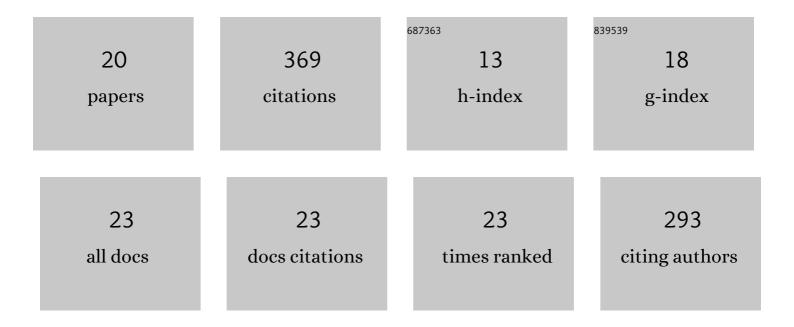
Qianqian Shi

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/3950494/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Overexpression of Ps-CHI1, a homologue of the chalcone isomerase gene from tree peony (Paeonia) Tj ETQq1	0.784314	4 rgBT /Overlo 43
1	and Organ Culture, 2014, 116, 285-295.	2.0	70
2	Transcriptomic Analysis of Paeonia delavayi 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 Paeonia qiui. 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 (Paeonia suffruticosa 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 Eucommia ulmoides. 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 (Ziziphus jujuba Mill.). Forests, 2019, 10, 346.	2.1	19
10	Biochemical and Comparative Transcriptomic Analyses Identify Candidate Genes Related to Variegation Formation in Paeonia rockii. Molecules, 2017, 22, 1364.	3.8	18
11	Characterization of Metabolites and Transcripts Involved in Flower Pigmentation in Primula vulgaris. 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 Primula vulgaris 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 Zanthoxylum bungeanum, 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 Zanthoxylum bungeanum 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 Paeonia rockii 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. Industrial Crops and Products, 2021, 171, 113865.	5.2	3
20	Pollination promotes ABA synthesis but not sexual reproduction in the apomictic species <i>Zanthoxylum bungeanum</i> Maxim Tree Physiology, 2021, 41, 1497-1509.	3.1	1