

Xitong Fei

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4290352/publications.pdf>

Version: 2024-02-01

14
papers

223
citations

1163117

8
h-index

1058476

14
g-index

14
all docs

14
docs citations

14
times ranked

171
citing authors

#	ARTICLE	IF	CITATIONS
1	Expression Stabilities of Ten Candidate Reference Genes for RT-qPCR in <i>Zanthoxylum bungeanum</i> Maxim. <i>Molecules</i> , 2018, 23, 802.	3.8	46
2	Transcriptome and Metabolome Dynamics Explain Aroma Differences between Green and Red Prickly Ash Fruit. <i>Foods</i> , 2021, 10, 391.	4.3	28
3	miRNAs and their target genes regulate the antioxidant system of <i>Zanthoxylum bungeanum</i> under drought stress. <i>Plant Physiology and Biochemistry</i> , 2020, 150, 196-203.	5.8	23
4	The steps from sexual reproduction to apomixis. <i>Planta</i> , 2019, 249, 1715-1730.	3.2	22
5	Patterns of Drought Response of 38 WRKY Transcription Factors of <i>Zanthoxylum bungeanum</i> Maxim.. <i>International Journal of Molecular Sciences</i> , 2019, 20, 68.	4.1	22
6	Effects of location, climate, soil conditions and plant species on levels of potentially toxic elements in Chinese Prickly Ash pericarps from the main cultivation regions in China. <i>Chemosphere</i> , 2020, 244, 125501.	8.2	16
7	Identification of Key Genes in the Synthesis Pathway of Volatile Terpenoids in Fruit of <i>Zanthoxylum bungeanum</i> Maxim. <i>Forests</i> , 2019, 10, 328.	2.1	15
8	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
9	Integrated Analysis of Metabolome and Transcriptome Data for Uncovering Flavonoid Components of <i>Zanthoxylum bungeanum</i> Maxim. Leaves Under Drought Stress. <i>Frontiers in Nutrition</i> , 2021, 8, 801244.	3.7	14
10	Genome-Wide Identification of the NAC Gene Family in <i>Zanthoxylum bungeanum</i> and Their Transcriptional Responses to Drought Stress. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4769.	4.1	8
11	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
12	Small RNA sequencing provides candidate miRNA-target pairs for revealing the mechanism of apomixis in <i>Zanthoxylum bungeanum</i> . <i>BMC Plant Biology</i> , 2021, 21, 178.	3.6	5
13	Integrated LC-MS/MS and Transcriptome Sequencing Analysis Reveals the Mechanism of Color Formation During Prickly Ash Fruit Ripening. <i>Frontiers in Nutrition</i> , 2022, 9, 847823.	3.7	2
14	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