

Xiaopeng Wen

List of Publications by Year in descending order

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Version: 2024-02-01

30
papers

440
citations

759233

12
h-index

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20
g-index

31
all docs

31
docs citations

31
times ranked

575
citing authors

#	ARTICLE	IF	CITATIONS
1	Changes in the quality of fruits of four sweet cherry cultivars grown under rain-shelter cultivation during storage at room temperature. <i>Journal of Food Measurement and Characterization</i> , 2022, 16, 2571-2581.	3.2	4
2	Cross-talk between Transcriptome Analysis and Physiological Characterization Identifies the Genes in Response to the Low Phosphorus Stress in <i>Malus mandshurica</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 4896.	4.1	1
3	Identification of VOCs in essential oils extracted using ultrasound- and microwave-assisted methods from sweet cherry flower. <i>Scientific Reports</i> , 2021, 11, 1167.	3.3	9
4	Cross-talk between transcriptome, phytohormone and HD-ZIP gene family analysis illuminates the molecular mechanism underlying fruitlet abscission in sweet cherry (<i>Prunus avium</i> L.). <i>BMC Plant Biology</i> , 2021, 21, 173.	3.6	11
5	Genetic diversity and population structure of masson pine (<i>Pinus massoniana</i> Lamb.) superior clones in South China as revealed by EST-SSR markers. <i>Genetic Resources and Crop Evolution</i> , 2021, 68, 1987-2002.	1.6	8
6	Physiological and Proteomic Responses of Pitaya to PEG-Induced Drought Stress. <i>Agriculture (Switzerland)</i> , 2021, 11, 632.	3.1	11
7	Effects of different rain shelter coverings on volatile organic compounds in mature fruit and postharvest quality of sweet cherry. <i>CYTA - Journal of Food</i> , 2021, 19, 465-475.	1.9	0
8	The Effects of Rain-shelter Cultivation on the Photosynthetic Characteristics and Chlorophyll Fluorescence of Sweet Cherry (<i>Prunus avium</i> L.). <i>Erwerbs-Obstbau</i> , 2021, 63, 359.	1.3	2
9	Genome-Wide Identification of ARF Gene Family Suggests a Functional Expression Pattern during Fruitlet Abscission in <i>Prunus avium</i> L.. <i>International Journal of Molecular Sciences</i> , 2021, 22, 11968.	4.1	10
10	Transcriptome-wide identification and expression profiling of <i>Pinus massoniana</i> MYB transcription factors responding to phosphorus deficiency. <i>Journal of Forestry Research</i> , 2020, 31, 909-919.	3.6	15
11	Trace macroelement content and speciation analysis in leaves of sweet cherry trees by elemental analysis and X-ray photoelectron spectroscopy. <i>Spectroscopy Letters</i> , 2020, 53, 572-579.	1.0	2
12	Comparative Transcriptome Analysis Combining SMRT- and Illumina-Based RNA-Seq Identifies Potential Candidate Genes Involved in Betalain Biosynthesis in Pitaya Fruit. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3288.	4.1	23
13	Identification and functional study of oleoresin terpenoid biosynthesis-related genes in masson pine (<i>Pinus massoniana</i> L.) based on transcriptome analysis. <i>Tree Genetics and Genomes</i> , 2020, 16, 1.	1.6	13
14	Comparative transcriptome analysis reveals the molecular regulation underlying the adaptive mechanism of cherry (<i>Cerasus pseudocerasus</i> Lindl.) to shelter covering. <i>BMC Plant Biology</i> , 2020, 20, 27.	3.6	19
15	Over-Expression of Masson Pine PmPT1 Gene in Transgenic Tobacco Confers Tolerance Enhancement to Pi Deficiency by Ameliorating P Level and the Antioxidants. <i>Plant Molecular Biology Reporter</i> , 2020, 38, 238-249.	1.8	1
16	Optimizing the supercritical carbon dioxide extraction of sweet cherry (<i>Prunus avium</i> L.) leaves and UPLC-MS/MS analysis. <i>Analytical Methods</i> , 2020, 12, 3004-3013.	2.7	13
17	Pitaya: a potential plant resource of citramalic acid. <i>CYTA - Journal of Food</i> , 2020, 18, 249-256.	1.9	8
18	Genetic diversity, linkage disequilibrium, and population structure analysis of the tea plant (<i>Camellia</i>) by genotyping-by-sequencing. <i>BMC Plant Biology</i> , 2019, 19, 328.	3.6	65

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19	Metabolic Profiling of Pitaya (<i>Hylocereus polyrhizus</i>) during Fruit Development and Maturation. <i>Molecules</i> , 2019, 24, 1114.	3.8	56
20	Protocols for miRNA Target Prediction in Plants. <i>Methods in Molecular Biology</i> , 2019, 1970, 65-73.	0.9	3
21	Diff isomiRs: Large-scale detection of differential isomiRs for understanding non-coding regulated stress omics in plants. <i>Scientific Reports</i> , 2019, 9, 1406.	3.3	9
22	Transcriptional activation of long terminal repeat retrotransposon sequences in the genome of pitaya under abiotic stress. <i>Plant Physiology and Biochemistry</i> , 2019, 135, 460-468.	5.8	21
23	Method for the Large-Scale Identification of phasiRNAs in <i>Brachypodium distachyon</i> . <i>Methods in Molecular Biology</i> , 2018, 1667, 187-194.	0.9	5
24	Plant IsomiR Atlas: Large Scale Detection, Profiling, and Target Repertoire of IsomiRs in Plants. <i>Frontiers in Plant Science</i> , 2018, 9, 1881.	3.6	7
25	Proteomic analyses provide new insights into the responses of <i>Pinus massoniana</i> seedlings to phosphorus deficiency. <i>Proteomics</i> , 2016, 16, 504-515.	2.2	22
26	The Temporal Transcriptomic Response of <i>Pinus massoniana</i> Seedlings to Phosphorus Deficiency. <i>PLoS ONE</i> , 2014, 9, e105068.	2.5	32
27	LTR-retrotransposon activation, IRAP marker development and its potential in genetic diversity assessment of masson pine (<i>Pinus massoniana</i>). <i>Tree Genetics and Genomes</i> , 2014, 10, 213-222.	1.6	27
28	Isolation, identification, and characterization of genomic LTR retrotransposon sequences from masson pine (<i>Pinus massoniana</i>). <i>Tree Genetics and Genomes</i> , 2013, 9, 1237-1246.	1.6	9
29	Identification of differentially expressed genes preferably related to drought response in pigeon pea (<i>Cajanus cajan</i>) inoculated by arbuscular mycorrhizae fungi (AMF). <i>Acta Physiologiae Plantarum</i> , 2012, 34, 1711-1721.	2.1	18
30	Cloning of two classes of PR genes and the development of SNAP markers for powdery mildew resistance loci in chestnut rose (<i>Rosa roxburghii</i> Tratt). <i>Molecular Breeding</i> , 2007, 19, 179-191.	2.1	16