

Qinghe Cao

List of Publications by Year in descending order

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#	ARTICLE	IF	CITATIONS
1	Melatonin is a potential target for improving horticultural crop resistance to abiotic stress. <i>Scientia Horticulturae</i> , 2022, 291, 110560.	3.6	55
2	Overexpression of IbMPK3 increases low-temperature tolerance in transgenic sweetpotato. <i>Plant Biotechnology Reports</i> , 2022, 16, 91-100.	1.5	1
3	Exogenous melatonin alleviates browning of fresh-cut sweetpotato by enhancing anti-oxidative process. <i>Scientia Horticulturae</i> , 2022, 297, 110937.	3.6	17
4	Metabolomic and Transcriptomic Analyses of the Flavonoid Biosynthetic Pathway for the Accumulation of Anthocyanins and Other Flavonoids in Sweetpotato Root Skin and Leaf Vein Base. <i>Journal of Agricultural and Food Chemistry</i> , 2022, 70, 2574-2588.	5.2	15
5	Sizes, Components, Crystalline Structure, and Thermal Properties of Starches from Sweet Potato Varieties Originating from Different Countries. <i>Molecules</i> , 2022, 27, 1905.	3.8	8
6	Relationships between X-ray Diffraction Peaks, Molecular Components, and Heat Properties of C-Type Starches from Different Sweet Potato Varieties. <i>Molecules</i> , 2022, 27, 3385.	3.8	3
7	Comparative Transcriptome and Interaction Protein Analysis Reveals the Mechanism of IbMPK3-Overexpressing Transgenic Sweet Potato Response to Low-Temperature Stress. <i>Genes</i> , 2022, 13, 1247.	2.4	1
8	QTL analysis of root diameter in a wild diploid relative of sweetpotato (<i>Ipomoea batatas</i> (L.) Lam.) using a SNP-based genetic linkage map generated by genotyping-by-sequencing. <i>Genetic Resources and Crop Evolution</i> , 2021, 68, 1375-1388.	1.6	3
9	Comparative analysis of chloroplast genomes of cultivars and wild species of sweetpotato (<i>Ipomoea</i>) Tj ETQq1 1 0.784314 rgBT /Ove 2.8 17		
10	Identification and function analysis of bHLH genes in response to cold stress in sweetpotato. <i>Plant Physiology and Biochemistry</i> , 2021, 169, 224-235.	5.8	19
11	A-, B- and C-type starch granules coexist in root tuber of sweet potato. <i>Food Hydrocolloids</i> , 2020, 98, 105279.	10.7	32
12	Genome-wide analysis of expression quantitative trait loci (eQTLs) reveals the regulatory architecture of gene expression variation in the storage roots of sweet potato. <i>Horticulture Research</i> , 2020, 7, 90.	6.3	38
13	A systematic comparison of eight new plastome sequences from <i>Ipomoea</i> L. PeerJ, 2019, 7, e6563.	2.0	10
14	Genome sequences of two diploid wild relatives of cultivated sweetpotato reveal targets for genetic improvement. <i>Nature Communications</i> , 2018, 9, 4580.	12.8	181
15	Transcriptome Sequencing of the Sweet Potato Progenitor (<i>Ipomoea Trifida</i> (H.B.K.) G. Don.) and Discovery of Drought Tolerance Genes. <i>Tropical Plant Biology</i> , 2016, 9, 63-72.	1.9	21
16	Novel interspecific hybridization between sweetpotato (<i>Ipomoea batatas</i> (L.) Lam.) and its two diploid wild relatives. <i>Euphytica</i> , 2009, 169, 345-352.	1.2	18