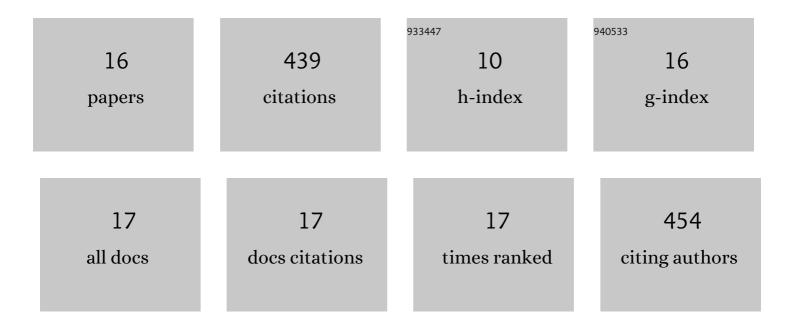
Qinghe Cao

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/9095336/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Genome sequences of two diploid wild relatives of cultivated sweetpotato reveal targets for genetic improvement. Nature Communications, 2018, 9, 4580.	12.8	181
2	Melatonin is a potential target for improving horticultural crop resistance to abiotic stress. Scientia Horticulturae, 2022, 291, 110560.	3.6	55
3	Genome-wide analysis of expression quantitative trait loci (eQTLs) reveals the regulatory architecture of gene expression variation in the storage roots of sweet potato. Horticulture Research, 2020, 7, 90.	6.3	38
4	A-, B- and C-type starch granules coexist in root tuber of sweet potato. Food Hydrocolloids, 2020, 98, 105279.	10.7	32
5	Transcriptome Sequencing of the Sweet Potato Progenitor (Ipomoea Trifida (H.B.K.) G. Don.) and Discovery of Drought Tolerance Genes. Tropical Plant Biology, 2016, 9, 63-72.	1.9	21
6	Identification and function analysis of bHLH genes in response to cold stress in sweetpotato. Plant Physiology and Biochemistry, 2021, 169, 224-235.	5.8	19
7	Novel interspecific hybridization between sweetpotato (Ipomoea batatas (L.) Lam.) and its two diploid wild relatives. Euphytica, 2009, 169, 345-352.	1.2	18
	Comparative analysis of chloroplast genomes of cultivars and wild species of sweetpotato (Inomora) Ti ETOp0.0		verlock 10 Tf

8 Comparative analysis of chloroplast genomes of cultivars and wild species of sweetpotato (Ipomoea) Tj ETQq0 0 0 rgBT /Overlock 10 Tf

9	Exogenous melatonin alleviates browning of fresh-cut sweetpotato by enhancing anti-oxidative process. Scientia Horticulturae, 2022, 297, 110937.	3.6	17
10	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. Journal of Agricultural and Food Chemistry, 2022, 70, 2574-2588.	5.2	15
11	A systematic comparison of eight new plastome sequences from <i>Ipomoea</i> L. PeerJ, 2019, 7, e6563.	2.0	10
12	Sizes, Components, Crystalline Structure, and Thermal Properties of Starches from Sweet Potato Varieties Originating from Different Countries. Molecules, 2022, 27, 1905.	3.8	8
13	QTL analysis of root diameter in a wild diploid relative of sweetpotato (Ipomoea batatas (L.) Lam.) using a SNP-based genetic linkage map generated by genotyping-by-sequencing. Genetic Resources and Crop Evolution, 2021, 68, 1375-1388.	1.6	3
14	Relationships between X-ray Diffraction Peaks, Molecular Components, and Heat Properties of C-Type Starches from Different Sweet Potato Varieties. Molecules, 2022, 27, 3385.	3.8	3
15	Overexpression of IbMPK3 increases low-temperature tolerance in transgenic sweetpotato. Plant Biotechnology Reports, 2022, 16, 91-100.	1.5	1
16	Comparative Transcriptome and Interaction Protein Analysis Reveals the Mechanism of IbMPK3-Overexpressing Transgenic Sweet Potato Response to Low-Temperature Stress. Genes, 2022, 13, 1247.	2.4	1