Jie Cui

List of Publications by Year in descending order

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		840776	713466
26	523	11	21
papers	citations	h-index	g-index
29	29	29	855
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#	Article	IF	Citations
1	Absorption mechanism of whey-protein-delivered curcumin using Caco-2 cell monolayers. Food Chemistry, 2015, 180, 48-54.	8.2	66
2	Preparation of corn starch–fatty acid complexes by highâ€pressure homogenization. Starch/Staerke, 2014, 66, 809-817.	2.1	63
3	Whey-protein-stabilized nanoemulsions as a potential delivery system for water-insoluble curcumin. LWT - Food Science and Technology, 2014, 59, 49-58.	5.2	58
4	Effects of milk protein-polysaccharide interactions on the stability ofÂice cream mix model systems. Food Hydrocolloids, 2015, 45, 327-336.	10.7	58
5	Effect of ball-milling on the physicochemical properties of maize starch. Biotechnology Reports (Amsterdam, Netherlands), 2014, 3, 54-59.	4.4	53
6	Whole-Transcriptome RNA Sequencing Reveals the Global Molecular Responses and CeRNA Regulatory Network of mRNAs, IncRNAs, miRNAs and circRNAs in Response to Salt Stress in Sugar Beet (Beta) Tj ETQq0 0 0	rg & T1/Ove	rlo ∉l s 10 Tf 50
7	Synergistic Radiation Protective Effect of Purified Auricularia auricular-judae Polysaccharide (AAP IV) with Grape Seed Procyanidins. Molecules, 2014, 19, 20675-20694.	3.8	36
8	The Effect of Yeast Species from Raw Milk in China on Proteolysis and Aroma Compound Formation in Camembert-Type Cheese. Food and Bioprocess Technology, 2012, 5, 2548-2556.	4.7	24
9	Goat and buffalo milk fat globule membranes exhibit better effects at inducing apoptosis and reduction the viability of HT-29 cells. Scientific Reports, 2019, 9, 2577.	3.3	15
10	Characterization of miRNA160/164 and Their Targets Expression of Beet (Beta vulgaris) Seedlings Under the Salt Tolerance. Plant Molecular Biology Reporter, 2018, 36, 790-799.	1.8	12
11	iTRAQ protein profile analysis of sugar beet under salt stress: different coping mechanisms in leaves and roots. BMC Plant Biology, 2020, 20, 347.	3.6	12
12	Characteristics of Cell Wall Structure of Green Beans During Controlled Freezing Point Storage. International Journal of Food Properties, 2015, 18, 1756-1772.	3.0	11
13	Proteomic analysis in different development stages on SPO generation of rice seeds after space flight. Life Sciences in Space Research, 2020, 26, 34-45.	2.3	10
14	Difference of proteomics vernalization-induced in bolting and flowering transitions of Beta vulgaris. Plant Physiology and Biochemistry, 2018, 123, 222-232.	5.8	9
15	Genome-wide sequence identification and expression analysis of <i>N⁶</i> -methyladenosine demethylase in sugar beet (<i>Beta vulgaris</i> L.) under salt stress. PeerJ, 2022, 10, e12719.	2.0	9
16	Photosynthetic Performance of Rice Seedlings Originated from Seeds Exposed to Spaceflight Conditions. Photochemistry and Photobiology, 2019, 95, 1205-1212.	2.5	8
17	Vernalisation mediated LncRNA-like gene expression in Beta vulgaris. Functional Plant Biology, 2017, 44, 720.	2.1	7
18	Metabolomics Analysis in Different Development Stages on SPO Generation of Rice Seeds After Spaceflight. Frontiers in Plant Science, 2021, 12, 700267.	3.6	7

#	Article	IF	CITATIONS
19	Identification of anthocyanin biosynthesis related microRNAs and total microRNAs in Lonicera edulis by high-throughput sequencing. Journal of Genetics, 2020, 99, 1.	0.7	6
20	Combining Proteomics and Metabolomics to Analyze the Effects of Spaceflight on Rice Progeny. Frontiers in Plant Science, 0, 13 , .	3.6	6
21	The Memory of Rice Response to Spaceflight Stress: From the Perspective of Metabolomics and Proteomics. International Journal of Molecular Sciences, 2022, 23, 3390.	4.1	5
22	Molecule studying on the diversity of cytoplasm fertility in Chinese sugar beet germplasm resource. , 2011, , .		1
23	Thermal Properties of Yak \hat{l} ±-Lactalbumin and \hat{l} ²-Lactoglobulin: a DSC Study. Food and Bioprocess Technology, 2017, 10, 2261-2267.	4.7	1
24	Cloning and function identification of the promoters and terminator of sugar beet chloroplast gene psbA. , $2011,$, .		0
25	Application of DNA fingerprint based on SSR in rice adulteration detection and origin traceability. , 2016, , .		0
26	Identification of anthocyanin biosynthesis related microRNAs and total microRNAs in by high-throughput sequencing. Journal of Genetics, 2020, 99, .	0.7	0