Fengde Wang

List of Publications by Year
in descending order

14	396	1163117 8	1058476 14
papers	citations	h-index	g-index

14	14	14	594
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Construction of an Intragenic SSR-Based Linkage Map and QTL Mapping for Agronomic Traits in Chinese Cabbage (Brassica rapa L. ssp. pekinensis). Horticulturae, 2022, 8, 165.	2.8	5
2	Genome-Wide Identification and Analysis of the Cytochrome B5 Protein Family in Chinese Cabbage (Brassica rapa L. ssp. Pekinensis). International Journal of Genomics, 2019, 2019, 1-16.	1.6	8
3	Identification of miRNAs and their targets in regulating tuberous root development in radish using small RNA and degradome analyses. 3 Biotech, 2018, 8, 311.	2.2	7
4	Ectopic expression of a Brassica rapa AINTEGUMENTA gene (BrANT-1) increases organ size and stomatal density in Arabidopsis. Scientific Reports, 2018, 8, 10528.	3.3	7
5	Physiological and Transcriptomic Responses of Chinese Cabbage (Brassica rapa L. ssp. Pekinensis) to Salt Stress. International Journal of Molecular Sciences, 2017, 18, 1953.	4.1	28
6	Transcriptome Analysis of Orange Head Chinese Cabbage (Brassica rapaL. ssp.pekinensis) and Molecular Marker Development. International Journal of Genomics, 2017, 2017, 1-8.	1.6	5
7	Comparative Transcriptome Analysis Reveals Effects of Exogenous Hematin on Anthocyanin Biosynthesis during Strawberry Fruit Ripening. International Journal of Genomics, 2016, 2016, 1-14.	1.6	8
8	Genome-Wide Identification and Analysis of the VQ Motif-Containing Protein Family in Chinese Cabbage (Brassica rapa L. ssp. Pekinensis). International Journal of Molecular Sciences, 2015, 16, 28683-28704.	4.1	43
9	Integrative Analysis of mRNA and miRNA Expression Profiles of the Tuberous Root Development at Seedling Stages in Turnips. PLoS ONE, 2015, 10, e0137983.	2.5	21
10	Characterization and Development of EST-SSRs by Deep Transcriptome Sequencing in Chinese Cabbage (Brassica rapaL. ssp.pekinensis). International Journal of Genomics, 2015, 2015, 1-11.	1.6	20
11	Genome-wide identification and analysis of the growth-regulating factor family in Chinese cabbage (Brassica rapa L. ssp. pekinensis). BMC Genomics, 2014, 15, 807.	2.8	80
12	MicroRNA expression analysis of rosette and folding leaves in Chinese cabbage using high-throughput Solexa sequencing. Gene, 2013, 532, 222-229.	2.2	20
13	Transcriptome analysis of rosette and folding leaves in Chinese cabbage using high-throughput RNA sequencing. Genomics, 2012, 99, 299-307.	2.9	48
14	Transcriptome analysis of the roots at early and late seedling stages using Illumina paired-end sequencing and development of EST-SSR markers in radish. Plant Cell Reports, 2012, 31, 1437-1447.	5.6	96