Rongzhan Guan

List of Publications by Year
in descending order

34 papers	1,220 citations	516710 16 h-index	395702 33 g-index
36 all docs	36 docs citations	36 times ranked	1450 citing authors

#	Article	IF	Citations
1	Enhanced Seed Oil Production in Canola by Conditional Expression of <i>Brassica napus LEAFY COTYLEDON1</i> and <i>LEC1-LIKE</i> in Developing Seeds Â Â. Plant Physiology, 2011, 156, 1577-1588.	4.8	216
2	Nitric Oxide Is Required for Melatonin-Enhanced Tolerance against Salinity Stress in Rapeseed (Brassica napus L.) Seedlings. International Journal of Molecular Sciences, 2018, 19, 1912.	4.1	136
3	An innovative procedure of genome-wide association analysis fits studies on germplasm population and plant breeding. Theoretical and Applied Genetics, 2017, 130, 2327-2343.	3.6	121
4	Substoichiometrically Different Mitotypes Coexist in Mitochondrial Genomes of Brassica napus L. PLoS ONE, 2011, 6, e17662.	2.5	99
5	Mitochondrial genome sequencing helps show the evolutionary mechanism of mitochondrial genome formation in Brassica. BMC Genomics, 2011, 12, 497.	2.8	99
6	BnHO1, a haem oxygenase-1 gene from Brassica napus, is required for salinity and osmotic stress-induced lateral root formation. Journal of Experimental Botany, 2011, 62, 4675-4689.	4.8	61
7	Nitrate reductase-dependent nitric oxide is crucial for multi-walled carbon nanotube-induced plant tolerance against salinity. Nanoscale, 2019, 11, 10511-10523.	5.6	60
8	l-Cysteine desulfhydrase-dependent hydrogen sulfide is required for methane-induced lateral root formation. Plant Molecular Biology, 2019, 99, 283-298.	3.9	52
9	Proteome Dynamics and Physiological Responses to Short-Term Salt Stress in Brassica napus Leaves. PLoS ONE, 2015, 10, e0144808.	2.5	48
10	Molecular Cloning, Characterization, and Expression Analysis of a Novel Gene Encoding l-Cysteine Desulfhydrase from Brassica napus. Molecular Biotechnology, 2013, 54, 737-746.	2.4	40
11	Fine mapping of a dominant gene conferring chlorophyll-deficiency in Brassica napus. Scientific Reports, 2016, 6, 31419.	3.3	30
12	Fine mapping of a major locus controlling plant height using a high-density single-nucleotide polymorphism map in Brassica napus. Theoretical and Applied Genetics, 2016, 129, 1479-1491.	3.6	28
13	Mapping a major QTL responsible for dwarf architecture in Brassica napus using a single-nucleotide polymorphism marker approach. BMC Plant Biology, 2016, 16, 178.	3.6	27
14	Genome-wide transcriptomic analysis uncovers the molecular basis underlying early flowering and apetalous characteristic in Brassica napus L. Scientific Reports, 2016, 6, 30576.	3.3	24
15	Cloning and expression analysis of three cDNAs encoding omega-3 fatty acid desaturases from Descurainia sophia. Biotechnology Letters, 2007, 29, 1417-1424.	2.2	18
16	Mapping of QTLs controlling seed weight and seed-shape traits in Brassica napus L. using a high-density SNP map. Euphytica, 2018, 214, 1.	1.2	18
17	Quantitative Trait Transcripts Mapping Coupled with Expression Quantitative Trait Loci Mapping Reveal the Molecular Network Regulating the Apetalous Characteristic in Brassica napus L.. Frontiers in Plant Science, 2018, 9, 89.	3.6	17
18	Fine mapping of the BnaC04.BIL1 gene controlling plant height in Brassica napus L. BMC Plant Biology, 2021, 21, 359.	3.6	14

#	Article	IF	Citations
19	Complete Mitochondrial Genome of Eruca sativa Mill. (Garden Rocket). PLoS ONE, 2014, 9, e105748.	2.5	13
20	Identification and physical mapping of QTLs associated with flowering time in Brassica napus L.. Euphytica, 2019, 215, 1.	1.2	13
21	Importance of hydrogen sulfide as the molecular basis of heterosis in hybrid Brassica napus: A case study in salinity response. Environmental and Experimental Botany, 2022, 193, 104693.	4.2	13
22	Fine mapping of an up-curling leaf locus (BnUC1) in Brassica napus. BMC Plant Biology, 2019, 19, 324.	3.6	10
23	The Mitochondrial Genome of Raphanus sativus and Gene Evolution of Cruciferous Mitochondrial Types. Journal of Genetics and Genomics, 2013, 40, 117-126.	3.9	9
24	Fine mapping of the BnUC2 locus related to leaf up-curling and plant semi-dwarfing in Brassica napus. BMC Genomics, 2020, 21, 530.	2.8	9
25	An RNA-seq transcriptome analysis of floral buds of an interspecific Brassica hybrid between B. carinata and B. napus. Plant Reproduction, 2014, 27, 225-237.	2.2	8
26	Histological, Physiological, and Comparative Proteomic Analyses Provide Insights into Leaf Rolling in <i>Brassica napus</i>. Journal of Proteome Research, 2018, 17, 1761-1772.	3.7	6
27	Genome-Wide Analysis Reveals the Role of Mediator Complex in the Soybeanâ€"Phytophthora sojae Interaction. International Journal of Molecular Sciences, 2019, 20, 4570.	4.1	6
28	A sulfotransferase gene BnSOT-like1 has a minor genetic effect on seed glucosinolate content in Brassica napus. Crop Journal, 2020, 8, 855-865.	5.2	6
29	Overâ€expression of a conserved RNAâ€binding motif (RRM) domain (<i>csRRM2</i>) improves components of <i>Brassica napus</i> yield by regulating cell size. Plant Breeding, 2012, 131, 614-619.	1.9	5
30	Multi-Walled Carbon Nanotubes Can Promote Brassica napus L. and Arabidopsis thaliana L. Root Hair Development through Nitric Oxide and Ethylene Pathways. International Journal of Molecular Sciences, 2020, 21, 9109.	4.1	5
31	Nitric Oxide Is Associated With Heterosis of Salinity Tolerance in Brassica napus L.. Frontiers in Plant Science, 2021, 12, 649888.	3.6	3
32	Composite Interval Mapping Based on Lattice Design for Error Control May Increase Power of Quantitative Trait Locus Detection. PLoS ONE, 2015, 10, e0130125.	2.5	3
33	Identification and Fine Mapping of a Locus Related to Leaf Up-Curling Trait (Bnuc3) in Brassica napus. International Journal of Molecular Sciences, 2021, 22, 11693.	4.1	2
34	Brassica Mitochondrial and Chloroplast Genomes. Compendium of Plant Genomes, 2018, , 159-176.	0.5	0