Jian Bo Song

List of Publications by Year
in descending order

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23	1,236	471509	610901
papers	citations	17 h-index	24 g-index

24	24	24	1396
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genome-wide identification of Brassica napus microRNAs and their targets in response to cadmium. Journal of Experimental Botany, 2012, 63, 4597-4613.	4.8	181
2	A set of miRNAs from Brassica napus in response to sulphate deficiency and cadmium stress. Plant Biotechnology Journal, 2010, 8, 887-899.	8.3	179
3	miR394 and LCR are involved in Arabidopsis salt and drought stress responses in an abscisic acid-dependent manner. BMC Plant Biology, 2013, 13, 210.	3.6	178
4	miR395 is involved in detoxification of cadmium in Brassica napus. Journal of Hazardous Materials, 2013, 250-251, 204-211.	12.4	114
5	Regulation of Leaf Morphology by MicroRNA394 and its Target LEAF CURLING RESPONSIVENESS. Plant and Cell Physiology, 2012, 53, 1283-1294.	3.1	107
6	The F-box family genes as key elements in response to salt, heavy mental, and drought stresses in Medicago truncatula. Functional and Integrative Genomics, 2015, 15, 495-507.	3.5	76
7	miR394 and its target gene LCR are involved in cold stress response in Arabidopsis. Plant Gene, 2016, 5, 56-64.	2.3	66
8	AtMYB20 is negatively involved in plant adaptive response to drought stress. Plant and Soil, 2014, 376, 433-443.	3.7	48
9	Identification of Cd-responsive RNA helicase genes and expression of a putative BnRH 24 mediated by miR158 in canola (Brassica napus). Ecotoxicology and Environmental Safety, 2018, 157, 159-168.	6.0	42
10	The U-box family genes in Medicago truncatula: Key elements in response to salt, cold, and drought stresses. PLoS ONE, 2017, 12, e0182402.	2.5	35
11	SWEET Gene Family in Medicago truncatula: Genome-Wide Identification, Expression and Substrate Specificity Analysis. Plants, 2019, 8, 338.	3.5	30
12	Genome-wide identification and characterization of stress-associated protein (SAP) gene family encoding A20/AN1 zinc-finger proteins in Medicago truncatula. Archives of Biological Sciences, 2018, 70, 87-98.	0.5	29
13	Uridylation and adenylation of RNAs. Science China Life Sciences, 2015, 58, 1057-1066.	4.9	25
14	In silico identification and expression analysis of superoxide dismutase (SOD) gene family in Medicago truncatula. 3 Biotech, 2018, 8, 348.	2.2	25
15	Altered Fruit and Seed Development of Transgenic Rapeseed (Brassica napus) Over-Expressing MicroRNA394. PLoS ONE, 2015, 10, e0125427.	2.5	23
16	An F-box E3 ubiquitin ligase-coding gene AtDIF1 is involved in Arabidopsis salt and drought stress responses in an abscisic acid-dependent manner. Environmental and Experimental Botany, 2017, 138, 21-35.	4.2	21
17	Prevalent cytidylation and uridylation of precursor miRNAs in Arabidopsis. Nature Plants, 2019, 5, 1260-1272.	9.3	19
18	Isolation and characterization of a MADS-box gene in cucumber (Cucumis sativus L.) that affects flowering time and leaf morphology in transgenic Arabidopsis. Biotechnology and Biotechnological Equipment, 2019, 33, 54-63.	1.3	13

#	Article	IF	Citations
19	The F-box E3 ubiquitin ligase AtSDR is involved in salt and drought stress responses in Arabidopsis. Gene, 2022, 809, 146011.	2.2	7
20	Identification of the trehalose-6-phosphate synthase gene family in Medicago truncatula and expression analysis under abiotic stresses. Gene, 2021, 787, 145641.	2.2	5
21	Identification and expression profiling of Oryza sativa nucleotidyl transferase protein (NTP) genes under various stress conditions. Gene, 2017, 628, 93-102.	2.2	4
22	Identification of RNA helicases in Medicago truncatula and their expression patterns under abiotic stress. Physiology and Molecular Biology of Plants, 2021, 27, 2283-2296.	3.1	2
23	Genome-Wide Analysis of the Growth-Regulating Factor Family in Medicago truncatula. Journal of Plant Growth Regulation, 2023, 42, 2305-2316.	5.1	2