

Yongjun Shu

List of Publications by Year in descending order

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Version: 2024-02-01

19
papers

516
citations

777949

13
h-index

889612

19
g-index

20
all docs

20
docs citations

20
times ranked

884
citing authors

#	ARTICLE	IF	CITATIONS
1	Transcriptome sequencing and expression profiling of genes involved in daylily (<i>Hemerocallis citrina</i>) Tj ETQq1 1 0.784314 rgBT /Over	0.5	16
2	Genome-wide identification and characterization of R2R3-MYB genes in <i>Medicago truncatula</i> . <i>Genetics and Molecular Biology</i> , 2019, 42, 611-623.	0.6	16
3	Genome-wide analysis of AP2/ERF transcription factors in zoysiagrass, <i>Zoysia japonica</i> . <i>Biotechnology and Biotechnological Equipment</i> , 2018, 32, 303-308.	0.5	27
4	Transcriptome sequencing and expression profiling of genes involved in the response to abiotic stress in <i>Medicago ruthenica</i> . <i>Genetics and Molecular Biology</i> , 2018, 41, 638-648.	0.6	22
5	Uncovering key small RNAs associated with gametocidal action in wheat. <i>Journal of Experimental Botany</i> , 2018, 69, 4739-4756.	2.4	4
6	Transcriptome sequencing analysis of alfalfa reveals CBF genes potentially playing important roles in response to freezing stress. <i>Genetics and Molecular Biology</i> , 2017, 40, 824-833.	0.6	27
7	Bioinformatics Analysis of MAPKKK Family Genes in <i>Medicago truncatula</i> . <i>Genes</i> , 2016, 7, 13.	1.0	11
8	Genome-Wide Investigation of MicroRNAs and Their Targets in Response to Freezing Stress in <i>Medicago sativa</i> L., Based on High-Throughput Sequencing. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 755-765.	0.8	48
9	Deep-sequencing transcriptome analysis of field-grown <i>Medicago sativa</i> L. crown buds acclimated to freezing stress. <i>Functional and Integrative Genomics</i> , 2016, 16, 495-511.	1.4	28
10	In silico identification, phylogeny and expression analysis of expansin superfamily in <i>Medicago truncatula</i> . <i>Biotechnology and Biotechnological Equipment</i> , 2016, 30, 197-203.	0.5	7
11	Genome-wide identification and characterization of the Dof gene family in <i>Medicago truncatula</i> . <i>Genetics and Molecular Research</i> , 2015, 14, 10645-10657.	0.3	24
12	Analysis of the <i>Thinopyrum elongatum</i> Transcriptome under Water Deficit Stress. <i>International Journal of Genomics</i> , 2015, 2015, 1-8.	0.8	8
13	Genome-Wide Analysis of the AP2/ERF Superfamily Genes and their Responses to Abiotic Stress in <i>Medicago truncatula</i> . <i>Frontiers in Plant Science</i> , 2015, 6, 1247.	1.7	128
14	Genome-wide survey and expression analysis of the MADS-box gene family in soybean. <i>Molecular Biology Reports</i> , 2013, 40, 3901-3911.	1.0	60
15	Genomic selection of seed weight based on low-density SCAR markers in soybean. <i>Genetics and Molecular Research</i> , 2013, 12, 2178-2188.	0.3	31
16	SNPs discovery and CAPS marker conversion in soybean. <i>Molecular Biology Reports</i> , 2011, 38, 1841-1846.	1.0	18
17	Identification and characterization of a new member of the SINE Au retroposon family (GmAu1) in the soybean, <i>Glycine max</i> (L.) Merr., genome and its potential application. <i>Plant Cell Reports</i> , 2011, 30, 2207-2213.	2.8	9
18	Genome-wide identification of intron fragment insertion mutations and their potential use as SCAR molecular markers in the soybean. <i>Theoretical and Applied Genetics</i> , 2010, 121, 1-8.	1.8	21

#	ARTICLE	IF	CITATIONS
19	Genome-wide identification of osmotic stress response gene in <i>Arabidopsis thaliana</i> . <i>Genomics</i> , 2008, 92, 488-493.	1.3	21