Xiaoxia Li

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/6162983/publications.pdf

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21	564	687363 13	677142 22
papers	citations	h-index	g-index

23	23	23	619
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Antibacterial and Cytotoxic Phenyltetracenoid Polyketides from Streptomyces morookaense. Journal of Natural Products, 2021, 84, 1806-1815.	3.0	10
2	Ectopic Expression of a Salt-Inducible Gene, LcSAIN3, from Sheepgrass Improves Seed Germination and Seedling Growth under Salt Stress in Arabidopsis. Genes, 2021, 12, 1994.	2.4	2
3	LcMYB4, an unknown function transcription factor gene from sheepgrass, as a positive regulator of chilling and freezing tolerance in transgenic Arabidopsis. BMC Plant Biology, 2020, 20, 238.	3.6	12
4	Evolutionary strategies drive a balance of the interacting gene products for the CBL and CIPK gene families. New Phytologist, 2020, 226, 1506-1516.	7.3	52
5	LcFIN2, a novel chloroplast protein gene from sheepgrass, enhances tolerance to low temperature in Arabidopsis and rice. Physiologia Plantarum, 2019, 166, 628-645.	5.2	12
6	Transcriptomic Analysis Reveals a Comprehensive Calcium- and Phytohormone-Dominated Signaling Response in Leymus chinensis Self-Incompatibility. International Journal of Molecular Sciences, 2019, 20, 2356.	4.1	16
7	Comparative transcriptome analysis provides insights into the distinct germination in sheepgrass (Leymus chinensis) during seed development. Plant Physiology and Biochemistry, 2019, 139, 446-458.	5.8	14
8	A MYB-related transcription factor from sheepgrass, LcMYB2, promotes seed germination and root growth under drought stress. BMC Plant Biology, 2019, 19, 564.	3.6	33
9	bHLH92from sheepgrass acts as a negative regulator of anthocyanin/proanthocyandin accumulation and influences seed dormancy. Journal of Experimental Botany, 2019, 70, 269-284.	4.8	41
10	Germination characteristics among different sheepgrass (Leymus chinensis) germplasm during the seed development and after-ripening stages. PeerJ, 2019, 7, e6688.	2.0	5
11	MADS-box family genes in sheepgrass and their involvement in abiotic stress responses. BMC Plant Biology, 2018, 18, 42.	3.6	45
12	New Insights on Drought Stress Response by Global Investigation of Gene Expression Changes in Sheepgrass (Leymus chinensis). Frontiers in Plant Science, 2016, 7, 954.	3.6	38
13	Overexpression of a novel coldâ€responsive transcript factor <scp>L</scp>c<scp>FIN</scp>1 from sheepgrass enhances tolerance to low temperature stress in transgenic plants. Plant Biotechnology Journal, 2016, 14, 861-874.	8.3	23
14	Transcriptome Analysis Reveals Common and Distinct Mechanisms for Sheepgrass (Leymus chinensis) Responses to Defoliation Compared to Mechanical Wounding. PLoS ONE, 2014, 9, e89495.	2.5	29
15	Molecular characterization and expression patterns of sucrose transport-related genes in sweet sorghum under defoliation. Acta Physiologiae Plantarum, 2014, 36, 1251-1259.	2.1	5
16	The large-scale investigation of gene expression in Leymus chinensis stigmas provides a valuable resource for understanding the mechanisms of poaceae self-incompatibility. BMC Genomics, 2014, 15, 399.	2.8	22
17	Molecular Characterization and Defoliation-Induced Expression of a Sucrose Transporter LcSUT1 Gene in Sheep Grass (Leymus chinensis). Plant Molecular Biology Reporter, 2013, 31, 1184-1191.	1.8	8
18	LcSAIN1, a Novel Salt-Induced Gene from SheepGrass, Confers Salt Stress Tolerance in Transgenic Arabidopsis and Rice. Plant and Cell Physiology, 2013, 54, 1172-1185.	3.1	32

#	Article	IF	Citations
19	Overexpression of sheepgrass R1-MYB transcription factor LcMYB1 confers salt tolerance in transgenic Arabidopsis. Plant Physiology and Biochemistry, 2013, 70, 252-260.	5.8	71
20	A novel salt-induced gene from sheepgrass, LcSAIN2, enhances salt tolerance in transgenic Arabidopsis. Plant Physiology and Biochemistry, 2013, 64, 52-59.	5.8	23
21	Transcriptome Analysis in Sheepgrass (Leymus chinensis): A Dominant Perennial Grass of the Eurasian Steppe. PLoS ONE, 2013, 8, e67974.	2.5	68