Dayong Li

List of Publications by Year in descending order

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DAVONGL

#	Article	IF	CITATIONS
1	MiR396â€ <i>GRF</i> module associates with switchgrass biomass yield and feedstock quality. Plant Biotechnology Journal, 2021, 19, 1523-1536.	8.3	35
2	The OsSPK1–OsRac1–RAI1 defense signaling pathway is shared by two distantly related NLR proteins in rice blast resistance. Plant Physiology, 2021, 187, 2852-2864.	4.8	5
3	Identification of GROWTH-REGULATING FACTOR transcription factors in lettuce (Lactuca sativa) genome and functional analysis of LsaGRF5 in leaf size regulation. BMC Plant Biology, 2021, 21, 485.	3.6	20
4	The bHLH transcription factor PPLS1 regulates the color of pulvinus and leaf sheath in foxtail millet (Setaria italica). Theoretical and Applied Genetics, 2020, 133, 1911-1926.	3.6	14
5	Heterologous expression of a chimeric gene, OsDST-SRDX, enhanced salt tolerance of transgenic switchgrass (Panicum virgatum L.). Plant Cell Reports, 2020, 39, 723-736.	5.6	1
6	MiR319 mediated salt tolerance by ethylene. Plant Biotechnology Journal, 2019, 17, 2370-2383.	8.3	64
7	Importance of OsRac1 and RAI1 in signalling of nucleotideâ€binding site leucineâ€rich repeat proteinâ€mediated resistance to rice blast disease. New Phytologist, 2019, 223, 828-838.	7.3	27
8	A novel antisense long noncoding <scp>RNA</scp> , <i><scp>TWISTED LEAF</scp></i> , maintains leaf blade flattening by regulating its associated sense R2R3â€ <scp>MYB</scp> gene in rice. New Phytologist, 2018, 218, 774-788.	7.3	96
9	An AT-hook protein DEPRESSED PALEA1 physically interacts with the TCP Family transcription factor RETARDED PALEA1 in rice. Biochemical and Biophysical Research Communications, 2018, 495, 487-492.	2.1	11
10	Overexpression of OsPIL1 enhanced biomass yield and saccharification efficiency in switchgrass. Plant Science, 2018, 276, 143-151.	3.6	11
11	WHITE PANICLE3, a Novel Nucleus-Encoded Mitochondrial Protein, Is Essential for Proper Development and Maintenance of Chloroplasts and Mitochondria in Rice. Frontiers in Plant Science, 2018, 9, 762.	3.6	10
12	Identification of a G2-like transcription factor, OsPHL3, functions as a negative regulator of flowering in rice by co-expression and reverse genetic analysis. BMC Plant Biology, 2018, 18, 157.	3.6	15
13	Enhanced Cold Tolerance and Tillering in Switchgrass (Panicum virgatum L.) by Heterologous Expression of Osa-miR393a. Plant and Cell Physiology, 2017, 58, 2226-2240.	3.1	44
14	MicroRNA319-regulated TCPs interact with FBHs and PFT1 to activate CO transcription and control flowering time in Arabidopsis. PLoS Genetics, 2017, 13, e1006833.	3.5	70
15	Constitutive expression of OsDof4, encoding a C2-C2 zinc finger transcription factor, confesses its distinct flowering effects under long- and short-day photoperiods in rice (Oryza sativa L.). BMC Plant Biology, 2017, 17, 166.	3.6	36
16	Overexpression of a Chimeric Gene, OsDST-SRDX, Improved Salt Tolerance of Perennial Ryegrass. Scientific Reports, 2016, 6, 27320.	3.3	24
17	Integrated analysis of phenome, genome, and transcriptome of hybrid rice uncovered multiple heterosis-related loci for yield increase. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E6026-E6035.	7.1	126
18	Overexpression of OsDof12 affects plant architecture in rice (Oryza sativa L.). Frontiers in Plant Science, 2015, 6, 833.	3.6	36

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19	Long Non-coding RNAs and Their Biological Roles in Plants. Genomics, Proteomics and Bioinformatics, 2015, 13, 137-147.	6.9	231
20	Constitutive Expression of Rice <i>MicroRNA528</i> Alters Plant Development and Enhances Tolerance to Salinity Stress and Nitrogen Starvation in Creeping Bentgrass. Plant Physiology, 2015, 169, 576-593.	4.8	136
21	OsMYB103L, an R2R3-MYB transcription factor, influences leaf rolling and mechanical strength in rice (Oryza sativaL.). BMC Plant Biology, 2014, 14, 158.	3.6	92
22	Identifying the Genome-Wide Sequence Variations and Developing New Molecular Markers for Genetics Research by Re-Sequencing a Landrace Cultivar of Foxtail Millet. PLoS ONE, 2013, 8, e73514.	2.5	62