## Dayong Li

List of Publications by Year in descending order

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DAVONGL

#	Article	IF	CITATIONS
1	Long Non-coding RNAs and Their Biological Roles in Plants. Genomics, Proteomics and Bioinformatics, 2015, 13, 137-147.	6.9	231
2	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
3	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
4	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
5	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
6	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
7	MiR319 mediated salt tolerance by ethylene. Plant Biotechnology Journal, 2019, 17, 2370-2383.	8.3	64
8	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
9	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
10	Overexpression of OsDof12 affects plant architecture in rice (Oryza sativa L.). Frontiers in Plant Science, 2015, 6, 833.	3.6	36
11	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
12	MiR396â€∢i>GRF module associates with switchgrass biomass yield and feedstock quality. Plant Biotechnology Journal, 2021, 19, 1523-1536.	8.3	35
13	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
14	Overexpression of a Chimeric Gene, OsDST-SRDX, Improved Salt Tolerance of Perennial Ryegrass. Scientific Reports, 2016, 6, 27320.	3.3	24
15	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
16	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
17	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
18	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

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19	Overexpression of OsPIL1 enhanced biomass yield and saccharification efficiency in switchgrass. Plant Science, 2018, 276, 143-151.	3.6	11
20	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
21	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
22	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