Zhiquan Wang

List of Publications by Year in descending order

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1163117 1058476 20 210 8 14 citations h-index g-index papers 22 22 22 156 all docs docs citations times ranked citing authors

#	Article	IF	CITATIONS
1	An Integrated Transcriptome and Proteome Analysis Reveals Putative Regulators of Adventitious Root Formation in Taxodium â€~Zhongshanshan'. International Journal of Molecular Sciences, 2019, 20, 1225.	4.1	32
2	De novo sequencing, assembly, and analysis of Iris lactea var. chinensis roots' transcriptome in response to salt stress. Plant Physiology and Biochemistry, 2018, 125, 1-12.	5.8	27
3	Identification of suitable reference genes in Taxodium †Zhongshanshan†under abiotic stresses. Trees - Structure and Function, 2017, 31, 1519-1530.	1.9	21
4	Identification and Functional Analysis of ThADH1 and ThADH4 Genes Involved in Tolerance to Waterlogging Stress in Taxodium hybrid â€~Zhongshanshan 406'. Genes, 2021, 12, 225.	2.4	17
5	Full-Length Transcriptome Sequencing and Comparative Transcriptome Analysis to Evaluate Drought and Salt Stress in Iris lactea var. chinensis. Genes, 2021, 12, 434.	2.4	14
6	Genome-wide Analysis of Basic Helix-Loop-Helix Family Genes and Expression Analysis in Response to Drought and Salt Stresses in Hibiscus hamabo Sieb. et Zucc. International Journal of Molecular Sciences, 2021, 22, 8748.	4.1	14
7	Genome-wide study of the GRAS gene family in Hibiscus hamabo Sieb. et Zucc and analysis of HhGRAS14-induced drought and salt stress tolerance in Arabidopsis. Plant Science, 2022, 319, 111260.	3.6	13
8	The genome of <i>Hibiscus hamabo</i> reveals its adaptation to saline and waterlogged habitat. Horticulture Research, 2022, 9, uhac067.	6.3	12
9	Selection and verification of candidate reference genes for gene expression by quantitative RT-PCR in Hibiscus hamabo Sieb.et Zucc Trees - Structure and Function, 2019, 33, 1591-1601.	1.9	10
10	Efficient virus-induced gene silencing in <i>Hibiscus hamabo</i> Sieb. et Zucc. using tobacco rattle virus. PeerJ, 2019, 7, e7505.	2.0	8
11	Genome-Wide Identification and Characterization of NAC Family in Hibiscus hamabo Sieb. et Zucc. under Various Abiotic Stresses. International Journal of Molecular Sciences, 2022, 23, 3055.	4.1	8
12	Molecular cloning and expression analysis of threeThERFs involved in the response to waterlogging stress ofTaxodium†Zhongshanshan406', and subcellular localization of the gene products. PeerJ, 2018, 6, e4434.	2.0	7
13	Cloning and Characterization of ThSHRs and ThSCR Transcription Factors in Taxodium Hybrid †Zhongshanshan 406'. Genes, 2017, 8, 185.	2.4	6
14	Phylogenetic and Transcription Analysis of Hibiscus hamabo Sieb. et Zucc. WRKY Transcription Factors. DNA and Cell Biology, 2020, 39, 1141-1154.	1.9	6
15	Influence of soil properties on the performance of the <i>Taxodium</i> hybrid â€~Zhongshanshan 407' in a short-term pot experiment. Soil Science and Plant Nutrition, 2017, 63, 145-152.	1.9	4
16	Transcriptome Analysis Reveals Regulatory Framework for Salt and Drought Tolerance in Hibiscus hamabo Siebold & Zuccarini. Forests, 2021, 12, 454.	2.1	4
17	Transcriptome Analysis of Salt Stress in Hibiscus hamabo Sieb. et Zucc Based on Pacbio Full-Length Transcriptome Sequencing. International Journal of Molecular Sciences, 2022, 23, 138.	4.1	4
18	Screening and Identification of Host Proteins Interacting with Iris lactea var. chinensis Metallothionein IlMT2a by Yeast Two-Hybrid Assay. Genes, 2021, 12, 554.	2.4	2

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#	Article	IF	CITATIONS
19	The complete chloroplast genome sequence of <i>Hibiscus coccineus</i> . Mitochondrial DNA Part B: Resources, 2022, 7, 217-218.	0.4	1
20	Complete chloroplast genome sequence of <i>Kosteletzkya pentacarpos</i> . Mitochondrial DNA Part B: Resources, 2022, 7, 1232-1233.	0.4	0