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	The complete chloroplast genome sequence of <i>Hibiscus coccineus</i> . Mitochondrial DNA Part B: Resources, 2022, 7, 217-218.	0.4	1
2	The genome of <i>Hibiscus hamabo</i> reveals its adaptation to saline and waterlogged habitat. Horticulture Research, 2022, 9, uhac067.	6.3	12
3	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
4	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
5	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
6	Complete chloroplast genome sequence of <i>Kosteletzkya pentacarpos</i> . Mitochondrial DNA Part B: Resources, 2022, 7, 1232-1233.	0.4	O
7	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
8	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
9	Transcriptome Analysis Reveals Regulatory Framework for Salt and Drought Tolerance in Hibiscus hamabo Siebold & Zuccarini. Forests, 2021, 12, 454.	2.1	4
10	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
11	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
12	Phylogenetic and Transcription Analysis of Hibiscus hamabo Sieb. et Zucc. WRKY Transcription Factors. DNA and Cell Biology, 2020, 39, 1141-1154.	1.9	6
13	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
14	An Integrated Transcriptome and Proteome Analysis Reveals Putative Regulators of Adventitious Root Formation in Taxodium †Zhongshanshan'. International Journal of Molecular Sciences, 2019, 20, 1225.	4.1	32
15	Efficient virus-induced gene silencing in <i>Hibiscus hamabo</i> Sieb. et Zucc. using tobacco rattle virus. PeerJ, 2019, 7, e7505.	2.0	8
16	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
17	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
18	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

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#	Article	lF	CITATIONS
19	Identification of suitable reference genes in Taxodium $\hat{a}\in \mathbb{Z}$ hongshanshan $\hat{a}\in \mathbb{Z}$ under abiotic stresses. Trees - Structure and Function, 2017, 31, 1519-1530.	1.9	21
20	Cloning and Characterization of ThSHRs and ThSCR Transcription Factors in Taxodium Hybrid †Zhongshanshan 406'. Genes, 2017, 8, 185.	2.4	6