

YuChun Wang

List of Publications by Year in descending order

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Version: 2024-02-01

11
papers

286
citations

1163117
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docs citations

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times ranked

296
citing authors

#	ARTICLE	IF	CITATIONS
1	Transcriptome Analysis of an Anthracnose-Resistant Tea Plant Cultivar Reveals Genes Associated with Resistance to <i>Colletotrichum camelliae</i> . PLoS ONE, 2016, 11, e0148535.	2.5	55
2	Transcriptional analysis and histochemistry reveal that hypersensitive cell death and H ₂ O ₂ have crucial roles in the resistance of tea plant (<i>Camellia sinensis</i> (L.) O. Kuntze) to anthracnose. Horticulture Research, 2018, 5, 18.	6.3	46
3	Differences in the Characteristics and Pathogenicity of <i>Colletotrichum camelliae</i> and <i>C. fructicola</i> Isolated From the Tea Plant [<i>Camellia sinensis</i> (L.) O. Kuntze]. Frontiers in Microbiology, 2018, 9, 3060.	3.5	44
4	The involvements of calcium-dependent protein kinases and catechins in tea plant [<i>Camellia sinensis</i> (L.) O. Kuntze] cold responses. Plant Physiology and Biochemistry, 2019, 143, 190-202.	5.8	32
5	Identification of the invertase gene family (INVs) in tea plant and their expression analysis under abiotic stress. Plant Cell Reports, 2016, 35, 2269-2283.	5.6	31
6	Diversity of <i>Pestalotiopsis</i> -Like Species Causing Gray Blight Disease of Tea Plants (<i>Camellia</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf Pathogenicity. Plant Disease, 2019, 103, 2548-2558.	1.4	31
7	Genome-wide identification of glutathione S-transferase gene family members in tea plant (<i>Camellia</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf Macromolecules, 2022, 205, 749-760.	7.5	17
8	Integrated transcriptomic and metabolomic analyses reveal the effects of callose deposition and multihormone signal transduction pathways on the tea plant- <i>Colletotrichum camelliae</i> interaction. Scientific Reports, 2020, 10, 12858.	3.3	14
9	Genome-wide identification, characterization, and expression analysis of nucleotide-binding leucine-rich repeats gene family under environmental stresses in tea (<i>Camellia sinensis</i>). Genomics, 2020, 112, 1351-1362.	2.9	7
10	Genome-wide identification of SULTR genes in tea plant and analysis of their expression in response to sulfur and selenium. Protoplasma, 2022, 259, 127-140.	2.1	7
11	Lifestyle Characteristics and Gene Expression Analysis of <i>Colletotrichum camelliae</i> Isolated from Tea Plant [<i>Camellia sinensis</i> (L.) O. Kuntze] Based on Transcriptome. Biomolecules, 2020, 10, 782.	4.0	2