

Darren Cj Wong

List of Publications by Year in descending order

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Version: 2024-02-01

15
papers

1,184
citations

623188

14
h-index

996533

15
g-index

15
all docs

15
docs citations

15
times ranked

1547
citing authors

#	ARTICLE	IF	CITATIONS
1	Network aggregation improves gene function prediction of grapevine gene co-expression networks. <i>Plant Molecular Biology</i> , 2020, 103, 425-441.	2.0	22
2	Ethylene receptors and related proteins in climacteric and non-climacteric fruits. <i>Plant Science</i> , 2018, 276, 63-72.	1.7	79
3	Identification, characterization, and expression analysis of calmodulin and calmodulin-like genes in grapevine (<i>Vitis vinifera</i>) reveal likely roles in stress responses. <i>Plant Physiology and Biochemistry</i> , 2018, 129, 221-237.	2.8	52
4	Complex Sexual Deception in an Orchid Is Achieved by Co-opting Two Independent Biosynthetic Pathways for Pollinator Attraction. <i>Current Biology</i> , 2017, 27, 1867-1877.e5.	1.8	67
5	Comprehensive Workflow for the Genome-wide Identification and Expression Meta-analysis of the ATL E3 Ubiquitin Ligase Gene Family in Grapevine. <i>Journal of Visualized Experiments</i> , 2017, , .	0.2	4
6	Constructing Integrated Networks for Identifying New Secondary Metabolic Pathway Regulators in Grapevine: Recent Applications and Future Opportunities. <i>Frontiers in Plant Science</i> , 2017, 8, 505.	1.7	77
7	Genome-wide characterisation and expression profile of the grapevine ATL ubiquitin ligase family reveal biotic and abiotic stress-responsive and development-related members. <i>Scientific Reports</i> , 2016, 6, 38260.	1.6	21
8	The photomorphogenic factors UV-B RECEPTOR 1, ELONGATED HYPOCOTYL 5, and HY5 HOMOLOGUE are part of the UV-B signalling pathway in grapevine and mediate flavonol accumulation in response to the environment. <i>Journal of Experimental Botany</i> , 2016, 67, 5429-5445.	2.4	100
9	Combined physiological, transcriptome, and cis-regulatory element analyses indicate that key aspects of ripening, metabolism, and transcriptional program in grapes (<i>Vitis vinifera</i> L.) are differentially modulated accordingly to fruit size. <i>BMC Genomics</i> , 2016, 17, 416.	1.2	88
10	A systems-oriented analysis of the grapevine R2R3-MYB transcription factor family uncovers new insights into the regulation of stilbene accumulation. <i>DNA Research</i> , 2016, 23, 451-466.	1.5	141
11	Transcriptome and metabolite profiling reveals that prolonged drought modulates the phenylpropanoid and terpenoid pathway in white grapes (<i>Vitis vinifera</i> L.). <i>BMC Plant Biology</i> , 2016, 16, 67.	1.6	269
12	New insights into the evolutionary history of plant sorbitol dehydrogenase. <i>BMC Plant Biology</i> , 2015, 15, 101.	1.6	26
13	Annotation of gene function in citrus using gene expression information and co-expression networks. <i>BMC Plant Biology</i> , 2014, 14, 186.	1.6	38
14	VTCdb: a gene co-expression database for the crop species <i>Vitis vinifera</i> (grapevine). <i>BMC Genomics</i> , 2013, 14, 882.	1.2	75
15	Transcriptome analysis at four developmental stages of grape berry (<i>Vitis vinifera</i> cv. Shiraz) provides insights into regulated and coordinated gene expression. <i>BMC Genomics</i> , 2012, 13, 691.	1.2	125