

Javier Canales

List of Publications by Year in descending order

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Version: 2024-02-01

29
papers

1,109
citations

430874

18
h-index

477307

29
g-index

34
all docs

34
docs citations

34
times ranked

1641
citing authors

#	ARTICLE	IF	CITATIONS
1	Allelic diversity of three anthocyanin synthesis genes in accessions of native <i>Solanum tuberosum</i> L. ssp. <i>tuberosum</i> at the Potato Genebank of the Universidad Austral de Chile. <i>Genetic Resources and Crop Evolution</i> , 2022, 69, 297-314.	1.6	2
2	Transcriptomic and Physiological Response of Durum Wheat Grain to Short-Term Heat Stress during Early Grain Filling. <i>Plants</i> , 2022, 11, 59.	3.5	9
3	Evolutionary and Gene Expression Analyses Reveal New Insights into the Role of LSU Gene-Family in Plant Responses to Sulfate-Deficiency. <i>Plants</i> , 2022, 11, 1526.	3.5	3
4	Transcriptome Analysis of Seed Weight Plasticity in <i>Brassica napus</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 4449.	4.1	6
5	Integrative Transcriptomic and Metabolomic Analysis at Organ Scale Reveals Gene Modules Involved in the Responses to Suboptimal Nitrogen Supply in Tomato. <i>Agronomy</i> , 2021, 11, 1320.	3.0	6
6	The Arabidopsis Transcription Factor CDF3 Is Involved in Nitrogen Responses and Improves Nitrogen Use Efficiency in Tomato. <i>Frontiers in Plant Science</i> , 2020, 11, 601558.	3.6	18
7	Transcriptomic analysis at organ and time scale reveals gene regulatory networks controlling the sulfate starvation response of <i>Solanum lycopersicum</i> . <i>BMC Plant Biology</i> , 2020, 20, 385.	3.6	13
8	Nitrate Defines Shoot Size through Compensatory Roles for Endoreplication and Cell Division in <i>Arabidopsis thaliana</i> . <i>Current Biology</i> , 2020, 30, 1988-2000.e3.	3.9	25
9	Expansin genes expression in growing ovaries and grains of sunflower are tissue-specific and associate with final grain weight. <i>BMC Plant Biology</i> , 2018, 18, 327.	3.6	10
10	Integrative Transcriptomic Analysis Uncovers Novel Gene Modules That Underlie the Sulfate Response in <i>Arabidopsis thaliana</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 470.	3.6	44
11	GENIUS: web server to predict local gene networks and key genes for biological functions. <i>Bioinformatics</i> , 2017, 33, 760-761.	4.1	4
12	Nitrate induction of root hair density is mediated by <i>TGA1</i> and <i>TGA4</i> and <i>CPC</i> transcription factors in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2017, 92, 305-316.	5.7	115
13	The Integration of Electrical Signals Originating in the Root of Vascular Plants. <i>Frontiers in Plant Science</i> , 2017, 8, 2173.	3.6	36
14	Poplar trees for phytoremediation of high levels of nitrate and applications in bioenergy. <i>Plant Biotechnology Journal</i> , 2016, 14, 299-312.	8.3	45
15	Use of transcriptomics and co-expression networks to analyze the interconnections between nitrogen assimilation and photorespiratory metabolism. <i>Journal of Experimental Botany</i> , 2016, 67, 3095-3108.	4.8	34
16	The overexpression of the pine transcription factor <i>PpDof5</i> in <i>Arabidopsis</i> leads to increased lignin content and affects carbon and nitrogen metabolism. <i>Physiologia Plantarum</i> , 2015, 155, 369-383.	5.2	18
17	Transcriptome analysis reveals regulatory networks underlying differential susceptibility to <i>Botrytis cinerea</i> in response to nitrogen availability in <i>Solanum lycopersicum</i> . <i>Frontiers in Plant Science</i> , 2015, 6, 911.	3.6	41
18	Understanding developmental and adaptive cues in pine through metabolite profiling and co-expression network analysis. <i>Journal of Experimental Botany</i> , 2015, 66, 3113-3127.	4.8	34

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19	Systems analysis of transcriptome data provides new hypotheses about Arabidopsis root response to nitrate treatments. <i>Frontiers in Plant Science</i> , 2014, 5, 22.	3.6	116
20	Transcriptome analysis in maritime pine using laser capture microdissection and 454 pyrosequencing. <i>Tree Physiology</i> , 2014, 34, 1278-1288.	3.1	38
21	Nitrogen control of developmental phase transitions in <i>Arabidopsis thaliana</i> . <i>Journal of Experimental Botany</i> , 2014, 65, 5611-5618.	4.8	108
22	<i>De novo</i> assembly of maritime pine transcriptome: implications for forest breeding and biotechnology. <i>Plant Biotechnology Journal</i> , 2014, 12, 286-299.	8.3	115
23	Identification of genes differentially expressed in ectomycorrhizal roots during the <i>Pinus pinaster</i> – <i>Laccaria bicolor</i> interaction. <i>Planta</i> , 2013, 237, 1637-1650.	3.2	18
24	Novel Insights into Regulation of Asparagine Synthetase in Conifers. <i>Frontiers in Plant Science</i> , 2012, 3, 100.	3.6	50
25	Gene expression profiling in the stem of young maritime pine trees: detection of ammonium stress-responsive genes in the apex. <i>Trees - Structure and Function</i> , 2012, 26, 609-619.	1.9	21
26	A maritime pine antimicrobial peptide involved in ammonium nutrition. <i>Plant, Cell and Environment</i> , 2011, 34, 1443-1453.	5.7	21
27	The glutamine synthetase gene family in <i>Populus</i> . <i>BMC Plant Biology</i> , 2011, 11, 119.	3.6	63
28	EuroPineDB: a high-coverage web database for maritime pine transcriptome. <i>BMC Genomics</i> , 2011, 12, 366.	2.8	59
29	Identification of genes regulated by ammonium availability in the roots of maritime pine trees. <i>Amino Acids</i> , 2010, 39, 991-1001.	2.7	30