

Jose V Die

List of Publications by Year in descending order

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34
papers

858
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471509

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37
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37
times ranked

1260
citing authors

#	ARTICLE	IF	CITATIONS
1	Aldehyde Dehydrogenase 3 Is an Expanded Gene Family with Potential Adaptive Roles in Chickpea. <i>Plants</i> , 2021, 10, 2429.	3.5	3
2	Characterization and Analysis of Anthocyanin-Related Genes in Wild-Type Blueberry and the Pink-Fruited Mutant Cultivar "Pink Lemonade": New Insights into Anthocyanin Biosynthesis. <i>Agronomy</i> , 2020, 10, 1296.	3.0	15
3	Genetic analysis reveals PDH1 as a candidate gene for control of pod dehiscence in chickpea. <i>Molecular Breeding</i> , 2020, 40, 1.	2.1	14
4	geneHummus: an R package to define gene families and their expression in legumes and beyond. <i>BMC Genomics</i> , 2019, 20, 591.	2.8	3
5	Candidate genes expression profiling during wilting in chickpea caused by <i>Fusarium oxysporum</i> f. sp. <i>ciceris</i> race 5. <i>PLoS ONE</i> , 2019, 14, e0224212.	2.5	18
6	Evidence of epistatic suppression of repeat fruiting in cultivated strawberry. <i>BMC Plant Biology</i> , 2019, 19, 386.	3.6	7
7	First RNA-seq approach to study fruit set and parthenocarpy in zucchini (<i>Cucurbita pepo</i> L.). <i>BMC Plant Biology</i> , 2019, 19, 61.	3.6	19
8	Transcriptome analysis identifies genes related to the waxy coating on blueberry fruit in two northern-adapted rabbiteye breeding populations. <i>BMC Plant Biology</i> , 2019, 19, 460.	3.6	22
9	Genome-scale examination of NBS-encoding genes in blueberry. <i>Scientific Reports</i> , 2018, 8, 3429.	3.3	18
10	Genome-wide identification of the auxin response factor gene family in <i>Cicer arietinum</i> . <i>BMC Genomics</i> , 2018, 19, 301.	2.8	40
11	Segmental and Tandem Duplications Driving the Recent NBS-LRR Gene Expansion in the Asparagus Genome. <i>Genes</i> , 2018, 9, 568.	2.4	18
12	Auxin signalling regulation during induced and parthenocarpic fruit set in zucchini. <i>Molecular Breeding</i> , 2017, 37, 1.	2.1	21
13	Selection of internal reference genes for normalization of reverse transcription quantitative polymerase chain reaction (RT-qPCR) analysis in the rumen epithelium. <i>PLoS ONE</i> , 2017, 12, e0172674.	2.5	15
14	Proteome dynamics of cold-acclimating <i>Rhododendron</i> species contrasting in their freezing tolerance and thermonasty behavior. <i>PLoS ONE</i> , 2017, 12, e0177389.	2.5	16
15	Design and Sampling Plan Optimization for RT-qPCR Experiments in Plants: A Case Study in Blueberry. <i>Frontiers in Plant Science</i> , 2016, 7, 271.	3.6	9
16	Global patterns of protein abundance during the development of cold hardiness in blueberry. <i>Environmental and Experimental Botany</i> , 2016, 124, 11-21.	4.2	11
17	Identification, cloning, and expression analysis of three phytoene synthase genes from <i>Cucurbita pepo</i> . <i>Biologia Plantarum</i> , 2015, 59, 201-210.	1.9	9
18	Elucidating cold acclimation pathway in blueberry by transcriptome profiling. <i>Environmental and Experimental Botany</i> , 2014, 106, 87-98.	4.2	30

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19	Carotenogenic Gene Expression and Carotenoid Accumulation in Three Varieties of <i>Cucurbita pepo</i> during Fruit Development. <i>Journal of Agricultural and Food Chemistry</i> , 2013, 61, 6393-6403.	5.2	33
20	Advent of genomics in blueberry. <i>Molecular Breeding</i> , 2013, 32, 493-504.	2.1	18
21	Superior Cross-Species Reference Genes: A Blueberry Case Study. <i>PLoS ONE</i> , 2013, 8, e73354.	2.5	35
22	RNA quality assessment: a view from plant qPCR studies. <i>Journal of Experimental Botany</i> , 2012, 63, 6069-6077.	4.8	52
23	Selection of reference genes for expression studies in <i>Cicer arietinum</i> L.: analysis of <i>cyp81E3</i> gene expression against <i>Ascochyta rabiei</i> . <i>Molecular Breeding</i> , 2012, 29, 261-274.	2.1	26
24	Selection of Reference Genes for Gene Expression Studies in Zucchini (<i>Cucurbita pepo</i>) Using qPCR. <i>Journal of Agricultural and Food Chemistry</i> , 2011, 59, 5402-5411.	5.2	74
25	Characterization of the ΔCt ratio for reliable determination of RNA quality. <i>Analytical Biochemistry</i> , 2011, 419, 336-338.	2.4	21
26	Selection of reference genes in <i>Hedysarum coronarium</i> under various stresses and stages of development. <i>Analytical Biochemistry</i> , 2011, 409, 236-243.	2.4	28
27	Evaluation of candidate reference genes for expression studies in <i>Pisum sativum</i> under different experimental conditions. <i>Planta</i> , 2010, 232, 145-153.	3.2	151
28	Gene expression profiling of <i>Medicago truncatula</i> roots in response to the parasitic plant <i>Orobanche crenata</i> . <i>Weed Research</i> , 2009, 49, 66-80.	1.7	26
29	Gene expression analysis of molecular mechanisms of defense induced in <i>Medicago truncatula</i> parasitized by <i>Orobanche crenata</i> . <i>Plant Physiology and Biochemistry</i> , 2009, 47, 635-641.	5.8	10
30	Expression analysis of <i>Pisum sativum</i> putative defence genes during <i>Orobanche crenata</i> infection. <i>Crop and Pasture Science</i> , 2009, 60, 490.	1.5	7
31	Selection of housekeeping genes for normalization by real-time RT-PCR: Analysis of <i>Or-MYB1</i> gene expression in <i>Orobanche ramosa</i> development. <i>Analytical Biochemistry</i> , 2008, 379, 176-181.	2.4	46
32	Isolation and expression analysis of a cobalamin-independent methionine synthase gene from the parasitic plant <i>Orobanche ramosa</i> . <i>Scientia Horticulturae</i> , 2008, 116, 337-341.	3.6	2
33	First Report of <i>Orobanche crenata</i> on <i>Sulla</i> (<i>Hedysarum coronarium</i>) in Andalusia, Southern Spain. <i>Plant Disease</i> , 2008, 92, 1709-1709.	1.4	2
34	Identification by suppression subtractive hybridization and expression analysis of <i>Medicago truncatula</i> putative defence genes in response to <i>Orobanche crenata</i> parasitization. <i>Physiological and Molecular Plant Pathology</i> , 2007, 70, 49-59.	2.5	37