

Rosa Figueroa-Balderas

List of Publications by Year in descending order

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Version: 2024-02-01

25
papers

3,051
citations

471371

17
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25
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docs citations

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times ranked

5892
citing authors

#	ARTICLE	IF	CITATIONS
1	Glutathione S-transferase: a candidate gene for berry color in muscadine grapes (<i>Vitis</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	0.8	5
2	Haplotype-resolved powdery mildew resistance loci reveal the impact of heterozygous structural variation on NLR genes in <i>Muscadinia rotundifolia</i> . G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	7
3	Fungal and bacterial communities of "Pinot noir" must: effects of vintage, growing region, climate, and basic must chemistry. PeerJ, 2021, 9, e10836.	0.9	12
4	Diploid chromosome-scale assembly of the <i>Muscadinia rotundifolia</i> genome supports chromosome fusion and disease resistance gene expansion during <i>Vitis</i> and <i>Muscadinia</i> divergence. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	35
5	Rootstock influences the effect of grapevine leafroll-associated viruses on berry development and metabolism via abscisic acid signalling. Molecular Plant Pathology, 2021, 22, 984-1005.	2.0	16
6	The genetic basis of sex determination in grapes. Nature Communications, 2020, 11, 2902.	5.8	118
7	Regulation of monocot and dicot plant development with constitutively active alleles of phytochrome B. Plant Direct, 2020, 4, e00210.	0.8	7
8	Independent Whole-Genome Duplications Define the Architecture of the Genomes of the Devastating West African Cacao Black Pod Pathogen <i>Phytophthora megakarya</i> and Its Close Relative <i>Phytophthora palmivora</i> . G3: Genes, Genomes, Genetics, 2020, 10, 2241-2255.	0.8	18
9	Diploid Genome Assembly of the Wine Grape Carm"re. G3: Genes, Genomes, Genetics, 2019, 9, 1331-1337. 0.8	0.8	84
10	The genomic diversification of grapevine clones. BMC Genomics, 2019, 20, 972.	1.2	66
11	Iso-Seq Allows Genome-Independent Transcriptome Profiling of Grape Berry Development. G3: Genes, Genomes, Genetics, 2019, 9, 755-767.	0.8	79
12	Strategies for Sequencing and Assembling Grapevine Genomes. Compendium of Plant Genomes, 2019, , 77-88.	0.3	14
13	Lipopolysaccharide O-antigen delays plant innate immune recognition of <i>Xylella fastidiosa</i> . Nature Communications, 2018, 9, 390.	5.8	91
14	Condition-dependent coregulation of genomic clusters of virulence factors in the grapevine trunk pathogen <i>Neofusicoccum parvum</i> . Molecular Plant Pathology, 2018, 19, 21-34.	2.0	55
15	Closed-reference metatranscriptomics enables <i>in planta</i> profiling of putative virulence activities in the grapevine trunk disease complex. Molecular Plant Pathology, 2018, 19, 490-503.	2.0	36
16	Profiling grapevine trunk pathogens in planta: a case for community-targeted DNA metabarcoding. BMC Microbiology, 2018, 18, 214.	1.3	23
17	Whole-Genome Resequencing and Pan-Transcriptome Reconstruction Highlight the Impact of Genomic Structural Variation on Secondary Metabolite Gene Clusters in the Grapevine Esca Pathogen <i>Phaeoacremonium minimum</i> . Frontiers in Microbiology, 2018, 9, 1784.	1.5	28
18	Red blotch disease alters grape berry development and metabolism by interfering with the transcriptional and hormonal regulation of ripening. Journal of Experimental Botany, 2017, 68, 1225-1238.	2.4	92

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19	<i>Neofusicoccum parvum</i> Colonization of the Grapevine Woody Stem Triggers Asynchronous Host Responses at the Site of Infection and in the Leaves. <i>Frontiers in Plant Science</i> , 2017, 8, 1117.	1.7	37
20	Phased diploid genome assembly with single-molecule real-time sequencing. <i>Nature Methods</i> , 2016, 13, 1050-1054.	9.0	1,658
21	Comparative transcriptomics of Central Asian <i>Vitis vinifera</i> accessions reveals distinct defense strategies against powdery mildew. <i>Horticulture Research</i> , 2015, 2, 15037.	2.9	47
22	<i>Uniform ripening</i> Encodes a <i>Golden 2-like</i> Transcription Factor Regulating Tomato Fruit Chloroplast Development. <i>Science</i> , 2012, 336, 1711-1715.	6.0	384
23	An intellectual property sharing initiative in agricultural biotechnology: development of broadly accessible technologies for plant transformation. <i>Plant Biotechnology Journal</i> , 2012, 10, 501-510.	4.1	32
24	Wounding and pathogen infection induce a chloroplast-targeted lipoxygenase in the common bean (<i>Phaseolus vulgaris</i> L.). <i>Planta</i> , 2007, 227, 363-373.	1.6	32
25	Hormonal and Stress Induction of the Gene Encoding Common Bean Acetyl-Coenzyme A Carboxylase. <i>Plant Physiology</i> , 2006, 142, 609-619.	2.3	36