

JÃ©rÃ©me Grimplet

List of Publications by Year in descending order

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Version: 2024-02-01

49
papers

4,132
citations

186265
28
h-index

254184
43
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53
all docs

53
docs citations

53
times ranked

3720
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic and Bioinformatic Resources for Perennial Fruit Species. <i>Current Genomics</i> , 2022, 23, .	1.6	0
2	Genetic variation and association analyses identify genes linked to fruit set-related traits in grapevine. <i>Plant Science</i> , 2021, 306, 110875.	3.6	5
3	Polymorphisms and gene expression in the almond IGT family are not correlated to variability in growth habit in major commercial almond cultivars. <i>PLoS ONE</i> , 2021, 16, e0252001.	2.5	1
4	VviUCC1 Nucleotide Diversity, Linkage Disequilibrium and Association with Rachis Architecture Traits in Grapevine. <i>Genes</i> , 2020, 11, 598.	2.4	7
5	Genetic and Genomic Approaches for Adaptation of Grapevine to Climate Change. , 2020, , 157-270.		26
6	Biochemical and transcriptomic analysis in berries of wild and cultivated grapevine (<i>Vitis) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 542 T	0.2	0
7	Genetic variation for grapevine reproductive development. <i>Acta Horticulturae</i> , 2019, , 319-326.	0.2	3
8	Characterization of the reproductive performance of a collection of grapevine cultivars. <i>Acta Horticulturae</i> , 2019, , 345-352.	0.2	3
9	The Grapevine Genome Annotation. <i>Compendium of Plant Genomes</i> , 2019, , 89-101.	0.5	13
10	Ethylene receptors and related proteins in climacteric and non-climacteric fruits. <i>Plant Science</i> , 2018, 276, 63-72.	3.6	79
11	Phenotypic, Hormonal, and Genomic Variation Among <i>Vitis vinifera</i> Clones With Different Cluster Compactness and Reproductive Performance. <i>Frontiers in Plant Science</i> , 2018, 9, 1917.	3.6	18
12	Transcriptional response to temperature of ripening microvine (DRCF) depends on daytime. <i>Acta Horticulturae</i> , 2017, , 321-328.	0.2	2
13	A new version of the grapevine reference genome assembly (12X.v2) and of its annotation (VCost.v3). <i>Genomics Data</i> , 2017, 14, 56-62.	1.3	248
14	Catastrophic Unbalanced Genome Rearrangements Cause Somatic Loss of Berry Color in Grapevine. <i>Plant Physiology</i> , 2017, 175, 786-801.	4.8	98
15	The LATERAL ORGAN BOUNDARIES Domain gene family in grapevine: genome-wide characterization and expression analyses during developmental processes and stress responses. <i>Scientific Reports</i> , 2017, 7, 15968.	3.3	33
16	Differences in Flower Transcriptome between Grapevine Clones Are Related to Their Cluster Compactness, Fruitfulness, and Berry Size. <i>Frontiers in Plant Science</i> , 2017, 8, 632.	3.6	37
17	Structural and Functional Analysis of the GRAS Gene Family in Grapevine Indicates a Role of GRAS Proteins in the Control of Development and Stress Responses. <i>Frontiers in Plant Science</i> , 2016, 7, 353.	3.6	101
18	Towards an open grapevine information system. <i>Horticulture Research</i> , 2016, 3, 16056.	6.3	34

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19	Comparative genome-wide transcriptome analysis of <i>Vitis vinifera</i> responses to adapted and non-adapted strains of two-spotted spider mite, <i>Tetranychus urticae</i> . <i>BMC Genomics</i> , 2016, 17, 74.	2.8	53
20	Structural and functional annotation of the MADS-box transcription factor family in grapevine. <i>BMC Genomics</i> , 2016, 17, 80.	2.8	64
21	Association analysis of grapevine bunch traits using a comprehensive approach. <i>Theoretical and Applied Genetics</i> , 2016, 129, 227-242.	3.6	28
22	Genome Sequence Initiatives. , 2016, , 239-262.		3
23	Short day transcriptomic programming during induction of dormancy in grapevine. <i>Frontiers in Plant Science</i> , 2015, 6, 834.	3.6	48
24	Polymorphisms and minihaplotypes in the VvNAC26 gene associate with berry size variation in grapevine. <i>BMC Plant Biology</i> , 2015, 15, 253.	3.6	41
25	The grapevine gene nomenclature system. <i>BMC Genomics</i> , 2014, 15, 1077.	2.8	108
26	Is Transcriptomic Regulation of Berry Development More Important at Night than During the Day?. <i>PLoS ONE</i> , 2014, 9, e88844.	2.5	53
27	Transcriptome variation along bud development in grapevine (<i>Vitis vinifera</i> L.). <i>BMC Plant Biology</i> , 2012, 12, 181.	3.6	83
28	Comparative analysis of grapevine whole-genome gene predictions, functional annotation, categorization and integration of the predicted gene sequences. <i>BMC Research Notes</i> , 2012, 5, 213.	1.4	176
29	Berry Flesh and Skin Ripening Features in <i>Vitis vinifera</i> as Assessed by Transcriptional Profiling. <i>PLoS ONE</i> , 2012, 7, e39547.	2.5	108
30	Transcript and metabolite analysis in Trincadeira cultivar reveals novel information regarding the dynamics of grape ripening. <i>BMC Plant Biology</i> , 2011, 11, 149.	3.6	133
31	Differential floral development and gene expression in grapevines during long and short photoperiods suggests a role for floral genes in dormancy transitioning. <i>Plant Molecular Biology</i> , 2010, 73, 191-205.	3.9	49
32	Proteomic analysis of shoot tissue during photoperiod induced growth cessation in <i>V. riparia</i> Michx. grapevines. <i>Proteome Science</i> , 2010, 8, 44.	1.7	23
33	Transcriptomics Analysis Methods: Microarray Data Processing, Analysis and Visualization Using the Affymetrix GenechipÃ Vitis Vinifera Genome Array. , 2010, , 317-334.		4
34	Water deficit alters differentially metabolic pathways affecting important flavor and quality traits in grape berries of Cabernet Sauvignon and Chardonnay. <i>BMC Genomics</i> , 2009, 10, 212.	2.8	418
35	Transcript profiling in <i>Vitis riparia</i> during chilling requirement fulfillment reveals coordination of gene expression patterns with optimized bud break. <i>Functional and Integrative Genomics</i> , 2009, 9, 81-96.	3.5	99
36	Proteomic and selected metabolite analysis of grape berry tissues under well-watered and water-deficit stress conditions. <i>Proteomics</i> , 2009, 9, 2503-2528.	2.2	136

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37	VitisNet: â€œOmicsâ€™Integration through Grapevine Molecular Networks. PLoS ONE, 2009, 4, e8365.	2.5	153
38	Combined Mass Mapping and Biochemical Characterization of Grape Î²-Glycosidase-enriched Extract. Protein Journal, 2008, 27, 258-266.	1.6	2
39	Integrating Functional Genomics With Salinity and Water Deficit Stress Responses in Wine Grape - Vitis Vinifera. , 2007, , 643-668.		9
40	Tissue-specific mRNA expression profiling in grape berry tissues. BMC Genomics, 2007, 8, 187.	2.8	193
41	Transcriptomic and metabolite analyses of Cabernet Sauvignon grape berry development. BMC Genomics, 2007, 8, 429.	2.8	391
42	Identification of genes associated with flesh morphogenesis during grapevine fruit development. Plant Molecular Biology, 2007, 63, 307-323.	3.9	78
43	Water and salinity stress in grapevines: early and late changes in transcript and metabolite profiles. Functional and Integrative Genomics, 2007, 7, 111-134.	3.5	474
44	Transcript abundance profiles reveal larger and more complex responses of grapevine to chilling compared to osmotic and salinity stress. Functional and Integrative Genomics, 2007, 7, 317-333.	3.5	120
45	Predominant Expression of Diploid Mandarin Leaf Proteome in Two Citrus Mandarin-Derived Somatic Allotetraploid Hybrids. Journal of Agricultural and Food Chemistry, 2006, 54, 6212-6218.	5.2	18
46	Transcriptomic study of apricot fruit (Prunus armeniaca) ripening among 13 006 expressed sequence tags. Physiologia Plantarum, 2005, 125, 281-292.	5.2	76
47	Isogene specific oligo arrays reveal multifaceted changes in gene expression during grape berry (Vitis) Tj ETQq1 1 0,784314 rgBT /Overd	3.2	246
48	Including mutations from conceptually translated expressed sequence tags into orthologous proteins improves the preliminary assignment of peptide mass fingerprints on non-model genomes. Proteomics, 2005, 5, 2769-2777.	2.2	4
49	TRANSCRIPTOMICS AND PROTEOMICS TOOLS TOWARDS RIPENING MARKERS FOR ASSISTED SELECTION IN APRICOT. Acta Horticulturae, 2004, , 291-296.	0.2	2