

# JÃ©rÃ©me Grimplet

## List of Publications by Year in descending order

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49  
papers

4,132  
citations

186265

28  
h-index

254184

43  
g-index

53  
all docs

53  
docs citations

53  
times ranked

3720  
citing authors

#	ARTICLE	IF	CITATIONS
1	Water and salinity stress in grapevines: early and late changes in transcript and metabolite profiles. <i>Functional and Integrative Genomics</i> , 2007, 7, 111-134.	3.5	474
2	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
3	Transcriptomic and metabolite analyses of Cabernet Sauvignon grape berry development. <i>BMC Genomics</i> , 2007, 8, 429.	2.8	391
4	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
5	Isogene specific oligo arrays reveal multifaceted changes in gene expression during grape berry ( <i>Vitis</i> ) Tj ETQq1 1 0,784314 rgBT /Oveid	3.2	246
6	Tissue-specific mRNA expression profiling in grape berry tissues. <i>BMC Genomics</i> , 2007, 8, 187.	2.8	193
7	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
8	VitisNet: Omics Integration through Grapevine Molecular Networks. <i>PLoS ONE</i> , 2009, 4, e8365.	2.5	153
9	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
10	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
11	Transcript abundance profiles reveal larger and more complex responses of grapevine to chilling compared to osmotic and salinity stress. <i>Functional and Integrative Genomics</i> , 2007, 7, 317-333.	3.5	120
12	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
13	The grapevine gene nomenclature system. <i>BMC Genomics</i> , 2014, 15, 1077.	2.8	108
14	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
15	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
16	Catastrophic Unbalanced Genome Rearrangements Cause Somatic Loss of Berry Color in Grapevine. <i>Plant Physiology</i> , 2017, 175, 786-801.	4.8	98
17	Transcriptome variation along bud development in grapevine ( <i>Vitis vinifera</i> L.). <i>BMC Plant Biology</i> , 2012, 12, 181.	3.6	83
18	Ethylene receptors and related proteins in climacteric and non-climacteric fruits. <i>Plant Science</i> , 2018, 276, 63-72.	3.6	79

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19	Identification of genes associated with flesh morphogenesis during grapevine fruit development. <i>Plant Molecular Biology</i> , 2007, 63, 307-323.	3.9	78
20	Transcriptomic study of apricot fruit ( <i>Prunus armeniaca</i> ) ripening among 13 006 expressed sequence tags. <i>Physiologia Plantarum</i> , 2005, 125, 281-292.	5.2	76
21	Structural and functional annotation of the MADS-box transcription factor family in grapevine. <i>BMC Genomics</i> , 2016, 17, 80.	2.8	64
22	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
23	Is Transcriptomic Regulation of Berry Development More Important at Night than During the Day?. <i>PLoS ONE</i> , 2014, 9, e88844.	2.5	53
24	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
25	Short day transcriptomic programming during induction of dormancy in grapevine. <i>Frontiers in Plant Science</i> , 2015, 6, 834.	3.6	48
26	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
27	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
28	Towards an open grapevine information system. <i>Horticulture Research</i> , 2016, 3, 16056.	6.3	34
29	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
30	Association analysis of grapevine bunch traits using a comprehensive approach. <i>Theoretical and Applied Genetics</i> , 2016, 129, 227-242.	3.6	28
31	Genetic and Genomic Approaches for Adaptation of Grapevine to Climate Change. , 2020, , 157-270.		26
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	Predominant Expression of Diploid Mandarin Leaf Proteome in Two Citrus Mandarin-Derived Somatic Allotetraploid Hybrids. <i>Journal of Agricultural and Food Chemistry</i> , 2006, 54, 6212-6218.	5.2	18
34	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
35	The Grapevine Genome Annotation. <i>Compendium of Plant Genomes</i> , 2019, , 89-101.	0.5	13
36	Integrating Functional Genomics With Salinity and Water Deficit Stress Responses in Wine Grape - <i>Vitis Vinifera</i> . , 2007, , 643-668.		9

#	ARTICLE	IF	CITATIONS
37	VviUCC1 Nucleotide Diversity, Linkage Disequilibrium and Association with Rachis Architecture Traits in Grapevine. <i>Genes</i> , 2020, 11, 598.	2.4	7
38	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
39	Including mutations from conceptually translated expressed sequence tags into orthologous proteins improves the preliminary assignment of peptide mass fingerprints on non-model genomes. <i>Proteomics</i> , 2005, 5, 2769-2777.	2.2	4
40	Transcriptomics Analysis Methods: Microarray Data Processing, Analysis and Visualization Using the Affymetrix Genechip® Vitis Vinifera Genome Array. , 2010, , 317-334.		4
41	Genetic variation for grapevine reproductive development. <i>Acta Horticulturae</i> , 2019, , 319-326.	0.2	3
42	Characterization of the reproductive performance of a collection of grapevine cultivars. <i>Acta Horticulturae</i> , 2019, , 345-352.	0.2	3
43	Genome Sequence Initiatives. , 2016, , 239-262.		3
44	TRANSCRIPTOMICS AND PROTEOMICS TOOLS TOWARDS RIPENING MARKERS FOR ASSISTED SELECTION IN APRICOT. <i>Acta Horticulturae</i> , 2004, , 291-296.	0.2	2
45	Combined Mass Mapping and Biochemical Characterization of Grape $\beta$ -Glycosidase-enriched Extract. <i>Protein Journal</i> , 2008, 27, 258-266.	1.6	2
46	Transcriptional response to temperature of ripening microvine (DRCF) depends on daytime. <i>Acta Horticulturae</i> , 2017, , 321-328.	0.2	2
47	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
48	Biochemical and transcriptomic analysis in berries of wild and cultivated grapevine (<i>Vitis) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 302 T	0.2	0
49	Genomic and Bioinformatic Resources for Perennial Fruit Species. <i>Current Genomics</i> , 2022, 23, .	1.6	0