

Mario Pezzotti

List of Publications by Year in descending order

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Version: 2024-02-01

59
papers

7,408
citations

147801

31
h-index

138484

58
g-index

61
all docs

61
docs citations

61
times ranked

8316
citing authors

#	ARTICLE	IF	CITATIONS
1	VviNAC33 promotes organ dea€greening and represses vegetative growth during the vegetativea€toa€mature phase transition in grapevine. <i>New Phytologist</i> , 2021, 231, 726-746.	7.3	16
2	Grapevine and Wine Metabolomics-Based Guidelines for FAIR Data and Metadata Management. <i>Metabolites</i> , 2021, 11, 757.	2.9	16
3	The Grape Gene Reference Catalogue as a Standard Resource for Gene Selection and Genetic Improvement. <i>Frontiers in Plant Science</i> , 2021, 12, 803977.	3.6	19
4	Prevention and treatment of autoimmune diseases with plant virus nanoparticles. <i>Science Advances</i> , 2020, 6, eaaz0295.	10.3	22
5	Auxin treatment of grapevine (<i>Vitis vinifera</i> L.) berries delays ripening onset by inhibiting cell expansion. <i>Plant Molecular Biology</i> , 2020, 103, 91-111.	3.9	21
6	Russell-Like Bodies in Plant Seeds Share Common Features With Prolamin Bodies and Occur Upon Recombinant Protein Production. <i>Frontiers in Plant Science</i> , 2019, 10, 777.	3.6	10
7	The <sc>MYB</sc>5a-driven <sc>MBW</sc> complex recruits a <sc>WRKY</sc> factor to enhance the expression of targets involved in vacuolar hypera€acidification and trafficking in grapevine. <i>Plant Journal</i> , 2019, 99, 1220-1241.	5.7	54
8	Regeneration of plants from embryogenic callus-derived protoplasts of Garganega and Sangiovese grapevine (<i>Vitis vinifera</i> L.) cultivars. <i>Plant Cell, Tissue and Organ Culture</i> , 2019, 138, 239-246.	2.3	28
9	Genetic, epigenetic and genomic effects on variation of gene expression among grape varieties. <i>Plant Journal</i> , 2019, 99, 895-909.	5.7	19
10	Towards the definition of a detailed transcriptomic map of berry development. <i>BIO Web of Conferences</i> , 2019, 13, 01001.	0.2	1
11	Plant-Made Bet v 1 for Molecular Diagnosis. <i>Frontiers in Plant Science</i> , 2019, 10, 1273.	3.6	12
12	Distinct Metabolic Signals Underlie Clone by Environment Interplay in a€œNebbioloa€•Grapes Over Ripening. <i>Frontiers in Plant Science</i> , 2019, 10, 1575.	3.6	15
13	Grape Transcriptomics and Viticulture. <i>Compendium of Plant Genomes</i> , 2019, , 275-299.	0.5	0
14	Grapevine field experiments reveal the contribution of genotype, the influence of environment and the effect of their interaction (GAE) on the berry transcriptome. <i>Plant Journal</i> , 2018, 93, 1143-1159.	5.7	75
15	Multilevel comparative bioinformatics to investigate evolutionary relationships and specificities in gene annotations: an example for tomato and grapevine. <i>BMC Bioinformatics</i> , 2018, 19, 435.	2.6	9
16	Timing and Order of the Molecular Events Marking the Onset of Berry Ripening in Grapevine. <i>Plant Physiology</i> , 2018, 178, 1187-1206.	4.8	84
17	Design of a Type-1 Diabetes Vaccine Candidate Using Edible Plants Expressing a Major Autoantigen. <i>Frontiers in Plant Science</i> , 2018, 9, 572.	3.6	6
18	Edible plants for oral delivery of biopharmaceuticals. <i>British Journal of Clinical Pharmacology</i> , 2017, 83, 71-81.	2.4	33

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19	Ripening Transcriptomic Program in Red and White Grapevine Varieties Correlates with Berry Skin Anthocyanin Accumulation. <i>Plant Physiology</i> , 2017, 174, 2376-2396.	4.8	121
20	Whole-genome sequencing and SNV genotyping of "Nebbiolo"™ (<i>Vitis vinifera</i> L.) clones. <i>Scientific Reports</i> , 2017, 7, 17294.	3.3	72
21	Prospect on Ionomic Signatures for the Classification of Grapevine Berries According to Their Geographical Origin. <i>Frontiers in Plant Science</i> , 2017, 8, 640.	3.6	17
22	Editorial: Molecular and Metabolic Mechanisms Associated with Fleshy Fruit Quality. <i>Frontiers in Plant Science</i> , 2017, 8, 1236.	3.6	7
23	Mediterranean Way of Drinking and Longevity. <i>Critical Reviews in Food Science and Nutrition</i> , 2016, 56, 635-640.	10.3	76
24	Plasticity of the Berry Ripening Program in a White Grape Variety. <i>Frontiers in Plant Science</i> , 2016, 7, 970.	3.6	68
25	The Influence of Genotype and Environment on Small RNA Profiles in Grapevine Berry. <i>Frontiers in Plant Science</i> , 2016, 7, 1459.	3.6	40
26	Pectins, Hemicelluloses and Celluloses Show Specific Dynamics in the Internal and External Surfaces of Grape Berry Skin During Ripening. <i>Plant and Cell Physiology</i> , 2016, 57, 1332-1349.	3.1	78
27	Disclosing the Molecular Basis of the Postharvest Life of Berry in Different Grapevine Genotypes. <i>Plant Physiology</i> , 2016, 172, 1821-1843.	4.8	75
28	The Terroir Concept Interpreted through Grape Berry Metabolomics and Transcriptomics. <i>Journal of Visualized Experiments</i> , 2016, , .	0.3	9
29	Enhanced GAD65 production in plants using the MagnICON transient expression system: Optimization of upstream production and downstream processing. <i>Biotechnology Journal</i> , 2016, 11, 542-553.	3.5	13
30	Reducing sampling bias in molecular studies of grapevine fruit ripening: transcriptomic assessment of the density sorting method. <i>Theoretical and Experimental Plant Physiology</i> , 2016, 28, 109-129.	2.4	16
31	Plant-Derived Chimeric Virus Particles for the Diagnosis of Primary Sjögren Syndrome. <i>Frontiers in Plant Science</i> , 2015, 6, 1080.	3.6	19
32	Integrated Network Analysis Identifies Fight-Club Nodes as a Class of Hubs Encompassing Key Putative Switch Genes That Induce Major Transcriptome Reprogramming during Grapevine Development. <i>Plant Cell</i> , 2015, 26, 4617-4635.	6.6	110
33	A Comparative Analysis of Recombinant Protein Expression in Different Biofactories: Bacteria, Insect Cells and Plant Systems. <i>Journal of Visualized Experiments</i> , 2015, , .	0.3	29
34	miRVine: a microRNA expression atlas of grapevine based on small RNA sequencing. <i>BMC Genomics</i> , 2015, 16, 393.	2.8	73
35	Towards a scientific interpretation of the terroir concept: plasticity of the grape berry metabolome. <i>BMC Plant Biology</i> , 2015, 15, 191.	3.6	106
36	Heterologous Expression of Moss Light-harvesting Complex Stress-related 1 (LHCSR1), the Chlorophyll a-Xanthophyll Pigment-protein Complex Catalyzing Non-photochemical Quenching, in <i>Nicotiana</i> sp.. <i>Journal of Biological Chemistry</i> , 2015, 290, 24340-24354.	3.4	26

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37	Transcriptomic analysis of the late stages of grapevine (<i>Vitis vinifera</i> cv. Cabernet Sauvignon) berry ripening reveals significant induction of ethylene signaling and flavor pathways in the skin. <i>BMC Plant Biology</i> , 2014, 14, 370.	3.6	105
38	Comparative Evaluation of Recombinant Protein Production in Different Biofactories: The Green Perspective. <i>BioMed Research International</i> , 2014, 2014, 1-14.	1.9	97
39	Comparative analysis of different biofactories for the production of a major diabetes autoantigen. <i>Transgenic Research</i> , 2014, 23, 281-291.	2.4	19
40	Metabolite and transcript profiling of berry skin during fruit development elucidates differential regulation between Cabernet Sauvignon and Shiraz cultivars at branching points in the polyphenol pathway. <i>BMC Plant Biology</i> , 2014, 14, 188.	3.6	135
41	A downstream process allowing the efficient isolation of a recombinant amphiphilic protein from tobacco leaves. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2014, 960, 34-42.	2.3	7
42	Genome and transcriptome analysis of the grapevine (<i>Vitis vinifera</i> L.) WRKY gene family. <i>Horticulture Research</i> , 2014, 1, 14016.	6.3	188
43	The plasticity of the grapevine berry transcriptome. <i>Genome Biology</i> , 2013, 14, r54.	8.8	168
44	Selective defoliation affects plant growth, fruit transcriptional ripening program and flavonoid metabolism in grapevine. <i>BMC Plant Biology</i> , 2013, 13, 30.	3.6	131
45	The High Polyphenol Content of Grapevine Cultivar Tannat Berries Is Conferred Primarily by Genes That Are Not Shared with the Reference Genome. <i>Plant Cell</i> , 2013, 25, 4777-4788.	6.6	138
46	Genome-Wide Analysis of the Expansin Gene Superfamily Reveals Grapevine-Specific Structural and Functional Characteristics. <i>PLoS ONE</i> , 2013, 8, e62206.	2.5	113
47	The Grapevine Expression Atlas Reveals a Deep Transcriptome Shift Driving the Entire Plant into a Maturation Program A. <i>Plant Cell</i> , 2012, 24, 3489-3505.	6.6	371
48	Non-food/feed seeds as biofactories for the high-yield production of recombinant pharmaceuticals. <i>Plant Biotechnology Journal</i> , 2011, 9, 911-921.	8.3	48
49	Revealing impaired pathways in the <i>an11</i> mutant by high-throughput characterization of <i>Petunia axillaris</i> and <i>Petunia inflata</i> transcriptomes. <i>Plant Journal</i> , 2011, 68, 11-27.	5.7	35
50	Overexpression of <i>PhEXPA1</i> increases cell size, modifies cell wall polymer composition and affects the timing of axillary meristem development in <i>Petunia hybrida</i> . <i>New Phytologist</i> , 2011, 191, 662-677.	7.3	58
51	Increasing the source/sink ratio in <i>Vitis vinifera</i> (cv Sangiovese) induces extensive transcriptome reprogramming and modifies berry ripening. <i>BMC Genomics</i> , 2011, 12, 631.	2.8	72
52	Novel aspects of grape berry ripening and post-harvest withering revealed by untargeted LC-ESI-MS metabolomics analysis. <i>Metabolomics</i> , 2011, 7, 424-436.	3.0	74
53	Genomic and transcriptomic analysis of the AP2/ERF superfamily in <i>Vitis vinifera</i> . <i>BMC Genomics</i> , 2010, 11, 719.	2.8	307
54	Recombinant human GAD65 accumulates to high levels in transgenic tobacco plants when expressed as an enzymatically inactive mutant. <i>Plant Biotechnology Journal</i> , 2010, 8, 862-872.	8.3	22

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55	Identification of Putative Stage-Specific Grapevine Berry Biomarkers and Omics Data Integration into Networks. Plant Physiology, 2010, 154, 1439-1459.	4.8	145
56	Characterization of Transcriptional Complexity during Berry Development in <i>Vitis vinifera</i> Using RNA-Seq. Plant Physiology, 2010, 152, 1787-1795.	4.8	330
57	The grapevine genome sequence suggests ancestral hexaploidization in major angiosperm phyla. Nature, 2007, 449, 463-467.	27.8	3,384
58	Improved in planta expression of the human islet autoantigen glutamic acid decarboxylase (GAD65). Transgenic Research, 2003, 12, 203-212.	2.4	31
59	Title is missing!. Molecular Breeding, 1999, 5, 553-560.	2.1	33