

Sara Zenoni

List of Publications by Year in descending order

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66
papers

4,875
citations

109137

35
h-index

118652

62
g-index

68
all docs

68
docs citations

68
times ranked

4658
citing authors

#	ARTICLE	IF	CITATIONS
1	The Grapevine Expression Atlas Reveals a Deep Transcriptome Shift Driving the Entire Plant into a Maturation Program. <i>Plant Cell</i> , 2012, 24, 3489-3505.	3.1	371
2	Characterization of Transcriptional Complexity during Berry Development in <i>Vitis vinifera</i> Using RNA-Seq. <i>Plant Physiology</i> , 2010, 152, 1787-1795.	2.3	330
3	Genomic and transcriptomic analysis of the AP2/ERF superfamily in <i>Vitis vinifera</i> . <i>BMC Genomics</i> , 2010, 11, 719.	1.2	307
4	Genome-wide analysis of the grapevine stilbene synthase multigenic family: genomic organization and expression profiles upon biotic and abiotic stresses. <i>BMC Plant Biology</i> , 2012, 12, 130.	1.6	275
5	The Phenylpropanoid Pathway Is Controlled at Different Branches by a Set of R2R3-MYB C2 Repressors in Grapevine. <i>Plant Physiology</i> , 2015, 167, 1448-1470.	2.3	272
6	Genome and transcriptome analysis of the grapevine (<i>Vitis vinifera</i> L.) WRKY gene family. <i>Horticulture Research</i> , 2014, 1, 14016.	2.9	188
7	The plasticity of the grapevine berry transcriptome. <i>Genome Biology</i> , 2013, 14, r54.	3.8	168
8	Identification of Putative Stage-Specific Grapevine Berry Biomarkers and Omics Data Integration into Networks. <i>Plant Physiology</i> , 2010, 154, 1439-1459.	2.3	145
9	Downregulation of the <i>Petunia hybrida</i> Expansin Gene PhEXP1 Reduces the Amount of Crystalline Cellulose in Cell Walls and Leads to Phenotypic Changes in Petal Limbs. <i>Plant Cell</i> , 2004, 16, 295-308.	3.1	134
10	The grapevine VviPrx31 peroxidase as a candidate gene involved in anthocyanin degradation in ripening berries under high temperature. <i>Journal of Plant Research</i> , 2016, 129, 513-526.	1.2	134
11	Selective defoliation affects plant growth, fruit transcriptional ripening program and flavonoid metabolism in grapevine. <i>BMC Plant Biology</i> , 2013, 13, 30.	1.6	131
12	Ripening Transcriptomic Program in Red and White Grapevine Varieties Correlates with Berry Skin Anthocyanin Accumulation. <i>Plant Physiology</i> , 2017, 174, 2376-2396.	2.3	121
13	Genome-Wide Analysis of the Expansin Gene Superfamily Reveals Grapevine-Specific Structural and Functional Characteristics. <i>PLoS ONE</i> , 2013, 8, e62206.	1.1	113
14	A grapevine anthocyanin acyltransferase, transcriptionally regulated by VvMYBA, can produce most acylated anthocyanins present in grape skins. <i>Plant Physiology</i> , 2015, 169, pp.01255.2015.	2.3	113
15	De novo transcriptome characterization of <i>Vitis vinifera</i> cv. Corvina unveils varietal diversity. <i>BMC Genomics</i> , 2013, 14, 41.	1.2	110
16	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.	3.1	110
17	A Grapevine TTG2-Like WRKY Transcription Factor Is Involved in Regulating Vacuolar Transport and Flavonoid Biosynthesis. <i>Frontiers in Plant Science</i> , 2016, 7, 1979.	1.7	110
18	Towards a scientific interpretation of the terroir concept: plasticity of the grape berry metabolome. <i>BMC Plant Biology</i> , 2015, 15, 191.	1.6	106

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19	Temperature stress differentially modulates transcription in meiotic anthers of heat-tolerant and heat-sensitive tomato plants. <i>BMC Genomics</i> , 2011, 12, 384.	1.2	105
20	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.	1.6	105
21	Whole Plant Temperature Manipulation Affects Flavonoid Metabolism and the Transcriptome of Grapevine Berries. <i>Frontiers in Plant Science</i> , 2017, 8, 929.	1.7	102
22	Timing and Order of the Molecular Events Marking the Onset of Berry Ripening in Grapevine. <i>Plant Physiology</i> , 2018, 178, 1187-1206.	2.3	84
23	Functional Diversification of Grapevine MYB5a and MYB5b in the Control of Flavonoid Biosynthesis in a <i>Petunia</i> Anthocyanin Regulatory Mutant. <i>Plant and Cell Physiology</i> , 2014, 55, 517-534.	1.5	83
24	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.	1.5	78
25	Disclosing the Molecular Basis of the Postharvest Life of Berry in Different Grapevine Genotypes. <i>Plant Physiology</i> , 2016, 172, 1821-1843.	2.3	75
26	Grapevine field experiments reveal the contribution of genotype, the influence of environment and the effect of their interaction (G×E) on the berry transcriptome. <i>Plant Journal</i> , 2018, 93, 1143-1159.	2.8	75
27	miRVine: a microRNA expression atlas of grapevine based on small RNA sequencing. <i>BMC Genomics</i> , 2015, 16, 393.	1.2	73
28	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.	1.2	72
29	Plasticity of the Berry Ripening Program in a White Grape Variety. <i>Frontiers in Plant Science</i> , 2016, 7, 970.	1.7	68
30	Patterns of cell division and expansion in developing petals of <i>Petunia hybrida</i> . <i>Sexual Plant Reproduction</i> , 2002, 15, 123-132.	2.2	66
31	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.	3.5	58
32	The MYB5-driven MBW complex recruits a WRKY factor to enhance the expression of targets involved in vacuolar hyperacidification and trafficking in grapevine. <i>Plant Journal</i> , 2019, 99, 1220-1241.	2.8	54
33	Skin pectin metabolism during the postharvest dehydration of berries from three distinct grapevine cultivars. <i>Australian Journal of Grape and Wine Research</i> , 2013, 19, 171-179.	1.0	53
34	Distinct transcriptome responses to water limitation in isohydric and anisohydric grapevine cultivars. <i>BMC Genomics</i> , 2016, 17, 815.	1.2	49
35	The <i>Arabidopsis thaliana</i> transcription factor MYB59 regulates calcium signalling during plant growth and stress response. <i>Plant Molecular Biology</i> , 2019, 99, 517-534.	2.0	47
36	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.	2.8	35

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37	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.	1.2	28
38	Selection of candidate genes controlling veraison time in grapevine through integration of meta-QTL and transcriptomic data. <i>BMC Genomics</i> , 2019, 20, 739.	1.2	24
39	Transcriptional Responses to Pre-flowering Leaf Defoliation in Grapevine Berry from Different Growing Sites, Years, and Genotypes. <i>Frontiers in Plant Science</i> , 2017, 8, 630.	1.7	23
40	Pistil Transcriptome Analysis to Disclose Genes and Gene Products Related to Aposporous Apomixis in <i>Hypericum perforatum</i> L.. <i>Frontiers in Plant Science</i> , 2017, 8, 79.	1.7	22
41	Specific molecular interactions between <i>Vitis vinifera</i> and <i>Botrytis cinerea</i> are required for noble rot development in grape berries. <i>Postharvest Biology and Technology</i> , 2019, 156, 110924.	2.9	22
42	Sporophytic and gametophytic functions of the cell cycle-associated <i>Mob1</i> gene in <i>Arabidopsis thaliana</i> L.. <i>Gene</i> , 2011, 484, 1-12.	1.0	21
43	Rapid dehydration of grape berries dampens the post-ripening transcriptomic program and the metabolite profile evolution. <i>Horticulture Research</i> , 2020, 7, 141.	2.9	21
44	A multivariate statistical analysis approach to highlight molecular processes in plant cell walls through ATR FT-IR microspectroscopy: The role of the β -expansin PhEXPA1 in <i>Petunia hybrida</i> . <i>Vibrational Spectroscopy</i> , 2013, 65, 36-43.	1.2	19
45	Genetic, epigenetic and genomic effects on variation of gene expression among grape varieties. <i>Plant Journal</i> , 2019, 99, 895-909.	2.8	19
46	The Grape Gene Reference Catalogue as a Standard Resource for Gene Selection and Genetic Improvement. <i>Frontiers in Plant Science</i> , 2021, 12, 803977.	1.7	19
47	Root physiological and transcriptional response to single and combined S and Fe deficiency in durum wheat. <i>Environmental and Experimental Botany</i> , 2017, 143, 172-184.	2.0	16
48	WiNAC33 promotes organ de-greening and represses vegetative growth during the vegetative-to-mature phase transition in grapevine. <i>New Phytologist</i> , 2021, 231, 726-746.	3.5	16
49	Active rearrangements in the cell wall follow polymer concentration during postharvest withering in the berry skin of <i>Vitis vinifera</i> cv. Corvina. <i>Plant Physiology and Biochemistry</i> , 2019, 135, 411-422.	2.8	15
50	The Signatures of Selection for Translational Accuracy in Plant Genes. <i>Genome Biology and Evolution</i> , 2013, 5, 1117-1126.	1.1	13
51	Stress responses and epigenomic instability mark the loss of somatic embryogenesis competence in grapevine. <i>Plant Physiology</i> , 2022, 188, 490-508.	2.3	12
52	Genomic Designing for Biotic Stress Resistant Grapevine. , 2022, , 87-255.		11
53	PhEXPA1, a <i>Petunia hybrida</i> expansin, is involved in cell wall metabolism and in plant architecture specification. <i>Plant Signaling and Behavior</i> , 2011, 6, 2031-2034.	1.2	10
54	The Terroir Concept Interpreted through Grape Berry Metabolomics and Transcriptomics. <i>Journal of Visualized Experiments</i> , 2016, , .	0.2	9

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55	Pomegranate (<i>Punica granatum</i> L.) Expresses Several nsLTP Isoforms Characterized by Different Immunoglobulin E-Binding Properties. International Archives of Allergy and Immunology, 2014, 164, 112-121.	0.9	8
56	A Major QTL is associated with berry grape texture characteristics. Oeno One, 2021, 55, 183-206.	0.7	8
57	Genetic dissection of grape berry ripening control: defining a role for NAC transcription factors. Acta Horticulturae, 2019, , 387-402.	0.1	5
58	Plant and fungus transcriptomic data from grapevine berries undergoing artificially-induced noble rot caused by Botrytis cinerea. Data in Brief, 2019, 25, 104150.	0.5	3
59	Grape Berry Transcriptome. , 2021, , 558-571.		3
60	The Role of Expansins A in Petunia Development. , 2009, , 247-267.		1
61	DIFFERENTIAL EXPRESSION OF GENES IN BERRIES OF CV. 'SANGIOVESE' (VITIS VINIFERA L.) DURING RIPENING FOLLOWING CLUSTER THINNING AT V&RAISON. Acta Horticulturae, 2014, , 441-448.	0.1	1
62	Changes in flavonoid biosynthesis and in the berry whole transcriptome of â€˜Sangioveseâ€™™ under moderate air temperature increase. Acta Horticulturae, 2017, , 157-164.	0.1	1
63	Phenolic contents and genome-wide expression profiling of grapevine berries (Vitis vinifera L.) Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.1	1
64	Towards the definition of a detailed transcriptomic map of berry development. BIO Web of Conferences, 2019, 13, 01001.	0.1	1
65	Unraveling the key molecular events of grape berry ripening. Acta Horticulturae, 2019, , 241-248.	0.1	1
66	Grape Transcriptomics and Viticulture. Compendium of Plant Genomes, 2019, , 275-299.	0.3	0