

# Sara Zenoni

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

64  
papers

3,268  
citations

33  
h-index

57  
g-index

68  
ext. papers

4,305  
ext. citations

5.1  
avg, IF

4.89  
L-index

#	Paper	IF	Citations
64	Genomic Designing for Biotic Stress Resistant Grapevine <b>2022</b> , 87-255		0
63	The Grape Gene Reference Catalogue as a Standard Resource for Gene Selection and Genetic Improvement.. <i>Frontiers in Plant Science</i> , <b>2021</b> , 12, 803977	6.2	2
62	VviNAC33 promotes organ de-greening and represses vegetative growth during the vegetative-to-mature phase transition in grapevine. <i>New Phytologist</i> , <b>2021</b> , 231, 726-746	9.8	2
61	Grape Berry Transcriptome <b>2021</b> , 558-571		
60	A Major QTL is associated with berry grape texture characteristics. <i>Oeno One</i> , <b>2021</b> , 55, 183-206	3.3	2
59	Rapid dehydration of grape berries dampens the post-ripening transcriptomic program and the metabolite profile evolution. <i>Horticulture Research</i> , <b>2020</b> , 7, 141	7.7	7
58	Selection of candidate genes controlling veraison time in grapevine through integration of meta-QTL and transcriptomic data. <i>BMC Genomics</i> , <b>2019</b> , 20, 739	4.5	9
57	The MYB5-driven MBW complex recruits a WRKY factor to enhance the expression of targets involved in vacuolar hyper-acidification and trafficking in grapevine. <i>Plant Journal</i> , <b>2019</b> , 99, 1220-1241	6.9	20
56	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> , <b>2019</b> , 156, 110924	6.2	11
55	Plant and fungus transcriptomic data from grapevine berries undergoing artificially-induced noble rot caused by. <i>Data in Brief</i> , <b>2019</b> , 25, 104150	1.2	3
54	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> , <b>2019</b> , 138, 239-246	2.7	11
53	Genetic, epigenetic and genomic effects on variation of gene expression among grape varieties. <i>Plant Journal</i> , <b>2019</b> , 99, 895-909	6.9	11
52	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> , <b>2019</b> , 135, 411-422	5.4	7
51	Towards the definition of a detailed transcriptomic map of berry development. <i>BIO Web of Conferences</i> , <b>2019</b> , 13, 01001	0.4	0
50	Genetic dissection of grape berry ripening control: defining a role for NAC transcription factors. <i>Acta Horticulturae</i> , <b>2019</b> , 387-402	0.3	4
49	Grape Transcriptomics and Viticulture. <i>Compendium of Plant Genomes</i> , <b>2019</b> , 275-299	0.8	
48	The <i>Arabidopsis thaliana</i> transcription factor MYB59 regulates calcium signalling during plant growth and stress response. <i>Plant Molecular Biology</i> , <b>2019</b> , 99, 517-534	4.6	24

47	Unraveling the key molecular events of grape berry ripening. <i>Acta Horticulturae</i> , <b>2019</b> , 241-248	0.3	1
46	Grapevine field experiments reveal the contribution of genotype, the influence of environment and the effect of their interaction (GE) on the berry transcriptome. <i>Plant Journal</i> , <b>2018</b> , 93, 1143-1159	6.9	37
45	Timing and Order of the Molecular Events Marking the Onset of Berry Ripening in Grapevine. <i>Plant Physiology</i> , <b>2018</b> , 178, 1187-1206	6.6	39
44	Root physiological and transcriptional response to single and combined S and Fe deficiency in durum wheat. <i>Environmental and Experimental Botany</i> , <b>2017</b> , 143, 172-184	5.9	13
43	Ripening Transcriptomic Program in Red and White Grapevine Varieties Correlates with Berry Skin Anthocyanin Accumulation. <i>Plant Physiology</i> , <b>2017</b> , 174, 2376-2396	6.6	68
42	Changes in flavonoid biosynthesis and in the berry whole transcriptome of <i>Bangiovese</i> under moderate air temperature increase. <i>Acta Horticulturae</i> , <b>2017</b> , 157-164	0.3	1
41	Phenolic contents and genome-wide expression profiling of grapevine berries ( <i>Vitis vinifera</i> L. <i>Bangiovese</i> ) ripened under two different temperature regimes. <i>Acta Horticulturae</i> , <b>2017</b> , 289-294	0.3	1
40	Pistil Transcriptome Analysis to Disclose Genes and Gene Products Related to Aposporous Apomixis in <i>L. Frontiers in Plant Science</i> , <b>2017</b> , 8, 79	6.2	13
39	Transcriptional Responses to Pre-flowering Leaf Defoliation in Grapevine Berry from Different Growing Sites, Years, and Genotypes. <i>Frontiers in Plant Science</i> , <b>2017</b> , 8, 630	6.2	20
38	Whole Plant Temperature Manipulation Affects Flavonoid Metabolism and the Transcriptome of Grapevine Berries. <i>Frontiers in Plant Science</i> , <b>2017</b> , 8, 929	6.2	58
37	Distinct transcriptome responses to water limitation in isohydric and anisohydric grapevine cultivars. <i>BMC Genomics</i> , <b>2016</b> , 17, 815	4.5	34
36	The Terroir Concept Interpreted through Grape Berry Metabolomics and Transcriptomics. <i>Journal of Visualized Experiments</i> , <b>2016</b> ,	1.6	6
35	The grapevine VviPrx31 peroxidase as a candidate gene involved in anthocyanin degradation in ripening berries under high temperature. <i>Journal of Plant Research</i> , <b>2016</b> , 129, 513-26	2.6	76
34	A Grapevine TTG2-Like WRKY Transcription Factor Is Involved in Regulating Vacuolar Transport and Flavonoid Biosynthesis. <i>Frontiers in Plant Science</i> , <b>2016</b> , 7, 1979	6.2	61
33	Plasticity of the Berry Ripening Program in a White Grape Variety. <i>Frontiers in Plant Science</i> , <b>2016</b> , 7, 9706.2	6.2	39
32	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> , <b>2016</b> , 57, 1332-49	4.9	60
31	Disclosing the Molecular Basis of the Postharvest Life of Berry in Different Grapevine Genotypes. <i>Plant Physiology</i> , <b>2016</b> , 172, 1821-1843	6.6	45
30	miRVine: a microRNA expression atlas of grapevine based on small RNA sequencing. <i>BMC Genomics</i> , <b>2015</b> , 16, 393	4.5	42

29	A Grapevine Anthocyanin Acyltransferase, Transcriptionally Regulated by VvMYBA, Can Produce Most Acylated Anthocyanins Present in Grape Skins. <i>Plant Physiology</i> , <b>2015</b> , 169, 1897-916	6.6	78
28	Towards a scientific interpretation of the terroir concept: plasticity of the grape berry metabolome. <i>BMC Plant Biology</i> , <b>2015</b> , 15, 191	5.3	70
27	The phenylpropanoid pathway is controlled at different branches by a set of R2R3-MYB C2 repressors in grapevine. <i>Plant Physiology</i> , <b>2015</b> , 167, 1448-70	6.6	167
26	Functional diversification of grapevine MYB5a and MYB5b in the control of flavonoid biosynthesis in a petunia anthocyanin regulatory mutant. <i>Plant and Cell Physiology</i> , <b>2014</b> , 55, 517-34	4.9	50
25	Genome and transcriptome analysis of the grapevine ( <i>Vitis vinifera</i> L.) WRKY gene family. <i>Horticulture Research</i> , <b>2014</b> , 1, 14016	7.7	124
24	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> , <b>2014</b> , 26, 4617-35	11.6	84
23	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> , <b>2014</b> , 14, 370	5.3	68
22	Pomegranate ( <i>Punica granatum</i> L.) expresses several nsLTP isoforms characterized by different immunoglobulin E-binding properties. <i>International Archives of Allergy and Immunology</i> , <b>2014</b> , 164, 112-237	3.7	7
21	The plasticity of the grapevine berry transcriptome. <i>Genome Biology</i> , <b>2013</b> , 14, r54	18.3	119
20	Selective defoliation affects plant growth, fruit transcriptional ripening program and flavonoid metabolism in grapevine. <i>BMC Plant Biology</i> , <b>2013</b> , 13, 30	5.3	79
19	A multivariate statistical analysis approach to highlight molecular processes in plant cell walls through ATR FT-IR microspectroscopy: The role of the expansin PhEXPA1 in <i>Petunia hybrida</i> . <i>Vibrational Spectroscopy</i> , <b>2013</b> , 65, 36-43	2.1	16
18	De novo transcriptome characterization of <i>Vitis vinifera</i> cv. Corvina unveils varietal diversity. <i>BMC Genomics</i> , <b>2013</b> , 14, 41	4.5	82
17	Skin pectin metabolism during the postharvest dehydration of berries from three distinct grapevine cultivars. <i>Australian Journal of Grape and Wine Research</i> , <b>2013</b> , 19, 171-179	2.4	38
16	The signatures of selection for translational accuracy in plant genes. <i>Genome Biology and Evolution</i> , <b>2013</b> , 5, 1117-26	3.9	11
15	Genome-wide analysis of the expansin gene superfamily reveals grapevine-specific structural and functional characteristics. <i>PLoS ONE</i> , <b>2013</b> , 8, e62206	3.7	79
14	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> , <b>2012</b> , 12, 130	5.3	189
13	The grapevine expression atlas reveals a deep transcriptome shift driving the entire plant into a maturation program. <i>Plant Cell</i> , <b>2012</b> , 24, 3489-505	11.6	252
12	Sporophytic and gametophytic functions of the cell cycle-associated Mob1 gene in <i>Arabidopsis thaliana</i> L. <i>Gene</i> , <b>2011</b> , 484, 1-12	3.8	16

11	Revealing impaired pathways in the an11 mutant by high-throughput characterization of <i>Petunia axillaris</i> and <i>Petunia inflata</i> transcriptomes. <i>Plant Journal</i> , <b>2011</b> , 68, 11-27	6.9	31
10	Overexpression of PhEXPA1 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> , <b>2011</b> , 191, 662-677	9.8	48
9	Increasing the source/sink ratio in <i>Vitis vinifera</i> (cv Sangiovese) induces extensive transcriptome reprogramming and modifies berry ripening. <i>BMC Genomics</i> , <b>2011</b> , 12, 631	4.5	58
8	Temperature stress differentially modulates transcription in meiotic anthers of heat-tolerant and heat-sensitive tomato plants. <i>BMC Genomics</i> , <b>2011</b> , 12, 384	4.5	76
7	PhEXPA1, a <i>Petunia hybrida</i> expansin, is involved in cell wall metabolism and in plant architecture specification. <i>Plant Signaling and Behavior</i> , <b>2011</b> , 6, 2031-4	2.5	9
6	Identification of putative stage-specific grapevine berry biomarkers and omics data integration into networks. <i>Plant Physiology</i> , <b>2010</b> , 154, 1439-59	6.6	123
5	Characterization of transcriptional complexity during berry development in <i>Vitis vinifera</i> using RNA-Seq. <i>Plant Physiology</i> , <b>2010</b> , 152, 1787-95	6.6	294
4	Genomic and transcriptomic analysis of the AP2/ERF superfamily in <i>Vitis vinifera</i> . <i>BMC Genomics</i> , <b>2010</b> , 11, 719	4.5	209
3	The Role of Expansins A in <i>Petunia</i> Development <b>2009</b> , 247-267		
2	Downregulation of the <i>Petunia hybrida</i> alpha-expansin gene PhEXP1 reduces the amount of crystalline cellulose in cell walls and leads to phenotypic changes in petal limbs. <i>Plant Cell</i> , <b>2004</b> , 16, 295-308	11.6	121
1	Patterns of cell division and expansion in developing petals of <i>Petunia hybrida</i> . <i>Sexual Plant Reproduction</i> , <b>2002</b> , 15, 123-132		42