

# Giovanni Battista Tornielli

## List of Publications by Year in descending order

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56  
papers

4,615  
citations

87886

38  
h-index

168376

53  
g-index

58  
all docs

58  
docs citations

58  
times ranked

4193  
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.	6.6	371
2	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.	4.8	272
3	Genome-wide analysis and expression profile of the bZIP transcription factor gene family in grapevine ( <i>Vitis vinifera</i> ). <i>BMC Genomics</i> , 2014, 15, 281.	2.8	221
4	Toward the Analysis of the Petunia MADS Box Gene Family by Reverse and Forward Transposon Insertion Mutagenesis Approaches: B, C, and D Floral Organ Identity Functions Require SEPALLATA-Like MADS Box Genes in Petunia. <i>Plant Cell</i> , 2003, 15, 2680-2693.	6.6	188
5	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
6	Stilbene Compounds and Stilbene Synthase Expression during Ripening, Wilting, and UV Treatment in Grape cv. Corvina. <i>Journal of Agricultural and Food Chemistry</i> , 2001, 49, 5531-5536.	5.2	172
7	The plasticity of the grapevine berry transcriptome. <i>Genome Biology</i> , 2013, 14, r54.	8.8	168
8	A systems-oriented analysis of the grapevine R2R3-MYB transcription factor family uncovers new insights into the regulation of stilbene accumulation. <i>DNA Research</i> , 2016, 23, 451-466.	3.4	141
9	Downregulation of the Petunia hybrida $\beta$ -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.	6.6	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.	2.4	134
11	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
12	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
13	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
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.	4.8	113
15	De novo transcriptome characterization of <i>Vitis vinifera</i> cv. Corvina unveils varietal diversity. <i>BMC Genomics</i> , 2013, 14, 41.	2.8	110
16	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.	3.6	110
17	Ethylene Evolution and 1-Aminocyclopropane-1-carboxylate Oxidase Gene Expression during Early Development and Ripening of Peach Fruit. <i>Journal of the American Society for Horticultural Science</i> , 1997, 122, 642-647.	1.0	109
18	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

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19	A group of grapevine <sc>MYBA</sc> transcription factors located in chromosome 14 control anthocyanin synthesis in vegetative organs with different specificities compared with the berry color locus. <i>Plant Journal</i> , 2017, 91, 220-236.	5.7	103
20	Whole Plant Temperature Manipulation Affects Flavonoid Metabolism and the Transcriptome of Grapevine Berries. <i>Frontiers in Plant Science</i> , 2017, 8, 929.	3.6	102
21	The photomorphogenic factors UV-B RECEPTOR 1, ELONGATED HYPOCOTYL 5, and HY5 HOMOLOGUE are part of the UV-B signalling pathway in grapevine and mediate flavonol accumulation in response to the environment. <i>Journal of Experimental Botany</i> , 2016, 67, 5429-5445.	4.8	100
22	Molecular analysis of post-harvest withering in grape by AFLP transcriptional profiling. <i>Journal of Experimental Botany</i> , 2008, 59, 4145-4159.	4.8	86
23	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
24	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.	3.1	83
25	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
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.	5.7	75
27	miRVine: a microRNA expression atlas of grapevine based on small RNA sequencing. <i>BMC Genomics</i> , 2015, 16, 393.	2.8	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.	2.8	72
29	Plasticity of the Berry Ripening Program in a White Grape Variety. <i>Frontiers in Plant Science</i> , 2016, 7, 970.	3.6	68
30	Expression of rolBin tobacco flowers affects the coordinated processes of anther dehiscence and style elongation. <i>Plant Journal</i> , 2004, 38, 512-525.	5.7	59
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.	7.3	58
32	The Evolutionary History and Diverse Physiological Roles of the Grapevine Calcium-Dependent Protein Kinase Gene Family. <i>PLoS ONE</i> , 2013, 8, e80818.	2.5	57
33	The <sc>MYB</sc>5-driven <sc>MBW</sc> complex recruits a <sc>WRKY</sc> factor to enhance the expression of targets involved in vacuolar hyperacidification and trafficking in grapevine. <i>Plant Journal</i> , 2019, 99, 1220-1241.	5.7	54
34	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.	2.1	53
35	Effect of various thermo-hygrometric conditions on the withering kinetics of grapes used for the production of "Amarone" and "Recioto" wines. <i>Journal of Food Engineering</i> , 2008, 85, 350-358.	5.2	52
36	Distinct transcriptome responses to water limitation in isohydric and anisohydric grapevine cultivars. <i>BMC Genomics</i> , 2016, 17, 815.	2.8	49

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37	Whole-Metagenome-Sequencing-Based Community Profiles of <i>Vitis vinifera</i> L. cv. Corvina Berries Withered in Two Post-harvest Conditions. <i>Frontiers in Microbiology</i> , 2016, 7, 937.	3.5	47
38	Inspection of the Grapevine BURP Superfamily Highlights an Expansion of RD22 Genes with Distinctive Expression Features in Berry Development and ABA-Mediated Stress Responses. <i>PLoS ONE</i> , 2014, 9, e110372.	2.5	42
39	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
40	The Induction of Noble Rot ( <i>Botrytis cinerea</i> ) Infection during Postharvest Withering Changes the Metabolome of Grapevine Berries ( <i>Vitis vinifera</i> L., cv. Garganega). <i>Frontiers in Plant Science</i> , 2017, 8, 1002.	3.6	34
41	Improved in planta expression of the human islet autoantigen glutamic acid decarboxylase (GAD65). <i>Transgenic Research</i> , 2003, 12, 203-212.	2.4	31
42	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
43	Selection of candidate genes controlling veraison time in grapevine through integration of meta-QTL and transcriptomic data. <i>BMC Genomics</i> , 2019, 20, 739.	2.8	24
44	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.	3.6	23
45	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.	6.0	22
46	Rapid dehydration of grape berries dampens the post-ripening transcriptomic program and the metabolite profile evolution. <i>Horticulture Research</i> , 2020, 7, 141.	6.3	21
47	Genetic, epigenetic and genomic effects on variation of gene expression among grape varieties. <i>Plant Journal</i> , 2019, 99, 895-909.	5.7	19
48	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
49	VviNAC33 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.	7.3	16
50	Validation by isolation and expression analyses of the mitogen-activated protein kinase gene family in the grapevine ( <i>Vitis vinifera</i> L.). <i>Australian Journal of Grape and Wine Research</i> , 2014, 20, 255-262.	2.1	14
51	Genomic Designing for Biotic Stress Resistant Grapevine. , 2022, , 87-255.		11
52	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.	2.4	10
53	Transcriptomics and Metabolomics for the Analysis of Grape Berry Development. , 2012, , 218-240.		5
54	Plant and fungus transcriptomic data from grapevine berries undergoing artificially-induced noble rot caused by <i>Botrytis cinerea</i> . <i>Data in Brief</i> , 2019, 25, 104150.	1.0	3

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55	Grape Berry Transcriptome. , 2021, , 558-571.		3
56	Towards the definition of a detailed transcriptomic map of berry development. BIO Web of Conferences, 2019, 13, 01001.	0.2	1