

Giovanni Battista Tornielli

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.

56 papers	3,043 citations	34 h-index	55 g-index
58 ext. papers	4,034 ext. citations	5.7 avg, IF	4.72 L-index

#	Paper	IF	Citations
56	Genomic Designing for Biotic Stress Resistant Grapevine 2022 , 87-255		0
55	The Grape Gene Reference Catalogue as a Standard Resource for Gene Selection and Genetic Improvement.. <i>Frontiers in Plant Science</i> , 2021 , 12, 803977	6.2	2
54	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	9.8	2
53	Grape Berry Transcriptome 2021 , 558-571		
52	Rapid dehydration of grape berries dampens the post-ripening transcriptomic program and the metabolite profile evolution. <i>Horticulture Research</i> , 2020 , 7, 141	7.7	7
51	Selection of candidate genes controlling veraison time in grapevine through integration of meta-QTL and transcriptomic data. <i>BMC Genomics</i> , 2019 , 20, 739	4.5	9
50	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> , 2019 , 99, 1220-1241	6.9	20
49	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	6.2	11
48	Plant and fungus transcriptomic data from grapevine berries undergoing artificially-induced noble rot caused by. <i>Data in Brief</i> , 2019 , 25, 104150	1.2	3
47	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	2.7	11
46	Genetic, epigenetic and genomic effects on variation of gene expression among grape varieties. <i>Plant Journal</i> , 2019 , 99, 895-909	6.9	11
45	Towards the definition of a detailed transcriptomic map of berry development. <i>BIO Web of Conferences</i> , 2019 , 13, 01001	0.4	0
44	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> , 2018 , 93, 1143-1159	6.9	37
43	Timing and Order of the Molecular Events Marking the Onset of Berry Ripening in Grapevine. <i>Plant Physiology</i> , 2018 , 178, 1187-1206	6.6	39
42	A group of grapevine MYBA 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	6.9	58
41	Ripening Transcriptomic Program in Red and White Grapevine Varieties Correlates with Berry Skin Anthocyanin Accumulation. <i>Plant Physiology</i> , 2017 , 174, 2376-2396	6.6	68
40	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	6.2	20

39	Whole Plant Temperature Manipulation Affects Flavonoid Metabolism and the Transcriptome of Grapevine Berries. <i>Frontiers in Plant Science</i> , 2017 , 8, 929	6.2	58
38	The Induction of Noble Rot () Infection during Postharvest Withering Changes the Metabolome of Grapevine Berries (L., cv. Garganega). <i>Frontiers in Plant Science</i> , 2017 , 8, 1002	6.2	21
37	Distinct transcriptome responses to water limitation in isohydric and anisohydric grapevine cultivars. <i>BMC Genomics</i> , 2016 , 17, 815	4.5	34
36	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	4.5	88
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> , 2016 , 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> , 2016 , 7, 1979	6.2	61
33	Whole-Metagenome-Sequencing-Based Community Profiles of Vitis vinifera L. cv. Corvina Berries Withered in Two Post-harvest Conditions. <i>Frontiers in Microbiology</i> , 2016 , 7, 937	5.7	33
32	Plasticity of the Berry Ripening Program in a White Grape Variety. <i>Frontiers in Plant Science</i> , 2016 , 7, 9706.2	6.2	39
31	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	7	64
30	Disclosing the Molecular Basis of the Postharvest Life of Berry in Different Grapevine Genotypes. <i>Plant Physiology</i> , 2016 , 172, 1821-1843	6.6	45
29	miRVine: a microRNA expression atlas of grapevine based on small RNA sequencing. <i>BMC Genomics</i> , 2015 , 16, 393	4.5	42
28	A Grapevine Anthocyanin Acyltransferase, Transcriptionally Regulated by VvMYBA, Can Produce Most Acylated Anthocyanins Present in Grape Skins. <i>Plant Physiology</i> , 2015 , 169, 1897-916	6.6	78
27	Towards a scientific interpretation of the terroir concept: plasticity of the grape berry metabolome. <i>BMC Plant Biology</i> , 2015 , 15, 191	5.3	70
26	The phenylpropanoid pathway is controlled at different branches by a set of R2R3-MYB C2 repressors in grapevine. <i>Plant Physiology</i> , 2015 , 167, 1448-70	6.6	167
25	Genome-wide analysis and expression profile of the bZIP transcription factor gene family in grapevine (Vitis vinifera). <i>BMC Genomics</i> , 2014 , 15, 281	4.5	129
24	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> , 2014 , 55, 517-34	4.9	50
23	Genome and transcriptome analysis of the grapevine (Vitis vinifera L.) WRKY gene family. <i>Horticulture Research</i> , 2014 , 1, 14016	7.7	124
22	Validation by isolation and expression analyses of the mitogen-activated protein kinase gene family in the grapevine (Vitis vinifera L.). <i>Australian Journal of Grape and Wine Research</i> , 2014 , 20, 255-262	2.4	11

21	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	3.7	31
20	The plasticity of the grapevine berry transcriptome. <i>Genome Biology</i> , 2013 , 14, r54	18.3	119
19	Selective defoliation affects plant growth, fruit transcriptional ripening program and flavonoid metabolism in grapevine. <i>BMC Plant Biology</i> , 2013 , 13, 30	5.3	79
18	De novo transcriptome characterization of Vitis vinifera cv. Corvina unveils varietal diversity. <i>BMC Genomics</i> , 2013 , 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> , 2013 , 19, 171-179	2.4	38
16	Genome-wide analysis of the expansin gene superfamily reveals grapevine-specific structural and functional characteristics. <i>PLoS ONE</i> , 2013 , 8, e62206	3.7	79
15	The evolutionary history and diverse physiological roles of the grapevine calcium-dependent protein kinase gene family. <i>PLoS ONE</i> , 2013 , 8, e80818	3.7	44
14	The grapevine expression atlas reveals a deep transcriptome shift driving the entire plant into a maturation program. <i>Plant Cell</i> , 2012 , 24, 3489-505	11.6	252
13	Transcriptomics and Metabolomics for the Analysis of Grape Berry Development 2012 , 218-240		4
12	Revealing impaired pathways in the an11 mutant by high-throughput characterization of Petunia axillaris and Petunia inflata transcriptomes. <i>Plant Journal</i> , 2011 , 68, 11-27	6.9	31
11	Overexpression of PhEXPA1 increases cell size, modifies cell wall polymer composition and affects the timing of axillary meristem development in Petunia hybrida. <i>New Phytologist</i> , 2011 , 191, 662-677	9.8	48
10	Increasing the source/sink ratio in Vitis vinifera (cv Sangiovese) induces extensive transcriptome reprogramming and modifies berry ripening. <i>BMC Genomics</i> , 2011 , 12, 631	4.5	58
9	PhEXPA1, a Petunia hybrida expansin, is involved in cell wall metabolism and in plant architecture specification. <i>Plant Signaling and Behavior</i> , 2011 , 6, 2031-4	2.5	9
8	Molecular analysis of post-harvest withering in grape by AFLP transcriptional profiling. <i>Journal of Experimental Botany</i> , 2008 , 59, 4145-59	7	73
7	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	6	40
6	Downregulation of the Petunia hybrida 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> , 2004 , 16, 295-308	11.6	121
5	Expression of rolB in tobacco flowers affects the coordinated processes of anther dehiscence and style elongation. <i>Plant Journal</i> , 2004 , 38, 512-25	6.9	57
4	Improved in planta expression of the human islet autoantigen glutamic acid decarboxylase (GAD65). <i>Transgenic Research</i> , 2003 , 12, 203-12	3.3	26

3	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, 2680-93	11.6	140
2	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, 5531-6	5.7	142
1	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	2.3	82