

# Stefania Pilati

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1007021/publications.pdf>

Version: 2024-02-01

16  
papers

1,091  
citations

759233

12  
h-index

940533

16  
g-index

16  
all docs

16  
docs citations

16  
times ranked

1506  
citing authors

#	ARTICLE	IF	CITATIONS
1	Endoplasmic Reticulum Oxidoreductin 1-L <sup>1</sup> (ERO1-L <sup>1</sup> ), a Human Gene Induced in the Course of the Unfolded Protein Response. <i>Journal of Biological Chemistry</i> , 2000, 275, 23685-23692.	3.4	239
2	Genome-wide transcriptional analysis of grapevine berry ripening reveals a set of genes similarly modulated during three seasons and the occurrence of an oxidative burst at v <sup>1</sup> raison. <i>BMC Genomics</i> , 2007, 8, 428.	2.8	216
3	Abscisic Acid Is a Major Regulator of Grape Berry Ripening Onset: New Insights into ABA Signaling Network. <i>Frontiers in Plant Science</i> , 2017, 8, 1093.	3.6	138
4	The onset of grapevine berry ripening is characterized by ROS accumulation and lipoxygenase-mediated membrane peroxidation in the skin. <i>BMC Plant Biology</i> , 2014, 14, 87.	3.6	87
5	A Common Structural Basis for pH- and Calmodulin-mediated Regulation in Plant Glutamate Decarboxylase. <i>Journal of Molecular Biology</i> , 2009, 392, 334-351.	4.2	71
6	VESPUCCI: Exploring Patterns of Gene Expression in Grapevine. <i>Frontiers in Plant Science</i> , 2016, 7, 633.	3.6	65
7	Grapevine cell early activation of specific responses to DIMEB, a resveratrol elicitor. <i>BMC Genomics</i> , 2009, 10, 363.	2.8	54
8	Gene expression profiling in susceptible interaction of grapevine with its fungal pathogen <i>Eutypa lata</i> : Extending MapMan ontology for grapevine. <i>BMC Plant Biology</i> , 2009, 9, 104.	3.6	51
9	The C-terminal domain of yeast Ero1p mediates membrane localization and is essential for function. <i>FEBS Letters</i> , 2001, 508, 117-120.	2.8	46
10	Molecular analysis of the early interaction between the grapevine flower and <i>Botrytis cinerea</i> reveals that prompt activation of specific host pathways leads to fungus quiescence. <i>Plant, Cell and Environment</i> , 2017, 40, 1409-1428.	5.7	44
11	Dual Transcriptome and Metabolic Analysis of <i>Vitis vinifera</i> cv. Pinot Noir Berry and <i>Botrytis cinerea</i> During Quiescence and Egressed Infection. <i>Frontiers in Plant Science</i> , 2019, 10, 1704.	3.6	26
12	Discovering Causal Relationships in Grapevine Expression Data to Expand Gene Networks. A Case Study: Four Networks Related to Climate Change. <i>Frontiers in Plant Science</i> , 2018, 9, 1385.	3.6	17
13	<i>Vitis</i> OneGenE: A Causality-Based Approach to Generate Gene Networks in <i>Vitis vinifera</i> Sheds Light on the Laccase and Dirigent Gene Families. <i>Biomolecules</i> , 2021, 11, 1744.	4.0	16
14	Grapevine DMR6-1 Is a Candidate Gene for Susceptibility to Downy Mildew. <i>Biomolecules</i> , 2022, 12, 182.	4.0	14
15	A Computing System for Discovering Causal Relationships Among Human Genes to Improve Drug Repositioning. <i>IEEE Transactions on Emerging Topics in Computing</i> , 2021, 9, 1667-1682.	4.6	5
16	A COMPASS for VESPUCCI: A FAIR Way to Explore the Grapevine Transcriptomic Landscape. <i>Frontiers in Plant Science</i> , 2022, 13, 815443.	3.6	2