

Stefano Pavan

List of Publications by Year in descending order

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Version: 2024-02-01

49
papers

2,534
citations

218592

26
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48
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all docs

52
docs citations

52
times ranked

2586
citing authors

#	ARTICLE	IF	CITATIONS
1	Merging genotyping-by-sequencing data from two ex situ collections provides insights on the pea evolutionary history. Horticulture Research, 2022, , .	2.9	3
2	Phenolic characterization of olive genotypes potentially resistant to <i>Xylella</i> . Journal of Plant Interactions, 2022, 17, 462-474.	1.0	5
3	Intra- and Inter-Population Genetic Diversity of <i>Triticum aestivum</i> and <i>Triticum durum</i> Landraces from Sicily: A Proxy towards the Identification of Favorable Alleles in Durum Wheat. Agronomy, 2022, 12, 1326.	1.3	9
4	Data on the proximate composition, bioactive compounds, physicochemical and functional properties of a collection of faba beans (<i>Vicia faba</i> L.) and lentils (<i>Lens culinaris</i> Medik.). Data in Brief, 2021, 34, 106660.	0.5	11
5	Almond diversity and homozygosity define structure, kinship, inbreeding, and linkage disequilibrium in cultivated germplasm, and reveal genomic associations with nut and seed weight. Horticulture Research, 2021, 8, 15.	2.9	16
6	Genotyping-by-Sequencing in <i>Vigna unguiculata</i> Landraces and Its Utility for Assessing Taxonomic Relationships. Plants, 2021, 10, 509.	1.6	10
7	Macro- and Micro-Nutrient Composition and Antioxidant Activity of Chickpea and Pea Accessions. Polish Journal of Food and Nutrition Sciences, 2021, , 177-185.	0.6	14
8	Screening of Olive Biodiversity Defines Genotypes Potentially Resistant to <i>Xylella fastidiosa</i> . Frontiers in Plant Science, 2021, 12, 723879.	1.7	20
9	Recommendations for Choosing the Genotyping Method and Best Practices for Quality Control in Crop Genome-Wide Association Studies. Frontiers in Genetics, 2020, 11, 447.	1.1	48
10	Assessment of Genetic Diversity of the <i>Acquaviva Red Onion</i> (<i>Allium cepa</i> L.) Apulian Landrace. Plants, 2020, 9, 260.	1.6	16
11	Whole Genome Scan Reveals Molecular Signatures of Divergence and Selection Related to Important Traits in Durum Wheat Germplasm. Frontiers in Genetics, 2020, 11, 217.	1.1	50
12	In Vitro and In Vivo Nutraceutical Characterization of Two Chickpea Accessions: Differential Effects on Hepatic Lipid Over-Accumulation. Antioxidants, 2020, 9, 268.	2.2	11
13	Genetic Characterization of Apulian Olive Germplasm as Potential Source in New Breeding Programs. Plants, 2019, 8, 268.	1.6	33
14	Data on the chemical composition, bioactive compounds, fatty acid composition, physico-chemical and functional properties of a global chickpea collection. Data in Brief, 2019, 27, 104612.	0.5	19
15	Nutritional, physico-chemical and functional characterization of a global chickpea collection. Journal of Food Composition and Analysis, 2019, 84, 103306.	1.9	48
16	Genotyping by Sequencing of Cultivated Lentil (<i>Lens culinaris</i> Medik.) Highlights Population Structure in the Mediterranean Gene Pool Associated With Geographic Patterns and Phenotypic Variables. Frontiers in Genetics, 2019, 10, 872.	1.1	35
17	Genotyping-by-Sequencing Reveals Molecular Genetic Diversity in Italian Common Bean Landraces. Diversity, 2019, 11, 154.	0.7	12
18	Mutation of a bHLH transcription factor allowed almond domestication. Science, 2019, 364, 1095-1098.	6.0	116

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19	Genetic Diversity in broccoli rabe (<i>Brassica rapa</i> L. subsp. <i>sylvestris</i> (L.) Janch.) from Southern Italy. <i>Scientia Horticulturae</i> , 2019, 253, 140-146.	1.7	9
20	Evolutionary conservation of MLO gene promoter signatures. <i>BMC Plant Biology</i> , 2019, 19, 150.	1.6	14
21	Biotechnological and Digital Revolution for Climate-Smart Plant Breeding. <i>Agronomy</i> , 2018, 8, 277.	1.3	58
22	Elucidation of the Amygdalin Pathway Reveals the Metabolic Basis of Bitter and Sweet Almonds (<i>Prunus dulcis</i>). <i>Plant Physiology</i> , 2018, 178, 1096-1111.	2.3	64
23	Genotyping-by-sequencing highlights patterns of genetic structure and domestication in artichoke and cardoon. <i>PLoS ONE</i> , 2018, 13, e0205988.	1.1	43
24	GBS-derived SNP catalogue unveiled wide genetic variability and geographical relationships of Italian olive cultivars. <i>Scientific Reports</i> , 2018, 8, 15877.	1.6	84
25	Syteny-Based Development of CAPS Markers Linked to the Sweet kernel LOCUS, Controlling Amygdalin Accumulation in Almond (<i>Prunus dulcis</i> (Mill.) D.A.Webb). <i>Genes</i> , 2018, 9, 385.	1.0	9
26	Single nucleotide polymorphism (SNP) diversity in an olive germplasm collection. <i>Acta Horticulturae</i> , 2018, , 27-32.	0.1	14
27	Genetic, Bio-Agronomic, and Nutritional Characterization of Kale (<i>Brassica Oleracea</i> L. var. <i>Acephala</i>) Diversity in Apulia, Southern Italy. <i>Diversity</i> , 2018, 10, 25.	0.7	14
28	Functional characterization of the powdery mildew susceptibility gene SmMLO1 in eggplant (<i>Solanum</i>) Tj ETQq0 0 0 rgBT /Overlock 10	1.3	2
29	Genetic variation of a global germplasm collection of chickpea (<i>Cicer arietinum</i> L.) including Italian accessions at risk of genetic erosion. <i>Physiology and Molecular Biology of Plants</i> , 2017, 23, 197-205.	1.4	40
30	Development and validation of breeder-friendly KASPar markers for er1, a powdery mildew resistance gene in pea (<i>Pisum sativum</i> L.). <i>Molecular Breeding</i> , 2017, 37, 1.	1.0	22
31	Genotyping-by-sequencing of a melon (<i>Cucumis melo</i> L.) germplasm collection from a secondary center of diversity highlights patterns of genetic variation and genomic features of different gene pools. <i>BMC Genomics</i> , 2017, 18, 59.	1.2	72
32	Functional Characterization of a Syntxin Involved in Tomato (<i>Solanum lycopersicum</i>) Resistance against Powdery Mildew. <i>Frontiers in Plant Science</i> , 2017, 8, 1573.	1.7	6
33	Polyphenol Oxidases in Crops: Biochemical, Physiological and Genetic Aspects. <i>International Journal of Molecular Sciences</i> , 2017, 18, 377.	1.8	270
34	A Distinct Genetic Cluster in Cultivated Chickpea as Revealed by Genome-wide Marker Discovery and Genotyping. <i>Plant Genome</i> , 2017, 10, plantgenome2016.11.0115.	1.6	54
35	Genome-Wide Study of the Tomato SIMLO Gene Family and Its Functional Characterization in Response to the Powdery Mildew Fungus <i>Oidium neolycopersici</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 380.	1.7	61
36	Characterization of Low-Strigolactone Germplasm in Pea (<i>Pisum sativum</i> L.) Resistant to Crenate Broomrape (<i>Orobanche crenata</i> Forsk.). <i>Molecular Plant-Microbe Interactions</i> , 2016, 29, 743-749.	1.4	37

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37	Monocot and dicot MLO powdery mildew susceptibility factors are functionally conserved in spite of the evolution of class-specific molecular features. <i>BMC Plant Biology</i> , 2015, 15, 257.	1.6	51
38	Structure, evolution and functional inference on the Mildew Locus O (MLO) gene family in three cultivated Cucurbitaceae spp.. <i>BMC Genomics</i> , 2015, 16, 1112.	1.2	45
39	Identification of candidate MLO powdery mildew susceptibility genes in cultivated Solanaceae and functional characterization of tobacco NtMLO1. <i>Transgenic Research</i> , 2015, 24, 847-858.	1.3	55
40	Genetics and molecular mechanisms of resistance to powdery mildews in tomato (<i>Solanum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 622 T	0.8	31
41	Characterization of the MLO gene family in Rosaceae and gene expression analysis in <i>Malus domestica</i> . <i>BMC Genomics</i> , 2014, 15, 618.	1.2	97
42	Identification of Traits, Genes, and Crops of the Future. , 2013, , 27-177.		1
43	Identification of a complete set of functional markers for the selection of er1 powdery mildew resistance in <i>Pisum sativum</i> L.. <i>Molecular Breeding</i> , 2013, 31, 247-253.	1.0	41
44	Loss of Function in Mlo Orthologs Reduces Susceptibility of Pepper and Tomato to Powdery Mildew Disease Caused by <i>Leveillula taurica</i> . <i>PLoS ONE</i> , 2013, 8, e70723.	1.1	113
45	Pea powdery mildew er1 resistance is associated to loss-of-function mutations at a MLO homologous locus. <i>Theoretical and Applied Genetics</i> , 2011, 123, 1425-1431.	1.8	140
46	Loss of susceptibility as a novel breeding strategy for durable and broad-spectrum resistance. <i>Molecular Breeding</i> , 2010, 25, 1-12.	1.0	300
47	Map- vs. homology-based cloning for the recessive gene ol-2 conferring resistance to tomato powdery mildew. <i>Euphytica</i> , 2008, 162, 91-98.	0.6	24
48	Naturally Occurring Broad-Spectrum Powdery Mildew Resistance in a Central American Tomato Accession Is Caused by Loss of <i>Mlo</i> Function. <i>Molecular Plant-Microbe Interactions</i> , 2008, 21, 30-39.	1.4	269
49	Further isolation of AFLP and LMS markers for the mapping of the Ol-2 locus related to powdery mildew (<i>Oidium neolycopersici</i>) resistance in tomato (<i>Solanum lycopersicum</i> L.). <i>Plant Science</i> , 2007, 172, 746-755.	1.7	8