

Giampiero ValÃ

List of Publications by Year in descending order

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76
papers

3,154
citations

159525

30
h-index

168321

53
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77
all docs

77
docs citations

77
times ranked

4237
citing authors

#	ARTICLE	IF	CITATIONS
1	High accuracy of genome-enabled prediction of belowground and physiological traits in barley seedlings. <i>G3: Genes, Genomes, Genetics</i> , 2022, , .	0.8	0
2	Effect of water management on microbial diversity and composition in an Italian rice field system. <i>FEMS Microbiology Ecology</i> , 2022, 98, .	1.3	11
3	Resistance of European Spring 2-Row Barley Cultivars to <i>Pyrenophora graminea</i> and Detection of Associated Loci. <i>Agronomy</i> , 2021, 11, 374.	1.3	7
4	Characterization of the Resistance to Powdery Mildew and Leaf Rust Carried by the Bread Wheat Cultivar Victo. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3109.	1.8	4
5	Analysis of Cadmium Root Retention for Two Contrasting Rice Accessions Suggests an Important Role for OsHMA2. <i>Plants</i> , 2021, 10, 806.	1.6	11
6	Genomic Prediction of Grain Yield in a Barley MAGIC Population Modeling Genotype per Environment Interaction. <i>Frontiers in Plant Science</i> , 2021, 12, 664148.	1.7	5
7	Effects of the application of a moderate alternate wetting and drying technique on the performance of different European varieties in Northern Italy rice system. <i>Field Crops Research</i> , 2021, 270, 108220.	2.3	16
8	Application of plant-derived bioactive compounds as seed treatments to manage the rice pathogen <i>Fusarium fujikuroi</i> . <i>Crop Protection</i> , 2021, 148, 105739.	1.0	11
9	Fitness Cost Shapes Differential Evolutionary Dynamics of Disease Resistance Genes in Cultivated and Wild Plants. <i>Molecular Plant</i> , 2020, 13, 1352-1354.	3.9	3
10	Genome wide association studies for japonica rice resistance to blast in field and controlled conditions. <i>Rice</i> , 2020, 13, 71.	1.7	14
11	Effects of water management and cultivar on carbon dynamics, plant productivity and biomass allocation in European rice systems. <i>Science of the Total Environment</i> , 2019, 685, 1139-1151.	3.9	23
12	Continuous Flooding or Alternate Wetting and Drying Differently Affect the Accumulation of Health-Promoting Phytochemicals and Minerals in Rice Brown Grain. <i>Agronomy</i> , 2019, 9, 628.	1.3	14
13	GWAS for Starch-Related Parameters in Japonica Rice (<i>Oryza sativa</i> L.). <i>Plants</i> , 2019, 8, 292.	1.6	30
14	Identification and mapping of expressed genes associated with the 2DL QTL for fusarium head blight resistance in the wheat line Wuhan 1. <i>BMC Genetics</i> , 2019, 20, 47.	2.7	16
15	Dissection of coleoptile elongation in japonica rice under submergence through integrated genome-wide association mapping and transcriptional analyses. <i>Plant, Cell and Environment</i> , 2019, 42, 1832-1846.	2.8	36
16	High-resolution mapping of the pericentromeric region on wheat chromosome arm 5AS harbouring the Fusarium head blight resistance QTL <i>Qfhs.ifa</i> . <i>Plant Biotechnology Journal</i> , 2018, 16, 1046-1056.	4.1	35
17	Rice diversity panel provides accurate genomic predictions for complex traits in the progenies of biparental crosses involving members of the panel. <i>Theoretical and Applied Genetics</i> , 2018, 131, 417-435.	1.8	29
18	Comparative Transcriptome Profiles of Near-Isogenic Hexaploid Wheat Lines Differing for Effective Alleles at the 2DL FHB Resistance QTL. <i>Frontiers in Plant Science</i> , 2018, 9, 37.	1.7	46

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19	Regulation and Evolution of NLR Genes: A Close Interconnection for Plant Immunity. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1662.	1.8	68
20	Seed Dormancy Involves a Transcriptional Program That Supports Early Plastid Functionality during Imbibition. <i>Plants</i> , 2018, 7, 35.	1.6	16
21	Genomic Prediction Accounting for Genotype by Environment Interaction Offers an Effective Framework for Breeding Simultaneously for Adaptation to an Abiotic Stress and Performance Under Normal Cropping Conditions in Rice. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2319-2332.	0.8	30
22	Genetic variability of <i>Fusarium fujikuroi</i> populations associated with bakanae of rice in Italy. <i>Plant Pathology</i> , 2017, 66, 469-479.	1.2	12
23	Identification of bakanae disease resistance loci in japonica rice through genome wide association study. <i>Rice</i> , 2017, 10, 29.	1.7	43
24	Genome-Wide Analysis of japonica Rice Performance under Limited Water and Permanent Flooding Conditions. <i>Frontiers in Plant Science</i> , 2017, 8, 1862.	1.7	38
25	Economic Performance of Traditional and Modern Rice Varieties under Different Water Management Systems. <i>Sustainability</i> , 2017, 9, 347.	1.6	20
26	Stratification of Diversity and Activity of Methanogenic and Methanotrophic Microorganisms in a Nitrogen-Fertilized Italian Paddy Soil. <i>Frontiers in Microbiology</i> , 2017, 8, 2127.	1.5	62
27	Water Management Options for Rice Cultivation in a Temperate Area: A Multi-Objective Model to Explore Economic and Water Saving Results. <i>Water (Switzerland)</i> , 2016, 8, 336.	1.2	25
28	Rootstock-scion interaction affecting citrus response to CTV infection: a proteomic view. <i>Physiologia Plantarum</i> , 2016, 156, 444-467.	2.6	14
29	Phenotype and gene expression analyses of the <i>Rfo1</i> resistant aubergine interaction with <i>Fusarium oxysporum</i> f. sp. <i>melongenae</i> and <i>Verticillium dahliae</i> . <i>Plant Pathology</i> , 2016, 65, 1297-1309.	1.2	8
30	Comparative transcriptome profiling of resistant and susceptible rice genotypes in response to the seedborne pathogen <i>Fusarium fujikuroi</i> . <i>BMC Genomics</i> , 2016, 17, 608.	1.2	99
31	Knockdown of MLO genes reduces susceptibility to powdery mildew in grapevine. <i>Horticulture Research</i> , 2016, 3, 16016.	2.9	145
32	Next generation breeding. <i>Plant Science</i> , 2016, 242, 3-13.	1.7	139
33	Genetic analysis of durable resistance to <i>Magnaporthe oryzae</i> in the rice accession Gigante Vercelli identified two blast resistance loci. <i>Molecular Genetics and Genomics</i> , 2016, 291, 17-32.	1.0	13
34	QTLs for Woolly Poplar Aphid (<i>Phloeomyzus passerinii</i> L.) Resistance Detected in an Inter-Specific <i>Populus deltoides</i> x <i>P. nigra</i> Mapping Population. <i>PLoS ONE</i> , 2016, 11, e0152569.	1.1	13
35	Genome-Wide Association Study for Traits Related to Plant and Grain Morphology, and Root Architecture in Temperate Rice Accessions. <i>PLoS ONE</i> , 2016, 11, e0155425.	1.1	80
36	Deep sequencing transcriptional fingerprinting of rice kernels for dissecting grain quality traits. <i>BMC Genomics</i> , 2015, 16, 1091.	1.2	18

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37	Physical Mapping of Bread Wheat Chromosome 5A: An Integrated Approach. <i>Plant Genome</i> , 2015, 8, eplantgenome2015.03.0011.	1.6	11
38	QTL Mapping in Eggplant Reveals Clusters of Yield-Related Loci and Orthology with the Tomato Genome. <i>PLoS ONE</i> , 2014, 9, e89499.	1.1	76
39	A new genetic and deletion map of wheat chromosome 5A to detect candidate genes for quantitative traits. <i>Molecular Breeding</i> , 2014, 34, 1599-1611.	1.0	13
40	Identification and mapping of quantitative trait loci for leaf rust resistance derived from a tetraploid wheat <i>Triticum dicoccum</i> accession. <i>Molecular Breeding</i> , 2014, 34, 1659-1675.	1.0	33
41	De novo genome assembly of the soil-borne fungus and tomato pathogen <i>Pyrenochaeta lycopersici</i> . <i>BMC Genomics</i> , 2014, 15, 313.	1.2	39
42	Improvement of marker-based predictability of Apparent Amylose Content in japonica rice through GBSSI allele mining. <i>Rice</i> , 2014, 7, 1.	1.7	147
43	Haplotype variability and identification of new functional alleles at the Rdg2a leaf stripe resistance gene locus. <i>Theoretical and Applied Genetics</i> , 2013, 126, 1575-1586.	1.8	9
44	An <i>Agrobacterium tumefaciens</i> -mediated gene silencing system for functional analysis in grapevine. <i>Plant Cell, Tissue and Organ Culture</i> , 2013, 114, 49-60.	1.2	12
45	Investigation of rice blast development in susceptible and resistant rice cultivars using a <i>Magnaporthe oryzae</i> isolate. <i>Plant Pathology</i> , 2013, 62, 1030-1037.	1.2	16
46	The CC-NB-LRR-type Rdg2a Resistance Gene Evolved Through Recombination and Confers Immunity to the Seed-Borne Barley Leaf Stripe Pathogen in the Absence of Hypersensitive Cell Death. , 2013, , 217-228.		4
47	Development of a deletion and genetic linkage map for the 5A and 5B chromosomes of wheat (<i>Triticum aestivum</i>). <i>Genome</i> , 2012, 55, 417-427.	0.9	9
48	Proteomic characterization of the Rph15 barley resistance gene-mediated defence responses to leaf rust. <i>BMC Genomics</i> , 2012, 13, 642.	1.2	17
49	A RAD Tag Derived Marker Based Eggplant Linkage Map and the Location of QTLs Determining Anthocyanin Pigmentation. <i>PLoS ONE</i> , 2012, 7, e43740.	1.1	119
50	Comparative Transcriptome Profiling of the Early Response to <i>Magnaporthe oryzae</i> in Durable Resistant vs Susceptible Rice (<i>Oryza sativa</i> L.) Genotypes. <i>PLoS ONE</i> , 2012, 7, e51609.	1.1	149
51	Emerging Knowledge from Genome Sequencing of Crop Species. <i>Molecular Biotechnology</i> , 2012, 50, 250-266.	1.3	35
52	Identification of SNP and SSR markers in eggplant using RAD tag sequencing. <i>BMC Genomics</i> , 2011, 12, 304.	1.2	193
53	Identification and mapping of the leaf stripe resistance gene Rdg1a in <i>Hordeum spontaneum</i> . <i>Theoretical and Applied Genetics</i> , 2010, 120, 1207-1218.	1.8	19
54	Polymorphism analysis of genomic regions associated with broad-spectrum effective blast resistance genes for marker development in rice. <i>Molecular Breeding</i> , 2010, 26, 595-617.	1.0	28

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55	Segregation distortion and linkage analysis in eggplant (<i>Solanum melongena</i> L.). <i>Genome</i> , 2010, 53, 805-815.	0.9	54
56	The CC-NB-LRR-Type Rdg2a Resistance Gene Confers Immunity to the Seed-Borne Barley Leaf Stripe Pathogen in the Absence of Hypersensitive Cell Death. <i>PLoS ONE</i> , 2010, 5, e12599.	1.1	56
57	Inheritance of Fusarium wilt resistance introgressed from <i>Solanum aethiopicum</i> Gilo and <i>Aculeatum</i> groups into cultivated eggplant (<i>S. melongena</i>) and development of associated PCR-based markers. <i>Molecular Breeding</i> , 2008, 22, 237-250.	1.0	95
58	Identification of differentially expressed genes in the flesh of blood and common oranges. <i>Tree Genetics and Genomes</i> , 2008, 4, 315-331.	0.6	33
59	Histological and molecular analysis of Rdg2a barley resistance to leaf stripe. <i>Molecular Plant Pathology</i> , 2008, 9, 463-478.	2.0	21
60	Haplotype structure around the nud locus in barley and its association with resistance to leaf stripe (<i>Pyrenophora graminea</i>). <i>Plant Breeding</i> , 2007, 126, 24-29.	1.0	2
61	In vitro antifungal activity of the tea tree (<i>Melaleuca alternifolia</i>) essential oil and its major components against plant pathogens. <i>Letters in Applied Microbiology</i> , 2007, 44, 613-618.	1.0	104
62	Haplotype characterization and markers at the barley Mlo powdery mildew resistance locus as tools for marker-assisted selection. <i>Genome</i> , 2006, 49, 864-872.	0.9	10
63	Current status in production and utilization of dihaploids from somatic hybrids between eggplant (<i>Solanum melongena</i> L.) and its wild relatives. <i>Acta Physiologiae Plantarum</i> , 2005, 27, 723-733.	1.0	32
64	Marker assisted selection in crop plants. <i>Plant Cell, Tissue and Organ Culture</i> , 2005, 82, 317-342.	1.2	176
65	High-resolution genetic mapping of the leaf stripe resistance gene Rdg2a in barley. <i>Theoretical and Applied Genetics</i> , 2004, 108, 1401-1408.	1.8	34
66	The PCR-Based Marker MWG2018 Linked to the RDG2A Leaf Stripe Resistance Gene Is a Useful Tool for Assessing Barley Resistance in Breeding Programs. <i>Crop Science</i> , 2003, 43, 1036-1042.	0.8	10
67	Genomic regions determining resistance to leaf stripe (<i>Pyrenophora graminea</i>) in barley. <i>Genome</i> , 2002, 45, 460-466.	0.9	24
68	The transcripts of several components of the protein synthesis machinery are cold-regulated in a chloroplast-dependent manner in barley and wheat. <i>Journal of Plant Physiology</i> , 2001, 158, 1541-1546.	1.6	20
69	Identification and mapping of a new leaf stripe resistance gene in barley (<i>Hordeum vulgare</i> L.). <i>Theoretical and Applied Genetics</i> , 2001, 102, 1286-1291.	1.8	34
70	Cell-Autonomous Expression of Barley Mla1 Confers Race-Specific Resistance to the Powdery Mildew Fungus via a Rar1-Independent Signaling Pathway. <i>Plant Cell</i> , 2001, 13, 337-350.	3.1	203
71	Barley-Pyrenophora graminea interaction: QTL analysis and gene mapping. <i>Plant Breeding</i> , 1999, 118, 29-35.	1.0	28
72	High expression level of a gene coding for a chloroplastic amino acid selective channel protein is correlated to cold acclimation in cereals. <i>Plant Molecular Biology</i> , 1999, 41, 233-243.	2.0	47

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73	Characterization of a hypovirulent insertional mutant of <i>Pyrenophora graminea</i> and analysis of the barley defence response after inoculation. <i>Plant Pathology</i> , 1998, 47, 657-664.	1.2	6
74	Quantitative resistance to barley leaf stripe (<i>Pyrenophora graminea</i>) is dominated by one major locus. <i>Theoretical and Applied Genetics</i> , 1996, 93-93, 97-101.	1.8	50
75	Quantitative resistance to barley leaf stripe (<i>Pyrenophora graminea</i>) is dominated by one major locus. <i>Theoretical and Applied Genetics</i> , 1996, 93, 97-101.	1.8	10
76	Activation of genes in barley roots in response to infection by two <i>Drechslera graminea</i> isolates. <i>Physiological and Molecular Plant Pathology</i> , 1994, 44, 207-215.	1.3	22