

Laura Rossini

List of Publications by Year in descending order

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68
papers

4,447
citations

136950

32
h-index

110387

64
g-index

68
all docs

68
docs citations

68
times ranked

4830
citing authors

#	ARTICLE	IF	CITATIONS
1	The barley mutant happy under the sun 1 (hus1): An additional contribution to pale green crops. <i>Environmental and Experimental Botany</i> , 2022, 196, 104795.	4.2	6
2	Less is more: natural variation disrupting a miR172 gene at the di locus underlies the recessive double-flower trait in peach (<i>P. persica</i> L. Batsch). <i>BMC Plant Biology</i> , 2022, 22, .	3.6	2
3	The <i>Di2/pet</i> Variant in the <i>PETALOSA</i> Gene Underlies a Major Heat Requirement-Related QTL for Blooming Date in Peach [<i>Prunus persica</i> (L.) Batsch]. <i>Plant and Cell Physiology</i> , 2021, 62, 356-365.	3.1	7
4	Meta-QTL and ortho-MQTL analyses identified genomic regions controlling rice yield, yield-related traits and root architecture under water deficit conditions. <i>Scientific Reports</i> , 2021, 11, 6942.	3.3	41
5	Many candidates for a single chair: a critical review of the genetic determinant of flat fruit shape trait in peach (<i>Prunus persica</i> L. Batsch). <i>Tree Genetics and Genomes</i> , 2021, 17, 1.	1.6	3
6	Genetic and phenotypic analyses reveal major quantitative loci associated to fruit size and shape traits in a non-flat peach collection (<i>P. persica</i> L. Batsch). <i>Horticulture Research</i> , 2021, 8, 232.	6.3	8
7	The Multisite <i>PeachRefPop</i> Collection: A True Cultural Heritage and International Scientific Tool for Fruit Trees. <i>Plant Physiology</i> , 2020, 184, 632-646.	4.8	12
8	Transcriptional Regulation of Sorghum Stem Composition: Key Players Identified Through Co-expression Gene Network and Comparative Genomics Analyses. <i>Frontiers in Plant Science</i> , 2020, 11, 224.	3.6	17
9	Mutations in orthologous <i>PETALOSA</i> TOE-type genes cause a dominant double-flower phenotype in phylogenetically distant eudicots. <i>Journal of Experimental Botany</i> , 2020, 71, 2585-2595.	4.8	20
10	Segmental duplications are hot spots of copy number variants affecting barley gene content. <i>Plant Journal</i> , 2020, 103, 1073-1088.	5.7	6
11	Detection of natural and induced mutations from next generation sequencing data in sweet orange bud sports. <i>Acta Horticulturae</i> , 2019, , 119-124.	0.2	2
12	Exome sequences and multi-environment field trials elucidate the genetic basis of adaptation in barley. <i>Plant Journal</i> , 2019, 99, 1172-1191.	5.7	50
13	Tracing the ancestry of modern bread wheats. <i>Nature Genetics</i> , 2019, 51, 905-911.	21.4	230
14	Genetics of barley tiller and leaf development. <i>Journal of Integrative Plant Biology</i> , 2019, 61, 226-256.	8.5	33
15	An integrated approach for increasing breeding efficiency in apple and peach in Europe. <i>Horticulture Research</i> , 2018, 5, 11.	6.3	98
16	PeachVar-DB: A Curated Collection of Genetic Variations for the Interactive Analysis of Peach Genome Data. <i>Plant and Cell Physiology</i> , 2018, 59, e2-e2.	3.1	12
17	High-density multi-population consensus genetic linkage map for peach. <i>PLoS ONE</i> , 2018, 13, e0207724.	2.5	19
18	Linkage and association mapping for the slow softening (SwS) trait in peach (<i>P. persica</i> L. Batsch) fruit. <i>Tree Genetics and Genomes</i> , 2018, 14, 1.	1.6	9

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19	Deletion of the miR172 target site in a <i>TOE</i> type gene is a strong candidate variant for dominant double-flower trait in Rosaceae. <i>Plant Journal</i> , 2018, 96, 358-371.	5.7	43
20	Genetics of Whole Plant Morphology and Architecture. <i>Compendium of Plant Genomes</i> , 2018, , 209-231.	0.5	0
21	Integrative genomics approaches validate <i>PpYUC11</i> -like as candidate gene for the stony hard trait in peach (<i>P. persica</i> L. Batsch). <i>BMC Plant Biology</i> , 2018, 18, 88.	3.6	21
22	QTL mapping and candidate genes for resistance to <i>Fusarium</i> ear rot and fumonisin contamination in maize. <i>BMC Plant Biology</i> , 2017, 17, 20.	3.6	93
23	Genome-enabled predictions for fruit weight and quality from repeated records in European peach progenies. <i>BMC Genomics</i> , 2017, 18, 432.	2.8	44
24	The Peach v2.0 release: high-resolution linkage mapping and deep resequencing improve chromosome-scale assembly and contiguity. <i>BMC Genomics</i> , 2017, 18, 225.	2.8	342
25	PocketPlant3D: Analysing canopy structure using a smartphone. <i>Biosystems Engineering</i> , 2017, 164, 1-12.	4.3	27
26	Integrated QTL detection for key breeding traits in multiple peach progenies. <i>BMC Genomics</i> , 2017, 18, 404.	2.8	75
27	Exploring and exploiting phenotypic and genetic diversity in peach: identification of major genes and QTLs by GWAS. <i>Acta Horticulturae</i> , 2017, , 419-424.	0.2	1
28	Discovering peach QTLs with multiple progeny analysis. <i>Acta Horticulturae</i> , 2017, , 405-410.	0.2	5
29	FruitBreedomics phenotypes and genotypes database and tools. <i>Acta Horticulturae</i> , 2017, , 429-434.	0.2	2
30	Genetic dissection of Sharka disease tolerance in peach (<i>P. persica</i> L. Batsch). <i>BMC Plant Biology</i> , 2017, 17, 192.	3.6	19
31	Identifying SNP markers tightly associated with six major genes in peach [<i>Prunus persica</i> (L.) Batsch] using a high-density SNP array with an objective of marker-assisted selection (MAS). <i>Tree Genetics and Genomes</i> , 2016, 12, 1.	1.6	28
32	Photoperiod-H1 (<i>Ppd-H1</i>) Controls Leaf Size. <i>Plant Physiology</i> , 2016, 172, 405-415.	4.8	77
33	Genetic dissection of heading date and yield under Mediterranean dry climate in barley (<i>Hordeum</i>) Tj ETQq1 1 0.784314 rgBT ₁₂ /Overlook	1.2	12
34	GENETIC VARIABILITY AND POPULATION STRUCTURE OF PEACH ACCESSIONS FROM MAS.PES GERMPLOSM BANK. <i>Acta Horticulturae</i> , 2015, , 233-239.	0.2	0
35	The Genetic Basis of Composite Spike Form in Barley and "Miracle-Wheat"™. <i>Genetics</i> , 2015, 201, 155-165.	2.9	109
36	Whole-Genome Analysis of Diversity and SNP-Major Gene Association in Peach Germplasm. <i>PLoS ONE</i> , 2015, 10, e0136803.	2.5	98

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37	The Barley <i>UcnL4</i> Gene Encodes a BLADE-ON-PETIOLE-Like Protein That Controls Tillering and Leaf Patterning. <i>Plant Physiology</i> , 2015, 168, 164-174.	4.8	85
38	Genetic dissection of fruit weight and size in an F2 peach (<i>Prunus persica</i> (L.) Batsch) progeny. <i>Molecular Breeding</i> , 2015, 35, 1.	2.1	48
39	Protein profiling and <i>tps23</i> induction in different maize lines in response to methyl jasmonate treatment and <i>Diabrotica virgifera</i> infestation. <i>Journal of Plant Physiology</i> , 2015, 175, 68-77.	3.5	9
40	Crossability of <i>Triticum urartu</i> and <i>Triticum monococcum</i> Wheats, Homoeologous Recombination, and Description of a Panel of Interspecific Introgression Lines. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 1931-1941.	1.8	25
41	Isolation, promoter analysis and expression profile of <i>Dreb2</i> in response to drought stress in wheat ancestors. <i>Gene</i> , 2014, 549, 24-32.	2.2	24
42	QTL mapping for brown rot (<i>Monilinia fructigena</i>) resistance in an intraspecific peach (<i>Prunus persica</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T	1.8	64
43	Interaction between the <i>GROWTH-REGULATING FACTOR</i> and <i>KNOTTED1-LIKE HOMEODOMAIN</i> Families of Transcription Factors. <i>Plant Physiology</i> , 2014, 164, 1952-1966.	4.8	143
44	Genetics of Tillering in Rice and Barley. <i>Plant Genome</i> , 2014, 7, plantgenome2013.10.0032.	2.8	75
45	Shoot and Inflorescence Architecture. <i>Biotechnology in Agriculture and Forestry</i> , 2014, , 55-80.	0.2	3
46	A Unique Mutation in a MYB Gene Cosegregates with the Nectarine Phenotype in Peach. <i>PLoS ONE</i> , 2014, 9, e90574.	2.5	86
47	Expression profiling of genes involved in the formation of aroma in two peach genotypes. <i>Plant Biology</i> , 2013, 15, 443-451.	3.8	33
48	Fine mapping and identification of a candidate gene for a major locus controlling maturity date in peach. <i>BMC Plant Biology</i> , 2013, 13, 166.	3.6	113
49	Genetic dissection of aroma volatile compounds from the essential oil of peach fruit: QTL analysis and identification of candidate genes using dense SNP maps. <i>Tree Genetics and Genomes</i> , 2013, 9, 189-204.	1.6	105
50	The high-quality draft genome of peach (<i>Prunus persica</i>) identifies unique patterns of genetic diversity, domestication and genome evolution. <i>Nature Genetics</i> , 2013, 45, 487-494.	21.4	1,031
51	Integrating cereal genomics to support innovation in the Triticeae. <i>Functional and Integrative Genomics</i> , 2012, 12, 573-583.	3.5	39
52	Saturating the <i>Prunus</i> (stone fruits) genome with candidate genes for fruit quality. <i>Molecular Breeding</i> , 2011, 28, 667-682.	2.1	53
53	QTL analysis of fruit quality traits in two peach intraspecific populations and importance of maturity date pleiotropic effect. <i>Tree Genetics and Genomes</i> , 2011, 7, 323-335.	1.6	154
54	Identification of key odor volatile compounds in the essential oil of nine peach accessions. <i>Journal of the Science of Food and Agriculture</i> , 2010, 90, 1146-1154.	3.5	100

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55	Cross Talk between the KNOX and Ethylene Pathways Is Mediated by Intron-Binding Transcription Factors in Barley. <i>Plant Physiology</i> , 2010, 154, 1616-1632.	4.8	51
56	Genetic variants of HvCbf14 are statistically associated with frost tolerance in a European germplasm collection of <i>Hordeum vulgare</i> . <i>Theoretical and Applied Genetics</i> , 2009, 119, 1335-1348.	3.6	54
57	Candidate genes for barley mutants involved in plant architecture: an in silico approach. <i>Theoretical and Applied Genetics</i> , 2006, 112, 1073-1085.	3.6	42
58	Genetics of Barley Hooded Suppression. <i>Genetics</i> , 2004, 167, 439-448.	2.9	28
59	Gene and Genome Changes During Domestication of Cereals. , 2004, , 165-198.		14
60	Patterns and symmetries in leaf development. <i>Seminars in Cell and Developmental Biology</i> , 2001, 12, 363-372.	5.0	13
61	The Maize Golden2 Gene Defines a Novel Class of Transcriptional Regulators in Plants. <i>Plant Cell</i> , 2001, 13, 1231-1244.	6.6	200
62	Alachlor Regulation of Maize Glutathione S-Transferase Genes. <i>Pesticide Biochemistry and Physiology</i> , 1998, 60, 205-211.	3.6	11
63	GOLDEN 2: A Novel Transcriptional Regulator of Cellular Differentiation in the Maize Leaf. <i>Plant Cell</i> , 1998, 10, 925-936.	6.6	163
64	Characterization of Glutathione S-Transferase Isoforms in Three Maize Inbred Lines Exhibiting Differential Sensitivity to Alachlor. <i>Plant Physiology</i> , 1996, 112, 1595-1600.	4.8	36
65	Molecular analysis and mapping of two genes encoding maize glutathione S-transferases (GST I and Tj ETQq1). <i>Plant Physiology</i> , 1994, 106, 1073-1085.	2.4	14
66	Detection of QTLs controlling pollen germination and growth in maize. <i>Heredity</i> , 1994, 72, 332-335.	2.6	15
67	Developmental expression of glutathione-S-transferase in maize and its possible connection with herbicide tolerance. <i>Euphytica</i> , 1993, 67, 221-230.	1.2	45
68	Identification of novel plant architecture mutants in barley. <i>Cereal Research Communications</i> , 0, , 1.	1.6	0