

# Laura Rossini

## List of Publications by Year in descending order

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68  
papers

4,447  
citations

136740

32  
h-index

110170

64  
g-index

68  
all docs

68  
docs citations

68  
times ranked

4830  
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	9.4	1,031
2	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.	1.2	342
3	Tracing the ancestry of modern bread wheats. <i>Nature Genetics</i> , 2019, 51, 905-911.	9.4	230
4	The Maize Golden2 Gene Defines a Novel Class of Transcriptional Regulators in Plants. <i>Plant Cell</i> , 2001, 13, 1231-1244.	3.1	200
5	GOLDEN 2: A Novel Transcriptional Regulator of Cellular Differentiation in the Maize Leaf. <i>Plant Cell</i> , 1998, 10, 925-936.	3.1	163
6	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.	0.6	154
7	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.	2.3	143
8	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.	1.6	113
9	The Genetic Basis of Composite Spike Form in Barley and "Miracle-Wheat". <i>Genetics</i> , 2015, 201, 155-165.	1.2	109
10	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.	0.6	105
11	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.	1.7	100
12	Whole-Genome Analysis of Diversity and SNP-Major Gene Association in Peach Germplasm. <i>PLoS ONE</i> , 2015, 10, e0136803.	1.1	98
13	An integrated approach for increasing breeding efficiency in apple and peach in Europe. <i>Horticulture Research</i> , 2018, 5, 11.	2.9	98
14	QTL mapping and candidate genes for resistance to Fusarium ear rot and fumonisin contamination in maize. <i>BMC Plant Biology</i> , 2017, 17, 20.	1.6	93
15	A Unique Mutation in a MYB Gene Cosegregates with the Nectarine Phenotype in Peach. <i>PLoS ONE</i> , 2014, 9, e90574.	1.1	86
16	The Barley <i>Ucn4</i> Gene Encodes a BLADE-ON-PETIOLE-Like Protein That Controls Tillering and Leaf Patterning. <i>Plant Physiology</i> , 2015, 168, 164-174.	2.3	85
17	Photoperiod-H1 (Ppd-H1) Controls Leaf Size. <i>Plant Physiology</i> , 2016, 172, 405-415.	2.3	77
18	Genetics of Tillering in Rice and Barley. <i>Plant Genome</i> , 2014, 7, plantgenome2013.10.0032.	1.6	75

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19	Integrated QTL detection for key breeding traits in multiple peach progenies. BMC Genomics, 2017, 18, 404.	1.2	75
20	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	0.6	64
21	Genetic variants of HvCbf14 are statistically associated with frost tolerance in a European germplasm collection of <i>Hordeum vulgare</i> . Theoretical and Applied Genetics, 2009, 119, 1335-1348.	1.8	54
22	Saturating the <i>Prunus</i> (stone fruits) genome with candidate genes for fruit quality. Molecular Breeding, 2011, 28, 667-682.	1.0	53
23	Cross Talk between the KNOX and Ethylene Pathways Is Mediated by Intron-Binding Transcription Factors in Barley $\hat{A}$ . Plant Physiology, 2010, 154, 1616-1632.	2.3	51
24	Exome sequences and multi $\hat{e}$ environment field trials elucidate the genetic basis of adaptation in barley. Plant Journal, 2019, 99, 1172-1191.	2.8	50
25	Genetic dissection of fruit weight and size in an F2 peach ( <i>Prunus persica</i> (L.) Batsch) progeny. Molecular Breeding, 2015, 35, 1.	1.0	48
26	Developmental expression of glutathione-S-transferase in maize and its possible connection with herbicide tolerance. Euphytica, 1993, 67, 221-230.	0.6	45
27	Genome-enabled predictions for fruit weight and quality from repeated records in European peach progenies. BMC Genomics, 2017, 18, 432.	1.2	44
28	Deletion of the miR172 target site in a $\langle scp \rangle$ TOE $\langle /scp \rangle$ $\hat{e}$ type gene is a strong candidate variant for dominant double $\hat{e}$ flower trait in Rosaceae. Plant Journal, 2018, 96, 358-371.	2.8	43
29	Candidate genes for barley mutants involved in plant architecture: an in silico approach. Theoretical and Applied Genetics, 2006, 112, 1073-1085.	1.8	42
30	Meta-QTL and ortho-MQTL analyses identified genomic regions controlling rice yield, yield-related traits and root architecture under water deficit conditions. Scientific Reports, 2021, 11, 6942.	1.6	41
31	Integrating cereal genomics to support innovation in the Triticeae. Functional and Integrative Genomics, 2012, 12, 573-583.	1.4	39
32	Characterization of Glutathione S-Transferase Isoforms in Three Maize Inbred Lines Exhibiting Differential Sensitivity to Alachlor. Plant Physiology, 1996, 112, 1595-1600.	2.3	36
33	Expression profiling of genes involved in the formation of aroma in two peach genotypes. Plant Biology, 2013, 15, 443-451.	1.8	33
34	Genetics of barley tiller and leaf development. Journal of Integrative Plant Biology, 2019, 61, 226-256.	4.1	33
35	Genetics of Barley Hooded Suppression. Genetics, 2004, 167, 439-448.	1.2	28
36	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). Tree Genetics and Genomes, 2016, 12, 1.	0.6	28

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37	PocketPlant3D: Analysing canopy structure using a smartphone. <i>Biosystems Engineering</i> , 2017, 164, 1-12.	1.9	27
38	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.	0.8	25
39	Isolation, promoter analysis and expression profile of Dreb2 in response to drought stress in wheat ancestors. <i>Gene</i> , 2014, 549, 24-32.	1.0	24
40	Integrative genomics approaches validate PpYUC11-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.	1.6	21
41	Mutations in orthologous PETALOSA TOE-type genes cause a dominant double-flower phenotype in phylogenetically distant eudicots. <i>Journal of Experimental Botany</i> , 2020, 71, 2585-2595.	2.4	20
42	Genetic dissection of Sharka disease tolerance in peach ( <i>P. persica</i> L. Batsch). <i>BMC Plant Biology</i> , 2017, 17, 192.	1.6	19
43	High-density multi-population consensus genetic linkage map for peach. <i>PLoS ONE</i> , 2018, 13, e0207724.	1.1	19
44	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.	1.7	17
45	Detection of QTLs controlling pollen germination and growth in maize. <i>Heredity</i> , 1994, 72, 332-335.	1.2	15
46	Molecular analysis and mapping of two genes encoding maize glutathione S-transferases (GST I and Tj ETQq0 0 0 rgBT /Overlock 10 Tf	2.4	14
47	Gene and Genome Changes During Domestication of Cereals. , 2004, , 165-198.		14
48	Patterns and symmetries in leaf development. <i>Seminars in Cell and Developmental Biology</i> , 2001, 12, 363-372.	2.3	13
49	Genetic dissection of heading date and yield under Mediterranean dry climate in barley ( <i>Hordeum</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 12	0.6	12
50	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.	1.5	12
51	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.	2.3	12
52	Alachlor Regulation of Maize Glutathione S-Transferase Genes. <i>Pesticide Biochemistry and Physiology</i> , 1998, 60, 205-211.	1.6	11
53	Protein profiling and tps23 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.	1.6	9
54	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.	0.6	9

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55	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.	2.9	8
56	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.	1.5	7
57	Segmental duplications are hot spots of copy number variants affecting barley gene content. <i>Plant Journal</i> , 2020, 103, 1073-1088.	2.8	6
58	The barley mutant happy under the sun 1 ( <i>hus1</i> ): An additional contribution to pale green crops. <i>Environmental and Experimental Botany</i> , 2022, 196, 104795.	2.0	6
59	Discovering peach QTLs with multiple progeny analysis. <i>Acta Horticulturae</i> , 2017, , 405-410.	0.1	5
60	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.	0.6	3
61	Shoot and Inflorescence Architecture. <i>Biotechnology in Agriculture and Forestry</i> , 2014, , 55-80.	0.2	3
62	FruitBreedomics phenotypes and genotypes database and tools. <i>Acta Horticulturae</i> , 2017, , 429-434.	0.1	2
63	Detection of natural and induced mutations from next generation sequencing data in sweet orange bud sports. <i>Acta Horticulturae</i> , 2019, , 119-124.	0.1	2
64	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, .	1.6	2
65	Exploring and exploiting phenotypic and genetic diversity in peach: identification of major genes and QTLs by GWAS. <i>Acta Horticulturae</i> , 2017, , 419-424.	0.1	1
66	GENETIC VARIABILITY AND POPULATION STRUCTURE OF PEACH ACCESSIONS FROM MAS.PES GERMPLOSM BANK. <i>Acta Horticulturae</i> , 2015, , 233-239.	0.1	0
67	Genetics of Whole Plant Morphology and Architecture. <i>Compendium of Plant Genomes</i> , 2018, , 209-231.	0.3	0
68	Identification of novel plant architecture mutants in barley. <i>Cereal Research Communications</i> , 0, , 1.	0.8	0