

Laura Rossini

List of Publications by Year in descending order

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Version: 2024-02-01

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 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 |
| 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. | 2.8 | 342 |
| 3 | Tracing the ancestry of modern bread wheats. <i>Nature Genetics</i> , 2019, 51, 905-911. | 21.4 | 230 |
| 4 | The Maize Golden2 Gene Defines a Novel Class of Transcriptional Regulators in Plants. <i>Plant Cell</i> , 2001, 13, 1231-1244. | 6.6 | 200 |
| 5 | GOLDEN 2: A Novel Transcriptional Regulator of Cellular Differentiation in the Maize Leaf. <i>Plant Cell</i> , 1998, 10, 925-936. | 6.6 | 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. | 1.6 | 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. | 4.8 | 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. | 3.6 | 113 |
| 9 | The Genetic Basis of Composite Spike Form in Barley and "Miracle-Wheat". <i>Genetics</i> , 2015, 201, 155-165. | 2.9 | 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. | 1.6 | 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. | 3.5 | 100 |
| 12 | Whole-Genome Analysis of Diversity and SNP-Major Gene Association in Peach Germplasm. <i>PLoS ONE</i> , 2015, 10, e0136803. | 2.5 | 98 |
| 13 | An integrated approach for increasing breeding efficiency in apple and peach in Europe. <i>Horticulture Research</i> , 2018, 5, 11. | 6.3 | 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. | 3.6 | 93 |
| 15 | A Unique Mutation in a MYB Gene Cosegregates with the Nectarine Phenotype in Peach. <i>PLoS ONE</i> , 2014, 9, e90574. | 2.5 | 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. | 4.8 | 85 |
| 17 | Photoperiod-H1 (Ppd-H1) Controls Leaf Size. <i>Plant Physiology</i> , 2016, 172, 405-415. | 4.8 | 77 |
| 18 | Genetics of Tillering in Rice and Barley. <i>Plant Genome</i> , 2014, 7, plantgenome2013.10.0032. | 2.8 | 75 |

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|----|--|-----|-----------|
| 19 | Integrated QTL detection for key breeding traits in multiple peach progenies. BMC Genomics, 2017, 18, 404. | 2.8 | 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 Tt | 1.6 | 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. | 3.6 | 54 |
| 22 | Saturating the <i>Prunus</i> (stone fruits) genome with candidate genes for fruit quality. Molecular Breeding, 2011, 28, 667-682. | 2.1 | 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. | 4.8 | 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. | 5.7 | 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. | 2.1 | 48 |
| 26 | Developmental expression of glutathione-S-transferase in maize and its possible connection with herbicide tolerance. Euphytica, 1993, 67, 221-230. | 1.2 | 45 |
| 27 | Genome-enabled predictions for fruit weight and quality from repeated records in European peach progenies. BMC Genomics, 2017, 18, 432. | 2.8 | 44 |
| 28 | Deletion of the miR172 target site in a \langle scp>TOE</scp> \hat{a} type gene is a strong candidate variant for dominant double \hat{a} flower trait in Rosaceae. Plant Journal, 2018, 96, 358-371. | 5.7 | 43 |
| 29 | Candidate genes for barley mutants involved in plant architecture: an in silico approach. Theoretical and Applied Genetics, 2006, 112, 1073-1085. | 3.6 | 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. | 3.3 | 41 |
| 31 | Integrating cereal genomics to support innovation in the Triticeae. Functional and Integrative Genomics, 2012, 12, 573-583. | 3.5 | 39 |
| 32 | Characterization of Glutathione S-Transferase Isoforms in Three Maize Inbred Lines Exhibiting Differential Sensitivity to Alachlor. Plant Physiology, 1996, 112, 1595-1600. | 4.8 | 36 |
| 33 | Expression profiling of genes involved in the formation of aroma in two peach genotypes. Plant Biology, 2013, 15, 443-451. | 3.8 | 33 |
| 34 | Genetics of barley tiller and leaf development. Journal of Integrative Plant Biology, 2019, 61, 226-256. | 8.5 | 33 |
| 35 | Genetics of Barley Hooded Suppression. Genetics, 2004, 167, 439-448. | 2.9 | 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. | 1.6 | 28 |

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|----|--|-----|-----------|
| 37 | PocketPlant3D: Analysing canopy structure using a smartphone. <i>Biosystems Engineering</i> , 2017, 164, 1-12. | 4.3 | 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. | 1.8 | 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. | 2.2 | 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. | 3.6 | 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. | 4.8 | 20 |
| 42 | 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 |
| 43 | High-density multi-population consensus genetic linkage map for peach. <i>PLoS ONE</i> , 2018, 13, e0207724. | 2.5 | 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. | 3.6 | 17 |
| 45 | Detection of QTLs controlling pollen germination and growth in maize. <i>Heredity</i> , 1994, 72, 332-335. | 2.6 | 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. | 5.0 | 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 Tf | 1.2 | 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. | 3.1 | 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. | 4.8 | 12 |
| 52 | Alachlor Regulation of Maize Glutathione S-Transferase Genes. <i>Pesticide Biochemistry and Physiology</i> , 1998, 60, 205-211. | 3.6 | 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. | 3.5 | 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. | 1.6 | 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. | 6.3 | 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. | 3.1 | 7 |
| 57 | Segmental duplications are hot spots of copy number variants affecting barley gene content. <i>Plant Journal</i> , 2020, 103, 1073-1088. | 5.7 | 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. | 4.2 | 6 |
| 59 | Discovering peach QTLs with multiple progeny analysis. <i>Acta Horticulturae</i> , 2017, , 405-410. | 0.2 | 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. | 1.6 | 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. | 0.2 | 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. | 0.2 | 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, . | 3.6 | 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. | 0.2 | 1 |
| 66 | GENETIC VARIABILITY AND POPULATION STRUCTURE OF PEACH ACCESSIONS FROM MAS.PES GERMPLOSM BANK. <i>Acta Horticulturae</i> , 2015, , 233-239. | 0.2 | 0 |
| 67 | Genetics of Whole Plant Morphology and Architecture. <i>Compendium of Plant Genomes</i> , 2018, , 209-231. | 0.5 | 0 |
| 68 | Identification of novel plant architecture mutants in barley. <i>Cereal Research Communications</i> , 0, , 1. | 1.6 | 0 |