

Genomic analyses provide insights into the history of t

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Identification of chilling stress-responsive tomato microRNAs and their target genes by high-throughput sequencing and degradome analysis. <i>BMC Genomics</i> , 2014, 15, 1130.	1.2	93
2	Diversity in global gene expression and morphology across a watercress (<i>Nasturtium officinale</i> R. Br.) germplasm collection: first steps to breeding. <i>Horticulture Research</i> , 2015, 2, 15029.	2.9	14
3	A Novel Route Controlling Begomovirus Resistance by the Messenger RNA Surveillance Factor Pelota. <i>PLoS Genetics</i> , 2015, 11, e1005538.	1.5	127
4	Association Mapping for Fruit, Plant and Leaf Morphology Traits in Eggplant. <i>PLoS ONE</i> , 2015, 10, e0135200.	1.1	57
5	Exploring a Tomato Landraces Collection for Fruit-Related Traits by the Aid of a High-Throughput Genomic Platform. <i>PLoS ONE</i> , 2015, 10, e0137139.	1.1	91
6	Successful Wide Hybridization and Introgression Breeding in a Diverse Set of Common Peppers (<i>Capsicum annuum</i>) Using Different Cultivated <i>AjÃ</i> -(<i>C. baccatum</i>) Accessions as Donor Parents. <i>PLoS ONE</i> , 2015, 10, e0144142.	1.1	40
7	Crop improvement using life cycle datasets acquired under field conditions. <i>Frontiers in Plant Science</i> , 2015, 6, 740.	1.7	16
8	Genomic variation in tomato, from wild ancestors to contemporary breeding accessions. <i>BMC Genomics</i> , 2015, 16, 257.	1.2	190
9	A DEMETER-like DNA demethylase governs tomato fruit ripening. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 10804-10809.	3.3	256
10	Assessing the genetic variation in cultivated tomatoes (<i>Solanum lycopersicum</i> L.) using genome-wide single nucleotide polymorphisms. <i>Horticulture Environment and Biotechnology</i> , 2015, 56, 800-810.	0.7	7
11	Insight into flower diversity in <i>Solanum lycopersicum</i> and <i>Solanum chilense</i> using comparative biological approaches. <i>Canadian Journal of Plant Science</i> , 2015, 95, 467-478.	0.3	3
12	Testing the SI Ã— SC rule: Pollenâ€pistil interactions in interspecific crosses between members of the tomato clade (<i>Solanum</i> section <i>Lycopersicon</i> , Solanaceae). <i>American Journal of Botany</i> , 2015, 102, 302-311.	0.8	65
13	Network-assisted crop systems genetics: network inference and integrative analysis. <i>Current Opinion in Plant Biology</i> , 2015, 24, 61-70.	3.5	40
14	Patterns of genomic changes with crop domestication and breeding. <i>Current Opinion in Plant Biology</i> , 2015, 24, 47-53.	3.5	83
15	Genome scans reveal candidate domestication and improvement genes in cultivated sunflower, as well as postâ€domestication introgression with wild relatives. <i>New Phytologist</i> , 2015, 206, 830-838.	3.5	79
16	Progress, challenges and the future of crop genomes. <i>Current Opinion in Plant Biology</i> , 2015, 24, 71-81.	3.5	197
17	Transposon Insertions, Structural Variations, and SNPs Contribute to the Evolution of the Melon Genome. <i>Molecular Biology and Evolution</i> , 2015, 32, 2760-2774.	3.5	80
18	Morphological and molecular characterization of local varieties, modern cultivars and wild relatives of an emerging vegetable crop, the pepino (<i>Solanum muricatum</i>), provides insight into its diversity, relationships and breeding history. <i>Euphytica</i> , 2015, 206, 301-318.	0.6	14

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19	Sequencing consolidates molecular markers with plant breeding practice. <i>Theoretical and Applied Genetics</i> , 2015, 128, 779-795.	1.8	96
20	Rapid and reliable identification of tomato fruit weight and locule number loci by QTL-seq. <i>Theoretical and Applied Genetics</i> , 2015, 128, 1329-1342.	1.8	153
21	Making the Bread: Insights from Newly Synthesized Allohexaploid Wheat. <i>Molecular Plant</i> , 2015, 8, 847-859.	3.9	59
22	Metabolic analyses of interspecific tomato recombinant inbred lines for fruit quality improvement. <i>Metabolomics</i> , 2015, 11, 1416-1431.	1.4	35
23	Genomic breeding for food, environment and livelihoods. <i>Food Security</i> , 2015, 7, 375-382.	2.4	23
24	Adaptive Horizontal Gene Transfers between Multiple Cheese-Associated Fungi. <i>Current Biology</i> , 2015, 25, 2562-2569.	1.8	110
25	Breeding Self-Fertilizing Plants: From Inbred to Hybrid Cultivars. , 2015, , 141-171.		0
26	Integrative Approaches to Enhance Understanding of Plant Metabolic Pathway Structure and Regulation. <i>Plant Physiology</i> , 2015, 169, 1499-1511.	2.3	40
27	A Rare SNP Identified a TCP Transcription Factor Essential for Tendril Development in Cucumber. <i>Molecular Plant</i> , 2015, 8, 1795-1808.	3.9	58
28	Wide-genome QTL mapping of fruit quality traits in a tomato RIL population derived from the wild-relative species <i>Solanum pimpinellifolium</i> L. <i>Theoretical and Applied Genetics</i> , 2015, 128, 2019-2035.	1.8	63
29	Metabolomics-Inspired Insight into Developmental, Environmental and Genetic Aspects of Tomato Fruit Chemical Composition and Quality: Fig. 1. <i>Plant and Cell Physiology</i> , 2015, 56, 1681-1696.	1.5	66
30	Population Genomics for Understanding Adaptation in Wild Plant Species. <i>Annual Review of Genetics</i> , 2015, 49, 315-338.	3.2	94
31	Candidate gene selection and detailed morphological evaluations of <i>fs8.1</i> , a quantitative trait locus controlling tomato fruit shape. <i>Journal of Experimental Botany</i> , 2015, 66, 6471-6482.	2.4	32
32	Resequencing at ~40-Fold Depth of the Parental Genomes of a <i>Solanum lycopersicum</i> × <i>S. pimpinellifolium</i> Recombinant Inbred Line Population and Characterization of Frame-Shift Indels That Are Highly Likely to Perturb Protein Function. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 971-981.	0.8	18
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34	Exploring Genetic Diversity in Plants Using High-Throughput Sequencing Techniques. <i>Current Genomics</i> , 2016, 17, 358-367.	0.7	51
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36	Differentiation of Tomato Seedlings with Different Mechanical Damage Severities Using E-Nose and GC-MS. <i>Transactions of the ASABE</i> , 2016, 59, 1069-1078.	1.1	6

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37	DNA Sequence Evolution and Rare Homoeologous Conversion in Tetraploid Cotton. <i>PLoS Genetics</i> , 2016, 12, e1006012.	1.5	27
38	QTL Location and Epistatic Effect Analysis of 100-Seed Weight Using Wild Soybean (<i>Glycine soja</i> Sieb.) Tj ETQq1 1 0,784314,rgBT /Ow	1.1	73
39	Tomato Fruits Show Wide Phenomic Diversity but Fruit Developmental Genes Show Low Genomic Diversity. <i>PLoS ONE</i> , 2016, 11, e0152907.	1.1	33
40	Metabolite Profiling of Italian Tomato Landraces with Different Fruit Types. <i>Frontiers in Plant Science</i> , 2016, 7, 664.	1.7	65
41	Autofluorescence as a Signal to Sort Developing Glandular Trichomes by Flow Cytometry. <i>Frontiers in Plant Science</i> , 2016, 7, 949.	1.7	29
42	Identification of Sesame Genomic Variations from Genome Comparison of Landrace and Variety. <i>Frontiers in Plant Science</i> , 2016, 7, 1169.	1.7	48
43	Exploring New Alleles Involved in Tomato Fruit Quality in an Introgression Line Library of <i>Solanum pimpinellifolium</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 1172.	1.7	50
44	Association Mapping of Main Tomato Fruit Sugars and Organic Acids. <i>Frontiers in Plant Science</i> , 2016, 7, 1286.	1.7	41
45	Identification of Loci Affecting Accumulation of Secondary Metabolites in Tomato Fruit of a <i>Solanum lycopersicum</i> Å— <i>Solanum chmielewskii</i> Introgression Line Population. <i>Frontiers in Plant Science</i> , 2016, 7, 1428.	1.7	45
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47	Sequence variation in <i>SIMYB12</i> is associated with fruit peel color in pink tomato cultivars. <i>Horticulture Environment and Biotechnology</i> , 2016, 57, 274-279.	0.7	10
48	Genome-wide Diversity and Association Mapping for Capsaicinoids and Fruit Weight in <i>Capsicum annuum</i> L. <i>Scientific Reports</i> , 2016, 6, 38081.	1.6	60
49	Gene Mapping in Tomato. <i>Compendium of Plant Genomes</i> , 2016, , 23-37.	0.3	7
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53	A simulation-based breeding design that uses whole-genome prediction in tomato. <i>Scientific Reports</i> , 2016, 6, 19454.	1.6	54
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56	Dissecting stelar responses to self-pollination in wild tomato self-compatible and self-incompatible species using comparative proteomics. <i>Plant Physiology and Biochemistry</i> , 2016, 106, 177-186.	2.8	6
57	Phenotypic and molecular diversity in a collection of "Pomodoro di Sorrento" Italian tomato landrace. <i>Scientia Horticulturae</i> , 2016, 203, 143-151.	1.7	16
58	Characterization of a New Pink-Fruited Tomato Mutant Results in the Identification of a Null Allele of the SIMYB12 Transcription Factor. <i>Plant Physiology</i> , 2016, 171, 1821-1836.	2.3	47
59	Fine mapping of the dialytic gene that controls multicellular trichome formation and stamen development in tomato. <i>Theoretical and Applied Genetics</i> , 2016, 129, 1531-1539.	1.8	14
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62	Diverse responses of wild and cultivated tomato to BABA, oligandrin and <i>Oidium neolycopersici</i> infection. <i>Annals of Botany</i> , 2017, 119, mcw188.	1.4	11
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65	Cisgenesis and genome editing: combining concepts and efforts for a smarter use of genetic resources in crop breeding. <i>Plant Breeding</i> , 2016, 135, 139-147.	1.0	80
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70	Spatiotemporal transcriptome provides insights into early fruit development of tomato (<i>Solanum</i>) Tj ETQq1 1 0.784314 rgBT./Overlook	1.6	39
71	A nuclear-replicating viroid antagonizes infectivity and accumulation of a geminivirus by upregulating methylation-related genes and inducing hypermethylation of viral DNA. <i>Scientific Reports</i> , 2016, 6, 35101.	1.6	29
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74	Global investigation of the co-evolution of <i>MIRNA</i> genes and microRNA targets during soybean domestication. <i>Plant Journal</i> , 2016, 85, 396-409.	2.8	36
75	Genome-wide association study using whole-genome sequencing rapidly identifies new genes influencing agronomic traits in rice. <i>Nature Genetics</i> , 2016, 48, 927-934.	9.4	600
76	Identification of an SNP variation of elite tomato (<i>Solanum lycopersicum</i> L.) lines using genome resequencing analysis. <i>Horticulture Environment and Biotechnology</i> , 2016, 57, 173-181.	0.7	4
77	Genomic signatures of domestication on neurogenetic genes in <i>Drosophila melanogaster</i> . <i>BMC Evolutionary Biology</i> , 2016, 16, 6.	3.2	23
78	1,135 Genomes Reveal the Global Pattern of Polymorphism in <i>Arabidopsis thaliana</i> . <i>Cell</i> , 2016, 166, 481-491.	13.5	1,107
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80	Phenotypic plasticity and its genetic regulation for yield, nitrogen fixation and $\delta^{13}C$ in chickpea crops under varying water regimes. <i>Journal of Experimental Botany</i> , 2016, 67, 4339-4351.	2.4	50
81	The completed eight chloroplast genomes of tomato from <i>Solanum</i> genus. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 4155-4157.	0.7	20
82	Genomics-based strategies for the use of natural variation in the improvement of crop metabolism. <i>Plant Science</i> , 2016, 242, 47-64.	1.7	60
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87	<i>Gr</i> and <i>hp-1</i> tomato mutants unveil unprecedented interactions between arbuscular mycorrhizal symbiosis and fruit ripening. <i>Planta</i> , 2016, 244, 155-165.	1.6	13
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89	Cultivated tomato clock runs slow. <i>Nature Genetics</i> , 2016, 48, 8-9.	9.4	3
90	The Omics Revolution in Agricultural Research. <i>Journal of Agricultural and Food Chemistry</i> , 2016, 64, 36-44.	2.4	104

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99	Genotyping-by-sequencing of pear (<i>Pyrus</i> spp.) accessions unravels novel patterns of genetic diversity and selection footprints. <i>Horticulture Research</i> , 2017, 4, 17015.	2.9	56
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104	Bypassing Negative Epistasis on Yield in Tomato Imposed by a Domestication Gene. <i>Cell</i> , 2017, 169, 1142-1155.e12.	13.5	286
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108	Past and Future Use of Wild Relatives in Crop Breeding. <i>Crop Science</i> , 2017, 57, 1070-1082.	0.8	446

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110	Genome-wide Association Studies in Maize: Praise and Stargaze. <i>Molecular Plant</i> , 2017, 10, 359-374.	3.9	334
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113	Population Genomics in Wild Tomatoes—The Interplay of Divergence and Admixture. <i>Genome Biology and Evolution</i> , 2017, 9, 3023-3038.	1.1	33
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117	The RNA Editing Factor SLORRM4 Is Required for Normal Fruit Ripening in Tomato. <i>Plant Physiology</i> , 2017, 175, 1690-1702.	2.3	78
118	Genome-wide association analysis of free glutamate content, a key factor conferring umami taste in the bottle gourd [<i>Lagenaria siceraria</i> (Mol.) Standl.]. <i>Scientia Horticulturae</i> , 2017, 225, 795-801.	1.7	14
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120	The Genetics of Plant Metabolism. <i>Annual Review of Genetics</i> , 2017, 51, 287-310.	3.2	118
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134	Association and Genetic Identification of Loci for Four Fruit Traits in Tomato Using InDel Markers. <i>Frontiers in Plant Science</i> , 2017, 8, 1269.	1.7	23
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136	Gene editing in tomatoes. <i>Emerging Topics in Life Sciences</i> , 2017, 1, 183-191.	1.1	2
137	Molecular Insights Reveal Psy1, SGR, and SIMYB12 Genes are Associated with Diverse Fruit Color Pigments in Tomato (<i>Solanum lycopersicum</i> L.). <i>Molecules</i> , 2017, 22, 2180.	1.7	21
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140	Review on Genetics and Breeding of Tomato (<i>Lycopersicon esculentum</i> Mill). <i>Advances in Crop Science and Technology</i> , 2017, 05, .	0.4	19
141	The antioxidant properties of plant flavonoids: their exploitation by molecular plant breeding. <i>Phytochemistry Reviews</i> , 2018, 17, 611-625.	3.1	91
142	Whole-genome re-sequencing of two Italian tomato landraces reveals sequence variations in genes associated with stress tolerance, fruit quality and long shelf-life traits. <i>DNA Research</i> , 2018, 25, 149-160.	1.5	68
143	Tomato quality as influenced by preharvest factors. <i>Scientia Horticulturae</i> , 2018, 233, 264-276.	1.7	97
144	Natural Variation Underlies Differences in ETHYLENE RESPONSE FACTOR17 Activity in Fruit Peel Degreening. <i>Plant Physiology</i> , 2018, 176, 2292-2304.	2.3	47
145	Genomic Analyses Yield Markers for Identifying Agronomically Important Genes in Potato. <i>Molecular Plant</i> , 2018, 11, 473-484.	3.9	73

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147	Efficient genome-wide genotyping strategies and data integration in crop plants. Theoretical and Applied Genetics, 2018, 131, 499-511.	1.8	62
148	Genetic mapping reveals a candidate gene (ClFS1) for fruit shape in watermelon (<i>Citrullus lanatus</i> L.). Theoretical and Applied Genetics, 2018, 131, 947-958.	1.8	94
149	Silencing <i>GRAS2</i> reduces fruit weight in tomato. Journal of Integrative Plant Biology, 2018, 60, 498-513.	4.1	29
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