

# James J Giovannoni

## List of Publications by Year in descending order

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Version: 2024-02-01

141  
papers

22,924  
citations

11651

70  
h-index

10158

140  
g-index

160  
all docs

160  
docs citations

160  
times ranked

15964  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic Regulation of Fruit Development and Ripening. <i>Plant Cell</i> , 2004, 16, S170-S180.	6.6	1,152
2	A naturally occurring epigenetic mutation in a gene encoding an SBP-box transcription factor inhibits tomato fruit ripening. <i>Nature Genetics</i> , 2006, 38, 948-952.	21.4	1,076
3	Genome sequence of the hot pepper provides insights into the evolution of pungency in <i>Capsicum</i> species. <i>Nature Genetics</i> , 2014, 46, 270-278.	21.4	867
4	Genetics and Control of Tomato Fruit Ripening and Quality Attributes. <i>Annual Review of Genetics</i> , 2011, 45, 41-59.	7.6	855
5	Genomic analyses provide insights into the history of tomato breeding. <i>Nature Genetics</i> , 2014, 46, 1220-1226.	21.4	801
6	iTAK: A Program for Genome-wide Prediction and Classification of Plant Transcription Factors, Transcriptional Regulators, and Protein Kinases. <i>Molecular Plant</i> , 2016, 9, 1667-1670.	8.3	735
7	The draft genome of watermelon ( <i>Citrullus lanatus</i> ) and resequencing of 20 diverse accessions. <i>Nature Genetics</i> , 2013, 45, 51-58.	21.4	731
8	Single-base resolution methylomes of tomato fruit development reveal epigenome modifications associated with ripening. <i>Nature Biotechnology</i> , 2013, 31, 154-159.	17.5	693
9	Transcriptome and Selected Metabolite Analyses Reveal Multiple Points of Ethylene Control during Tomato Fruit Development. <i>Plant Cell</i> , 2005, 17, 2954-2965.	6.6	474
10	Ethylene and Fruit Ripening. <i>Journal of Plant Growth Regulation</i> , 2007, 26, 143-159.	5.1	464
11	Fruit ripening mutants yield insights into ripening control. <i>Current Opinion in Plant Biology</i> , 2007, 10, 283-289.	7.1	463
12	The tomato pan-genome uncovers new genes and a rare allele regulating fruit flavor. <i>Nature Genetics</i> , 2019, 51, 1044-1051.	21.4	441
13	Fleshy Fruit Expansion and Ripening Are Regulated by the Tomato <i>SHATTERPROOF</i> Gene <i>TAGL1</i> . <i>Plant Cell</i> , 2009, 21, 3041-3062.	6.6	415
14	The genome of the stress-tolerant wild tomato species <i>Solanum pennellii</i> . <i>Nature Genetics</i> , 2014, 46, 1034-1038.	21.4	391
15	<i>Uniform ripening</i> Encodes a <i>Golden 2-like</i> Transcription Factor Regulating Tomato Fruit Chloroplast Development. <i>Science</i> , 2012, 336, 1711-1715.	12.6	384
16	High-Throughput Illumina Strand-Specific RNA Sequencing Library Preparation. <i>Cold Spring Harbor Protocols</i> , 2011, 2011, pdb.prot5652.	0.3	382
17	Isolation of molecular markers from specific chromosomal intervals using DNA pools from existing mapping populations. <i>Nucleic Acids Research</i> , 1991, 19, 6553-6568.	14.5	381
18	The Tomato MADS-Box Transcription Factor RIPENING INHIBITOR Interacts with Promoters Involved in Numerous Ripening Processes in a COLORLESS NONRIPENING-Dependent Manner. <i>Plant Physiology</i> , 2011, 157, 1568-1579.	4.8	375

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19	A tomato ( <i>Solanum lycopersicum</i> ) APETALA2/ERF gene, SlAP2a, is a negative regulator of fruit ripening. <i>Plant Journal</i> , 2010, 64, 936-947.	5.7	353
20	The Epigenome and Transcriptional Dynamics of Fruit Ripening. <i>Annual Review of Plant Biology</i> , 2017, 68, 61-84.	18.7	335
21	Systems Biology of Tomato Fruit Development: Combined Transcript, Protein, and Metabolite Analysis of Tomato Transcription Factor ( <i>nor</i> , <i>rin</i> ) and Ethylene Receptor ( <i>Nr</i> ) Mutants Reveals Novel Regulatory Interactions. <i>Plant Physiology</i> , 2011, 157, 405-425.	4.8	303
22	Tackling the plant proteome: practical approaches, hurdles and experimental tools. <i>Plant Journal</i> , 2004, 39, 715-733.	5.7	301
23	Molecular and genetic regulation of fruit ripening. <i>Plant Molecular Biology</i> , 2013, 82, 575-591.	3.9	300
24	Deductions about the Number, Organization, and Evolution of Genes in the Tomato Genome Based on Analysis of a Large Expressed Sequence Tag Collection and Selective Genomic Sequencing. <i>Plant Cell</i> , 2002, 14, 1441-1456.	6.6	283
25	Role of $\beta$ -Oxidation in Jasmonate Biosynthesis and Systemic Wound Signaling in Tomato. <i>Plant Cell</i> , 2005, 17, 971-986.	6.6	280
26	Combined transcriptome, genetic diversity and metabolite profiling in tomato fruit reveals that the ethylene response factor <i>SlERF6</i> plays an important role in ripening and carotenoid accumulation. <i>Plant Journal</i> , 2012, 70, 191-204.	5.7	268
27	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.	7.1	256
28	Genome encode analyses reveal the basis of convergent evolution of fleshy fruit ripening. <i>Nature Plants</i> , 2018, 4, 784-791.	9.3	256
29	High-resolution spatiotemporal transcriptome mapping of tomato fruit development and ripening. <i>Nature Communications</i> , 2018, 9, 364.	12.8	255
30	Branched-chain and aromatic amino acid catabolism into aroma volatiles in <i>Cucumis melo</i> L. fruit. <i>Journal of Experimental Botany</i> , 2010, 61, 1111-1123.	4.8	247
31	Amino Acid Substitutions in Homologs of the STAY-GREEN Protein Are Responsible for the <i>green-flesh</i> and <i>chlorophyll retainer</i> Mutations of Tomato and Pepper. <i>Plant Physiology</i> , 2008, 147, 179-187.	4.8	223
32	Comprehensive EST analysis of tomato and comparative genomics of fruit ripening. <i>Plant Journal</i> , 2004, 40, 47-59.	5.7	210
33	Chilling-induced tomato flavor loss is associated with altered volatile synthesis and transient changes in DNA methylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 12580-12585.	7.1	208
34	An InDel in the Promoter of <i>Al-ACTIVATED MALATE TRANSPORTER9</i> Selected during Tomato Domestication Determines Fruit Malate Contents and Aluminum Tolerance. <i>Plant Cell</i> , 2017, 29, 2249-2268.	6.6	207
35	From The Cover: Ripening in the tomato Green-ripe mutant is inhibited by ectopic expression of a protein that disrupts ethylene signaling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 7923-7928.	7.1	205
36	Molecular and Genetic Characterization of a Novel Pleiotropic Tomato-Ripening Mutant1. <i>Plant Physiology</i> , 1999, 120, 383-390.	4.8	202

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37	Tissue- and Cell-Type Specific Transcriptome Profiling of Expanding Tomato Fruit Provides Insights into Metabolic and Regulatory Specialization and Cuticle Formation. <i>Plant Cell</i> , 2011, 23, 3893-3910.	6.6	193
38	Tomato <i>GOLDEN2-LIKE</i> Transcription Factors Reveal Molecular Gradients That Function during Fruit Development and Ripening. <i>Plant Cell</i> , 2014, 26, 585-601.	6.6	193
39	Molecular biology of ethylene during tomato fruit development and maturation. <i>Plant Science</i> , 2008, 175, 106-113.	3.6	190
40	Phytohormones in fruit development and maturation. <i>Plant Journal</i> , 2021, 105, 446-458.	5.7	189
41	Cucurbit Genomics Database (CuGenDB): a central portal for comparative and functional genomics of cucurbit crops. <i>Nucleic Acids Research</i> , 2019, 47, D1128-D1136.	14.5	177
42	A <i>SEPALLATA</i> gene is involved in the development and ripening of strawberry ( <i>Fragaria</i> — <i>ananassa</i> Duch.) fruit, a non-climacteric tissue*. <i>Journal of Experimental Botany</i> , 2011, 62, 1179-1188.	4.8	174
43	Integrative Comparative Analyses of Transcript and Metabolite Profiles from Pepper and Tomato Ripening and Development Stages Uncovers Species-Specific Patterns of Network Regulatory Behavior. <i>Plant Physiology</i> , 2012, 159, 1713-1729.	4.8	174
44	Integrative Transcript and Metabolite Analysis of Nutritionally Enhanced <i>DE-ETIOLATED1</i> Downregulated Tomato Fruit. <i>Plant Cell</i> , 2010, 22, 1190-1215.	6.6	160
45	Plant MetGenMAP: An Integrative Analysis System for Plant Systems Biology. <i>Plant Physiology</i> , 2009, 151, 1758-1768.	4.8	156
46	A <i>STAYGREEN</i> protein <i>S</i> regulates lycopene and $\beta$ -carotene accumulation by interacting directly with <i>S</i> <i>PSY</i> 1 during ripening processes in tomato. <i>New Phytologist</i> , 2013, 198, 442-452.	7.3	149
47	<i>LeCTR1</i> , a Tomato <i>CTR1</i> -Like Gene, Demonstrates Ethylene Signaling Ability in Arabidopsis and Novel Expression Patterns in Tomato. <i>Plant Physiology</i> , 2002, 130, 1132-1142.	4.8	143
48	Catalyzing plant science research with RNA-seq. <i>Frontiers in Plant Science</i> , 2013, 4, 66.	3.6	136
49	Deciphering genetic factors that determine melon fruit quality traits using RNA-seq based high-resolution QTL and eQTL mapping. <i>Plant Journal</i> , 2018, 94, 169-191.	5.7	133
50	Involvement of an ethylene response factor in chlorophyll degradation during citrus fruit degreening. <i>Plant Journal</i> , 2016, 86, 403-412.	5.7	130
51	Ethylene suppresses tomato ( <i>Solanum lycopersicum</i> ) fruit set through modification of gibberellin metabolism. <i>Plant Journal</i> , 2015, 83, 237-251.	5.7	128
52	Functional diversification of <i>AGAMOUS</i> lineage genes in regulating tomato flower and fruit development. <i>Journal of Experimental Botany</i> , 2010, 61, 1795-1806.	4.8	123
53	Ethylene Insensitivity Conferred by the Green-ripe and Never-ripe 2 Ripening Mutants of Tomato. <i>Plant Physiology</i> , 2005, 138, 267-275.	4.8	118
54	Combined transcription factor profiling, microarray analysis and metabolite profiling reveals the transcriptional control of metabolic shifts occurring during tomato fruit development. <i>Plant Journal</i> , 2011, 68, 999-1013.	5.7	118

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55	Biology and genetic engineering of fruit maturation for enhanced quality and shelf-life. <i>Current Opinion in Biotechnology</i> , 2009, 20, 197-203.	6.6	116
56	Banana <i>MaMADS</i> Transcription Factors Are Necessary for Fruit Ripening and Molecular Tools to Promote Shelf-Life and Food Security. <i>Plant Physiology</i> , 2016, 171, 380-391.	4.8	114
57	The regulation of MADS-box gene expression during ripening of banana and their regulatory interaction with ethylene. <i>Journal of Experimental Botany</i> , 2010, 61, 1523-1535.	4.8	113
58	Transgenic analysis of tomato endo-beta-1,4-glucanase gene function. Role of cell1 in floral abscission. <i>Plant Journal</i> , 1998, 13, 303-310.	5.7	111
59	Folate synthesis in plants: The p-aminobenzoate branch is initiated by a bifunctional PabA-PabB protein that is targeted to plastids. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 1496-1501.	7.1	111
60	Utilization of tomato microarrays for comparative gene expression analysis in the Solanaceae. <i>Journal of Experimental Botany</i> , 2005, 56, 2885-2895.	4.8	105
61	Sequencing and Comparative Analysis of a Conserved Syntenic Segment in the Solanaceae. <i>Genetics</i> , 2008, 180, 391-408.	2.9	105
62	Identification of Genes in the Phenylalanine Metabolic Pathway by Ectopic Expression of a MYB Transcription Factor in Tomato Fruit. <i>Plant Cell</i> , 2011, 23, 2738-2753.	6.6	97
63	Transcriptomic and Reverse Genetic Analyses of Branched-Chain Fatty Acid and Acyl Sugar Production in <i>Solanum pennellii</i> and <i>Nicotiana benthamiana</i> . <i>Plant Physiology</i> , 2008, 148, 1830-1846.	4.8	95
64	The NAC transcription factor FaRIF controls fruit ripening in strawberry. <i>Plant Cell</i> , 2021, 33, 1574-1593.	6.6	95
65	Polygalacturonase Isozymes and Pectin Depolymerization in Transgenic <i>rin</i> Tomato Fruit. <i>Plant Physiology</i> , 1990, 94, 1882-1886.	4.8	90
66	Folate synthesis in plants: the last step of the p-aminobenzoate branch is catalyzed by a plastidial aminodeoxychorismate lyase. <i>Plant Journal</i> , 2004, 40, 453-461.	5.7	86
67	Genome of <i>Solanum pimpinellifolium</i> provides insights into structural variants during tomato breeding. <i>Nature Communications</i> , 2020, 11, 5817.	12.8	85
68	Ectopic expression of <i>ORANGE</i> promotes carotenoid accumulation and fruit development in tomato. <i>Plant Biotechnology Journal</i> , 2019, 17, 33-49.	8.3	83
69	Fluorescence <i>In Situ</i> Hybridization and Optical Mapping to Correct Scaffold Arrangement in the Tomato Genome. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 1395-1405.	1.8	81
70	Carotenoid profiling of the leaves of selected African eggplant accessions subjected to drought stress. <i>Food Science and Nutrition</i> , 2017, 5, 113-122.	3.4	79
71	Natural genetic variation for expression of a <i>SWEET</i> transporter among wild species of <i>Solanum lycopersicum</i> (tomato) determines the hexose composition of ripening tomato fruit. <i>Plant Journal</i> , 2018, 96, 343-357.	5.7	74
72	The molecular and biochemical basis for varietal variation in sesquiterpene content in melon ( <i>Cucumis melo</i> L.) rinds. <i>Plant Molecular Biology</i> , 2008, 66, 647-661.	3.9	73

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73	A physical map of the highly heterozygous <i>Populus</i> genome: integration with the genome sequence and genetic map and analysis of haplotype variation. <i>Plant Journal</i> , 2007, 50, 1063-1078.	5.7	70
74	Expression of ripening-related genes in cold-stored tomato fruit. <i>Postharvest Biology and Technology</i> , 2011, 61, 1-14.	6.0	68
75	Altered Chloroplast Development and Delayed Fruit Ripening Caused by Mutations in a Zinc Metalloprotease at the <i>lut</i> Locus of Tomato. <i>Plant Physiology</i> , 2012, 159, 1086-1098.	4.8	68
76	More than meets the eye: from carotenoid biosynthesis, to new insights into apocarotenoid signaling. <i>Current Opinion in Plant Biology</i> , 2015, 27, 172-179.	7.1	67
77	Genome-wide association analysis identifies a natural variation in basic helix-loop-helix transcription factor regulating ascorbate biosynthesis via D-mannose/L-galactose pathway in tomato. <i>PLoS Genetics</i> , 2019, 15, e1008149.	3.5	66
78	Sequencing-Based Bin Map Construction of a Tomato Mapping Population, Facilitating High-Resolution Quantitative Trait Loci Detection. <i>Plant Genome</i> , 2019, 12, 180010.	2.8	65
79	The Tomato Expression Atlas. <i>Bioinformatics</i> , 2017, 33, 2397-2398.	4.1	64
80	Enabling proteomic studies with RNA-Seq: The proteome of tomato pollen as a test case. <i>Proteomics</i> , 2012, 12, 761-774.	2.2	62
81	Tomato Multiomics Reveals Consequences of Crop Domestication and Improvement. <i>Cell</i> , 2018, 172, 6-8.	28.9	60
82	Overexpression of the class D MADS-box gene <i>Sl-AGL11</i> impacts fleshy tissue differentiation and structure in tomato fruits. <i>Journal of Experimental Botany</i> , 2017, 68, 4869-4884.	4.8	59
83	<i>AtPDS</i> overexpression in tomato: exposing unique patterns of carotenoid self-regulation and an alternative strategy for the enhancement of fruit carotenoid content. <i>Plant Biotechnology Journal</i> , 2018, 16, 482-494.	8.3	58
84	Expression of a Chimeric Polygalacturonase Gene in Transgenic <i>rin</i> (Ripening Inhibitor) Tomato Fruit Results in Polyuronide Degradation but Not Fruit Softening. <i>Plant Cell</i> , 1989, 1, 53.	6.6	58
85	Genomic Analysis of Wild Tomato Introgressions Determining Metabolism- and Yield-Associated Traits. <i>Plant Physiology</i> , 2010, 152, 1772-1786.	4.8	57
86	<i>SlERF.F12</i> modulates the transition to ripening in tomato fruit by recruiting the co-repressor <i>TOPLESS</i> and histone deacetylases to repress key ripening genes. <i>Plant Cell</i> , 2022, 34, 1250-1272.	6.6	57
87	Molecular genetic analysis of the ripening-inhibitor and non-ripening loci of tomato: A first step in genetic map-based cloning of fruit ripening genes. <i>Molecular Genetics and Genomics</i> , 1995, 248, 195-206.	2.4	55
88	Understanding development and ripening of fruit crops in an omics era. <i>Horticulture Research</i> , 2014, 1, 14034.	6.3	53
89	Cell wall metabolism in cold-stored tomato fruit. <i>Postharvest Biology and Technology</i> , 2010, 57, 106-113.	6.0	52
90	Regulatory control of high levels of carotenoid accumulation in potato tubers. <i>Plant, Cell and Environment</i> , 2011, 34, 1020-1030.	5.7	52

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91	Analysis of the Ethylene Response in the epinastic Mutant of Tomato. <i>Plant Physiology</i> , 2001, 127, 58-66.	4.8	51
92	Conserved Changes in the Dynamics of Metabolic Processes during Fruit Development and Ripening across Species <i>À À À</i> . <i>Plant Physiology</i> , 2014, 164, 55-68.	4.8	50
93	Transcriptomic Analysis of <i>Petunia hybrida</i> in Response to Salt Stress Using High Throughput RNA Sequencing. <i>PLoS ONE</i> , 2014, 9, e94651.	2.5	46
94	Relationships between genome methylation, levels of non-coding RNAs, mRNAs and metabolites in ripening tomato fruit. <i>Plant Journal</i> , 2020, 103, 980-994.	5.7	46
95	Characterization of a major latex protein (MLP) gene down-regulated by ethylene during peach fruitlet abscission. <i>Plant Science</i> , 2002, 163, 265-272.	3.6	44
96	Developmental and Feedforward Control of the Expression of Folate Biosynthesis Genes in Tomato Fruit. <i>Molecular Plant</i> , 2010, 3, 66-77.	8.3	44
97	Fruit carotenoid-deficient mutants in tomato reveal a function of the plastidial isopentenyl diphosphate isomerase ( <i>IDI1</i> ) in carotenoid biosynthesis. <i>Plant Journal</i> , 2016, 88, 82-94.	5.7	44
98	Manipulation of ZDS in tomato exposes carotenoid- and ABA-specific effects on fruit development and ripening. <i>Plant Biotechnology Journal</i> , 2020, 18, 2210-2224.	8.3	44
99	Completing a pathway to plant vitamin C synthesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 9109-9110.	7.1	41
100	Differential metabolism of L-phenylalanine in the formation of aromatic volatiles in melon ( <i>Cucumis</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 T 2.95 41	2.95	41
101	A tomato LATERAL ORGAN BOUNDARIES transcription factor, <i>SILOB1</i> , predominantly regulates cell wall and softening components of ripening. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	41
102	Molecular analysis of softening and ethylene synthesis and signaling pathways in a non-softening apple cultivar, "Honeycrisp"™ and a rapidly softening cultivar, "McIntosh"™. <i>Postharvest Biology and Technology</i> , 2012, 64, 94-103.	6.0	39
103	Genetic and metabolic effects of ripening mutations and vine detachment on tomato fruit quality. <i>Plant Biotechnology Journal</i> , 2020, 18, 106-118.	8.3	39
104	The <i>Ptr1</i> Locus of <i>Solanum lycopersicoides</i> Confers Resistance to Race 1 Strains of <i>Pseudomonas syringae</i> pv. <i>tomato</i> and to <i>Ralstonia pseudosolanacearum</i> by Recognizing the Type III Effectors AvrRpt2 and RipBN. <i>Molecular Plant-Microbe Interactions</i> , 2019, 32, 949-960.	2.6	37
105	Metabolomic analyses to evaluate the effect of drought stress on selected African Eggplant accessions. <i>Journal of the Science of Food and Agriculture</i> , 2018, 98, 205-216.	3.5	36
106	Differential Control of Ethylene Responses by <i>GREEN-RIPE</i> and <i>GREEN-RIPE LIKE1</i> Provides Evidence for Distinct Ethylene Signaling Modules in Tomato <i>À À</i> . <i>Plant Physiology</i> , 2012, 160, 1968-1984.	4.8	35
107	Identification of a <i>Solanum pennellii</i> Chromosome 4 Fruit Flavor and Nutritional Quality-Associated Metabolite QTL. <i>Frontiers in Plant Science</i> , 2016, 7, 1671.	3.6	35
108	Differential Regulation of <i>Salmonella</i> Typhimurium Genes Involved in O-Antigen Capsule Production and Their Role in Persistence Within Tomato Fruit. <i>Molecular Plant-Microbe Interactions</i> , 2013, 26, 793-800.	2.6	33

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109	Differential fruit gene expression in two strawberry cultivars in response to elevated CO <sub>2</sub> during storage revealed by a heterologous fruit microarray approach. <i>Postharvest Biology and Technology</i> , 2009, 51, 131-140.	6.0	32
110	Features of a unique intronless cluster of class I small heat shock protein genes in tandem with box C/D snoRNA genes on chromosome 6 in tomato ( <i>Solanum lycopersicum</i> ). <i>Planta</i> , 2012, 235, 453-471.	3.2	31
111	Transmission modes affect the population structure of potato virus Y in potato. <i>PLoS Pathogens</i> , 2020, 16, e1008608.	4.7	31
112	Metabolomics should be deployed in the identification and characterization of gene-edited crops. <i>Plant Journal</i> , 2020, 102, 897-902.	5.7	30
113	Comparative genomics of muskmelon reveals a potential role for retrotransposons in the modification of gene expression. <i>Communications Biology</i> , 2020, 3, 432.	4.4	29
114	Ectopic expression of miRNA172 in tomato ( <i>Solanum lycopersicum</i> ) reveals novel function in fruit development through regulation of an AP2 transcription factor. <i>BMC Plant Biology</i> , 2020, 20, 283.	3.6	29
115	Breeding new life into plant metabolism. <i>Nature Biotechnology</i> , 2006, 24, 418-419.	17.5	27
116	Modest calcium increase in tomatoes expressing a variant of Arabidopsis cation/H <sup>+</sup> antiporter. <i>Plant Biotechnology Reports</i> , 2010, 4, 15-21.	1.5	25
117	Characterizing the involvement of <i>FaMADS9</i> in the regulation of strawberry fruit receptacle development. <i>Plant Biotechnology Journal</i> , 2020, 18, 929-943.	8.3	25
118	Longitudinal Transcriptomic, Proteomic, and Metabolomic Analysis of <i>Citrus limon</i> Response to Graft Inoculation by <i>Candidatus Liberibacter asiaticus</i> . <i>Journal of Proteome Research</i> , 2020, 19, 2247-2263.	3.7	25
119	A modified procedure for PCR-based differential display and demonstration of use in plants for isolation of genes related to fruit ripening. <i>Plant Molecular Biology Reporter</i> , 1995, 13, 70-81.	1.8	20
120	The tomato HIGH PIGMENT1/DAMAGED DNA BINDING PROTEIN 1 gene contributes to regulation of fruit ripening. <i>Horticulture Research</i> , 2019, 6, 15.	6.3	20
121	Tomato $\beta$ -Glucanase: Expression, Characterization, and Evidence for Heterodimer Formation. <i>Plant Physiology</i> , 2008, 148, 775-785.	4.8	19
122	Application of Genetic Bit Analysis (GBATM) for allelic selection in plant breeding. <i>Molecular Breeding</i> , 1997, 3, 495-502.	2.1	18
123	Tomato fruit as a model for tissue-specific gene silencing in crop plants. <i>Horticulture Research</i> , 2020, 7, 142.	6.3	18
124	Genome-wide association study reveals the genetic architecture of 27 agronomic traits in tomato. <i>Plant Physiology</i> , 2021, 186, 2078-2092.	4.8	18
125	Tissue specificity and differential expression of transcription factors in tomato provide hints of unique regulatory networks during fruit ripening. <i>Plant Signaling and Behavior</i> , 2012, 7, 1639-1647.	2.4	16
126	Plant Viruses Transmitted in Two Different Modes Produce Differing Effects on Small RNA-Mediated Processes in Their Aphid Vector. <i>Phytobiomes Journal</i> , 2019, 3, 71-81.	2.7	16

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127	A <i>Solanum lycopersicoides</i> reference genome facilitates insights into tomato specialized metabolism and immunity. <i>Plant Journal</i> , 2022, 110, 1791-1810.	5.7	16
128	GWAS Based on RNA-Seq SNPs and High-Throughput Phenotyping Combined with Climatic Data Highlights the Reservoir of Valuable Genetic Diversity in Regional Tomato Landraces. <i>Genes</i> , 2020, 11, 1387.	2.4	14
129	Gr and hp-1 tomato mutants unveil unprecedented interactions between arbuscular mycorrhizal symbiosis and fruit ripening. <i>Planta</i> , 2016, 244, 155-165.	3.2	13
130	Determining the Physical Limits of the Brassica S Locus by Recombinational Analysis. <i>Plant Cell</i> , 2000, 12, 23.	6.6	11
131	Harvesting the apple genome. <i>Nature Genetics</i> , 2010, 42, 822-823.	21.4	9
132	A comparative transcriptomics and eQTL approach identifies <i>SlWD40</i> as a tomato fruit ripening regulator. <i>Plant Physiology</i> , 2022, 190, 250-266.	4.8	9
133	Identification of Plastome Variants useful for Cytoplasmic Selection and Cultivar Identification in Onion. <i>Journal of the American Society for Horticultural Science</i> , 1999, 124, 122-127.	1.0	8
134	Rapid and reliable screening of a tomato YAC library exclusively based on PCR. <i>Plant Molecular Biology Reporter</i> , 1996, 14, 58-67.	1.8	6
135	The pineapple <i>AcMADS1</i> promoter confers high level expression in tomato and <i>Arabidopsis</i> flowering and fruiting tissues, but <i>AcMADS1</i> does not complement the tomato <i>LeMADS-RIN (rin)</i> mutant. <i>Plant Molecular Biology</i> , 2014, 86, 395-407.	3.9	6
136	Harnessing epigenome modifications for better crops. <i>Journal of Experimental Botany</i> , 2016, 67, 2535-2537.	4.8	6
137	Ripening activator turned repressor. <i>Nature Plants</i> , 2017, 3, 920-921.	9.3	6
138	Molecular and Genetic Analysis of Tomato Fruit Development and Ripening. <i>Methods in Plant Biochemistry</i> , 1993, 10, 251-285.	0.2	5
139	Genetic Control of Fruit Quality, and Prospects for Nutrient Modification. <i>Hortscience: A Publication of the American Society for Horticultural Science</i> , 2002, 37, 453-456.	1.0	3
140	Rapid isolation of terminal sequences from cloned plant DNA fragments. <i>Plant Molecular Biology Reporter</i> , 1995, 13, 369-376.	1.8	1
141	Laser capture of tomato pericarp tissues for microscale carotenoid analysis by supercritical fluid chromatography. <i>Methods in Enzymology</i> , 2022, , 213-233.	1.0	0