James J Giovannoni

List of Publications by Citations

149 papers	16,101 citations	63 h-index	126 g-index
160 ext. papers	20,271 ext. citations	10 avg, IF	6.74 L-index

#	Paper	IF	Citations
149	Genetic regulation of fruit development and ripening. *Plant Cell*, **2004**, 16 Suppl, S170-80	11.6	904
148	A naturally occurring epigenetic mutation in a gene encoding an SBP-box transcription factor inhibits tomato fruit ripening. *Nature Genetics*, **2006**, 38, 948-52	36.3	861
147	Genetics and control of tomato fruit ripening and quality attributes. *Annual Review of Genetics*, **2011**, 45, 41-59	14.5	613
146	Genome sequence of the hot pepper provides insights into the evolution of pungency in Capsicum species. *Nature Genetics*, **2014**, 46, 270-8	36.3	594
145	The draft genome of watermelon (Citrullus lanatus) and resequencing of 20 diverse accessions. *Nature Genetics*, **2013**, 45, 51-8	36.3	503
144	Single-base resolution methylomes of tomato fruit development reveal epigenome modifications associated with ripening. *Nature Biotechnology*, **2013**, 31, 154-9	44.5	493
143	Genomic analyses provide insights into the history of tomato breeding. *Nature Genetics*, **2014**, 46, 1220-6	36.3	490
142	Transcriptome and selected metabolite analyses reveal multiple points of ethylene control during tomato fruit development. *Plant Cell*, **2005**, 17, 2954-65	11.6	400
141	Fruit ripening mutants yield insights into ripening control. *Current Opinion in Plant Biology*, **2007**, 10, 283-9	9.9	377
140	iTAK: A Program for Genome-wide Prediction and Classification of Plant Transcription Factors, Transcriptional Regulators, and Protein Kinases. *Molecular Plant*, **2016**, 9, 1667-1670	14.4	352
139	Ethylene and Fruit Ripening. *Journal of Plant Growth Regulation*, **2007**, 26, 143-159	4.7	342
138	Fleshy fruit expansion and ripening are regulated by the Tomato SHATTERPROOF gene TAGL1. *Plant Cell*, **2009**, 21, 3041-62	11.6	311
137	High-throughput illumina strand-specific RNA sequencing library preparation. *Cold Spring Harbor Protocols*, **2011**, 2011, 940-9	1.2	310
136	Isolation of molecular markers from specific chromosomal intervals using DNA pools from existing mapping populations. *Nucleic Acids Research*, **1991**, 19, 6553-8	20.1	294
135	The tomato MADS-box transcription factor RIPENING INHIBITOR interacts with promoters involved in numerous ripening processes in a COLORLESS NONRIPENING-dependent manner. *Plant Physiology*, **2011**, 157, 1568-79	6.6	287
134	The genome of the stress-tolerant wild tomato species Solanum pennellii. *Nature Genetics*, **2014**, 46, 1034-8	36.3	269
133	A tomato (Solanum lycopersicum) APETALA2/ERF gene, SlAP2a, is a negative regulator of fruit ripening. *Plant Journal*, **2010**, 64, 936-47	6.9	269

132	Tackling the plant proteome: practical approaches, hurdles and experimental tools. *Plant Journal*, **2004**, 39, 715-33	6.9	264
131	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. *Plant Cell*, **2002**, 14, 1441-56	11.6	259
130	Uniform ripening encodes a Golden 2-like transcription factor regulating tomato fruit chloroplast development. *Science*, **2012**, 336, 1711-5	33.3	253
129	Systems biology of tomato fruit development: combined transcript, protein, and metabolite analysis of tomato transcription factor (nor, rin) and ethylene receptor (Nr) mutants reveals novel regulatory interactions. *Plant Physiology*, **2011**, 157, 405-25	6.6	245
128	Role of beta-oxidation in jasmonate biosynthesis and systemic wound signaling in tomato. *Plant Cell*, **2005**, 17, 971-86	11.6	239
127	The tomato pan-genome uncovers new genes and a rare allele regulating fruit flavor. *Nature Genetics*, **2019**, 51, 1044-1051	36.3	218
126	Combined transcriptome, genetic diversity and metabolite profiling in tomato fruit reveals that the ethylene response factor SlERF6 plays an important role in ripening and carotenoid accumulation. *Plant Journal*, **2012**, 70, 191-204	6.9	214
125	The Epigenome and Transcriptional Dynamics of Fruit Ripening. *Annual Review of Plant Biology*, **2017**, 68, 61-84	30.7	204
124	Molecular and genetic regulation of fruit ripening. *Plant Molecular Biology*, **2013**, 82, 575-91	4.6	200
123	Comprehensive EST analysis of tomato and comparative genomics of fruit ripening. *Plant Journal*, **2004**, 40, 47-59	6.9	196
122	Branched-chain and aromatic amino acid catabolism into aroma volatiles in Cucumis melo L. fruit. *Journal of Experimental Botany*, **2010**, 61, 1111-23	7	183
121	Ripening in the tomato Green-ripe mutant is inhibited by ectopic expression of a protein that disrupts ethylene signaling. *Proceedings of the National Academy of Sciences of the United States of America*, **2006**, 103, 7923-8	11.5	182
120	A DEMETER-like DNA demethylase governs tomato fruit ripening. *Proceedings of the National Academy of Sciences of the United States of America*, **2015**, 112, 10804-9	11.5	173
119	Molecular and genetic characterization of a novel pleiotropic tomato-ripening mutant. *Plant Physiology*, **1999**, 120, 383-90	6.6	172
118	Amino acid substitutions in homologs of the STAY-GREEN protein are responsible for the green-flesh and chlorophyll retainer mutations of tomato and pepper. *Plant Physiology*, **2008**, 147, 179-87	6.6	166
117	Tissue- and cell-type specific transcriptome profiling of expanding tomato fruit provides insights into metabolic and regulatory specialization and cuticle formation. *Plant Cell*, **2011**, 23, 3893-910	11.6	162
116	Molecular biology of ethylene during tomato fruit development and maturation. *Plant Science*, **2008**, 175, 106-113	5.3	150
115	A SEPALLATA gene is involved in the development and ripening of strawberry (Fragaria x ananassa Duch.) fruit, a non-climacteric tissue. *Journal of Experimental Botany*, **2011**, 62, 1179-88	7	145

114	Integrative transcript and metabolite analysis of nutritionally enhanced DE-ETIOLATED1 downregulated tomato fruit. *Plant Cell*, **2010**, 22, 1190-215	11.6	136
113	High-resolution spatiotemporal transcriptome mapping of tomato fruit development and ripening. *Nature Communications*, **2018**, 9, 364	17.4	131
112	Integrative comparative analyses of transcript and metabolite profiles from pepper and tomato ripening and development stages uncovers species-specific patterns of network regulatory behavior. *Plant Physiology*, **2012**, 159, 1713-29	6.6	131
111	Chilling-induced tomato flavor loss is associated with altered volatile synthesis and transient changes in DNA methylation. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, 12580-12585	11.5	129
110	Genome encode analyses reveal the basis of convergent evolution of fleshy fruit ripening. *Nature Plants*, **2018**, 4, 784-791	11.5	123
109	LeCTR1, a tomato CTR1-like gene, demonstrates ethylene signaling ability in Arabidopsis and novel expression patterns in tomato. *Plant Physiology*, **2002**, 130, 1132-42	6.6	122
108	Plant MetGenMAP: an integrative analysis system for plant systems biology. *Plant Physiology*, **2009**, 151, 1758-68	6.6	120
107	An InDel in the Promoter of Selected during Tomato Domestication Determines Fruit Malate Contents and Aluminum Tolerance. *Plant Cell*, **2017**, 29, 2249-2268	11.6	115
106	Tomato GOLDEN2-LIKE transcription factors reveal molecular gradients that function during fruit development and ripening. *Plant Cell*, **2014**, 26, 585-601	11.6	107
105	Biology and genetic engineering of fruit maturation for enhanced quality and shelf-life. *Current Opinion in Biotechnology*, **2009**, 20, 197-203	11.4	103
104	Catalyzing plant science research with RNA-seq. *Frontiers in Plant Science*, **2013**, 4, 66	6.2	102
103	The regulation of MADS-box gene expression during ripening of banana and their regulatory interaction with ethylene. *Journal of Experimental Botany*, **2010**, 61, 1523-35	7	101
102	Ethylene insensitivity conferred by the Green-ripe and Never-ripe 2 ripening mutants of tomato. *Plant Physiology*, **2005**, 138, 267-75	6.6	100
101	Folate synthesis in plants: the p-aminobenzoate branch is initiated by a bifunctional PabA-PabB protein that is targeted to plastids. *Proceedings of the National Academy of Sciences of the United States of America*, **2004**, 101, 1496-501	11.5	99
100	Combined transcription factor profiling, microarray analysis and metabolite profiling reveals the transcriptional control of metabolic shifts occurring during tomato fruit development. *Plant Journal*, **2011**, 68, 999-1013	6.9	98
99	Functional diversification of AGAMOUS lineage genes in regulating tomato flower and fruit development. *Journal of Experimental Botany*, **2010**, 61, 1795-806	7	97
98	Transgenic analysis of tomato endo-β1,4-glucanase gene function. Role of cel1 in floral abscission. *Plant Journal*, **1998**, 13, 303-310	6.9	94
97	Utilization of tomato microarrays for comparative gene expression analysis in the Solanaceae. *Journal of Experimental Botany*, **2005**, 56, 2885-95	7	93

96	Cucurbit Genomics Database (CuGenDB): a central portal for comparative and functional genomics of cucurbit crops. *Nucleic Acids Research*, **2019**, 47, D1128-D1136	20.1	93
95	A STAY-GREEN protein SlSGR1 regulates lycopene and β-carotene accumulation by interacting directly with SlPSY1 during ripening processes in tomato. *New Phytologist*, **2013**, 198, 442-452	9.8	91
94	Involvement of an ethylene response factor in chlorophyll degradation during citrus fruit degreening. *Plant Journal*, **2016**, 86, 403-12	6.9	89
93	Sequencing and comparative analysis of a conserved syntenic segment in the Solanaceae. *Genetics*, **2008**, 180, 391-408	4	84
92	Identification of genes in the phenylalanine metabolic pathway by ectopic expression of a MYB transcription factor in tomato fruit. *Plant Cell*, **2011**, 23, 2738-53	11.6	82
91	Polygalacturonase Isozymes and Pectin Depolymerization in Transgenic rin Tomato Fruit. *Plant Physiology*, **1990**, 94, 1882-6	6.6	80
90	Ethylene suppresses tomato (Solanum lycopersicum) fruit set through modification of gibberellin metabolism. *Plant Journal*, **2015**, 83, 237-51	6.9	76
89	Transcriptomic and reverse genetic analyses of branched-chain fatty acid and acyl sugar production in Solanum pennellii and Nicotiana benthamiana. *Plant Physiology*, **2008**, 148, 1830-46	6.6	75
88	Banana MaMADS Transcription Factors Are Necessary for Fruit Ripening and Molecular Tools to Promote Shelf-Life and Food Security. *Plant Physiology*, **2016**, 171, 380-91	6.6	67
87	A physical map of the highly heterozygous Populus genome: integration with the genome sequence and genetic map and analysis of haplotype variation. *Plant Journal*, **2007**, 50, 1063-78	6.9	63
86	Folate synthesis in plants: the last step of the p-aminobenzoate branch is catalyzed by a plastidial aminodeoxychorismate lyase. *Plant Journal*, **2004**, 40, 453-61	6.9	62
85	Fluorescence in situ hybridization and optical mapping to correct scaffold arrangement in the tomato genome. *G3: Genes, Genomes, Genetics*, **2014**, 4, 1395-405	3.2	61
84	The molecular and biochemical basis for varietal variation in sesquiterpene content in melon (Cucumis melo L.) rinds. *Plant Molecular Biology*, **2008**, 66, 647-61	4.6	60
83	Deciphering genetic factors that determine melon fruit-quality traits using RNA-Seq-based high-resolution QTL and eQTL mapping. *Plant Journal*, **2018**, 94, 169-191	6.9	57
82	Enabling proteomic studies with RNA-Seq: The proteome of tomato pollen as a test case. *Proteomics*, **2012**, 12, 761-74	4.8	56
81	Expression of ripening-related genes in cold-stored tomato fruit. *Postharvest Biology and Technology*, **2011**, 61, 1-14	6.2	54
80	Carotenoid profiling of the leaves of selected African eggplant accessions subjected to drought stress. *Food Science and Nutrition*, **2017**, 5, 113-122	3.2	49
79	Altered chloroplast development and delayed fruit ripening caused by mutations in a zinc metalloprotease at the lutescent2 locus of tomato. *Plant Physiology*, **2012**, 159, 1086-98	6.6	48

78	Phytohormones in fruit development and maturation. *Plant Journal*, **2021**, 105, 446-458	6.9	48
77	Ectopic expression of ORANGE promotes carotenoid accumulation and fruit development in tomato. *Plant Biotechnology Journal*, **2019**, 17, 33-49	11.6	46
76	Regulatory control of high levels of carotenoid accumulation in potato tubers. *Plant, Cell and Environment*, **2011**, 34, 1020-1030	8.4	45
75	Genomic analysis of wild tomato introgressions determining metabolism- and yield-associated traits. *Plant Physiology*, **2010**, 152, 1772-86	6.6	45
74	More than meets the eye: from carotenoid biosynthesis, to new insights into apocarotenoid signaling. *Current Opinion in Plant Biology*, **2015**, 27, 172-9	9.9	44
73	Understanding development and ripening of fruit crops in an 'omics' era. *Horticulture Research*, **2014**, 1, 14034	7.7	43
72	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. *Molecular Genetics and Genomics*, **1995**, 248, 195-206		43
71	Conserved changes in the dynamics of metabolic processes during fruit development and ripening across species. *Plant Physiology*, **2014**, 164, 55-68	6.6	42
70	Analysis of the ethylene response in the epinastic mutant of tomato. *Plant Physiology*, **2001**, 127, 58-66	6.6	42
69	The Tomato Expression Atlas. *Bioinformatics*, **2017**, 33, 2397-2398	7.2	39
68	Cell wall metabolism in cold-stored tomato fruit. *Postharvest Biology and Technology*, **2010**, 57, 106-113	6.2	38
67	Developmental and feedforward control of the expression of folate biosynthesis genes in tomato fruit. *Molecular Plant*, **2010**, 3, 66-77	14.4	36
66	An improved de novo assembly and annotation of the tomato reference genome using single-molecule sequencing, Hi-C proximity ligation and optical maps		36
65	Natural genetic variation for expression of a SWEET transporter among wild species of Solanum lycopersicum (tomato) determines the hexose composition of ripening tomato fruit. *Plant Journal*, **2018**, 96, 343-357	6.9	35
64	Transcriptomic analysis of Petunia hybrida in response to salt stress using high throughput RNA sequencing. *PLoS ONE*, **2014**, 9, e94651	3.7	34
63	Differential control of ethylene responses by GREEN-RIPE and GREEN-RIPE LIKE1 provides evidence for distinct ethylene signaling modules in tomato. *Plant Physiology*, **2012**, 160, 1968-84	6.6	33
62	Characterization of a major latex protein (MLP) gene down-regulated by ethylene during peach fruitlet abscission. *Plant Science*, **2002**, 163, 265-272	5.3	33
61	Fruit carotenoid-deficient mutants in tomato reveal a function of the plastidial isopentenyl diphosphate isomerase (IDI1) in carotenoid biosynthesis. *Plant Journal*, **2016**, 88, 82-94	6.9	33

60	Sequencing-Based Bin Map Construction of a Tomato Mapping Population, Facilitating High-Resolution Quantitative Trait Loci Detection. *Plant Genome*, **2019**, 12, 180010	4.4	32
59	Ethylene and the Control of Fruit Ripening **2013**, 43-73		32
58	Expression of a Chimeric Polygalacturonase Gene in Transgenic rin (Ripening Inhibitor) Tomato Fruit Results in Polyuronide Degradation but Not Fruit Softening. *Plant Cell*, **1989**, 1, 53	11.6	32
57	AtPDS overexpression in tomato: exposing unique patterns of carotenoid self-regulation and an alternative strategy for the enhancement of fruit carotenoid content. *Plant Biotechnology Journal*, **2018**, 16, 482-494	11.6	31
56	Molecular analysis of softening and ethylene synthesis and signaling pathways in a non-softening apple cultivar, Honeycrisp and a rapidly softening cultivar, McIntosh *Postharvest Biology and Technology*, **2012**, 64, 94-103	6.2	31
55	Differential fruit gene expression in two strawberry cultivars in response to elevated CO2 during storage revealed by a heterologous fruit microarray approach. *Postharvest Biology and Technology*, **2009**, 51, 131-140	6.2	30
54	Completing a pathway to plant vitamin C synthesis. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 9109-10	11.5	30
53	Overexpression of the class D MADS-box gene Sl-AGL11 impacts fleshy tissue differentiation and structure in tomato fruits. *Journal of Experimental Botany*, **2017**, 68, 4869-4884	7	29
52	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. *PLoS Genetics*, **2019**, 15, e1008149	6	28
51	Metabolomic analyses to evaluate the effect of drought stress on selected African Eggplant accessions. *Journal of the Science of Food and Agriculture*, **2018**, 98, 205-216	4.3	27
50	Differential metabolism of L-phenylalanine in the formation of aromatic volatiles in melon (Cucumis melo L.) fruit. *Phytochemistry*, **2018**, 148, 122-131	4	24
49	Metabolomics should be deployed in the identification and characterization of gene-edited crops. *Plant Journal*, **2020**, 102, 897-902	6.9	24
48	Genome of Solanum pimpinellifolium provides insights into structural variants during tomato breeding. *Nature Communications*, **2020**, 11, 5817	17.4	24
47	Differential regulation of Salmonella typhimurium genes involved in O-antigen capsule production and their role in persistence within tomato fruit. *Molecular Plant-Microbe Interactions*, **2013**, 26, 793-800	3.6	23
46	Genetic and metabolic effects of ripening mutations and vine detachment on tomato fruit quality. *Plant Biotechnology Journal*, **2020**, 18, 106-118	11.6	23
45	Modest calcium increase in tomatoes expressing a variant of Arabidopsis cation/H+ antiporter. *Plant Biotechnology Reports*, **2010**, 4, 15-21	2.5	22
44	Manipulation of ZDS in tomato exposes carotenoid- and ABA-specific effects on fruit development and ripening. *Plant Biotechnology Journal*, **2020**, 18, 2210-2224	11.6	21
43	Tomato Multiomics Reveals Consequences of Crop Domestication and Improvement. *Cell*, **2018**, 172, 6-8	56.2	20

42	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 (Solanum lycopersicum). *Planta*, **2012**, 235, 453-71	4.7	20
41	Relationships between genome methylation, levels of non-coding RNAs, mRNAs and metabolites in ripening tomato fruit. *Plant Journal*, **2020**, 103, 980-994	6.9	20
40	Identification of a Chromosome 4 Fruit Flavor and Nutritional Quality-Associated Metabolite QTL. *Frontiers in Plant Science*, **2016**, 7, 1671	6.2	19
39	A modified procedure for PCR-based differential display and demonstration of use in plants for isolation of genes related to fruit ripening. *Plant Molecular Biology Reporter*, **1995**, 13, 70-81	1.7	18
38	Biochemistry of Fruit Ripening **2013**, 1-19		17
37	Tomato gamma-glutamylhydrolases: expression, characterization, and evidence for heterodimer formation. *Plant Physiology*, **2008**, 148, 775-85	6.6	17
36	The Locus of Confers Resistance to Race 1 Strains of pv. and to by Recognizing the Type III Effectors AvrRpt2 and RipBN. *Molecular Plant-Microbe Interactions*, **2019**, 32, 949-960	3.6	17
35	The NAC transcription factor FaRIF controls fruit ripening in strawberry. *Plant Cell*, **2021**, 33, 1574-1593	11.6	14
34	Gr and hp-1 tomato mutants unveil unprecedented interactions between arbuscular mycorrhizal symbiosis and fruit ripening. *Planta*, **2016**, 244, 155-65	4.7	13
33	Longitudinal Transcriptomic, Proteomic, and Metabolomic Analysis of Response to Graft Inoculation by. *Journal of Proteome Research*, **2020**, 19, 2247-2263	5.6	12
32	Biosynthesis of Volatile Compounds **2013**, 135-161		12
31	The tomato gene contributes to regulation of fruit ripening. *Horticulture Research*, **2019**, 6, 15	7.7	10
30	Application of Genetic Bit Analysis (GBATM) for allelic selection in plant breeding. *Molecular Breeding*, **1997**, 3, 495-502	3.4	10
29	Characterizing the involvement of FaMADS9 in the regulation of strawberry fruit receptacle development. *Plant Biotechnology Journal*, **2020**, 18, 929-943	11.6	10
28	Ectopic expression of miRNA172 in tomato (Solanum lycopersicum) reveals novel function in fruit development through regulation of an AP2 transcription factor. *BMC Plant Biology*, **2020**, 20, 283	5.3	9
27	Tissue specificity and differential expression of transcription factors in tomato provide hints of unique regulatory networks during fruit ripening. *Plant Signaling and Behavior*, **2012**, 7, 1639-47	2.5	9
26	Carotenoid Biosynthesis and Chlorophyll Degradation **2013**, 75-116		9
25	Comparative genomics of muskmelon reveals a potential role for retrotransposons in the modification of gene expression. *Communications Biology*, **2020**, 3, 432	6.7	9

24	Plant Viruses Transmitted in Two Different Modes Produce Differing Effects on Small RNA-Mediated Processes in Their Aphid Vector. *Phytobiomes Journal*, **2019**, 3, 71-81	4.8	8
23	Transmission modes affect the population structure of potato virus Y in potato. *PLoS Pathogens*, **2020**, 16, e1008608	7.6	7
22	Cell Wall Architecture and Metabolism in Ripening Fruit and the Complex Relationship with Softening **2013**, 163-187		7
21	Tomato fruit as a model for tissue-specific gene silencing in crop plants. *Horticulture Research*, **2020**, 7, 142	7.7	7
20	Rapid and reliable screening of a tomato YAC library exclusively based on PCR. *Plant Molecular Biology Reporter*, **1996**, 14, 58-67	1.7	6
19	The pineapple AcMADS1 promoter confers high level expression in tomato and Arabidopsis flowering and fruiting tissues, but AcMADS1 does not complement the tomato LeMADS-RIN (rin) mutant. *Plant Molecular Biology*, **2014**, 86, 395-407	4.6	5
18	Harnessing epigenome modifications for better crops. *Journal of Experimental Botany*, **2016**, 67, 2535-7	7	5
17	Ripening activator turned repressor. *Nature Plants*, **2017**, 3, 920-921	11.5	4
16	Fruit: An Angiosperm Innovation **2013**, 21-42		4
15	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. *Genes*, **2020**, 11,	4.2	4
14	Phenylpropanoid Metabolism and Biosynthesis of Anthocyanins **2013**, 117-134		3
13	Genetic Control of Fruit Quality, and Prospects for Nutrient Modification. *Hortscience: A Publication of the American Society for Hortcultural Science*, **2002**, 37, 453-456	2.4	3
12	Identification of Plastome Variants useful for Cytoplasmic Selection and Cultivar Identification in Onion. *Journal of the American Society for Horticultural Science*, **1999**, 124, 122-127	2.3	3
11	Molecular and Genetic Analysis of Tomato Fruit Development and Ripening. *Methods in Plant Biochemistry*, **1993**, 10, 251-285		3
10	A tomato LATERAL ORGAN BOUNDARIES transcription factor, , predominantly regulates cell wall and softening components of ripening. *Proceedings of the National Academy of Sciences of the United States of America*, **2021**, 118,	11.5	3
9	Determining the Physical Limits of the Brassica S Locus by Recombinational Analysis. *Plant Cell*, **2000**, 12, 23	11.6	2
8	SlERF.F12 modulates the transition to ripening in tomato fruit by recruiting the co-repressor Topless and histone deacetylases to repress key ripening genes.. *Plant Cell*, **2022**,	11.6	2
7	Regulatory Networks Controlling Ripening **2013**, 189-206		1

6	Rapid isolation of terminal sequences from cloned plant DNA fragments. *Plant Molecular Biology Reporter*, **1995**, 13, 369-376	1.7	1
5	Melon ethylene-mediated transcriptome and methylome dynamics provide insights to volatile production		1
4	Genome of Solanum pimpinellifolium provides insights into structural variants during tomato breeding		1
3	Genome-wide association study reveals the genetic architecture of 27 agronomic traits in tomato. *Plant Physiology*, **2021**, 186, 2078-2092	6.6	1
2	Fruit Ripening and its Manipulation **2018**, 278-303		
1	Fruit Ripening **2018**, 164-182		