James J Giovannoni

List of Publications by Year
in descending order

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141 papers	22,924 citations	13332 70 h-index	11608 140 g-index
160 all docs	160 docs citations	160 times ranked	17558 citing authors

#	ARTICLE	IF	CITATIONS
1	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, 34, 1250-1272.	3.1	57
2	Laser capture of tomato pericarp tissues for microscale carotenoid analysis by supercritical fluid chromatography. Methods in Enzymology, 2022, , 213-233.	0.4	0
3	A <i>Solanum lycopersicoides</i> reference genome facilitates insights into tomato specialized metabolism and immunity. Plant Journal, 2022, 110, 1791-1810.	2.8	16
4	A comparative transcriptomics and eQTL approach identifies<i>SlWD40</i>as a tomato fruit ripening regulator. Plant Physiology, 2022, 190, 250-266.	2.3	9
5	Phytohormones in fruit development and maturation. Plant Journal, 2021, 105, 446-458.	2.8	189
6	The NAC transcription factor FaRIF controls fruit ripening in strawberry. Plant Cell, 2021, 33, 1574-1593.	3.1	95
7	Genome-wide association study reveals the genetic architecture of 27 agronomic traits in tomato. Plant Physiology, 2021, 186, 2078-2092.	2.3	18
8	A tomato LATERAL ORGAN BOUNDARIES transcription factor, <i>SlLOB1</i> , predominantly regulates cell wall and softening components of ripening. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	41
9	Genetic and metabolic effects of ripening mutations and vine detachment on tomato fruit quality. Plant Biotechnology Journal, 2020, 18, 106-118.	4.1	39
10	Characterizing the involvement of <i>FaMADS9</i> in the regulation of strawberry fruit receptacle development. Plant Biotechnology Journal, 2020, 18, 929-943.	4.1	25
11	Metabolomics should be deployed in the identification and characterization of geneâ€•edited crops. Plant Journal, 2020, 102, 897-902.	2.8	30
12	Genome of Solanum pimpinellifolium provides insights into structural variants during tomato breeding. Nature Communications, 2020, 11, 5817.	5.8	85
13	Comparative genomics of muskmelon reveals a potential role for retrotransposons in the modification of gene expression. Communications Biology, 2020, 3, 432.	2.0	29
14	Tomato fruit as a model for tissue-specific gene silencing in crop plants. Horticulture Research, 2020, 7, 142.	2.9	18
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, 1387.	1.0	14
16	Transmission modes affect the population structure of potato virus Y in potato. PLoS Pathogens, 2020, 16, e1008608.	2.1	31
17	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.	1.6	29
18	Manipulation of ZDS in tomato exposes carotenoidâ€•and ABAâ€•specific effects on fruit development and ripening. Plant Biotechnology Journal, 2020, 18, 2210-2224.	4.1	44

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19	Longitudinal Transcriptomic, Proteomic, and Metabolomic Analysis of <i>Citrus limon</i> Response to Graft Inoculation by <i>Candidatus Liberibacter asiaticus</i>. Journal of Proteome Research, 2020, 19, 2247-2263.	1.8	25
20	Relationships between genome methylation, levels of nonâ€coding RNAs, mRNAs and metabolites in ripening tomato fruit. Plant Journal, 2020, 103, 980-994.	2.8	46
21	Ectopic expression of <i><scp>ORANGE</scp></i> promotes carotenoid accumulation and fruit development in tomato. Plant Biotechnology Journal, 2019, 17, 33-49.	4.1	83
22	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.	1.4	16
23	Sequencingâ€Based Bin Map Construction of a Tomato Mapping Population, Facilitating Highâ€Resolution Quantitative Trait Loci Detection. Plant Genome, 2019, 12, 180010.	1.6	65
24	The tomato HIGH PIGMENT1/DAMAGED DNA BINDING PROTEIN 1 gene contributes to regulation of fruit ripening. Horticulture Research, 2019, 6, 15.	2.9	20
25	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.	1.5	66
26	The tomato pan-genome uncovers new genes and a rare allele regulating fruit flavor. Nature Genetics, 2019, 51, 1044-1051.	9.4	441
27	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. Molecular Plant-Microbe Interactions, 2019, 32, 949-960.	1.4	37
28	Cucurbit Genomics Database (CuGenDB): a central portal for comparative and functional genomics of cucurbit crops. Nucleic Acids Research, 2019, 47, D1128-D1136.	6.5	177
29	Differential metabolism of Lâ€“phenylalanine in the formation of aromatic volatiles in melon (Cucumis) Tj ETQq1 1 0.784314 rgBT /Ov	1.4	41
30	High-resolution spatiotemporal transcriptome mapping of tomato fruit development and ripening. Nature Communications, 2018, 9, 364.	5.8	255
31	Deciphering genetic factors that determine melon fruitâ€quality traits using RNA â€Seqâ€based highâ€resolution QTL and eQTL mapping. Plant Journal, 2018, 94, 169-191.	2.8	133
32	Tomato Multiomics Reveals Consequences of Crop Domestication and Improvement. Cell, 2018, 172, 6-8.	13.5	60
33	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.	1.7	36
34	<i>AtPDS</i> overexpression in tomato: exposing unique patterns of carotenoid selfâ€regulation and an alternative strategy for the enhancement of fruit carotenoid content. Plant Biotechnology Journal, 2018, 16, 482-494.	4.1	58
35	Genome encode analyses reveal the basis of convergent evolution of fleshy fruit ripening. Nature Plants, 2018, 4, 784-791.	4.7	256
36	Natural genetic variation for expression of a <scp>SWEET</scp> transporter among wild species of <i>Solanum lycopersicum</i> (tomato) determines the hexose composition of ripening tomato fruit. Plant Journal, 2018, 96, 343-357.	2.8	74

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37	The Epigenome and Transcriptional Dynamics of Fruit Ripening. Annual Review of Plant Biology, 2017, 68, 61-84.	8.6	335
38	The Tomato Expression Atlas. Bioinformatics, 2017, 33, 2397-2398.	1.8	64
39	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.	2.4	59
40	An InDel in the Promoter of <i>Al-ACTIVATED MALATE TRANSPORTER9</i> Selected during Tomato Domestication Determines Fruit Malate Contents and Aluminum Tolerance. Plant Cell, 2017, 29, 2249-2268.	3.1	207
41	Ripening activator turned repressor. Nature Plants, 2017, 3, 920-921.	4.7	6
42	Carotenoid profiling of the leaves of selected African eggplant accessions subjected to drought stress. Food Science and Nutrition, 2017, 5, 113-122.	1.5	79
43	Identification of a Solanum pennellii Chromosome 4 Fruit Flavor and Nutritional Quality-Associated Metabolite QTL. Frontiers in Plant Science, 2016, 7, 1671.	1.7	35
44	Involvement of an ethylene response factor in chlorophyll degradation during citrus fruit degreening. Plant Journal, 2016, 86, 403-412.	2.8	130
45	Fruit carotenoidâ€deficient mutants in tomato reveal a function of the plastidial isopentenyl diphosphate isomerase (<scp>IDI</scp>1) in carotenoid biosynthesis. Plant Journal, 2016, 88, 82-94.	2.8	44
46	Harnessing epigenome modifications for better crops. Journal of Experimental Botany, 2016, 67, 2535-2537.	2.4	6
47	iTAK: A Program for Genome-wide Prediction andÂClassification of Plant Transcription Factors, Transcriptional Regulators, and Protein Kinases. Molecular Plant, 2016, 9, 1667-1670.	3.9	735
48	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.	3.3	208
49	Gr and hp-1 tomato mutants unveil unprecedented interactions between arbuscular mycorrhizal symbiosis and fruit ripening. Planta, 2016, 244, 155-165.	1.6	13
50	Banana <i>MaMADS</i> Transcription Factors Are Necessary for Fruit Ripening and Molecular Tools to Promote Shelf-Life and Food Security. Plant Physiology, 2016, 171, 380-391.	2.3	114
51	Ethylene suppresses tomato (<i>Solanum lycopersicum</i>) fruit set through modification of gibberellin metabolism. Plant Journal, 2015, 83, 237-251.	2.8	128
52	A DEMETER-like DNA demethylase governs tomato fruit ripening. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 10804-10809.	3.3	256
53	More than meets the eye: from carotenoid biosynthesis, to new insights into apocarotenoid signaling. Current Opinion in Plant Biology, 2015, 27, 172-179.	3.5	67
54	Transcriptomic Analysis of Petunia hybrida in Response to Salt Stress Using High Throughput RNA Sequencing. PLoS ONE, 2014, 9, e94651.	1.1	46

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55	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.	2.0	6
56	Fluorescence<i>In Situ</i>Hybridization and Optical Mapping to Correct Scaffold Arrangement in the Tomato Genome. G3: Genes, Genomes, Genetics, 2014, 4, 1395-1405.	0.8	81
57	Tomato <i>GOLDEN2-LIKE</i> Transcription Factors Reveal Molecular Gradients That Function during Fruit Development and Ripening. Plant Cell, 2014, 26, 585-601.	3.1	193
58	Conserved Changes in the Dynamics of Metabolic Processes during Fruit Development and Ripening across Species Â Â Â. Plant Physiology, 2014, 164, 55-68.	2.3	50
59	Genome sequence of the hot pepper provides insights into the evolution of pungency in Capsicum species. Nature Genetics, 2014, 46, 270-278.	9.4	867
60	The genome of the stress-tolerant wild tomato species Solanum pennellii. Nature Genetics, 2014, 46, 1034-1038.	9.4	391
61	Genomic analyses provide insights into the history of tomato breeding. Nature Genetics, 2014, 46, 1220-1226.	9.4	801
62	Understanding development and ripening of fruit crops in an â€˜omicsâ€™ era. Horticulture Research, 2014, 1, 14034.	2.9	53
63	The draft genome of watermelon (Citrullus lanatus) and resequencing of 20 diverse accessions. Nature Genetics, 2013, 45, 51-58.	9.4	731
64	Single-base resolution methylomes of tomato fruit development reveal epigenome modifications associated with ripening. Nature Biotechnology, 2013, 31, 154-159.	9.4	693
65	A STAYâ€GREEN protein <scp>S</scp>l<scp>SGR</scp>1 regulates lycopene and Î²â€carotene accumulation by interacting directly with <scp>S</scp>l<scp>PSY</scp>1 during ripening processes in tomato. New Phytologist, 2013, 198, 442-452.	3.5	149
66	Molecular and genetic regulation of fruit ripening. Plant Molecular Biology, 2013, 82, 575-591.	2.0	300
67	Catalyzing plant science research with RNA-seq. Frontiers in Plant Science, 2013, 4, 66.	1.7	136
68	Differential Regulation of <i>Salmonella</i> Typhimurium Genes Involved in O-Antigen Capsule Production and Their Role in Persistence Within Tomato Fruit. Molecular Plant-Microbe Interactions, 2013, 26, 793-800.	1.4	33
69	Integrative Comparative Analyses of Transcript and Metabolite Profiles from Pepper and Tomato Ripening and Development Stages Uncovers Species-Specific Patterns of Network Regulatory Behavior Â. Plant Physiology, 2012, 159, 1713-1729.	2.3	174
70	Altered Chloroplast Development and Delayed Fruit Ripening Caused by Mutations in a Zinc Metalloprotease at the <i>lutescent2</i> Locus of Tomato Â Â. Plant Physiology, 2012, 159, 1086-1098.	2.3	68
71	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 Â Â. Plant Physiology, 2012, 160, 1968-1984.	2.3	35
72	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, 1639-1647.	1.2	16

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73	Enabling proteomic studies with RNAâ€Seq: The proteome of tomato pollen as a test case. Proteomics, 2012, 12, 761-774.	1.3	62
74	<i>Uniform ripening</i> Encodes a <i>Golden 2-like</i> Transcription Factor Regulating Tomato Fruit Chloroplast Development. Science, 2012, 336, 1711-1715.	6.0	384
75	Molecular analysis of softening and ethylene synthesis and signaling pathways in a non-softening apple cultivar, â€˜Honeycrispâ€™ and a rapidly softening cultivar, â€˜McIntoshâ€™. Postharvest Biology and Technology, 2012, 64, 94-103.	2.9	39
76	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. Plant Journal, 2012, 70, 191-204.	2.8	268
77	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, 453-471.	1.6	31
78	Genetics and Control of Tomato Fruit Ripening and Quality Attributes. Annual Review of Genetics, 2011, 45, 41-59.	3.2	855
79	Regulatory control of high levels of carotenoid accumulation in potato tubers. Plant, Cell and Environment, 2011, 34, 1020-1030.	2.8	52
80	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.	2.8	118
81	Expression of ripening-related genes in cold-stored tomato fruit. Postharvest Biology and Technology, 2011, 61, 1-14.	2.9	68
82	High-Throughput Illumina Strand-Specific RNA Sequencing Library Preparation. Cold Spring Harbor Protocols, 2011, 2011, pdb.prot5652.	0.2	382
83	The Tomato MADS-Box Transcription Factor RIPENING INHIBITOR Interacts with Promoters Involved in Numerous Ripening Processes in a COLORLESS NONRIPENING-Dependent Manner Â Â. Plant Physiology, 2011, 157, 1568-1579.	2.3	375
84	Identification of Genes in the Phenylalanine Metabolic Pathway by Ectopic Expression of a MYB Transcription Factor in Tomato Fruit. Plant Cell, 2011, 23, 2738-2753.	3.1	97
85	Systems Biology of Tomato Fruit Development: Combined Transcript, Protein, and Metabolite Analysis of Tomato Transcription Factor (<i>nor, rin</i>) and Ethylene Receptor (<i>Nr</i>) Mutants Reveals Novel Regulatory Interactions Â Â. Plant Physiology, 2011, 157, 405-425.	2.3	303
86	Tissue- and Cell-Type Specific Transcriptome Profiling of Expanding Tomato Fruit Provides Insights into Metabolic and Regulatory Specialization and Cuticle Formation Â. Plant Cell, 2011, 23, 3893-3910.	3.1	193
87	A SEPALLATA gene is involved in the development and ripening of strawberry (FragariaÃ—ananassa Duch.) fruit, a non-climacteric tissue*. Journal of Experimental Botany, 2011, 62, 1179-1188.	2.4	174
88	Modest calcium increase in tomatoes expressing a variant of Arabidopsis cation/H+ antiporter. Plant Biotechnology Reports, 2010, 4, 15-21.	0.9	25
89	Cell wall metabolism in cold-stored tomato fruit. Postharvest Biology and Technology, 2010, 57, 106-113.	2.9	52
90	A tomato (Solanum lycopersicum) APETALA2/ERF gene, SlAP2a, is a negative regulator of fruit ripening. Plant Journal, 2010, 64, 936-947.	2.8	353

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91	Harvesting the apple genome. Nature Genetics, 2010, 42, 822-823.	9.4	9
92	Genomic Analysis of Wild Tomato Introgressions Determining Metabolism- and Yield-Associated Traits. Plant Physiology, 2010, 152, 1772-1786.	2.3	57
93	Integrative Transcript and Metabolite Analysis of Nutritionally Enhanced <i>DE-ETIOLATED1</i> Downregulated Tomato Fruit. Plant Cell, 2010, 22, 1190-1215.	3.1	160
94	Developmental and Feedforward Control of the Expression of Folate Biosynthesis Genes in Tomato Fruit. Molecular Plant, 2010, 3, 66-77.	3.9	44
95	Branched-chain and aromatic amino acid catabolism into aroma volatiles in Cucumis melo L. fruit. Journal of Experimental Botany, 2010, 61, 1111-1123.	2.4	247
96	Functional diversification of AGAMOUS lineage genes in regulating tomato flower and fruit development. Journal of Experimental Botany, 2010, 61, 1795-1806.	2.4	123
97	The regulation of MADS-box gene expression during ripening of banana and their regulatory interaction with ethylene. Journal of Experimental Botany, 2010, 61, 1523-1535.	2.4	113
98	Fleshy Fruit Expansion and Ripening Are Regulated by the Tomato <i>SHATTERPROOF</i> Gene <i>TAGL1</i> Â Â. Plant Cell, 2009, 21, 3041-3062.	3.1	415
99	Plant MetGenMAP: An Integrative Analysis System for Plant Systems Biology Â Â. Plant Physiology, 2009, 151, 1758-1768.	2.3	156
100	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.	2.9	32
101	Biology and genetic engineering of fruit maturation for enhanced quality and shelf-life. Current Opinion in Biotechnology, 2009, 20, 197-203.	3.3	116
102	The molecular and biochemical basis for varietal variation in sesquiterpene content in melon (Cucumis melo L.) rinds. Plant Molecular Biology, 2008, 66, 647-661.	2.0	73
103	Molecular biology of ethylene during tomato fruit development and maturation. Plant Science, 2008, 175, 106-113.	1.7	190
104	Sequencing and Comparative Analysis of a Conserved Syntenic Segment in the Solanaceae. Genetics, 2008, 180, 391-408.	1.2	105
105	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 Â Â. Plant Physiology, 2008, 147, 179-187.	2.3	223
106	Tomato <i>Î³</i>-Glutamylhydrolases: Expression, Characterization, and Evidence for Heterodimer Formation Â. Plant Physiology, 2008, 148, 775-785.	2.3	19
107	Transcriptomic and Reverse Genetic Analysesof Branched-Chain Fatty Acid and Acyl Sugar Production in<i>Solanum pennellii</i>and<i>Nicotiana benthamiana</i>Â Â. Plant Physiology, 2008, 148, 1830-1846.	2.3	95
108	Completing a pathway to plant vitamin C synthesis. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 9109-9110.	3.3	41

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109	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, 1063-1078.	2.8	70
110	Fruit ripening mutants yield insights into ripening control. Current Opinion in Plant Biology, 2007, 10, 283-289.	3.5	463
111	Ethylene and Fruit Ripening. Journal of Plant Growth Regulation, 2007, 26, 143-159.	2.8	464
112	A naturally occurring epigenetic mutation in a gene encoding an SBP-box transcription factor inhibits tomato fruit ripening. Nature Genetics, 2006, 38, 948-952.	9.4	1,076
113	Breeding new life into plant metabolism. Nature Biotechnology, 2006, 24, 418-419.	9.4	27
114	From The Cover: 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, 7923-7928.	3.3	205
115	Transcriptome and Selected Metabolite Analyses Reveal Multiple Points of Ethylene Control during Tomato Fruit Development. Plant Cell, 2005, 17, 2954-2965.	3.1	474
116	Ethylene Insensitivity Conferred by the Green-ripe and Never-ripe 2 Ripening Mutants of Tomato. Plant Physiology, 2005, 138, 267-275.	2.3	118
117	Utilization of tomato microarrays for comparative gene expression analysis in the Solanaceae. Journal of Experimental Botany, 2005, 56, 2885-2895.	2.4	105
118	Role of Î²-Oxidation in Jasmonate Biosynthesis and Systemic Wound Signaling in Tomato. Plant Cell, 2005, 17, 971-986.	3.1	280
119	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, 1496-1501.	3.3	111
120	Tackling the plant proteome: practical approaches, hurdles and experimental tools. Plant Journal, 2004, 39, 715-733.	2.8	301
121	Comprehensive EST analysis of tomato and comparative genomics of fruit ripening. Plant Journal, 2004, 40, 47-59.	2.8	210
122	Folate synthesis in plants: the last step of the p-aminobenzoate branch is catalyzed by a plastidial aminodeoxychorismate lyase. Plant Journal, 2004, 40, 453-461.	2.8	86
123	Genetic Regulation of Fruit Development and Ripening. Plant Cell, 2004, 16, S170-S180.	3.1	1,152
124	LeCTR1, a Tomato CTR1-Like Gene, Demonstrates Ethylene Signaling Ability in Arabidopsis and Novel Expression Patterns in Tomato. Plant Physiology, 2002, 130, 1132-1142.	2.3	143
125	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, 1441-1456.	3.1	283
126	Characterization of a major latex protein (MLP) gene down-regulated by ethylene during peach fruitlet abscission. Plant Science, 2002, 163, 265-272.	1.7	44

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127	Genetic Control of Fruit Quality, and Prospects for Nutrient Modification. Hortscience: A Publication of the American Society for Hortcultural Science, 2002, 37, 453-456.	0.5	3
128	Analysis of the Ethylene Response in theepinastic Mutant of Tomato. Plant Physiology, 2001, 127, 58-66.	2.3	51
129	Determining the Physical Limits of the Brassica S Locus by Recombinational Analysis. Plant Cell, 2000, 12, 23.	3.1	11
130	Molecular and Genetic Characterization of a Novel Pleiotropic Tomato-Ripening Mutant1. Plant Physiology, 1999, 120, 383-390.	2.3	202
131	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.	0.5	8
132	Transgenic analysis of tomato endo-beta-1,4-glucanase gene function. Role of cel1 in floral abscission. Plant Journal, 1998, 13, 303-310.	2.8	111
133	Application of Genetic Bit Analysis (GBATM) for allelic selection in plant breeding. Molecular Breeding, 1997, 3, 495-502.	1.0	18
134	Rapid and reliable screening of a tomato YAC library exclusively based on PCR. Plant Molecular Biology Reporter, 1996, 14, 58-67.	1.0	6
135	Molecular genetic analysis of theripening-inhibitor andnon-ripening loci of tomato: A first step in genetic map-based cloning of fruit ripening genes. Molecular Genetics and Genomics, 1995, 248, 195-206.	2.4	55
136	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.	1.0	20
137	Rapid isolation of terminal sequences from cloned plant DNA fragments. Plant Molecular Biology Reporter, 1995, 13, 369-376.	1.0	1
138	Molecular and Genetic Analysis of Tomato Fruit Development and Ripening. Methods in Plant Biochemistry, 1993, 10, 251-285.	0.2	5
139	Isolation of molecular markers from specific chromosomal intervals using DNA pools from existing mapping populations. Nucleic Acids Research, 1991, 19, 6553-6568.	6.5	381
140	Polygalacturonase Isozymes and Pectin Depolymerization in Transgenic rin Tomato Fruit. Plant Physiology, 1990, 94, 1882-1886.	2.3	90
141	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.	3.1	58