

# James J Giovannoni

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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

| #   | Paper   | IF   | Citations |
|-----|---|------|-----------|
| 149 | SLERF.F12 modulates the transition to ripening in tomato fruit by recruiting the co-repressor Topless and histone deacetylases to repress key ripening genes.. <i>Plant Cell</i> , <b>2022</b> ,  | 11.6 | 2         |
| 148 | Genome-wide association study reveals the genetic architecture of 27 agronomic traits in tomato. <i>Plant Physiology</i> , <b>2021</b> , 186, 2078-2092   | 6.6  | 1         |
| 147 | Phytohormones in fruit development and maturation. <i>Plant Journal</i> , <b>2021</b> , 105, 446-458  | 6.9  | 48        |
| 146 | The NAC transcription factor FaRIF controls fruit ripening in strawberry. <i>Plant Cell</i> , <b>2021</b> , 33, 1574-1593   | 11.6 | 14        |
| 145 | A tomato LATERAL ORGAN BOUNDARIES transcription factor, , predominantly regulates cell wall and softening components of ripening. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2021</b> , 118, | 11.5 | 3         |
| 144 | Transmission modes affect the population structure of potato virus Y in potato. <i>PLoS Pathogens</i> , <b>2020</b> , 16, e1008608  | 7.6  | 7         |
| 143 | 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> , <b>2020</b> , 20, 283                      | 5.3  | 9         |
| 142 | Manipulation of ZDS in tomato exposes carotenoid- and ABA-specific effects on fruit development and ripening. <i>Plant Biotechnology Journal</i> , <b>2020</b> , 18, 2210-2224  | 11.6 | 21        |
| 141 | Longitudinal Transcriptomic, Proteomic, and Metabolomic Analysis of Response to Graft Inoculation by. <i>Journal of Proteome Research</i> , <b>2020</b> , 19, 2247-2263   | 5.6  | 12        |
| 140 | Metabolomics should be deployed in the identification and characterization of gene-edited crops. <i>Plant Journal</i> , <b>2020</b> , 102, 897-902  | 6.9  | 24        |
| 139 | Genome of <i>Solanum pimpinellifolium</i> provides insights into structural variants during tomato breeding. <i>Nature Communications</i> , <b>2020</b> , 11, 5817  | 17.4 | 24        |
| 138 | Comparative genomics of muskmelon reveals a potential role for retrotransposons in the modification of gene expression. <i>Communications Biology</i> , <b>2020</b> , 3, 432  | 6.7  | 9         |
| 137 | Tomato fruit as a model for tissue-specific gene silencing in crop plants. <i>Horticulture Research</i> , <b>2020</b> , 7, 142  | 7.7  | 7         |
| 136 | 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> , <b>2020</b> , 11,                                  | 4.2  | 4         |
| 135 | Genetic and metabolic effects of ripening mutations and vine detachment on tomato fruit quality. <i>Plant Biotechnology Journal</i> , <b>2020</b> , 18, 106-118   | 11.6 | 23        |
| 134 | Characterizing the involvement of FaMADS9 in the regulation of strawberry fruit receptacle development. <i>Plant Biotechnology Journal</i> , <b>2020</b> , 18, 929-943  | 11.6 | 10        |
| 133 | Relationships between genome methylation, levels of non-coding RNAs, mRNAs and metabolites in ripening tomato fruit. <i>Plant Journal</i> , <b>2020</b> , 103, 980-994  | 6.9  | 20        |

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| 132 | Plant Viruses Transmitted in Two Different Modes Produce Differing Effects on Small RNA-Mediated Processes in Their Aphid Vector. <i>Phytobiomes Journal</i> , <b>2019</b> , 3, 71-81   | 4.8  | 8   |
| 131 | Sequencing-Based Bin Map Construction of a Tomato Mapping Population, Facilitating High-Resolution Quantitative Trait Loci Detection. <i>Plant Genome</i> , <b>2019</b> , 12, 180010  | 4.4  | 32  |
| 130 | The tomato gene contributes to regulation of fruit ripening. <i>Horticulture Research</i> , <b>2019</b> , 6, 15   | 7.7  | 10  |
| 129 | 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> , <b>2019</b> , 15, e1008149 | 6    | 28  |
| 128 | The tomato pan-genome uncovers new genes and a rare allele regulating fruit flavor. <i>Nature Genetics</i> , <b>2019</b> , 51, 1044-1051  | 36.3 | 218 |
| 127 | Ectopic expression of ORANGE promotes carotenoid accumulation and fruit development in tomato. <i>Plant Biotechnology Journal</i> , <b>2019</b> , 17, 33-49   | 11.6 | 46  |
| 126 | The Locus of Confers Resistance to Race 1 Strains of pv. and to by Recognizing the Type III Effectors AvrRpt2 and RipBN. <i>Molecular Plant-Microbe Interactions</i> , <b>2019</b> , 32, 949-960  | 3.6  | 17  |
| 125 | Cucurbit Genomics Database (CuGenDB): a central portal for comparative and functional genomics of cucurbit crops. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, D1128-D1136   | 20.1 | 93  |
| 124 | Differential metabolism of L-phenylalanine in the formation of aromatic volatiles in melon ( <i>Cucumis melo</i> L.) fruit. <i>Phytochemistry</i> , <b>2018</b> , 148, 122-131  | 4    | 24  |
| 123 | High-resolution spatiotemporal transcriptome mapping of tomato fruit development and ripening. <i>Nature Communications</i> , <b>2018</b> , 9, 364  | 17.4 | 131 |
| 122 | Deciphering genetic factors that determine melon fruit-quality traits using RNA-Seq-based high-resolution QTL and eQTL mapping. <i>Plant Journal</i> , <b>2018</b> , 94, 169-191  | 6.9  | 57  |
| 121 | Tomato Multiomics Reveals Consequences of Crop Domestication and Improvement. <i>Cell</i> , <b>2018</b> , 172, 6-8  | 56.2 | 20  |
| 120 | Metabolomic analyses to evaluate the effect of drought stress on selected African Eggplant accessions. <i>Journal of the Science of Food and Agriculture</i> , <b>2018</b> , 98, 205-216  | 4.3  | 27  |
| 119 | AtPDS 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> , <b>2018</b> , 16, 482-494              | 11.6 | 31  |
| 118 | Natural genetic variation for expression of a SWEET transporter among wild species of <i>Solanum lycopersicum</i> (tomato) determines the hexose composition of ripening tomato fruit. <i>Plant Journal</i> , <b>2018</b> , 96, 343-357         | 6.9  | 35  |
| 117 | Fruit Ripening and its Manipulation <b>2018</b> , 278-303   |      |     |
| 116 | Fruit Ripening <b>2018</b> , 164-182  |      |     |
| 115 | Genome encode analyses reveal the basis of convergent evolution of fleshy fruit ripening. <i>Nature Plants</i> , <b>2018</b> , 4, 784-791   | 11.5 | 123 |

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|-----|---|------|-----|
| 114 | The Epigenome and Transcriptional Dynamics of Fruit Ripening. <i>Annual Review of Plant Biology</i> , <b>2017</b> , 68, 61-84   | 30.7 | 204 |
| 113 | The Tomato Expression Atlas. <i>Bioinformatics</i> , <b>2017</b> , 33, 2397-2398  | 7.2  | 39  |
| 112 | Overexpression of the class D MADS-box gene Sl-AGL11 impacts fleshy tissue differentiation and structure in tomato fruits. <i>Journal of Experimental Botany</i> , <b>2017</b> , 68, 4869-4884  | 7    | 29  |
| 111 | An InDel in the Promoter of Selected during Tomato Domestication Determines Fruit Malate Contents and Aluminum Tolerance. <i>Plant Cell</i> , <b>2017</b> , 29, 2249-2268   | 11.6 | 115 |
| 110 | Ripening activator turned repressor. <i>Nature Plants</i> , <b>2017</b> , 3, 920-921  | 11.5 | 4   |
| 109 | Carotenoid profiling of the leaves of selected African eggplant accessions subjected to drought stress. <i>Food Science and Nutrition</i> , <b>2017</b> , 5, 113-122  | 3.2  | 49  |
| 108 | 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> , <b>2016</b> , 113, 12580-12585 | 11.5 | 129 |
| 107 | Gr and hp-1 tomato mutants unveil unprecedented interactions between arbuscular mycorrhizal symbiosis and fruit ripening. <i>Planta</i> , <b>2016</b> , 244, 155-65   | 4.7  | 13  |
| 106 | Banana MaMADS Transcription Factors Are Necessary for Fruit Ripening and Molecular Tools to Promote Shelf-Life and Food Security. <i>Plant Physiology</i> , <b>2016</b> , 171, 380-91   | 6.6  | 67  |
| 105 | Identification of a Chromosome 4 Fruit Flavor and Nutritional Quality-Associated Metabolite QTL. <i>Frontiers in Plant Science</i> , <b>2016</b> , 7, 1671  | 6.2  | 19  |
| 104 | Involvement of an ethylene response factor in chlorophyll degradation during citrus fruit degreening. <i>Plant Journal</i> , <b>2016</b> , 86, 403-12   | 6.9  | 89  |
| 103 | Fruit carotenoid-deficient mutants in tomato reveal a function of the plastidial isopentenyl diphosphate isomerase (IDI1) in carotenoid biosynthesis. <i>Plant Journal</i> , <b>2016</b> , 88, 82-94  | 6.9  | 33  |
| 102 | Harnessing epigenome modifications for better crops. <i>Journal of Experimental Botany</i> , <b>2016</b> , 67, 2535-7   | 7    | 5   |
| 101 | iTAK: A Program for Genome-wide Prediction and Classification of Plant Transcription Factors, Transcriptional Regulators, and Protein Kinases. <i>Molecular Plant</i> , <b>2016</b> , 9, 1667-1670  | 14.4 | 352 |
| 100 | More than meets the eye: from carotenoid biosynthesis, to new insights into apocarotenoid signaling. <i>Current Opinion in Plant Biology</i> , <b>2015</b> , 27, 172-9  | 9.9  | 44  |
| 99  | Ethylene suppresses tomato ( <i>Solanum lycopersicum</i> ) fruit set through modification of gibberellin metabolism. <i>Plant Journal</i> , <b>2015</b> , 83, 237-51  | 6.9  | 76  |
| 98  | A DEMETER-like DNA demethylase governs tomato fruit ripening. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2015</b> , 112, 10804-9   | 11.5 | 173 |
| 97  | Tomato GOLDEN2-LIKE transcription factors reveal molecular gradients that function during fruit development and ripening. <i>Plant Cell</i> , <b>2014</b> , 26, 585-601   | 11.6 | 107 |

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|----|---|------|-----|
| 96 | Conserved changes in the dynamics of metabolic processes during fruit development and ripening across species. <i>Plant Physiology</i> , <b>2014</b> , 164, 55-68   | 6.6  | 42  |
| 95 | Genome sequence of the hot pepper provides insights into the evolution of pungency in Capsicum species. <i>Nature Genetics</i> , <b>2014</b> , 46, 270-8  | 36.3 | 594 |
| 94 | The genome of the stress-tolerant wild tomato species Solanum pennellii. <i>Nature Genetics</i> , <b>2014</b> , 46, 1034-8  | 36.3 | 269 |
| 93 | Genomic analyses provide insights into the history of tomato breeding. <i>Nature Genetics</i> , <b>2014</b> , 46, 1220-6  | 36.3 | 490 |
| 92 | Understanding development and ripening of fruit crops in an 'omics' era. <i>Horticulture Research</i> , <b>2014</b> , 1, 14034  | 7.7  | 43  |
| 91 | Transcriptomic analysis of Petunia hybrida in response to salt stress using high throughput RNA sequencing. <i>PLoS ONE</i> , <b>2014</b> , 9, e94651   | 3.7  | 34  |
| 90 | 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. <i>Plant Molecular Biology</i> , <b>2014</b> , 86, 395-407 | 4.6  | 5   |
| 89 | Fluorescence in situ hybridization and optical mapping to correct scaffold arrangement in the tomato genome. <i>G3: Genes, Genomes, Genetics</i> , <b>2014</b> , 4, 1395-405  | 3.2  | 61  |
| 88 | The draft genome of watermelon (Citrullus lanatus) and resequencing of 20 diverse accessions. <i>Nature Genetics</i> , <b>2013</b> , 45, 51-8   | 36.3 | 503 |
| 87 | Single-base resolution methylomes of tomato fruit development reveal epigenome modifications associated with ripening. <i>Nature Biotechnology</i> , <b>2013</b> , 31, 154-9  | 44.5 | 493 |
| 86 | Fruit An Angiosperm Innovation <b>2013</b> , 21-42  |      | 4   |
| 85 | Ethylene and the Control of Fruit Ripening <b>2013</b> , 43-73  |      | 32  |
| 84 | Carotenoid Biosynthesis and Chlorophyll Degradation <b>2013</b> , 75-116  |      | 9   |
| 83 | Phenylpropanoid Metabolism and Biosynthesis of Anthocyanins <b>2013</b> , 117-134   |      | 3   |
| 82 | Biosynthesis of Volatile Compounds <b>2013</b> , 135-161  |      | 12  |
| 81 | Cell Wall Architecture and Metabolism in Ripening Fruit and the Complex Relationship with Softening <b>2013</b> , 163-187   |      | 7   |
| 80 | Regulatory Networks Controlling Ripening <b>2013</b> , 189-206  |      | 1   |
| 79 | A STAY-GREEN protein SISGR1 regulates lycopene and $\beta$ -carotene accumulation by interacting directly with SLPY1 during ripening processes in tomato. <i>New Phytologist</i> , <b>2013</b> , 198, 442-452   | 9.8  | 91  |

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|----|---|------|-----|
| 78 | Molecular and genetic regulation of fruit ripening. <i>Plant Molecular Biology</i> , <b>2013</b> , 82, 575-91   | 4.6  | 200 |
| 77 | Biochemistry of Fruit Ripening <b>2013</b> , 1-19   |      | 17  |
| 76 | Catalyzing plant science research with RNA-seq. <i>Frontiers in Plant Science</i> , <b>2013</b> , 4, 66   | 6.2  | 102 |
| 75 | Differential regulation of Salmonella typhimurium genes involved in O-antigen capsule production and their role in persistence within tomato fruit. <i>Molecular Plant-Microbe Interactions</i> , <b>2013</b> , 26, 793-800                           | 3.6  | 23  |
| 74 | 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> , <b>2012</b> , 64, 94-103          | 6.2  | 31  |
| 73 | 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. <i>Plant Journal</i> , <b>2012</b> , 70, 191-204 | 6.9  | 214 |
| 72 | 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> , <b>2012</b> , 235, 453-71                            | 4.7  | 20  |
| 71 | 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> , <b>2012</b> , 7, 1639-47                                   | 2.5  | 9   |
| 70 | Enabling proteomic studies with RNA-Seq: The proteome of tomato pollen as a test case. <i>Proteomics</i> , <b>2012</b> , 12, 761-74   | 4.8  | 56  |
| 69 | Uniform ripening encodes a Golden 2-like transcription factor regulating tomato fruit chloroplast development. <i>Science</i> , <b>2012</b> , 336, 1711-5   | 33.3 | 253 |
| 68 | 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> , <b>2012</b> , 159, 1713-29 | 6.6  | 131 |
| 67 | Altered chloroplast development and delayed fruit ripening caused by mutations in a zinc metalloprotease at the lutescent2 locus of tomato. <i>Plant Physiology</i> , <b>2012</b> , 159, 1086-98  | 6.6  | 48  |
| 66 | Differential control of ethylene responses by GREEN-RIPE and GREEN-RIPE LIKE1 provides evidence for distinct ethylene signaling modules in tomato. <i>Plant Physiology</i> , <b>2012</b> , 160, 1968-84   | 6.6  | 33  |
| 65 | Genetics and control of tomato fruit ripening and quality attributes. <i>Annual Review of Genetics</i> , <b>2011</b> , 45, 41-59  | 14.5 | 613 |
| 64 | Regulatory control of high levels of carotenoid accumulation in potato tubers. <i>Plant, Cell and Environment</i> , <b>2011</b> , 34, 1020-1030   | 8.4  | 45  |
| 63 | 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> , <b>2011</b> , 68, 999-1013            | 6.9  | 98  |
| 62 | Expression of ripening-related genes in cold-stored tomato fruit. <i>Postharvest Biology and Technology</i> , <b>2011</b> , 61, 1-14  | 6.2  | 54  |
| 61 | High-throughput illumina strand-specific RNA sequencing library preparation. <i>Cold Spring Harbor Protocols</i> , <b>2011</b> , 2011, 940-9  | 1.2  | 310 |

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|----|--|------|-----|
| 60 | 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> , <b>2011</b> , 157, 1568-79   | 6.6  | 287 |
| 59 | Identification of genes in the phenylalanine metabolic pathway by ectopic expression of a MYB transcription factor in tomato fruit. <i>Plant Cell</i> , <b>2011</b> , 23, 2738-53  | 11.6 | 82  |
| 58 | 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. <i>Plant Physiology</i> , <b>2011</b> , 157, 405-25 | 6.6  | 245 |
| 57 | 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> , <b>2011</b> , 23, 3893-910  | 11.6 | 162 |
| 56 | A SEPALLATA gene is involved in the development and ripening of strawberry ( <i>Fragaria x ananassa</i> Duch.) fruit, a non-climacteric tissue. <i>Journal of Experimental Botany</i> , <b>2011</b> , 62, 1179-88  | 7    | 145 |
| 55 | A tomato ( <i>Solanum lycopersicum</i> ) APETALA2/ERF gene, SLAP2a, is a negative regulator of fruit ripening. <i>Plant Journal</i> , <b>2010</b> , 64, 936-47   | 6.9  | 269 |
| 54 | Genomic analysis of wild tomato introgressions determining metabolism- and yield-associated traits. <i>Plant Physiology</i> , <b>2010</b> , 152, 1772-86   | 6.6  | 45  |
| 53 | Integrative transcript and metabolite analysis of nutritionally enhanced DE-ETIOLATED1 downregulated tomato fruit. <i>Plant Cell</i> , <b>2010</b> , 22, 1190-215  | 11.6 | 136 |
| 52 | Developmental and feedforward control of the expression of folate biosynthesis genes in tomato fruit. <i>Molecular Plant</i> , <b>2010</b> , 3, 66-77  | 14.4 | 36  |
| 51 | Branched-chain and aromatic amino acid catabolism into aroma volatiles in <i>Cucumis melo</i> L. fruit. <i>Journal of Experimental Botany</i> , <b>2010</b> , 61, 1111-23  | 7    | 183 |
| 50 | Functional diversification of AGAMOUS lineage genes in regulating tomato flower and fruit development. <i>Journal of Experimental Botany</i> , <b>2010</b> , 61, 1795-806  | 7    | 97  |
| 49 | The regulation of MADS-box gene expression during ripening of banana and their regulatory interaction with ethylene. <i>Journal of Experimental Botany</i> , <b>2010</b> , 61, 1523-35   | 7    | 101 |
| 48 | Modest calcium increase in tomatoes expressing a variant of Arabidopsis cation/H <sup>+</sup> antiporter. <i>Plant Biotechnology Reports</i> , <b>2010</b> , 4, 15-21  | 2.5  | 22  |
| 47 | Cell wall metabolism in cold-stored tomato fruit. <i>Postharvest Biology and Technology</i> , <b>2010</b> , 57, 106-113  | 6.2  | 38  |
| 46 | Fleshy fruit expansion and ripening are regulated by the Tomato SHATTERPROOF gene TAGL1. <i>Plant Cell</i> , <b>2009</b> , 21, 3041-62   | 11.6 | 311 |
| 45 | Plant MetGenMAP: an integrative analysis system for plant systems biology. <i>Plant Physiology</i> , <b>2009</b> , 151, 1758-68  | 6.6  | 120 |
| 44 | 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> , <b>2009</b> , 51, 131-140                          | 6.2  | 30  |
| 43 | Biology and genetic engineering of fruit maturation for enhanced quality and shelf-life. <i>Current Opinion in Biotechnology</i> , <b>2009</b> , 20, 197-203   | 11.4 | 103 |



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|----|--|------|-----|
| 42 | Molecular biology of ethylene during tomato fruit development and maturation. <i>Plant Science</i> , <b>2008</b> , 175, 106-113  | 5.3  | 150 |
| 41 | Sequencing and comparative analysis of a conserved syntenic segment in the Solanaceae. <i>Genetics</i> , <b>2008</b> , 180, 391-408  | 4    | 84  |
| 40 | Amino acid substitutions in homologs of the STAY-GREEN protein are responsible for the green-flesh and chlorophyll retainer mutations of tomato and pepper. <i>Plant Physiology</i> , <b>2008</b> , 147, 179-87  | 6.6  | 166 |
| 39 | Tomato gamma-glutamylhydrolases: expression, characterization, and evidence for heterodimer formation. <i>Plant Physiology</i> , <b>2008</b> , 148, 775-85   | 6.6  | 17  |
| 38 | 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> , <b>2008</b> , 148, 1830-46                                     | 6.6  | 75  |
| 37 | The molecular and biochemical basis for varietal variation in sesquiterpene content in melon ( <i>Cucumis melo</i> L.) rinds. <i>Plant Molecular Biology</i> , <b>2008</b> , 66, 647-61  | 4.6  | 60  |
| 36 | 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> , <b>2007</b> , 50, 1063-78  | 6.9  | 63  |
| 35 | Fruit ripening mutants yield insights into ripening control. <i>Current Opinion in Plant Biology</i> , <b>2007</b> , 10, 283-9   | 9.9  | 377 |
| 34 | Ethylene and Fruit Ripening. <i>Journal of Plant Growth Regulation</i> , <b>2007</b> , 26, 143-159   | 4.7  | 342 |
| 33 | Completing a pathway to plant vitamin C synthesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2007</b> , 104, 9109-10   | 11.5 | 30  |
| 32 | 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> , <b>2006</b> , 103, 7923-8              | 11.5 | 182 |
| 31 | A naturally occurring epigenetic mutation in a gene encoding an SBP-box transcription factor inhibits tomato fruit ripening. <i>Nature Genetics</i> , <b>2006</b> , 38, 948-52   | 36.3 | 861 |
| 30 | Transcriptome and selected metabolite analyses reveal multiple points of ethylene control during tomato fruit development. <i>Plant Cell</i> , <b>2005</b> , 17, 2954-65   | 11.6 | 400 |
| 29 | Ethylene insensitivity conferred by the Green-ripe and Never-ripe 2 ripening mutants of tomato. <i>Plant Physiology</i> , <b>2005</b> , 138, 267-75  | 6.6  | 100 |
| 28 | Utilization of tomato microarrays for comparative gene expression analysis in the Solanaceae. <i>Journal of Experimental Botany</i> , <b>2005</b> , 56, 2885-95  | 7    | 93  |
| 27 | Role of beta-oxidation in jasmonate biosynthesis and systemic wound signaling in tomato. <i>Plant Cell</i> , <b>2005</b> , 17, 971-86  | 11.6 | 239 |
| 26 | 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> , <b>2004</b> , 101, 1496-501 | 11.5 | 99  |
| 25 | Tackling the plant proteome: practical approaches, hurdles and experimental tools. <i>Plant Journal</i> , <b>2004</b> , 39, 715-33   | 6.9  | 264 |



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|----|---|------|-----|
| 24 | Comprehensive EST analysis of tomato and comparative genomics of fruit ripening. <i>Plant Journal</i> , <b>2004</b> , 40, 47-59   | 6.9  | 196 |
| 23 | Folate synthesis in plants: the last step of the p-aminobenzoate branch is catalyzed by a plastidial aminodeoxychorismate lyase. <i>Plant Journal</i> , <b>2004</b> , 40, 453-61  | 6.9  | 62  |
| 22 | Genetic regulation of fruit development and ripening. <i>Plant Cell</i> , <b>2004</b> , 16 Suppl, S170-80   | 11.6 | 904 |
| 21 | LeCTR1, a tomato CTR1-like gene, demonstrates ethylene signaling ability in Arabidopsis and novel expression patterns in tomato. <i>Plant Physiology</i> , <b>2002</b> , 130, 1132-42   | 6.6  | 122 |
| 20 | 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> , <b>2002</b> , 14, 1441-56 | 11.6 | 259 |
| 19 | Characterization of a major latex protein (MLP) gene down-regulated by ethylene during peach fruitlet abscission. <i>Plant Science</i> , <b>2002</b> , 163, 265-272   | 5.3  | 33  |
| 18 | Genetic Control of Fruit Quality, and Prospects for Nutrient Modification. <i>Hortscience: A Publication of the American Society for Horticultural Science</i> , <b>2002</b> , 37, 453-456  | 2.4  | 3   |
| 17 | Analysis of the ethylene response in the epinastic mutant of tomato. <i>Plant Physiology</i> , <b>2001</b> , 127, 58-66   | 6.6  | 42  |
| 16 | Determining the Physical Limits of the Brassica S Locus by Recombinational Analysis. <i>Plant Cell</i> , <b>2000</b> , 12, 23   | 11.6 | 2   |
| 15 | Molecular and genetic characterization of a novel pleiotropic tomato-ripening mutant. <i>Plant Physiology</i> , <b>1999</b> , 120, 383-90   | 6.6  | 172 |
| 14 | Identification of Plastome Variants useful for Cytoplasmic Selection and Cultivar Identification in Onion. <i>Journal of the American Society for Horticultural Science</i> , <b>1999</b> , 124, 122-127                              | 2.3  | 3   |
| 13 | Transgenic analysis of tomato endo- $\beta$ ,4-glucanase gene function. Role of cel1 in floral abscission. <i>Plant Journal</i> , <b>1998</b> , 13, 303-310   | 6.9  | 94  |
| 12 | Application of Genetic Bit Analysis (GBATM) for allelic selection in plant breeding. <i>Molecular Breeding</i> , <b>1997</b> , 3, 495-502   | 3.4  | 10  |
| 11 | Rapid and reliable screening of a tomato YAC library exclusively based on PCR. <i>Plant Molecular Biology Reporter</i> , <b>1996</b> , 14, 58-67  | 1.7  | 6   |
| 10 | 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> , <b>1995</b> , 13, 70-81                        | 1.7  | 18  |
| 9  | Rapid isolation of terminal sequences from cloned plant DNA fragments. <i>Plant Molecular Biology Reporter</i> , <b>1995</b> , 13, 369-376  | 1.7  | 1   |
| 8  | 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> , <b>1995</b> , 248, 195-206          |      | 43  |
| 7  | Molecular and Genetic Analysis of Tomato Fruit Development and Ripening. <i>Methods in Plant Biochemistry</i> , <b>1993</b> , 10, 251-285   |      | 3   |

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|---|---|------|-----|
| 6 | Isolation of molecular markers from specific chromosomal intervals using DNA pools from existing mapping populations. <i>Nucleic Acids Research</i> , <b>1991</b> , 19, 6553-8                          | 20.1 | 294 |
| 5 | Polygalacturonase Isozymes and Pectin Depolymerization in Transgenic rin Tomato Fruit. <i>Plant Physiology</i> , <b>1990</b> , 94, 1882-6   | 6.6  | 80  |
| 4 | Expression of a Chimeric Polygalacturonase Gene in Transgenic rin (Ripening Inhibitor) Tomato Fruit Results in Polyuronide Degradation but Not Fruit Softening. <i>Plant Cell</i> , <b>1989</b> , 1, 53 | 11.6 | 32  |
| 3 | Melon ethylene-mediated transcriptome and methylome dynamics provide insights to volatile production  |      | 1   |
| 2 | Genome of <i>Solanum pimpinellifolium</i> provides insights into structural variants during tomato breeding   |      | 1   |
| 1 | An improved de novo assembly and annotation of the tomato reference genome using single-molecule sequencing, Hi-C proximity ligation and optical maps   |      | 36  |