

List of Publications by Citations

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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.

76 papers	7,431 citations	40 h-index	80 g-index
80 ext. papers	9,748 ext. citations	8.7 avg, IF	6.64 L-index

#	Paper	IF	Citations
76	The tomato genome sequence provides insights into fleshy fruit evolution. <i>Nature</i> , 2012 , 485, 635-41	50.4	2138
75	The draft genome of watermelon (<i>Citrullus lanatus</i>) and resequencing of 20 diverse accessions. <i>Nature Genetics</i> , 2013 , 45, 51-8	36.3	503
74	Single-base resolution methylomes of tomato fruit development reveal epigenome modifications associated with ripening. <i>Nature Biotechnology</i> , 2013 , 31, 154-9	44.5	493
73	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	14.4	352
72	High-throughput illumina strand-specific RNA sequencing library preparation. <i>Cold Spring Harbor Protocols</i> , 2011 , 2011, 940-9	1.2	310
71	The draft genome of whitefly <i>Bemisia tabaci</i> MEAM1, a global crop pest, provides novel insights into virus transmission, host adaptation, and insecticide resistance. <i>BMC Biology</i> , 2016 , 14, 110	7.3	178
70	Evolution and expression analysis of the grape (<i>Vitis vinifera</i> L.) WRKY gene family. <i>Journal of Experimental Botany</i> , 2014 , 65, 1513-28	7	169
69	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, 3893-910	11.6	162
68	Transcriptome sequencing and comparative analysis of cucumber flowers with different sex types. <i>BMC Genomics</i> , 2010 , 11, 384	4.5	146
67	High-resolution spatiotemporal transcriptome mapping of tomato fruit development and ripening. <i>Nature Communications</i> , 2018 , 9, 364	17.4	131
66	VirusDetect: An automated pipeline for efficient virus discovery using deep sequencing of small RNAs. <i>Virology</i> , 2017 , 500, 130-138	3.6	115
65	iAssembler: a package for de novo assembly of Roche-454/Sanger transcriptome sequences. <i>BMC Bioinformatics</i> , 2011 , 12, 453	3.6	111
64	Tomato GOLDEN2-LIKE transcription factors reveal molecular gradients that function during fruit development and ripening. <i>Plant Cell</i> , 2014 , 26, 585-601	11.6	107
63	Characterization of transcriptome dynamics during watermelon fruit development: sequencing, assembly, annotation and gene expression profiles. <i>BMC Genomics</i> , 2011 , 12, 454	4.5	97
62	Cucurbit Genomics Database (CuGenDB): a central portal for comparative and functional genomics of cucurbit crops. <i>Nucleic Acids Research</i> , 2019 , 47, D1128-D1136	20.1	93
61	Transcriptomics-based screen for genes induced by flagellin and repressed by pathogen effectors identifies a cell wall-associated kinase involved in plant immunity. <i>Genome Biology</i> , 2013 , 14, R139	18.3	92
60	Genome-wide identification and analysis of the SBP-box family genes in apple (<i>Malus domestica</i> Borkh.). <i>Plant Physiology and Biochemistry</i> , 2013 , 70, 100-14	5.4	92

59	Draft genome of spinach and transcriptome diversity of 120 <i>Spinacia</i> accessions. <i>Nature Communications</i> , 2017 , 8, 15275	17.4	90
58	RhNAC2 and RhEXPA4 are involved in the regulation of dehydration tolerance during the expansion of rose petals. <i>Plant Physiology</i> , 2012 , 160, 2064-82	6.6	90
57	TAL effector driven induction of a SWEET gene confers susceptibility to bacterial blight of cotton. <i>Nature Communications</i> , 2017 , 8, 15588	17.4	88
56	An NAC transcription factor controls ethylene-regulated cell expansion in flower petals. <i>Plant Physiology</i> , 2013 , 163, 775-91	6.6	87
55	Comprehensive Tissue-Specific Transcriptome Analysis Reveals Distinct Regulatory Programs during Early Tomato Fruit Development. <i>Plant Physiology</i> , 2015 , 168, 1684-701	6.6	86
54	Tomato Functional Genomics Database: a comprehensive resource and analysis package for tomato functional genomics. <i>Nucleic Acids Research</i> , 2011 , 39, D1156-63	20.1	83
53	Vascular-mediated signalling involved in early phosphate stress response in plants. <i>Nature Plants</i> , 2016 , 2, 16033	11.5	80
52	Comparative genomics reveals candidate carotenoid pathway regulators of ripening watermelon fruit. <i>BMC Genomics</i> , 2013 , 14, 781	4.5	77
51	Ethylene suppresses tomato (<i>Solanum lycopersicum</i>) fruit set through modification of gibberellin metabolism. <i>Plant Journal</i> , 2015 , 83, 237-51	6.9	76
50	Comprehensive Transcriptome Analyses Reveal that Potato Spindle Tuber Viroid Triggers Genome-Wide Changes in Alternative Splicing, Inducible -Acting Activity of Phased Secondary Small Interfering RNAs, and Immune Responses. <i>Journal of Virology</i> , 2017 , 91,	6.6	73
49	Distinct Mechanisms of the ORANGE Protein in Controlling Carotenoid Flux. <i>Plant Physiology</i> , 2017 , 173, 376-389	6.6	69
48	Comparative Transcriptome Analysis of Cultivated and Wild Watermelon during Fruit Development. <i>PLoS ONE</i> , 2015 , 10, e0130267	3.7	61
47	Integrative analysis of miRNA and mRNA profiles in response to ethylene in rose petals during flower opening. <i>PLoS ONE</i> , 2013 , 8, e64290	3.7	60
46	Genome-wide identification, evolutionary and expression analysis of the aspartic protease gene superfamily in grape. <i>BMC Genomics</i> , 2013 , 14, 554	4.5	59
45	Genome-wide Identification and Expression Analysis of the CDPK Gene Family in Grape, <i>Vitis</i> spp. <i>BMC Plant Biology</i> , 2015 , 15, 164	5.3	57
44	Comprehensive Transcriptome Profiling Reveals Long Noncoding RNA Expression and Alternative Splicing Regulation during Fruit Development and Ripening in Kiwifruit (<i>Actinidia chinensis</i>). <i>Frontiers in Plant Science</i> , 2016 , 7, 335	6.2	54
43	Transcriptomic analysis reveals tomato genes whose expression is induced specifically during effector-triggered immunity and identifies the Epk1 protein kinase which is required for the host response to three bacterial effector proteins. <i>Genome Biology</i> , 2014 , 15, 492	18.3	52
42	A dynamic evolutionary and functional landscape of plant phased small interfering RNAs. <i>BMC Biology</i> , 2015 , 13, 32	7.3	50

41	Modulation of RNA polymerase II phosphorylation downstream of pathogen perception orchestrates plant immunity. <i>Cell Host and Microbe</i> , 2014 , 16, 748-58	23.4	47
40	Analysis of expressed sequence tags generated from full-length enriched cDNA libraries of melon. <i>BMC Genomics</i> , 2011 , 12, 252	4.5	47
39	A cost-effective method for Illumina small RNA-Seq library preparation using T4 RNA ligase 1 adenylated adapters. <i>Plant Methods</i> , 2012 , 8, 41	5.8	45
38	Elucidation of the Mechanisms of Long-Distance mRNA Movement in a /Tomato Heterograft System. <i>Plant Physiology</i> , 2018 , 177, 745-758	6.6	44
37	A tomato phloem-mobile protein regulates the shoot-to-root ratio by mediating the auxin response in distant organs. <i>Plant Journal</i> , 2015 , 83, 853-63	6.9	44
36	The Tomato Expression Atlas. <i>Bioinformatics</i> , 2017 , 33, 2397-2398	7.2	39
35	Use of RNA-seq data to identify and validate RT-qPCR reference genes for studying the tomato-Pseudomonas pathosystem. <i>Scientific Reports</i> , 2017 , 7, 44905	4.9	39
34	A bulk segregant transcriptome analysis reveals metabolic and cellular processes associated with Orange allelic variation and fruit β -carotene accumulation in melon fruit. <i>BMC Plant Biology</i> , 2015 , 15, 274	5.3	35
33	De novo and comparative transcriptome analysis of cultivated and wild spinach. <i>Scientific Reports</i> , 2015 , 5, 17706	4.9	34
32	Genome-wide identification and analysis of the apple (<i>Malus domestica</i> Borkh.) TIFY gene family. <i>Tree Genetics and Genomes</i> , 2015 , 11, 1	2.1	32
31	Transcriptome Analysis of Mango (<i>Mangifera indica</i> L.) Fruit Epidermal Peel to Identify Putative Cuticle-Associated Genes. <i>Scientific Reports</i> , 2017 , 7, 46163	4.9	31
30	Evolutionary and expression analysis of a MADS-box gene superfamily involved in ovule development of seeded and seedless grapevines. <i>Molecular Genetics and Genomics</i> , 2015 , 290, 825-46	3.1	29
29	Transcriptome analysis of the whitefly, <i>Bemisia tabaci</i> MEAM1 during feeding on tomato infected with the crinivirus, Tomato chlorosis virus, identifies a temporal shift in gene expression and differential regulation of novel orphan genes. <i>BMC Genomics</i> , 2017 , 18, 370	4.5	28
28	Incomplete transfer of accessory loci influencing SbMATE expression underlies genetic background effects for aluminum tolerance in sorghum. <i>Plant Journal</i> , 2013 , 73, 276-88	6.9	27
27	Genome-wide identification and analysis of the aldehyde dehydrogenase (ALDH) gene superfamily in apple (<i>Malus domestica</i> Borkh.). <i>Plant Physiology and Biochemistry</i> , 2013 , 71, 268-82	5.4	26
26	RadishBase: a database for genomics and genetics of radish. <i>Plant and Cell Physiology</i> , 2013 , 54, e3	4.9	26
25	Identification of miRNAs and their targets through high-throughput sequencing and degradome analysis in male and female <i>Asparagus officinalis</i> . <i>BMC Plant Biology</i> , 2016 , 16, 80	5.3	23
24	Comparative Transcriptomes Analysis of Red- and White-Fleshed Apples in an F1 Population of <i>Malus sieversii</i> f. <i>niedzwetzkyana</i> Crossed with <i>M. domestica</i> 'Fuji' <i>PLoS ONE</i> , 2015 , 10, e0133468	3.7	22

23	Suppressing Sorbitol Synthesis Substantially Alters the Global Expression Profile of Stress Response Genes in Apple (<i>Malus domestica</i>) Leaves. <i>Plant and Cell Physiology</i> , 2015 , 56, 1748-61	4.9	21
22	Identification of a Chromosome 4 Fruit Flavor and Nutritional Quality-Associated Metabolite QTL. <i>Frontiers in Plant Science</i> , 2016 , 7, 1671	6.2	19
21	Transcriptome-based identification and validation of reference genes for plant-bacteria interaction studies using <i>Nicotiana benthamiana</i> . <i>Scientific Reports</i> , 2019 , 9, 1632	4.9	18
20	The SAFEGUARD1 suppresses singlet oxygen-induced stress responses by protecting grana margins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 6918-6927	11.5	18
19	Plant lncRNAs are enriched in and move systemically through the phloem in response to phosphate deficiency. <i>Journal of Integrative Plant Biology</i> , 2019 , 61, 492-508	8.3	17
18	SpinachBase: a central portal for spinach genomics. <i>Database: the Journal of Biological Databases and Curation</i> , 2019 , 2019,	5	16
17	Comprehensive analysis of expressed sequence tags from cultivated and wild radish (<i>Raphanus</i> spp.). <i>BMC Genomics</i> , 2013 , 14, 721	4.5	15
16	Complete Genome Sequence of Southern tomato virus Identified in China Using Next-Generation Sequencing. <i>Genome Announcements</i> , 2015 , 3,		14
15	Transcriptomic and functional analysis of cucumber (<i>Cucumis sativus</i> L.) fruit phloem during early development. <i>Plant Journal</i> , 2018 , 96, 982-996	6.9	14
14	Kiwifruit Genome Database (KGD): a comprehensive resource for kiwifruit genomics. <i>Horticulture Research</i> , 2020 , 7, 117	7.7	13
13	Comprehensive transcriptome analyses reveal tomato plant responses to tobacco rattle virus-based gene silencing vectors. <i>Scientific Reports</i> , 2017 , 7, 9771	4.9	11
12	First complete genome sequence of an emerging cucumber green mottle mosaic virus isolate in north america. <i>Genome Announcements</i> , 2015 , 3,		10
11	Identification of Conserved Gene-Regulatory Networks that Integrate Environmental Sensing and Growth in the Root Cambium. <i>Current Biology</i> , 2020 , 30, 2887-2900.e7	6.3	10
10	Complete Genome Sequence of Southern tomato virus Naturally Infecting Tomatoes in Bangladesh. <i>Genome Announcements</i> , 2015 , 3,		9
9	Complete Genome Sequence of a Tomato-Infecting Tomato Mottle Mosaic Virus in New York. <i>Genome Announcements</i> , 2015 , 3,		7
8	A novel method of transcriptome interpretation reveals a quantitative suppressive effect on tomato immune signaling by two domains in a single pathogen effector protein. <i>BMC Genomics</i> , 2016 , 17, 229	4.5	5
7	Comparative transcriptome analyses shed light on carotenoid production and plastid development in melon fruit. <i>Horticulture Research</i> , 2021 , 8, 112	7.7	5
6	Complete Genome Sequence of an Emerging Melon Necrotic Spot Virus Isolate Infecting Greenhouse Cucumber in North America. <i>Genome Announcements</i> , 2015 , 3,		4

5	Integration of Metabolome and Transcriptome Studies Reveals Flavonoids, Absciscic Acid, and Nitric Oxide Comodulating the Freezing Tolerance in .. <i>Frontiers in Plant Science</i> , 2021 , 12, 764625	6.2	3
4	Identification of Phloem Mobile mRNAs Using the Solanaceae Heterograft System. <i>Methods in Molecular Biology</i> , 2019 , 2014, 421-431	1.4	2
3	Natural Genetic Diversity in Tomato Flavor Genes. <i>Frontiers in Plant Science</i> , 2021 , 12, 642828	6.2	1
2	The tomato yellow leaf curl virus C4 protein alters the expression of plant developmental genes correlating to leaf upward cupping phenotype in tomato.. <i>PLoS ONE</i> , 2022 , 17, e0257936	3.7	0
1	Beta-Amylase and Phosphatidic Acid Involved in Recalcitrant Seed Germination of Chinese Chestnut.. <i>Frontiers in Plant Science</i> , 2022 , 13, 828270	6.2	