Yi Zheng

List of Publications by Year
in descending order

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		53794	71685
77 papers	10,916 citations	45 h-index	76 g-index
80 all docs	80 docs citations	80 times ranked	12623 citing authors

#	Article	IF	Citations
1	The tomato genome sequence provides insights into fleshy fruit evolution. Nature, 2012, 485, 635-641.	27.8	2,860
2	iTAK: A Program for Genome-wide Prediction andÂClassification of Plant Transcription Factors, Transcriptional Regulators, and Protein Kinases. Molecular Plant, 2016, 9, 1667-1670.	8.3	735
3	The draft genome of watermelon (Citrullus lanatus) and resequencing of 20 diverse accessions. Nature Genetics, 2013, 45, 51-58.	21.4	731
4	Single-base resolution methylomes of tomato fruit development reveal epigenome modifications associated with ripening. Nature Biotechnology, 2013, 31, 154-159.	17.5	693
5	High-Throughput Illumina Strand-Specific RNA Sequencing Library Preparation. Cold Spring Harbor Protocols, 2011, 2011, pdb.prot5652.	0.3	382
6	The draft genome of whitefly Bemisia tabaci MEAM1, a global crop pest, provides novel insights into virus transmission, host adaptation, and insecticide resistance. BMC Biology, 2016, 14, 110.	3.8	265
7	High-resolution spatiotemporal transcriptome mapping of tomato fruit development and ripening. Nature Communications, 2018, 9, 364.	12.8	255
8	Evolution and expression analysis of the grape (Vitis vinifera L.) WRKY gene family. Journal of Experimental Botany, 2014, 65, 1513-1528.	4.8	246
9	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.	6.6	193
10	Tomato <i>GOLDEN2-LIKE</i> Transcription Factors Reveal Molecular Gradients That Function during Fruit Development and Ripening. Plant Cell, 2014, 26, 585-601.	6.6	193
11	VirusDetect: An automated pipeline for efficient virus discovery using deep sequencing of small RNAs. Virology, 2017, 500, 130-138.	2.4	191
12	Cucurbit Genomics Database (CuGenDB): a central portal for comparative and functional genomics of cucurbit crops. Nucleic Acids Research, 2019, 47, D1128-D1136.	14.5	177
13	Transcriptome sequencing and comparative analysis of cucumber flowers with different sex types. BMC Genomics, 2010, 11, 384.	2.8	161
14	Draft genome of spinach and transcriptome diversity of 120 Spinacia accessions. Nature Communications, 2017, 8, 15275.	12.8	156
15	Genome-wide identification and analysis of the SBP-box family genes in apple (MalusÂÃ—Âdomestica) Tj ETQq1 1 0.784314 rgBT /Overl	5.8	145
16	TAL effector driven induction of a SWEET gene confers susceptibility to bacterial blight of cotton. Nature Communications, 2017, 8, 15588.	12.8	144
17	Comprehensive Tissue-Specific Transcriptome Analysis Reveals Distinct Regulatory Programs during Early Tomato Fruit Development. Plant Physiology, 2015, 168, 1684-1701.	4.8	142
18	Transcriptomics-based screen for genes induced by flagellin and repressed by pathogen effectors identifies a cell wall-associated kinase involved in plant immunity. Genome Biology, 2013, 14, R139.	9.6	137

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19	Ethylene suppresses tomato (<i>Solanum lycopersicum</i>) fruit set through modification of gibberellin metabolism. Plant Journal, 2015, 83, 237-251.	5.7	128
20	Characterization of transcriptome dynamics during watermelon fruit development: sequencing, assembly, annotation and gene expression profiles. BMC Genomics, 2011, 12, 454.	2.8	126
21	Vascular-mediated signalling involved in early phosphate stress response in plants. Nature Plants, 2016, 2, 16033.	9.3	124
22	An NAC Transcription Factor Controls Ethylene-Regulated Cell Expansion in Flower Petals. Plant Physiology, 2013, 163, 775-791.	4.8	122
23	iAssembler: a package for de novo assembly of Roche-454/Sanger transcriptome sequences. BMC Bioinformatics, 2011, 12, 453.	2.6	120
24	Tomato Functional Genomics Database: a comprehensive resource and analysis package for tomato functional genomics. Nucleic Acids Research, 2011, 39, D1156-D1163.	14.5	113
25	<i>RhNAC2</i> and <i>RhEXPA4</i> Are Involved in the Regulation of Dehydration Tolerance during the Expansion of Rose Petals. Plant Physiology, 2012, 160, 2064-2082.	4.8	110
26	Comprehensive Transcriptome Analyses Reveal that Potato Spindle Tuber Viroid Triggers Genome-Wide Changes in Alternative Splicing, Inducible <i>trans</i> -Acting Activity of Phased Secondary Small Interfering RNAs, and Immune Responses. Journal of Virology, 2017, 91, .	3.4	107
27	Comparative Transcriptome Analysis of Cultivated and Wild Watermelon during Fruit Development. PLoS ONE, 2015, 10, e0130267.	2.5	106
28	Comparative genomics reveals candidate carotenoid pathway regulators of ripening watermelon fruit. BMC Genomics, 2013, 14, 781.	2.8	103
29	Distinct Mechanisms of the ORANGE Protein in Controlling Carotenoid Flux. Plant Physiology, 2017, 173, 376-389.	4.8	97
30	Comprehensive Transcriptome Profiling Reveals Long Noncoding RNA Expression and Alternative Splicing Regulation during Fruit Development and Ripening in Kiwifruit (Actinidia chinensis). Frontiers in Plant Science, 2016, 7, 335.	3.6	89
31	Genome-wide identification, evolutionary and expression analysis of the aspartic protease gene superfamily in grape. BMC Genomics, 2013, 14, 554.	2.8	85
32	Genome-wide Identification and Expression Analysis of the CDPK Gene Family in Grape, Vitis spp. BMC Plant Biology, 2015, 15, 164.	3.6	85
33	Use of RNA-seq data to identify and validate RT-qPCR reference genes for studying the tomato-Pseudomonas pathosystem. Scientific Reports, 2017, 7, 44905.	3.3	85
34	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. Genome Biology, 2014, 15, 492.	8.8	75
35	Elucidation of the Mechanisms of Long-Distance mRNA Movement in a <i>Nicotiana benthamiana</i>/Tomato Heterograft System. Plant Physiology, 2018, 177, 745-758.	4.8	72
36	Modulation of RNA Polymerase II Phosphorylation Downstream of Pathogen Perception Orchestrates Plant Immunity. Cell Host and Microbe, 2014, 16, 748-758.	11.0	70

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37	Integrative Analysis of miRNA and mRNA Profiles in Response to Ethylene in Rose Petals during Flower Opening. PLoS ONE, 2013, 8, e64290.	2.5	70
38	Transcriptome Analysis of Mango (Mangifera indica L.) Fruit Epidermal Peel to Identify Putative Cuticle-Associated Genes. Scientific Reports, 2017, 7, 46163.	3.3	68
39	The Tomato Expression Atlas. Bioinformatics, 2017, 33, 2397-2398.	4.1	64
40	A bulk segregant transcriptome analysis reveals metabolic and cellular processes associated with Orange allelic variation and fruit Î²-carotene accumulation in melon fruit. BMC Plant Biology, 2015, 15, 274.	3.6	58
41	A dynamic evolutionary and functional landscape of plant phased small interfering RNAs. BMC Biology, 2015, 13, 32.	3.8	57
42	A cost-effective method for Illumina small RNA-Seq library preparation using T4 RNA ligase 1 adenylated adapters. Plant Methods, 2012, 8, 41.	4.3	56
43	Genome-wide identification and analysis of the apple (Malus Ã— domestica Borkh.) TIFY gene family. Tree Genetics and Genomes, 2015, 11, 1.	1.6	51
44	A tomato phloemâ€mobile protein regulates the shootâ€toâ€root ratio by mediating the auxin response in distant organs. Plant Journal, 2015, 83, 853-863.	5.7	50
45	Analysis of expressed sequence tags generated from full-length enriched cDNA libraries of melon. BMC Genomics, 2011, 12, 252.	2.8	49
46	Transcriptome analysis of the whitefly, Bemisia tabaci 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. BMC Genomics, 2017, 18, 370.	2.8	49
47	Kiwifruit Genome Database (KGD): a comprehensive resource for kiwifruit genomics. Horticulture Research, 2020, 7, 117.	6.3	47
48	Evolutionary and expression analysis of a MADS-box gene superfamily involved in ovule development of seeded and seedless grapevines. Molecular Genetics and Genomics, 2015, 290, 825-846.	2.1	46
49	De novo and comparative transcriptome analysis of cultivated and wild spinach. Scientific Reports, 2016, 5, 17706.	3.3	41
50	The <i>Arabidopsis</i> SAFEGUARD1 suppresses singlet oxygen-induced stress responses by protecting grana margins. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 6918-6927.	7.1	41
51	Plant lncRNAs are enriched in and move systemically through the phloem in response to phosphate deficiency. Journal of Integrative Plant Biology, 2019, 61, 492-508.	8.5	37
52	Genome-wide identification and analysis of the aldehyde dehydrogenase (ALDH) gene superfamily in apple (MalusÂÃ—Âdomestica Borkh.). Plant Physiology and Biochemistry, 2013, 71, 268-282.	5.8	36
53	Identification of a Solanum pennellii Chromosome 4 Fruit Flavor and Nutritional Quality-Associated Metabolite QTL. Frontiers in Plant Science, 2016, 7, 1671.	3.6	35
54	Transcriptome-based identification and validation of reference genes for plant-bacteria interaction studies using Nicotiana benthamiana. Scientific Reports, 2019, 9, 1632.	3.3	34

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55	RadishBase: A Database for Genomics and Genetics of Radish. Plant and Cell Physiology, 2013, 54, e3-e3.	3.1	32
56	Incomplete transfer of accessory loci influencing <i><scp>S</scp>b<scp>MATE</scp></i> expression underlies genetic background effects for aluminum tolerance in sorghum. Plant Journal, 2013, 73, 276-288.	5.7	31
57	Identification of miRNAs and their targets through high-throughput sequencing and degradome analysis in male and female Asparagus officinalis. BMC Plant Biology, 2016, 16, 80.	3.6	31
58	Transcriptomic and functional analysis of cucumber (<i>Cucumis sativus</i> L.) fruit phloem during early development. Plant Journal, 2018, 96, 982-996.	5.7	30
59	SpinachBase: a central portal for spinach genomics. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	30
60	Comparative Transcriptomes Analysis of Red- and White-Fleshed Apples in an F1 Population of Malus sieversii f. niedzwetzkyana Crossed with M. domestica â€˜Fujiâ€™. PLoS ONE, 2015, 10, e0133468.	2.5	29
61	Suppressing Sorbitol Synthesis Substantially Alters the Global Expression Profile of Stress Response Genes in Apple (<i>Malus domestica</i>) Leaves. Plant and Cell Physiology, 2015, 56, 1748-1761.	3.1	29
62	Identification of Conserved Gene-Regulatory Networks that Integrate Environmental Sensing and Growth in the Root Cambium. Current Biology, 2020, 30, 2887-2900.e7.	3.9	22
63	Comparative transcriptome analyses shed light on carotenoid production and plastid development in melon fruit. Horticulture Research, 2021, 8, 112.	6.3	22
64	Comprehensive transcriptome analyses reveal tomato plant responses to tobacco rattle virus-based gene silencing vectors. Scientific Reports, 2017, 7, 9771.	3.3	21
65	Integration of Metabolome and Transcriptome Studies Reveals Flavonoids, Abscisic Acid, and Nitric Oxide Comodulating the Freezing Tolerance in Liriope spicata. Frontiers in Plant Science, 2021, 12, 764625.	3.6	17
66	Comprehensive analysis of expressed sequence tags from cultivated and wild radish (Raphanus spp.). BMC Genomics, 2013, 14, 721.	2.8	16
67	Complete Genome Sequence of Southern tomato virus Identified in China Using Next-Generation Sequencing. Genome Announcements, 2015, 3, .	0.8	16
68	Natural Genetic Diversity in Tomato Flavor Genes. Frontiers in Plant Science, 2021, 12, 642828.	3.6	16
69	First Complete Genome Sequence of an Emerging Cucumber Green Mottle Mosaic Virus Isolate in North America. Genome Announcements, 2015, 3, .	0.8	14
70	Complete Genome Sequence of <i>Southern tomato virus</i> Naturally Infecting Tomatoes in Bangladesh. Genome Announcements, 2015, 3, .	0.8	12
71	Complete Genome Sequence of a Tomato-Infecting Tomato Mottle Mosaic Virus in New York. Genome Announcements, 2015, 3, .	0.8	10
72	A novel method of transcriptome interpretation reveals a quantitative suppressive effect on tomato immune signaling by two domains in a single pathogen effector protein. BMC Genomics, 2016, 17, 229.	2.8	9

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73	The tomato yellow leaf curl virus C4 protein alters the expression of plant developmental genes correlating to leaf upward cupping phenotype in tomato. PLoS ONE, 2022, 17, e0257936.	2.5	7
74	Complete Genome Sequence of an Emerging Melon Necrotic Spot Virus Isolate Infecting Greenhouse Cucumber in North America. Genome Announcements, 2015, 3, .	0.8	4
75	Identification of Phloem Mobile mRNAs Using the Solanaceae Heterograft System. Methods in Molecular Biology, 2019, 2014, 421-431.	0.9	3
76	Beta-Amylase and Phosphatidic Acid Involved in Recalcitrant Seed Germination of Chinese Chestnut. Frontiers in Plant Science, 2022, 13, 828270.	3.6	1
77	Dynamically expressed small <scp>RNAs</scp>, substantially driven by genomic structural variants, contribute to transcriptomic changes during tomato domestication. Plant Journal, 2022, 110, 1536-1550.	5.7	1