Yi Zheng

List of Publications by Year in Descending Order

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	Beta-Amylase and Phosphatidic Acid Involved in Recalcitrant Seed Germination of Chinese Chestnut.. *Frontiers in Plant Science*, **2022**, 13, 828270	6.2	
75	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	3.7	0
74	Integration of Metabolome and Transcriptome Studies Reveals Flavonoids, Abscisic Acid, and Nitric Oxide Comodulating the Freezing Tolerance in .. *Frontiers in Plant Science*, **2021**, 12, 764625	6.2	3
73	Comparative transcriptome analyses shed light on carotenoid production and plastid development in melon fruit. *Horticulture Research*, **2021**, 8, 112	7.7	5
72	Natural Genetic Diversity in Tomato Flavor Genes. *Frontiers in Plant Science*, **2021**, 12, 642828	6.2	1
71	Identification of Conserved Gene-Regulatory Networks that Integrate Environmental Sensing and Growth in the Root Cambium. *Current Biology*, **2020**, 30, 2887-2900.e7	6.3	10
70	The 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	11.5	18
69	Kiwifruit Genome Database (KGD): a comprehensive resource for kiwifruit genomics. *Horticulture Research*, **2020**, 7, 117	7.7	13
68	Identification of Phloem Mobile mRNAs Using the Solanaceae Heterograft System. *Methods in Molecular Biology*, **2019**, 2014, 421-431	1.4	2
67	SpinachBase: a central portal for spinach genomics. *Database: the Journal of Biological Databases and Curation*, **2019**, 2019,	5	16
66	Transcriptome-based identification and validation of reference genes for plant-bacteria interaction studies using Nicotiana benthamiana. *Scientific Reports*, **2019**, 9, 1632	4.9	18
65	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	8.3	17
64	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
63	High-resolution spatiotemporal transcriptome mapping of tomato fruit development and ripening. *Nature Communications*, **2018**, 9, 364	17.4	131
62	Elucidation of the Mechanisms of Long-Distance mRNA Movement in a /Tomato Heterograft System. *Plant Physiology*, **2018**, 177, 745-758	6.6	44
61	Transcriptomic and functional analysis of cucumber (Cucumis sativus L.) fruit phloem during early development. *Plant Journal*, **2018**, 96, 982-996	6.9	14
60	Transcriptome Analysis of Mango (Mangifera indica L.) Fruit Epidermal Peel to Identify Putative Cuticle-Associated Genes. *Scientific Reports*, **2017**, 7, 46163	4.9	31

59	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	4.5	28
58	Draft genome of spinach and transcriptome diversity of 120 Spinacia accessions. *Nature Communications*, **2017**, 8, 15275	17.4	90
57	TAL effector driven induction of a SWEET gene confers susceptibility to bacterial blight of cotton. *Nature Communications*, **2017**, 8, 15588	17.4	88
56	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. *Journal of Virology*, **2017**, 91,	6.6	73
55	The Tomato Expression Atlas. *Bioinformatics*, **2017**, 33, 2397-2398	7.2	39
54	Use of RNA-seq data to identify and validate RT-qPCR reference genes for studying the tomato-Pseudomonas pathosystem. *Scientific Reports*, **2017**, 7, 44905	4.9	39
53	Comprehensive transcriptome analyses reveal tomato plant responses to tobacco rattle virus-based gene silencing vectors. *Scientific Reports*, **2017**, 7, 9771	4.9	11
52	Distinct Mechanisms of the ORANGE Protein in Controlling Carotenoid Flux. *Plant Physiology*, **2017**, 173, 376-389	6.6	69
51	VirusDetect: An automated pipeline for efficient virus discovery using deep sequencing of small RNAs. *Virology*, **2017**, 500, 130-138	3.6	115
50	Vascular-mediated signalling involved in early phosphate stress response in plants. *Nature Plants*, **2016**, 2, 16033	11.5	80
49	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	4.5	5
48	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	5.3	23
47	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	6.2	54
46	Identification of a Chromosome 4 Fruit Flavor and Nutritional Quality-Associated Metabolite QTL. *Frontiers in Plant Science*, **2016**, 7, 1671	6.2	19
45	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	7.3	178
44	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
43	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, 825-46	3.1	29
42	Suppressing Sorbitol Synthesis Substantially Alters the Global Expression Profile of Stress Response Genes in Apple (Malus domestica) Leaves. *Plant and Cell Physiology*, **2015**, 56, 1748-61	4.9	21

41	Genome-wide Identification and Expression Analysis of the CDPK Gene Family in Grape, Vitis spp. *BMC Plant Biology*, **2015**, 15, 164	5.3	57
40	First complete genome sequence of an emerging cucumber green mottle mosaic virus isolate in north america. *Genome Announcements*, **2015**, 3,		10
39	Complete Genome Sequence of an Emerging Melon Necrotic Spot Virus Isolate Infecting Greenhouse Cucumber in North America. *Genome Announcements*, **2015**, 3,		4
38	A dynamic evolutionary and functional landscape of plant phased small interfering RNAs. *BMC Biology*, **2015**, 13, 32	7.3	50
37	Comprehensive Tissue-Specific Transcriptome Analysis Reveals Distinct Regulatory Programs during Early Tomato Fruit Development. *Plant Physiology*, **2015**, 168, 1684-701	6.6	86
36	Complete Genome Sequence of a Tomato-Infecting Tomato Mottle Mosaic Virus in New York. *Genome Announcements*, **2015**, 3,		7
35	A bulk segregant transcriptome analysis reveals metabolic and cellular processes associated with Orange allelic variation and fruit ɛ-carotene accumulation in melon fruit. *BMC Plant Biology*, **2015**, 15, 274	5.3	35
34	A tomato phloem-mobile protein regulates the shoot-to-root ratio by mediating the auxin response in distant organs. *Plant Journal*, **2015**, 83, 853-63	6.9	44
33	Complete Genome Sequence of Southern tomato virus Identified in China Using Next-Generation Sequencing. *Genome Announcements*, **2015**, 3,		14
32	Ethylene suppresses tomato (Solanum lycopersicum) fruit set through modification of gibberellin metabolism. *Plant Journal*, **2015**, 83, 237-51	6.9	76
31	Comparative Transcriptome Analysis of Cultivated and Wild Watermelon during Fruit Development. *PLoS ONE*, **2015**, 10, e0130267	3.7	61
30	Comparative Transcriptomes Analysis of Red- and White-Fleshed Apples in an F1 Population of Malus sieversii f. niedzwetzkyana Crossed with M. domestica ‖Fuji‖ *PLoS ONE*, **2015**, 10, e0133468	3.7	22
29	Complete Genome Sequence of Southern tomato virus Naturally Infecting Tomatoes in Bangladesh. *Genome Announcements*, **2015**, 3,		9
28	Genome-wide identification and analysis of the apple (Malus ×domestica Borkh.) TIFY gene family. *Tree Genetics and Genomes*, **2015**, 11, 1	2.1	32
27	De novo and comparative transcriptome analysis of cultivated and wild spinach. *Scientific Reports*, **2015**, 5, 17706	4.9	34
26	Tomato GOLDEN2-LIKE transcription factors reveal molecular gradients that function during fruit development and ripening. *Plant Cell*, **2014**, 26, 585-601	11.6	107
25	Evolution and expression analysis of the grape (Vitis vinifera L.) WRKY gene family. *Journal of Experimental Botany*, **2014**, 65, 1513-28	7	169
24	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	18.3	52

23	Modulation of RNA polymerase II phosphorylation downstream of pathogen perception orchestrates plant immunity. *Cell Host and Microbe*, **2014**, 16, 748-58	23.4	47
22	Comprehensive analysis of expressed sequence tags from cultivated and wild radish (Raphanus spp.). *BMC Genomics*, **2013**, 14, 721	4.5	15
21	Genome-wide identification, evolutionary and expression analysis of the aspartic protease gene superfamily in grape. *BMC Genomics*, **2013**, 14, 554	4.5	59
20	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	18.3	92
19	Comparative genomics reveals candidate carotenoid pathway regulators of ripening watermelon fruit. *BMC Genomics*, **2013**, 14, 781	4.5	77
18	The draft genome of watermelon (Citrullus lanatus) and resequencing of 20 diverse accessions. *Nature Genetics*, **2013**, 45, 51-8	36.3	503
17	Genome-wide identification and analysis of the SBP-box family genes in apple (Malus domestica Borkh.). *Plant Physiology and Biochemistry*, **2013**, 70, 100-14	5.4	92
16	Genome-wide identification and analysis of the aldehyde dehydrogenase (ALDH) gene superfamily in apple (Malus domestica Borkh.). *Plant Physiology and Biochemistry*, **2013**, 71, 268-82	5.4	26
15	Single-base resolution methylomes of tomato fruit development reveal epigenome modifications associated with ripening. *Nature Biotechnology*, **2013**, 31, 154-9	44.5	493
14	Incomplete transfer of accessory loci influencing SbMATE expression underlies genetic background effects for aluminum tolerance in sorghum. *Plant Journal*, **2013**, 73, 276-88	6.9	27
13	An NAC transcription factor controls ethylene-regulated cell expansion in flower petals. *Plant Physiology*, **2013**, 163, 775-91	6.6	87
12	RadishBase: a database for genomics and genetics of radish. *Plant and Cell Physiology*, **2013**, 54, e3	4.9	26
11	Integrative analysis of miRNA and mRNA profiles in response to ethylene in rose petals during flower opening. *PLoS ONE*, **2013**, 8, e64290	3.7	60
10	A cost-effective method for Illumina small RNA-Seq library preparation using T4 RNA ligase 1 adenylated adapters. *Plant Methods*, **2012**, 8, 41	5.8	45
9	The tomato genome sequence provides insights into fleshy fruit evolution. *Nature*, **2012**, 485, 635-41	50.4	2138
8	RhNAC2 and RhEXPA4 are involved in the regulation of dehydration tolerance during the expansion of rose petals. *Plant Physiology*, **2012**, 160, 2064-82	6.6	90
7	High-throughput illumina strand-specific RNA sequencing library preparation. *Cold Spring Harbor Protocols*, **2011**, 2011, 940-9	1.2	310
6	iAssembler: a package for de novo assembly of Roche-454/Sanger transcriptome sequences. *BMC Bioinformatics*, **2011**, 12, 453	3.6	111

5	Analysis of expressed sequence tags generated from full-length enriched cDNA libraries of melon. *BMC Genomics*, **2011**, 12, 252	4.5	47
4	Characterization of transcriptome dynamics during watermelon fruit development: sequencing, assembly, annotation and gene expression profiles. *BMC Genomics*, **2011**, 12, 454	4.5	97
3	Tomato Functional Genomics Database: a comprehensive resource and analysis package for tomato functional genomics. *Nucleic Acids Research*, **2011**, 39, D1156-63	20.1	83
2	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
1	Transcriptome sequencing and comparative analysis of cucumber flowers with different sex types. *BMC Genomics*, **2010**, 11, 384	4.5	146