

Yi Zheng

List of Publications by Year in descending order

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77
papers

10,916
citations

53794

45
h-index

71685

76
g-index

80
all docs

80
docs citations

80
times ranked

12623
citing authors

#	ARTICLE	IF	CITATIONS
1	Beta-Amylase and Phosphatidic Acid Involved in Recalcitrant Seed Germination of Chinese Chestnut. <i>Frontiers in Plant Science</i> , 2022, 13, 828270.	3.6	1
2	Dynamically expressed small <scp>RNAs</scp>, substantially driven by genomic structural variants, contribute to transcriptomic changes during tomato domestication. <i>Plant Journal</i> , 2022, 110, 1536-1550.	5.7	1
3	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.	2.5	7
4	Comparative transcriptome analyses shed light on carotenoid production and plastid development in melon fruit. <i>Horticulture Research</i> , 2021, 8, 112.	6.3	22
5	Natural Genetic Diversity in Tomato Flavor Genes. <i>Frontiers in Plant Science</i> , 2021, 12, 642828.	3.6	16
6	Integration of Metabolome and Transcriptome Studies Reveals Flavonoids, Abscisic Acid, and Nitric Oxide Comodulating the Freezing Tolerance in <i>Liriope spicata</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 764625.	3.6	17
7	Kiwifruit Genome Database (KGD): a comprehensive resource for kiwifruit genomics. <i>Horticulture Research</i> , 2020, 7, 117.	6.3	47
8	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.	3.9	22
9	The <i>Arabidopsis</i> 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.	7.1	41
10	Identification of Phloem Mobile mRNAs Using the Solanaceae Heterograft System. <i>Methods in Molecular Biology</i> , 2019, 2014, 421-431.	0.9	3
11	SpinachBase: a central portal for spinach genomics. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	3.0	30
12	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.	3.3	34
13	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.	8.5	37
14	Cucurbit Genomics Database (CuGenDB): a central portal for comparative and functional genomics of cucurbit crops. <i>Nucleic Acids Research</i> , 2019, 47, D1128-D1136.	14.5	177
15	High-resolution spatiotemporal transcriptome mapping of tomato fruit development and ripening. <i>Nature Communications</i> , 2018, 9, 364.	12.8	255
16	Elucidation of the Mechanisms of Long-Distance mRNA Movement in a <i>Nicotiana benthamiana</i>/Tomato Heterograft System. <i>Plant Physiology</i> , 2018, 177, 745-758.	4.8	72
17	Transcriptomic and functional analysis of cucumber (<i>Cucumis sativus</i> L.) fruit phloem during early development. <i>Plant Journal</i> , 2018, 96, 982-996.	5.7	30
18	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.	3.3	68

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19	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.	2.8	49
20	Draft genome of spinach and transcriptome diversity of 120 <i>Spinacia</i> accessions. <i>Nature Communications</i> , 2017, 8, 15275.	12.8	156
21	TAL effector driven induction of a SWEET gene confers susceptibility to bacterial blight of cotton. <i>Nature Communications</i> , 2017, 8, 15588.	12.8	144
22	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. <i>Journal of Virology</i> , 2017, 91, .	3.4	107
23	The Tomato Expression Atlas. <i>Bioinformatics</i> , 2017, 33, 2397-2398.	4.1	64
24	Use of RNA-seq data to identify and validate RT-qPCR reference genes for studying the tomato- <i>Pseudomonas</i> pathosystem. <i>Scientific Reports</i> , 2017, 7, 44905.	3.3	85
25	Comprehensive transcriptome analyses reveal tomato plant responses to tobacco rattle virus-based gene silencing vectors. <i>Scientific Reports</i> , 2017, 7, 9771.	3.3	21
26	Distinct Mechanisms of the ORANGE Protein in Controlling Carotenoid Flux. <i>Plant Physiology</i> , 2017, 173, 376-389.	4.8	97
27	VirusDetect: An automated pipeline for efficient virus discovery using deep sequencing of small RNAs. <i>Virology</i> , 2017, 500, 130-138.	2.4	191
28	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.	3.6	89
29	Identification of a <i>Solanum pennellii</i> Chromosome 4 Fruit Flavor and Nutritional Quality-Associated Metabolite QTL. <i>Frontiers in Plant Science</i> , 2016, 7, 1671.	3.6	35
30	De novo and comparative transcriptome analysis of cultivated and wild spinach. <i>Scientific Reports</i> , 2016, 5, 17706.	3.3	41
31	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.	3.8	265
32	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.	8.3	735
33	Vascular-mediated signalling involved in early phosphate stress response in plants. <i>Nature Plants</i> , 2016, 2, 16033.	9.3	124
34	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.	2.8	9
35	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.	3.6	31
36	Complete Genome Sequence of a Tomato-Infecting Tomato Mottle Mosaic Virus in New York. <i>Genome Announcements</i> , 2015, 3, .	0.8	10

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37	A bulk segregant transcriptome analysis reveals metabolic and cellular processes associated with Orange allelic variation and fruit Î²-carotene accumulation in melon fruit. <i>BMC Plant Biology</i> , 2015, 15, 274.	3.6	58
38	A tomato phloemâ€mobile protein regulates the shootâ€toâ€root ratio by mediating the auxin response in distant organs. <i>Plant Journal</i> , 2015, 83, 853-863.	5.7	50
39	Complete Genome Sequence of Southern tomato virus Identified in China Using Next-Generation Sequencing. <i>Genome Announcements</i> , 2015, 3, .	0.8	16
40	Ethylene suppresses tomato (<i>Solanum lycopersicum</i>) fruit set through modification of gibberellin metabolism. <i>Plant Journal</i> , 2015, 83, 237-251.	5.7	128
41	Comparative Transcriptome Analysis of Cultivated and Wild Watermelon during Fruit Development. <i>PLoS ONE</i> , 2015, 10, e0130267.	2.5	106
42	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> â€Fujiâ€™. <i>PLoS ONE</i> , 2015, 10, e0133468.	2.5	29
43	Complete Genome Sequence of <i>Southern tomato virus</i> Naturally Infecting Tomatoes in Bangladesh. <i>Genome Announcements</i> , 2015, 3, .	0.8	12
44	Genome-wide identification and analysis of the apple (<i>Malus</i> Æ– <i>domestica</i> Borkh.) TIFY gene family. <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	1.6	51
45	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, 825-846.	2.1	46
46	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, 1748-1761.	3.1	29
47	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.	3.6	85
48	First Complete Genome Sequence of an Emerging Cucumber Green Mottle Mosaic Virus Isolate in North America. <i>Genome Announcements</i> , 2015, 3, .	0.8	14
49	Complete Genome Sequence of an Emerging Melon Necrotic Spot Virus Isolate Infecting Greenhouse Cucumber in North America. <i>Genome Announcements</i> , 2015, 3, .	0.8	4
50	A dynamic evolutionary and functional landscape of plant phased small interfering RNAs. <i>BMC Biology</i> , 2015, 13, 32.	3.8	57
51	Comprehensive Tissue-Specific Transcriptome Analysis Reveals Distinct Regulatory Programs during Early Tomato Fruit Development. <i>Plant Physiology</i> , 2015, 168, 1684-1701.	4.8	142
52	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.	8.8	75
53	Modulation of RNA Polymerase II Phosphorylation Downstream of Pathogen Perception Orchestrates Plant Immunity. <i>Cell Host and Microbe</i> , 2014, 16, 748-758.	11.0	70
54	Tomato <i>GOLDEN2-LIKE</i> Transcription Factors Reveal Molecular Gradients That Function during Fruit Development and Ripening. <i>Plant Cell</i> , 2014, 26, 585-601.	6.6	193

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55	Evolution and expression analysis of the grape (<i>Vitis vinifera</i> L.) WRKY gene family. <i>Journal of Experimental Botany</i> , 2014, 65, 1513-1528.	4.8	246
56	Comprehensive analysis of expressed sequence tags from cultivated and wild radish (<i>Raphanus</i> spp.). <i>BMC Genomics</i> , 2013, 14, 721.	2.8	16
57	Genome-wide identification, evolutionary and expression analysis of the aspartic protease gene superfamily in grape. <i>BMC Genomics</i> , 2013, 14, 554.	2.8	85
58	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.	9.6	137
59	Comparative genomics reveals candidate carotenoid pathway regulators of ripening watermelon fruit. <i>BMC Genomics</i> , 2013, 14, 781.	2.8	103
60	The draft genome of watermelon (<i>Citrullus lanatus</i>) and resequencing of 20 diverse accessions. <i>Nature Genetics</i> , 2013, 45, 51-58.	21.4	731
61	Genome-wide identification and analysis of the SBP-box family genes in apple (<i>Malus domestica</i>) Tj ETQq1 1 0,784314 rgBT /Overl P45	5.8	145
62	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, 268-282.	5.8	36
63	Single-base resolution methylomes of tomato fruit development reveal epigenome modifications associated with ripening. <i>Nature Biotechnology</i> , 2013, 31, 154-159.	17.5	693
64	Incomplete transfer of accessory loci influencing <i>SbMATE</i> expression underlies genetic background effects for aluminum tolerance in sorghum. <i>Plant Journal</i> , 2013, 73, 276-288.	5.7	31
65	An NAC Transcription Factor Controls Ethylene-Regulated Cell Expansion in Flower Petals. <i>Plant Physiology</i> , 2013, 163, 775-791.	4.8	122
66	RadishBase: A Database for Genomics and Genetics of Radish. <i>Plant and Cell Physiology</i> , 2013, 54, e3-e3.	3.1	32
67	Integrative Analysis of miRNA and mRNA Profiles in Response to Ethylene in Rose Petals during Flower Opening. <i>PLoS ONE</i> , 2013, 8, e64290.	2.5	70
68	<i>RhNAC2</i> and <i>RhEXPA4</i> Are Involved in the Regulation of Dehydration Tolerance during the Expansion of Rose Petals. <i>Plant Physiology</i> , 2012, 160, 2064-2082.	4.8	110
69	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.	4.3	56
70	The tomato genome sequence provides insights into fleshy fruit evolution. <i>Nature</i> , 2012, 485, 635-641.	27.8	2,860
71	Tomato Functional Genomics Database: a comprehensive resource and analysis package for tomato functional genomics. <i>Nucleic Acids Research</i> , 2011, 39, D1156-D1163.	14.5	113
72	High-Throughput Illumina Strand-Specific RNA Sequencing Library Preparation. <i>Cold Spring Harbor Protocols</i> , 2011, 2011, pdb.prot5652.	0.3	382

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73	iAssembler: a package for de novo assembly of Roche-454/Sanger transcriptome sequences. BMC Bioinformatics, 2011, 12, 453.	2.6	120
74	Analysis of expressed sequence tags generated from full-length enriched cDNA libraries of melon. BMC Genomics, 2011, 12, 252.	2.8	49
75	Characterization of transcriptome dynamics during watermelon fruit development: sequencing, assembly, annotation and gene expression profiles. BMC Genomics, 2011, 12, 454.	2.8	126
76	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, 3893-3910.	6.6	193
77	Transcriptome sequencing and comparative analysis of cucumber flowers with different sex types. BMC Genomics, 2010, 11, 384.	2.8	161