

Zhangjun Fei

List of Publications by Year in descending order

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Version: 2024-02-01

247
papers

24,346
citations

4960

84
h-index

9861

141
g-index

270
all docs

270
docs citations

270
times ranked

20281
citing authors

#	ARTICLE	IF	CITATIONS
1	The genome of the cucumber, <i>Cucumis sativus</i> L.. <i>Nature Genetics</i> , 2009, 41, 1275-1281.	21.4	1,317
2	Genomic analyses provide insights into the history of tomato breeding. <i>Nature Genetics</i> , 2014, 46, 1220-1226.	21.4	801
3	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
4	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
5	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
6	A genomic variation map provides insights into the genetic basis of cucumber domestication and diversity. <i>Nature Genetics</i> , 2013, 45, 1510-1515.	21.4	472
7	The tomato pan-genome uncovers new genes and a rare allele regulating fruit flavor. <i>Nature Genetics</i> , 2019, 51, 1044-1051.	21.4	441
8	Draft genome of the kiwifruit <i>Actinidia chinensis</i> . <i>Nature Communications</i> , 2013, 4, 2640.	12.8	423
9	The genome of the stress-tolerant wild tomato species <i>Solanum pennellii</i> . <i>Nature Genetics</i> , 2014, 46, 1034-1038.	21.4	391
10	High-Throughput Illumina Strand-Specific RNA Sequencing Library Preparation. <i>Cold Spring Harbor Protocols</i> , 2011, 2011, pdb.prot5652.	0.3	382
11	The Epigenome and Transcriptional Dynamics of Fruit Ripening. <i>Annual Review of Plant Biology</i> , 2017, 68, 61-84.	18.7	335
12	Interdependence of threonine, methionine and isoleucine metabolism in plants: accumulation and transcriptional regulation under abiotic stress. <i>Amino Acids</i> , 2010, 39, 933-947.	2.7	305
13	Systems Biology of Tomato Fruit Development: Combined Transcript, Protein, and Metabolite Analysis of Tomato Transcription Factor (<i>rin</i>) and Ethylene Receptor (<i>Nr</i>) Mutants Reveals Novel Regulatory Interactions. <i>Plant Physiology</i> , 2011, 157, 405-425.	4.8	303
14	Genome re-sequencing reveals the history of apple and supports a two-stage model for fruit enlargement. <i>Nature Communications</i> , 2017, 8, 249.	12.8	286
15	Combined transcriptome, genetic diversity and metabolite profiling in tomato fruit reveals that the ethylene response factor <i>SIERF6</i> plays an important role in ripening and carotenoid accumulation. <i>Plant Journal</i> , 2012, 70, 191-204.	5.7	268
16	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
17	Karyotype Stability and Unbiased Fractionation in the Paleo-Allotetraploid Cucurbita Genomes. <i>Molecular Plant</i> , 2017, 10, 1293-1306.	8.3	263
18	Genome encode analyses reveal the basis of convergent evolution of fleshy fruit ripening. <i>Nature Plants</i> , 2018, 4, 784-791.	9.3	256

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19	High-resolution spatiotemporal transcriptome mapping of tomato fruit development and ripening. <i>Nature Communications</i> , 2018, 9, 364.	12.8	255
20	RNA-Seq improves annotation of protein-coding genes in the cucumber genome. <i>BMC Genomics</i> , 2011, 12, 540.	2.8	232
21	Resequencing of 414 cultivated and wild watermelon accessions identifies selection for fruit quality traits. <i>Nature Genetics</i> , 2019, 51, 1616-1623.	21.4	226
22	ESTs, cDNA microarrays, and gene expression profiling: tools for dissecting plant physiology and development. <i>Plant Journal</i> , 2004, 39, 697-714.	5.7	225
23	Down-regulation of AUXIN RESPONSE FACTORS 6 and 8 by microRNA 167 leads to floral development defects and female sterility in tomato. <i>Journal of Experimental Botany</i> , 2014, 65, 2507-2520.	4.8	223
24	Comprehensive EST analysis of tomato and comparative genomics of fruit ripening. <i>Plant Journal</i> , 2004, 40, 47-59.	5.7	210
25	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> , 2016, 113, 12580-12585.	7.1	208
26	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, 3893-3910.	6.6	193
27	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
28	Transcriptional profiles of drought-responsive genes in modulating transcription signal transduction, and biochemical pathways in tomato. <i>Journal of Experimental Botany</i> , 2010, 61, 3563-3575.	4.8	192
29	VirusDetect: An automated pipeline for efficient virus discovery using deep sequencing of small RNAs. <i>Virology</i> , 2017, 500, 130-138.	2.4	191
30	Antagonistic Basic Helix-Loop-Helix/bZIP Transcription Factors Form Transcriptional Modules That Integrate Light and Reactive Oxygen Species Signaling in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2013, 25, 1657-1673.	6.6	188
31	Identification of early salt stress response genes in tomato root by suppression subtractive hybridization and microarray analysis. <i>Journal of Experimental Botany</i> , 2007, 58, 507-520.	4.8	183
32	Genome sequences of two diploid wild relatives of cultivated sweetpotato reveal targets for genetic improvement. <i>Nature Communications</i> , 2018, 9, 4580.	12.8	181
33	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
34	A "golden" SNP in <i>CmOr</i> governs the fruit flesh color of melon (<i>Cucumis melo</i>). <i>Plant Cell</i> , 2017, 29, 173-183.	5.7	173
35	A Zinc Finger Protein Regulates Flowering Time and Abiotic Stress Tolerance in Chrysanthemum by Modulating Gibberellin Biosynthesis. <i>Plant Cell</i> , 2014, 26, 2038-2054.	6.6	172
36	Phased diploid genome assemblies and pan-genomes provide insights into the genetic history of apple domestication. <i>Nature Genetics</i> , 2020, 52, 1423-1432.	21.4	168

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37	Transcriptome sequencing and comparative analysis of cucumber flowers with different sex types. <i>BMC Genomics</i> , 2010, 11, 384.	2.8	161
38	Metabolic Coevolution in the Bacterial Symbiosis of Whiteflies and Related Plant Sap-Feeding Insects. <i>Genome Biology and Evolution</i> , 2015, 7, 2635-2647.	2.5	161
39	Plant MetGenMAP: An Integrative Analysis System for Plant Systems Biology. <i>Plant Physiology</i> , 2009, 151, 1758-1768.	4.8	156
40	Draft genome of spinach and transcriptome diversity of 120 <i>Spinacia</i> accessions. <i>Nature Communications</i> , 2017, 8, 15275.	12.8	156
41	Impact of intestinal colonization and invasion on the <i>Entamoeba histolytica</i> transcriptome. <i>Molecular and Biochemical Parasitology</i> , 2006, 147, 163-176.	1.1	153
42	A comprehensive genome variation map of melon identifies multiple domestication events and loci influencing agronomic traits. <i>Nature Genetics</i> , 2019, 51, 1607-1615.	21.4	153
43	The <i>Penium margaritaceum</i> Genome: Hallmarks of the Origins of Land Plants. <i>Cell</i> , 2020, 181, 1097-1111.e12.	28.9	153
44	Flavour compounds in tomato fruits: identification of loci and potential pathways affecting volatile composition. <i>Journal of Experimental Botany</i> , 2009, 60, 325-337.	4.8	152
45	The Transcriptome of the <i>Baculovirus Autographa californica</i> Multiple Nucleopolyhedrovirus in <i>Trichoplusia ni</i> Cells. <i>Journal of Virology</i> , 2013, 87, 6391-6405.	3.4	152
46	Diversification and independent domestication of Asian and European pears. <i>Genome Biology</i> , 2018, 19, 77.	8.8	149
47	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
48	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
49	Deep Sequencing of Small RNAs in Tomato for Virus and Viroid Identification and Strain Differentiation. <i>PLoS ONE</i> , 2012, 7, e37127.	2.5	138
50	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
51	Catalyzing plant science research with RNA-seq. <i>Frontiers in Plant Science</i> , 2013, 4, 66.	3.6	136
52	The Jujube Genome Provides Insights into Genome Evolution and the Domestication of Sweetness/Acidity Taste in Fruit Trees. <i>PLoS Genetics</i> , 2016, 12, e1006433.	3.5	136
53	A MYB-bHLH complex regulates tissue-specific anthocyanin biosynthesis in the inner pericarp of red-actinidia kiwifruit <i>Actinidia chinensis</i> cv. Hongyang. <i>Plant Journal</i> , 2019, 99, 359-378.	5.7	136
54	Deciphering genetic factors that determine melon fruit quality traits using RNA-seq-based high-resolution QTL and eQTL mapping. <i>Plant Journal</i> , 2018, 94, 169-191.	5.7	133

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55	Graph pangenome captures missing heritability and empowers tomato breeding. <i>Nature</i> , 2022, 606, 527-534.	27.8	131
56	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
57	Characterization of transcriptome dynamics during watermelon fruit development: sequencing, assembly, annotation and gene expression profiles. <i>BMC Genomics</i> , 2011, 12, 454.	2.8	126
58	Cutin and suberin: assembly and origins of specialized lipidic cell wall scaffolds. <i>Current Opinion in Plant Biology</i> , 2020, 55, 11-20.	7.1	126
59	Genome-Wide Mapping of Structural Variations Reveals a Copy Number Variant That Determines Reproductive Morphology in Cucumber. <i>Plant Cell</i> , 2015, 27, 1595-1604.	6.6	125
60	Messenger RNA exchange between scions and rootstocks in grafted grapevines. <i>BMC Plant Biology</i> , 2015, 15, 251.	3.6	124
61	Vascular-mediated signalling involved in early phosphate stress response in plants. <i>Nature Plants</i> , 2016, 2, 16033.	9.3	124
62	An NAC Transcription Factor Controls Ethylene-Regulated Cell Expansion in Flower Petals. <i>Plant Physiology</i> , 2013, 163, 775-791.	4.8	122
63	iAssembler: a package for de novo assembly of Roche-454/Sanger transcriptome sequences. <i>BMC Bioinformatics</i> , 2011, 12, 453.	2.6	120
64	Genomic analyses of an extensive collection of wild and cultivated accessions provide new insights into peach breeding history. <i>Genome Biology</i> , 2019, 20, 36.	8.8	120
65	Identification of multiple salicylic acid-binding proteins using two high throughput screens. <i>Frontiers in Plant Science</i> , 2014, 5, 777.	3.6	119
66	Host-secreted antimicrobial peptide enforces symbiotic selectivity in <i>Medicago truncatula</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 6854-6859.	7.1	119
67	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> , 2011, 68, 999-1013.	5.7	118
68	The pomegranate (<i>Punica granatum</i> L.) genome provides insights into fruit quality and ovule developmental biology. <i>Plant Biotechnology Journal</i> , 2018, 16, 1363-1374.	8.3	115
69	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
70	Genome Sequence of <i>Brucella abortus</i> Vaccine Strain S19 Compared to Virulent Strains Yields Candidate Virulence Genes. <i>PLoS ONE</i> , 2008, 3, e2193.	2.5	108
71	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
72	Comparative Transcriptome Analysis of Cultivated and Wild Watermelon during Fruit Development. <i>PLoS ONE</i> , 2015, 10, e0130267.	2.5	106

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73	Comparative genomics reveals candidate carotenoid pathway regulators of ripening watermelon fruit. <i>BMC Genomics</i> , 2013, 14, 781.	2.8	103
74	Genomic Organization, Phylogenetic Comparison and Differential Expression of the SBP-Box Family Genes in Grape. <i>PLoS ONE</i> , 2013, 8, e59358.	2.5	102
75	The USDA cucumber (<i>Cucumis sativus</i> L.) collection: genetic diversity, population structure, genome-wide association studies, and core collection development. <i>Horticulture Research</i> , 2018, 5, 64.	6.3	102
76	Metabolism of soluble sugars in developing melon fruit: a global transcriptional view of the metabolic transition to sucrose accumulation. <i>Plant Molecular Biology</i> , 2011, 76, 1-18.	3.9	101
77	The bottle gourd genome provides insights into Cucurbitaceae evolution and facilitates mapping of a <i>Papaya ring-spot virus</i> resistance locus. <i>Plant Journal</i> , 2017, 92, 963-975.	5.7	101
78	Transcriptome sequencing and whole genome expression profiling of chrysanthemum under dehydration stress. <i>BMC Genomics</i> , 2013, 14, 662.	2.8	100
79	The PH gene determines fruit acidity and contributes to the evolution of sweet melons. <i>Nature Communications</i> , 2014, 5, 4026.	12.8	100
80	Root and shoot transcriptome analysis of two ecotypes of <i>Nocca caerulescens</i> uncovers the role of <i>Ncramp1</i> in <i>Nc</i> hyperaccumulation. <i>Plant Journal</i> , 2014, 78, 398-410.	5.7	97
81	Distinct Mechanisms of the ORANGE Protein in Controlling Carotenoid Flux. <i>Plant Physiology</i> , 2017, 173, 376-389.	4.8	97
82	Genome of 'Charleston Gray', the principal American watermelon cultivar, and genetic characterization of 1,365 accessions in the U.S. National Plant Germplasm System watermelon collection. <i>Plant Biotechnology Journal</i> , 2019, 17, 2246-2258.	8.3	96
83	Gene expression in developing watermelon fruit. <i>BMC Genomics</i> , 2008, 9, 275.	2.8	94
84	Genome-Wide Identification and Analysis of Grape Aldehyde Dehydrogenase (ALDH) Gene Superfamily. <i>PLoS ONE</i> , 2012, 7, e32153.	2.5	91
85	A Single Amino Acid Substitution in an ORANGE Protein Promotes Carotenoid Overaccumulation in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2015, 169, 421-431.	4.8	91
86	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
87	Genome and evolution of the arbuscular mycorrhizal fungus <i>Diversispora epigaea</i> (formerly) <i>Tj ETQq1 1 0.784314 rgBT / Overlock</i>	7.3	88
88	Proteomic analysis of chromoplasts from six crop species reveals insights into chromoplast function and development. <i>Journal of Experimental Botany</i> , 2013, 64, 949-961.	4.8	85
89	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
90	Genome of <i>Solanum pimpinellifolium</i> provides insights into structural variants during tomato breeding. <i>Nature Communications</i> , 2020, 11, 5817.	12.8	85

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91	A high-density genetic map for anchoring genome sequences and identifying QTLs associated with dwarf vine in pumpkin (<i>Cucurbita maxima</i> Duch.). <i>BMC Genomics</i> , 2015, 16, 1101.	2.8	84
92	Ectopic expression of <i>ORANGE</i> promotes carotenoid accumulation and fruit development in tomato. <i>Plant Biotechnology Journal</i> , 2019, 17, 33-49.	8.3	83
93	Catabolism of L-methionine in the formation of sulfur and other volatiles in melon (<i>Cucumis melo</i> L.) fruit. <i>Plant Journal</i> , 2013, 74, 458-472.	5.7	78
94	Gibberellin-induced changes in the transcriptome of grapevine (<i>Vitis labrusca</i> L. cv. Kyoho) flowers. <i>BMC Genomics</i> , 2015, 16, 128.	2.8	77
95	A Kelch domain-containing F-box coding gene negatively regulates flavonoid accumulation in <i>Cucumis melo</i> L.. <i>Plant Physiology</i> , 2015, 169, pp.01008.2015.	4.8	77
96	Transcriptional dynamics of <i>Phytophthora infestans</i> during sequential stages of hemibiotrophic infection of tomato. <i>Molecular Plant Pathology</i> , 2016, 17, 29-41.	4.2	77
97	An integrated peach genome structural variation map uncovers genes associated with fruit traits. <i>Genome Biology</i> , 2020, 21, 258.	8.8	77
98	Arabidopsis Pollen Fertility Requires the Transcription Factors CITF1 and SPL7 That Regulate Copper Delivery to Anthers and Jasmonic Acid Synthesis. <i>Plant Cell</i> , 2017, 29, 3012-3029.	6.6	76
99	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
100	Tomato Expression Database (TED): a suite of data presentation and analysis tools. <i>Nucleic Acids Research</i> , 2006, 34, D766-D770.	14.5	72
101	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
102	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
103	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
104	High frequency oligonucleotides: targeting active gene (HFO-TAG) markers revealed wide genetic diversity among <i>Citrullus</i> spp. accessions useful for enhancing disease or pest resistance in watermelon cultivars. <i>Genetic Resources and Crop Evolution</i> , 2013, 60, 427-440.	1.6	66
105	Exploring key cellular processes and candidate genes regulating the primary thickening growth of <i>Moss</i> underground shoots. <i>New Phytologist</i> , 2017, 214, 81-96.	7.3	66
106	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> , 2019, 15, e1008149.	3.5	66
107	A CLE module regulates strigolactone content and fungal colonization in arbuscular mycorrhiza. <i>Nature Plants</i> , 2019, 5, 933-939.	9.3	65
108	Sequencing-Based Bin Map Construction of a Tomato Mapping Population, Facilitating High-Resolution Quantitative Trait Loci Detection. <i>Plant Genome</i> , 2019, 12, 180010.	2.8	65

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109	Chromosome-scale genome assembly of kiwifruit (<i>Actinidia chinensis</i>) with single-molecule sequencing and chromatin interaction mapping. <i>GigaScience</i> , 2019, 8, .	6.4	65
110	Early Blood Profiles of Virus Infection in a Monkey Model for Lassa Fever. <i>Journal of Virology</i> , 2007, 81, 7960-7973.	3.4	64
111	The Tomato Expression Atlas. <i>Bioinformatics</i> , 2017, 33, 2397-2398.	4.1	64
112	Diversity, Distribution, and Evolution of Tomato Viruses in China Uncovered by Small RNA Sequencing. <i>Journal of Virology</i> , 2017, 91, .	3.4	63
113	Transcriptome Responses of the Host <i>Trichoplusia ni</i> to Infection by the Baculovirus <i>Autographa californica</i> Multiple Nucleopolyhedrovirus. <i>Journal of Virology</i> , 2014, 88, 13781-13797.	3.4	60
114	Characterization of the developmental dynamics of the elongation of a bamboo internode during the fast growth stage. <i>Tree Physiology</i> , 2019, 39, 1201-1214.	3.1	60
115	Comprehensive transcriptome analysis and functional characterization of PR-5 for its involvement in tomato Sw-7 resistance to tomato spotted wilt tospovirus. <i>Scientific Reports</i> , 2019, 9, 7673.	3.3	60
116	Genome sequence of the corn leaf aphid (<i>Rhopalosiphum maidis</i> Fitch). <i>GigaScience</i> , 2019, 8, .	6.4	60
117	Dissecting the molecular signatures of apical cell-type shoot meristems from two ancient land plant lineages. <i>New Phytologist</i> , 2015, 207, 893-904.	7.3	59
118	Maternal Inheritance of a Single Somatic Animal Cell Displayed by the Bacteriocyte in the Whitefly <i>Bemisia tabaci</i> . <i>Current Biology</i> , 2018, 28, 459-465.e3.	3.9	59
119	Quantitative trait loci and differential gene expression analyses reveal the genetic basis for negatively associated β -carotene and starch content in hexaploid sweetpotato [<i>Ipomoea batatas</i> (L.) Lam.]. <i>Theoretical and Applied Genetics</i> , 2020, 133, 23-36.	3.6	59
120	Graph-based pan-genome reveals structural and sequence variations related to agronomic traits and domestication in cucumber. <i>Nature Communications</i> , 2022, 13, 682.	12.8	59
121	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.	3.6	58
122	A dynamic evolutionary and functional landscape of plant phased small interfering RNAs. <i>BMC Biology</i> , 2015, 13, 32.	3.8	57
123	Unravelling the Genetic Diversity among Cassava <i>Bemisia tabaci</i> Whiteflies Using NextRAD Sequencing. <i>Genome Biology and Evolution</i> , 2017, 9, 2958-2973.	2.5	57
124	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
125	Complete Genome Sequence of a New Tobamovirus Naturally Infecting Tomatoes in Mexico. <i>Genome Announcements</i> , 2013, 1, .	0.8	56
126	<i>Rosa hybrida</i> Rh _{ERF} 1 and Rh _{ERF} 4 mediate ethylene- and auxin-regulated petal abscission by influencing pectin degradation. <i>Plant Journal</i> , 2019, 99, 1159-1171.	5.7	56

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127	Analysis of the tomato leaf transcriptome during successive hemibiotrophic stages of a compatible interaction with the oomycete pathogen <i>Phytophthora infestans</i> . <i>Molecular Plant Pathology</i> , 2016, 17, 42-54.	4.2	55
128	Regulatory control of high levels of carotenoid accumulation in potato tubers. <i>Plant, Cell and Environment</i> , 2011, 34, 1020-1030.	5.7	52
129	Fastq_clean: An optimized pipeline to clean the Illumina sequencing data with quality control. , 2014, , .		51
130	Loss of function mutation of the calcium sensor <i>CBL1</i> increases aluminum sensitivity in <i>Arabidopsis</i> . <i>New Phytologist</i> , 2017, 214, 830-841.	7.3	50
131	Rapid growth of Moso bamboo (<i>Phyllostachys edulis</i>): Cellular roadmaps, transcriptome dynamics, and environmental factors. <i>Plant Cell</i> , 2022, 34, 3577-3610.	6.6	50
132	Analysis of expressed sequence tags generated from full-length enriched cDNA libraries of melon. <i>BMC Genomics</i> , 2011, 12, 252.	2.8	49
133	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
134	Comparative transcriptome analysis reveals networks of genes activated in the whitefly, <i>Bemisia tabaci</i> when fed on tomato plants infected with Tomato yellow leaf curl virus. <i>Virology</i> , 2018, 513, 52-64.	2.4	48
135	Genome of the African cassava whitefly <i>Bemisia tabaci</i> and distribution and genetic diversity of cassava-colonizing whiteflies in Africa. <i>Insect Biochemistry and Molecular Biology</i> , 2019, 110, 112-120.	2.7	47
136	Tomato stigma exertion induced by high temperature is associated with the jasmonate signalling pathway. <i>Plant, Cell and Environment</i> , 2019, 42, 1205-1221.	5.7	47
137	A high-quality chromosome-level genome assembly of a generalist herbivore, <i>Trichoplusia ni</i> . <i>Molecular Ecology Resources</i> , 2019, 19, 485-496.	4.8	47
138	Kiwifruit Genome Database (KGD): a comprehensive resource for kiwifruit genomics. <i>Horticulture Research</i> , 2020, 7, 117.	6.3	47
139	Unraveling a genetic roadmap for improved taste in the domesticated apple. <i>Molecular Plant</i> , 2021, 14, 1454-1471.	8.3	47
140	Manipulation of ZDS in tomato exposes carotenoid- and ABA-specific effects on fruit development and ripening. <i>Plant Biotechnology Journal</i> , 2020, 18, 2210-2224.	8.3	44
141	Genome-wide association studies provide insights into the genetic determination of fruit traits of pear. <i>Nature Communications</i> , 2021, 12, 1144.	12.8	44
142	Transcriptome Profiling of Petal Abscission Zone and Functional Analysis of an Aux/IAA Family Gene <i>RhIAA16</i> Involved in Petal Shedding in Rose. <i>Frontiers in Plant Science</i> , 2016, 7, 1375.	3.6	43
143	Auxin Regulates Sucrose Transport to Repress Petal Abscission in Rose (<i>Rosa hybrida</i>). <i>Plant Cell</i> , 2020, 32, 3485-3499.	6.6	43
144	Ethylene-regulated asymmetric growth of the petal base promotes flower opening in rose (<i>Rosa</i>)	8.6	43

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