

# Zhangjun Fei

## List of Publications by Year in descending order

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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	Cellular and molecular characterizations of the irregular internode division zone formation of a slow-growing bamboo variant. <i>Tree Physiology</i> , 2022, 42, 570-584.	3.1	10
2	Bt Cry1Ac resistance in <i>Trichoplusia ni</i> is conferred by multi-gene mutations. <i>Insect Biochemistry and Molecular Biology</i> , 2022, 140, 103678.	2.7	10
3	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
4	A <i>Solanum lycopersicoides</i> reference genome facilitates insights into tomato specialized metabolism and immunity. <i>Plant Journal</i> , 2022, 110, 1791-1810.	5.7	16
5	Genomic insights into the origin, adaptive evolution, and herbicide resistance of <i>Leptochloa chinensis</i> , a devastating tetraploid weedy grass in rice fields. <i>Molecular Plant</i> , 2022, 15, 1045-1058.	8.3	15
6	Dynamically expressed small <i>scp</i> RNAs, substantially driven by genomic structural variants, contribute to transcriptomic changes during tomato domestication. <i>Plant Journal</i> , 2022, 110, 1536-1550.	5.7	1
7	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
8	Chromosome-scale genome assemblies of wild tomato relatives <i>Solanum habrochaites</i> and <i>Solanum galapagense</i> reveal structural variants associated with stress tolerance and terpene biosynthesis. <i>Horticulture Research</i> , 2022, 9, .	6.3	4
9	Graph pangenome captures missing heritability and empowers tomato breeding. <i>Nature</i> , 2022, 606, 527-534.	27.8	131
10	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
11	Loss of function of the bHLH transcription factor Nrd1 in tomato enhances resistance to <i>Pseudomonas syringae</i> . <i>Plant Physiology</i> , 2022, 190, 1334-1348.	4.8	7
12	Combined nature and human selections reshaped peach fruit metabolome. <i>Genome Biology</i> , 2022, 23, .	8.8	23
13	QTL associated with gummy stem blight resistance in watermelon. <i>Theoretical and Applied Genetics</i> , 2021, 134, 573-584.	3.6	20
14	Ethylene-regulated asymmetric growth of the petal base promotes flower opening in rose ( <i>Rosa</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	8.6	48
15	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
16	Genomic analyses provide insights into peach local adaptation and responses to climate change. <i>Genome Research</i> , 2021, 31, 592-606.	5.5	30
17	Spelling Changes and Fluorescent Tagging With Prime Editing Vectors for Plants. <i>Frontiers in Genome Editing</i> , 2021, 3, 617553.	5.2	30
18	Comparative transcriptome profiling of Chinese wild grapes provides insights into powdery mildew resistance. <i>Phytopathology</i> , 2021, , PHYTO01210006R.	2.2	7

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19	Transcriptome analysis provides insights into the responses of sweet potato to sweet potato virus disease (SPVD). <i>Virus Research</i> , 2021, 295, 198293.	2.2	14
20	Genome sequencing sheds light on the contribution of structural variants to <i>Brassica oleracea</i> diversification. <i>BMC Biology</i> , 2021, 19, 93.	3.8	41
21	Comparative transcriptome analyses shed light on carotenoid production and plastid development in melon fruit. <i>Horticulture Research</i> , 2021, 8, 112.	6.3	22
22	A chromosome-level genome of a Kordofan melon illuminates the origin of domesticated watermelons. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	37
23	PIF4 negatively modulates cold tolerance in tomato anthers via temperature-dependent regulation of tapetal cell death. <i>Plant Cell</i> , 2021, 33, 2320-2339.	6.6	27
24	Genome-wide association study reveals the genetic architecture of 27 agronomic traits in tomato. <i>Plant Physiology</i> , 2021, 186, 2078-2092.	4.8	18
25	Natural Genetic Diversity in Tomato Flavor Genes. <i>Frontiers in Plant Science</i> , 2021, 12, 642828.	3.6	16
26	Genetic Resources and Vulnerabilities of Major Cucurbit Crops. <i>Genes</i> , 2021, 12, 1222.	2.4	36
27	A tomato LATERAL ORGAN BOUNDARIES transcription factor, <i>SlLOB1</i> , predominantly regulates cell wall and softening components of ripening. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	41
28	Unraveling a genetic roadmap for improved taste in the domesticated apple. <i>Molecular Plant</i> , 2021, 14, 1454-1471.	8.3	47
29	Genetic characterization of melon accessions in the U.S. National Plant Germplasm System and construction of a melon core collection. <i>Molecular Horticulture</i> , 2021, 1, .	5.8	12
30	Interspecific Recombination Between Zucchini Tigre Mosaic Virus and Papaya Ringspot Virus Infecting Cucurbits in China. <i>Frontiers in Microbiology</i> , 2021, 12, 773992.	3.5	3
31	A systems genetics approach reveals PbrNSC as a regulator of lignin and cellulose biosynthesis in stone cells of pear fruit. <i>Genome Biology</i> , 2021, 22, 313.	8.8	32
32	Genomic analyses provide insights into spinach domestication and the genetic basis of agronomic traits. <i>Nature Communications</i> , 2021, 12, 7246.	12.8	34
33	Quantitative trait loci and differential gene expression analyses reveal the genetic basis for negatively associated $\beta$ -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
34	Genetic mapping of green curd gene Gr in cauliflower. <i>Theoretical and Applied Genetics</i> , 2020, 133, 353-364.	3.6	12
35	QTL mapping of resistance to <i>Fusarium oxysporum</i> f. sp. <i>niveum</i> race 2 and Papaya ringspot virus in <i>Citrullus amarus</i> . <i>Theoretical and Applied Genetics</i> , 2020, 133, 677-687.	3.6	18
36	An integrated peach genome structural variation map uncovers genes associated with fruit traits. <i>Genome Biology</i> , 2020, 21, 258.	8.8	77

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37	The genome and transcriptome analysis of snake gourd provide insights into its evolution and fruit development and ripening. Horticulture Research, 2020, 7, 199.	6.3	22
38	Genome of <i>Solanum pimpinellifolium</i> provides insights into structural variants during tomato breeding. Nature Communications, 2020, 11, 5817.	12.8	85
39	Kiwifruit Genome Database (KGD): a comprehensive resource for kiwifruit genomics. Horticulture Research, 2020, 7, 117.	6.3	47
40	Phased diploid genome assemblies and pan-genomes provide insights into the genetic history of apple domestication. Nature Genetics, 2020, 52, 1423-1432.	21.4	168
41	Assembly of whole-chromosome pseudomolecules for polyploid plant genomes using outbred mapping populations. Nature Genetics, 2020, 52, 1256-1264.	21.4	13
42	Auxin Regulates Sucrose Transport to Repress Petal Abscission in Rose ( <i>Rosa hybrida</i> ). Plant Cell, 2020, 32, 3485-3499.	6.6	43
43	<i>Setaria viridis</i> chlorotic and seedling-lethal mutants define critical functions for chloroplast gene expression. Plant Journal, 2020, 104, 917-931.	5.7	2
44	Deep Sequencing of Small RNAs in the Whitefly <i>Bemisia tabaci</i> Reveals Novel MicroRNAs Potentially Associated with Begomovirus Acquisition and Transmission. Insects, 2020, 11, 562.	2.2	4
45	CWAS Based on RNA-Seq SNPs and High-Throughput Phenotyping Combined with Climatic Data Highlights the Reservoir of Valuable Genetic Diversity in Regional Tomato Landraces. Genes, 2020, 11, 1387.	2.4	14
46	KASP Genotyping as a Molecular Tool for Diagnosis of Cassava-Colonizing <i>Bemisia tabaci</i> . Insects, 2020, 11, 305.	2.2	9
47	Localization shift of a sugar transporter contributes to phloem unloading in sweet watermelons. New Phytologist, 2020, 227, 1858-1871.	7.3	32
48	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
49	Cutin and suberin: assembly and origins of specialized lipidic cell wall scaffolds. Current Opinion in Plant Biology, 2020, 55, 11-20.	7.1	126
50	Chromosome-level genome assembly of the greenhouse whitefly ( <i>Trialeurodes vaporariorum</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 T	4.8	21
51	Manipulation of ZDS in tomato exposes carotenoid- and ABA-specific effects on fruit development and ripening. Plant Biotechnology Journal, 2020, 18, 2210-2224.	8.3	44
52	<i>Citrullus lanatus</i> . Trends in Genetics, 2020, 36, 456-457.	6.7	5
53	Methylation of <i>MdMYB1</i> locus mediated by RdDM pathway regulates anthocyanin biosynthesis in apple. Plant Biotechnology Journal, 2020, 18, 1736-1748.	8.3	42
54	A key "foxy" aroma gene is regulated by homology-induced promoter indels in the iconic juice grape "Concord". Horticulture Research, 2020, 7, 67.	6.3	12

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55	The <i>Penium margaritaceum</i> Genome: Hallmarks of the Origins of Land Plants. <i>Cell</i> , 2020, 181, 1097-1111.e12.	28.9	153
56	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
57	Differences in gene expression in whitefly associated with CYSDV-infected and virus-free melon, and comparison with expression in whiteflies fed on ToCV- and TYLCV-infected tomato. <i>BMC Genomics</i> , 2019, 20, 654.	2.8	10
58	Mutation of ABC transporter ABCA2 confers resistance to Bt toxin Cry2Ab in <i>Trichoplusia ni</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2019, 112, 103209.	2.7	38
59	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
60	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
61	A CLE <sup>+</sup> SUNN module regulates strigolactone content and fungal colonization in arbuscular mycorrhiza. <i>Nature Plants</i> , 2019, 5, 933-939.	9.3	65
62	Plant Viruses Transmitted in Two Different Modes Produce Differing Effects on Small RNA-Mediated Processes in Their Aphid Vector. <i>Phytobiomes Journal</i> , 2019, 3, 71-81.	2.7	16
63	Plant Genome Editing Database (PGED): A Call for Submission of Information about Genome-Edited Plant Mutants. <i>Molecular Plant</i> , 2019, 12, 127-129.	8.3	20
64	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
65	The tomato HIGH PIGMENT1/DAMAGED DNA BINDING PROTEIN 1 gene contributes to regulation of fruit ripening. <i>Horticulture Research</i> , 2019, 6, 15.	6.3	20
66	Identification of Phloem Mobile mRNAs Using the Solanaceae Heterograft System. <i>Methods in Molecular Biology</i> , 2019, 2014, 421-431.	0.9	3
67	SpinachBase: a central portal for spinach genomics. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	3.0	30
68	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
69	<i>Rosa hybrida</i> Rh <sup>+</sup> ERF <sup>+</sup> 1 and Rh <sup>+</sup> ERF <sup>+</sup> 4 mediate ethylene- and auxin-regulated petal abscission by influencing pectin degradation. <i>Plant Journal</i> , 2019, 99, 1159-1171.	5.7	56
70	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
71	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
72	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

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73	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
74	Cellular and molecular characterization of a thick-walled variant reveal a pivotal role of shoot apical meristem in transverse development of bamboo culm. <i>Journal of Experimental Botany</i> , 2019, 70, 3911-3926.	4.8	29
75	Transcriptional Responses of the <i>Trichoplusia ni</i> Midgut to Oral Infection by the Baculovirus <i>Autographa californica</i> Multiple Nucleopolyhedrovirus. <i>Journal of Virology</i> , 2019, 93, .	3.4	20
76	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
77	Genome-wide profiling of piRNAs in the whitefly <i>Bemisia tabaci</i> reveals cluster distribution and association with begomovirus transmission. <i>PLoS ONE</i> , 2019, 14, e0213149.	2.5	7
78	A MYB/bHLH complex regulates tissue-specific anthocyanin biosynthesis in the inner pericarp of red-centered kiwifruit <i>Actinidia chinensis</i> cv. Hongyang. <i>Plant Journal</i> , 2019, 99, 359-378.	5.7	136
79	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
80	Genome sequence of the corn leaf aphid ( <i>Rhopalosiphum maidis</i> Fitch). <i>GigaScience</i> , 2019, 8, .	6.4	60
81	Chromosome-scale genome assembly of kiwifruit <i>Actinidia eriantha</i> with single-molecule sequencing and chromatin interaction mapping. <i>GigaScience</i> , 2019, 8, .	6.4	65
82	Differential gene regulatory pathways and co-expression networks associated with fire blight infection in apple ( <i>Malus domestica</i> ). <i>Horticulture Research</i> , 2019, 6, 35.	6.3	20
83	Transcriptome analysis provides insights into the regulation of metabolic processes during postharvest cold storage of loquat ( <i>Eriobotrya japonica</i> ) fruit. <i>Horticulture Research</i> , 2019, 6, 49.	6.3	29
84	Complete Genome Sequence of <i>Dickeya dianthicola</i> ME23, a Pathogen Causing Blackleg and Soft Rot Diseases of Potato. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	13
85	Integrated single-base resolution maps of transcriptome, sRNAome and methylome of Tomato yellow leaf curl virus (TYLCV) in tomato. <i>Scientific Reports</i> , 2019, 9, 2863.	3.3	26
86	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
87	QTL and Transcriptomic Analyses Implicate Cuticle Transcription Factor SHINE as a Source of Natural Variation for Epidermal Traits in Cucumber Fruit. <i>Frontiers in Plant Science</i> , 2019, 10, 1536.	3.6	12
88	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
89	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
90	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

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91	Morphological dissection and cellular and transcriptome characterizations of bamboo pith cavity formation reveal a pivotal role of genes related to programmed cell death. <i>Plant Biotechnology Journal</i> , 2019, 17, 982-997.	8.3	30
92	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
93	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
94	Differential metabolism of L-phenylalanine in the formation of aromatic volatiles in melon ( <i>Cucumis</i> ) <i>Tj ETQq0 0 0 rgBT /Overlock 10 T</i>	2.98	41
95	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
96	High-resolution spatiotemporal transcriptome mapping of tomato fruit development and ripening. <i>Nature Communications</i> , 2018, 9, 364.	12.8	255
97	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
98	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
99	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
100	Cellular and molecular characterizations of a slow-growth variant provide insights into the fast growth of bamboo. <i>Tree Physiology</i> , 2018, 38, 641-654.	3.1	42
101	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
102	Construction of genetic linkage map using genotyping-by-sequencing and identification of QTLs associated with leaf color in spinach. <i>Euphytica</i> , 2018, 214, 1.	1.2	9
103	Genome encode analyses reveal the basis of convergent evolution of fleshy fruit ripening. <i>Nature Plants</i> , 2018, 4, 784-791.	9.3	256
104	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
105	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
106	Global Analysis of Baculovirus <i>Autographa californica</i> Multiple Nucleopolyhedrovirus Gene Expression in the Midgut of the Lepidopteran Host <i>Trichoplusia ni</i> . <i>Journal of Virology</i> , 2018, 92, .	3.4	21
107	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
108	Diversification and independent domestication of Asian and European pears. <i>Genome Biology</i> , 2018, 19, 77.	8.8	149

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109	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
110	The Epigenome and Transcriptional Dynamics of Fruit Ripening. <i>Annual Review of Plant Biology</i> , 2017, 68, 61-84.	18.7	335
111	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
112	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
113	The complete mitochondrial genome sequence of spinach, <i>Spinacia oleracea</i> L. Mitochondrial DNA Part B: Resources, 2017, 2, 339-340.	0.4	5
114	The Tomato Kinase Pti1 Contributes to Production of Reactive Oxygen Species in Response to Two Flagellin-Derived Peptides and Promotes Resistance to <i>Pseudomonas syringae</i> Infection. <i>Molecular Plant-Microbe Interactions</i> , 2017, 30, 725-738.	2.6	22
115	Draft genome of spinach and transcriptome diversity of 120 <i>Spinacia</i> accessions. <i>Nature Communications</i> , 2017, 8, 15275.	12.8	156
116	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
117	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
118	Diversity, Distribution, and Evolution of Tomato Viruses in China Uncovered by Small RNA Sequencing. <i>Journal of Virology</i> , 2017, 91, .	3.4	63
119	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
120	The Tomato Expression Atlas. <i>Bioinformatics</i> , 2017, 33, 2397-2398.	4.1	64
121	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
122	Molecular and Biological Characterization of <i>Tomato mottle mosaic virus</i> and Development of RT-PCR Detection. <i>Plant Disease</i> , 2017, 101, 704-711.	1.4	28
123	Karyotype Stability and Unbiased Fractionation in the Paleo-Allotetraploid Cucurbita Genomes. <i>Molecular Plant</i> , 2017, 10, 1293-1306.	8.3	263
124	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
125	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
126	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



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127	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
128	Distinct Mechanisms of the ORANGE Protein in Controlling Carotenoid Flux. <i>Plant Physiology</i> , 2017, 173, 376-389.	4.8	97
129	Exploring key cellular processes and candidate genes regulating the primary thickening growth of <i>Scopolia</i> underground shoots. <i>New Phytologist</i> , 2017, 214, 81-96.	7.3	66
130	VirusDetect: An automated pipeline for efficient virus discovery using deep sequencing of small RNAs. <i>Virology</i> , 2017, 500, 130-138.	2.4	191
131	Using Small RNA-seq Data to Detect siRNA Duplexes Induced by Plant Viruses. <i>Genes</i> , 2017, 8, 163.	2.4	22
132	Identification and expression profiling of microRNAs involved in the stigma exertion under high-temperature stress in tomato. <i>BMC Genomics</i> , 2017, 18, 843.	2.8	42
133	Unravelling the Genetic Diversity among Cassava Bemisia tabaci Whiteflies Using NextRAD Sequencing. <i>Genome Biology and Evolution</i> , 2017, 9, 2958-2973.	2.5	57
134	Using Small RNA Deep Sequencing Data to Detect Human Viruses. <i>BioMed Research International</i> , 2016, 2016, 1-9.	1.9	33
135	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
136	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
137	Insights into the Mechanisms Underlying Ultraviolet-C Induced Resveratrol Metabolism in Grapevine ( <i>V. amurensis</i> Rupr.) cv. 'Tonghua-3'. <i>Frontiers in Plant Science</i> , 2016, 7, 503.	3.6	38
138	Transcriptome Profiling of Petal Abscission Zone and Functional Analysis of an Aux/IAA Family Gene RHIAA16 Involved in Petal Shedding in Rose. <i>Frontiers in Plant Science</i> , 2016, 7, 1375.	3.6	43
139	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
140	Transcriptome analyses of seed development in grape hybrids reveals a possible mechanism influencing seed size. <i>BMC Genomics</i> , 2016, 17, 898.	2.8	39
141	De novo and comparative transcriptome analysis of cultivated and wild spinach. <i>Scientific Reports</i> , 2016, 5, 17706.	3.3	41
142	Databases and Bioinformatics for Cucurbit Species. <i>Plant Genetics and Genomics: Crops and Models</i> , 2016, , 253-267.	0.3	2
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