

Xiuxin Deng

List of Publications by Year in descending order

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250
papers

10,504
citations

34105

52
h-index

54911

84
g-index

259
all docs

259
docs citations

259
times ranked

7852
citing authors

#	ARTICLE	IF	CITATIONS
1	The draft genome of sweet orange (<i>Citrus sinensis</i>). <i>Nature Genetics</i> , 2013, 45, 59-66.	21.4	837
2	Genomic analyses of primitive, wild and cultivated citrus provide insights into asexual reproduction. <i>Nature Genetics</i> , 2017, 49, 765-772.	21.4	316
3	A novel bud mutation that confers abnormal patterns of lycopene accumulation in sweet orange fruit (<i>Citrus sinensis</i> L. Osbeck). <i>Journal of Experimental Botany</i> , 2007, 58, 4161-4171.	4.8	185
4	The Citrus Transcription Factor CsMADS6 Modulates Carotenoid Metabolism by Directly Regulating Carotenogenic Genes. <i>Plant Physiology</i> , 2018, 176, 2657-2676.	4.8	184
5	Comparative proteomic and metabolomic profiling of citrus fruit with enhancement of disease resistance by postharvest heat treatment. <i>BMC Plant Biology</i> , 2013, 13, 44.	3.6	155
6	An R2R3- <i>MYB</i> transcription factor represses the transformation of β - and γ -branch carotenoids by negatively regulating expression of <i>CrBCH2</i> and <i>CrNCED5</i> in flavedo of <i>Citrus reticulata</i> . <i>New Phytologist</i> , 2017, 216, 178-192.	7.3	145
7	Transcriptome changes during fruit development and ripening of sweet orange (<i>Citrus sinensis</i>). <i>BMC Genomics</i> , 2012, 13, 10.	2.8	134
8	Genome of Wild Mandarin and Domestication History of Mandarin. <i>Molecular Plant</i> , 2018, 11, 1024-1037.	8.3	130
9	An integrative analysis of the transcriptome and proteome of the pulp of a spontaneous late-ripening sweet orange mutant and its wild type improves our understanding of fruit ripening in citrus. <i>Journal of Experimental Botany</i> , 2014, 65, 1651-1671.	4.8	129
10	Subfunctionalization of the Ruby2-Ruby1 gene cluster during the domestication of citrus. <i>Nature Plants</i> , 2018, 4, 930-941.	9.3	121
11	Discovery and comparative profiling of microRNAs in a sweet orange red-flesh mutant and its wild type. <i>BMC Genomics</i> , 2010, 11, 246.	2.8	120
12	The Or Gene Enhances Carotenoid Accumulation and Stability During Post-Harvest Storage of Potato Tubers. <i>Molecular Plant</i> , 2012, 5, 339-352.	8.3	120
13	Comprehensive comparative analysis of volatile compounds in citrus fruits of different species. <i>Food Chemistry</i> , 2017, 230, 316-326.	8.2	117
14	Exogenous β -aminobutyric acid treatment affects citrate and amino acid accumulation to improve fruit quality and storage performance of postharvest citrus fruit. <i>Food Chemistry</i> , 2017, 216, 138-145.	8.2	115
15	Comparative transcriptomics and proteomics analysis of citrus fruit, to improve understanding of the effect of low temperature on maintaining fruit quality during lengthy post-harvest storage. <i>Journal of Experimental Botany</i> , 2012, 63, 2873-2893.	4.8	110
16	Characterization and Metabolic Diversity of Flavonoids in Citrus Species. <i>Scientific Reports</i> , 2017, 7, 10549.	3.3	103
17	Natural Variation in CCD4 Promoter Underpins Species-Specific Evolution of Red Coloration in Citrus Peel. <i>Molecular Plant</i> , 2019, 12, 1294-1307.	8.3	102
18	In vitro induction of tetraploid in pomegranate (<i>Punica granatum</i>). <i>Plant Cell, Tissue and Organ Culture</i> , 2003, 75, 241-246.	2.3	101

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19	Comparative analysis of surface wax in mature fruits between Satsuma mandarin (<i>Citrus unshiu</i>) and 'Newhall' navel orange (<i>Citrus sinensis</i>) from the perspective of crystal morphology, chemical composition and key gene expression. <i>Food Chemistry</i> , 2014, 153, 177-185.	8.2	101
20	A <i>Medicago truncatula</i> SWEET transporter implicated in arbuscule maintenance during arbuscular mycorrhizal symbiosis. <i>New Phytologist</i> , 2019, 224, 396-408.	7.3	101
21	Comprehending crystalline β -carotene accumulation by comparing engineered cell models and the natural carotenoid-rich system of citrus. <i>Journal of Experimental Botany</i> , 2012, 63, 4403-4417.	4.8	100
22	Regulation of cuticle formation during fruit development and ripening in 'Newhall' navel orange () Tj ETQq0 0 0 rgBT /Overlock 10 131-144.	3.6	100
23	Mechanisms of action for 2-phenylethanol isolated from <i>Kloeckera apiculata</i> in control of <i>Penicillium</i> molds of citrus fruits. <i>BMC Microbiology</i> , 2014, 14, 242.	3.3	98
24	Network Analysis of Postharvest Senescence Process in Citrus Fruits Revealed by Transcriptomic and Metabolomic Profiling. <i>Plant Physiology</i> , 2015, 168, 357-376.	4.8	96
25	Volatile Constituents of Wild Citrus Mangshanyegan (<i>Citrus nobilis</i> Lauriro) Peel Oil. <i>Journal of Agricultural and Food Chemistry</i> , 2012, 60, 2617-2628.	5.2	94
26	Characterization of a Citrus R2R3-MYB Transcription Factor that Regulates the Flavonol and Hydroxycinnamic Acid Biosynthesis. <i>Scientific Reports</i> , 2016, 6, 25352.	3.3	93
27	Changes in Anthocyanin Production during Domestication of <i>Citrus</i> . <i>Plant Physiology</i> , 2017, 173, 2225-2242.	4.8	92
28	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
29	Genome sequencing and CRISPR/Cas9 gene editing of an early flowering Mini-Citrus (<i>Fortunella hindsii</i>). <i>Plant Biotechnology Journal</i> , 2019, 17, 2199-2210.	8.3	90
30	Proteomic analysis of somatic embryogenesis in Valencia sweet orange (<i>Citrus sinensis</i> Osbeck). <i>Plant Cell Reports</i> , 2009, 28, 281-289.	5.6	87
31	Evolution of self-compatibility by a mutant Sm-RNase in citrus. <i>Nature Plants</i> , 2020, 6, 131-142.	9.3	85
32	A set of primers for analyzing chloroplast DNA diversity in Citrus and related genera. <i>Tree Physiology</i> , 2005, 25, 661-672.	3.1	76
33	Phylogenetic relationships within Citrus and its related genera as inferred from AFLP markers. <i>Genetic Resources and Crop Evolution</i> , 2007, 54, 429-436.	1.6	74
34	An integrative analysis of transcriptome and proteome provides new insights into carotenoid biosynthesis and regulation in sweet orange fruits. <i>Journal of Proteomics</i> , 2012, 75, 2670-2684.	2.4	74
35	Expression of phytoene synthase gene (<i>Psy</i>) is enhanced during fruit ripening of Cara Cara navel orange (<i>Citrus sinensis</i> Osbeck). <i>Plant Cell Reports</i> , 2007, 26, 837-843.	5.6	71
36	Comprehensive insights on how 2,4-dichlorophenoxyacetic acid retards senescence in post-harvest citrus fruits using transcriptomic and proteomic approaches. <i>Journal of Experimental Botany</i> , 2014, 65, 61-74.	4.8	71

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37	Genome-wide comparison of microRNAs and their targeted transcripts among leaf, flower and fruit of sweet orange. <i>BMC Genomics</i> , 2014, 15, 695.	2.8	70
38	Comparative transcripts profiling reveals new insight into molecular processes regulating lycopene accumulation in a sweet orange (<i>Citrus sinensis</i>) red-flesh mutant. <i>BMC Genomics</i> , 2009, 10, 540.	2.8	69
39	Transcriptome analysis of a spontaneous mutant in sweet orange [<i>Citrus sinensis</i> (L.) Osbeck] during fruit development. <i>Journal of Experimental Botany</i> , 2009, 60, 801-813.	4.8	68
40	Volatile chemical and carotenoid profiles in watermelons [<i>Citrullus vulgaris</i> (Thunb.) Schrad (<i>Cucurbitaceae</i>)] with different flesh colors. <i>Food Science and Biotechnology</i> , 2012, 21, 531-541.	2.6	68
41	PtSVP, an SVP homolog from trifoliate orange (<i>Poncirus trifoliata</i> L. Raf.), shows seasonal periodicity of meristem determination and affects flower development in transgenic <i>Arabidopsis</i> and tobacco plants. <i>Plant Molecular Biology</i> , 2010, 74, 129-142.	3.9	67
42	CsCYT75B1, a Citrus CYTOCHROME P450 Gene, Is Involved in Accumulation of Antioxidant Flavonoids and Induces Drought Tolerance in Transgenic <i>Arabidopsis</i> . <i>Antioxidants</i> , 2020, 9, 161.	5.1	65
43	L-Ascorbic acid metabolism during fruit development in an ascorbate-rich fruit crop chestnut rose (<i>Rosa roxburghii</i> Tratt). <i>Journal of Plant Physiology</i> , 2014, 171, 1205-1216.	3.5	64
44	Isolation, phylogenetic relationship and expression profiling of sugar transporter genes in sweet orange (<i>Citrus sinensis</i>). <i>Plant Cell, Tissue and Organ Culture</i> , 2014, 119, 609-624.	2.3	63
45	iTRAQ-Based Quantitative Proteomics Analysis Revealed Alterations of Carbohydrate Metabolism Pathways and Mitochondrial Proteins in a Male Sterile Cybrid Pummelo. <i>Journal of Proteome Research</i> , 2014, 13, 2998-3015.	3.7	61
46	Genome-wide identification of sweet orange (<i>Citrus sinensis</i>) histone modification gene families and their expression analysis during the fruit development and fruit-blue mold infection process. <i>Frontiers in Plant Science</i> , 2015, 6, 607.	3.6	61
47	Salicylic acid treatment reduces the rot of postharvest citrus fruit by inducing the accumulation of H ₂ O ₂ , primary metabolites and lipophilic polymethoxylated flavones. <i>Food Chemistry</i> , 2016, 207, 68-74.	8.2	61
48	Comparative proteomics of a lycopene-accumulating mutant reveals the important role of oxidative stress on carotenogenesis in sweet orange (<i>Citrus sinensis</i> [L.] osbeck). <i>Proteomics</i> , 2009, 9, 5455-5470.	2.2	59
49	Functional characterization of Citrus PSY gene in Hongkong kumquat (<i>Fortunella hindsii</i> Swingle). <i>Plant Cell Reports</i> , 2009, 28, 1737-1746.	5.6	58
50	Utility of RAPD, ISSR, IRAP and REMAP markers for the genetic analysis of Citrus spp.. <i>Scientia Horticulturae</i> , 2010, 124, 254-261.	3.6	58
51	Isolation of TIR and nonTIR NBS-LRR resistance gene analogues and identification of molecular markers linked to a powdery mildew resistance locus in chestnut rose (<i>Rosa roxburghii</i> Tratt). <i>Theoretical and Applied Genetics</i> , 2005, 111, 819-830.	3.6	56
52	A proteomic analysis of the chromoplasts isolated from sweet orange fruits [<i>Citrus sinensis</i> (L.) Osbeck]. <i>Journal of Experimental Botany</i> , 2011, 62, 5297-5309.	4.8	56
53	Comparative Transcript Profiling of a Male Sterile Cybrid Pummelo and Its Fertile Type Revealed Altered Gene Expression Related to Flower Development. <i>PLoS ONE</i> , 2012, 7, e43758.	2.5	56
54	The effects of low boron on growth, gas exchange, boron concentration and distribution of 'Newhall' navel orange (<i>Citrus sinensis</i> Osb.) plants grafted on two rootstocks. <i>Scientia Horticulturae</i> , 2009, 121, 278-283.	3.6	53

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55	Carotenoid accumulation affects redox status, starch metabolism, and flavonoid/anthocyanin accumulation in citrus. BMC Plant Biology, 2015, 15, 27.	3.6	53
56	Ethylene activation of carotenoid biosynthesis by a novel transcription factor CsERF061. Journal of Experimental Botany, 2021, 72, 3137-3154.	4.8	53
57	Occurrence of chromosomal variations and plant regeneration from long-term-cultured citrus callus. In Vitro Cellular and Developmental Biology - Plant, 2002, 38, 472-476.	2.1	52
58	Genome-wide analysis of the R2R3-MYB transcription factor gene family in sweet orange (Citrus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 6	2.3	52
59	CsMYB3 and CsRuby1 form an "Activator-and-Repressor"™ Loop for the Regulation of Anthocyanin Biosynthesis in Citrus. Plant and Cell Physiology, 2020, 61, 318-330.	3.1	52
60	Comparative analysis of genetic diversity in Citrus germplasm collection using AFLP, SSAP, SAMPL and SSR markers. Scientia Horticulturae, 2011, 129, 798-803.	3.6	51
61	Genome Wide Characterization of Short Tandem Repeat Markers in Sweet Orange (Citrus sinensis). PLoS ONE, 2014, 9, e104182.	2.5	50
62	Involvement of polyamine biosynthesis in somatic embryogenesis of Valencia sweet orange (Citrus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 6	3.5	49
63	Identification of miRNAs and Their Target Genes Using Deep Sequencing and Degradome Analysis in Trifoliate Orange [Poncirus trifoliata (L.) Raf]. Molecular Biotechnology, 2012, 51, 44-57.	2.4	49
64	Integrated transcriptomic and metabolomic analyses of a wax deficient citrus mutant exhibiting jasmonic acid-mediated defense against fungal pathogens. Horticulture Research, 2018, 5, 43.	6.3	49
65	Identification of 2,4-D-responsive proteins in embryogenic callus of Valencia sweet orange (Citrus) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 6	2.3	48
66	Somatic variations led to the selection of acidic and acidless orange cultivars. Nature Plants, 2021, 7, 954-965.	9.3	48
67	Citrus sinensis Annotation Project (CAP): A Comprehensive Database for Sweet Orange Genome. PLoS ONE, 2014, 9, e87723.	2.5	47
68	Comparative study of flavonoid production in lycopene-accumulated and blonde-flesh sweet oranges (Citrus sinensis) during fruit development. Food Chemistry, 2015, 184, 238-246.	8.2	47
69	Effects of exogenous 24-epibrassinolide treatment on postharvest quality and resistance of Satsuma mandarin (Citrus unshiu). Postharvest Biology and Technology, 2015, 100, 8-15.	6.0	47
70	GABA Pathway Rate-Limit Citrate Degradation in Postharvest Citrus Fruit Evidence from HB Pumelo (<i>Citrus grandis</i>) Å— Fairchild (<i>Citrus reticulata</i>) Hybrid Population. Journal of Agricultural and Food Chemistry, 2017, 65, 1669-1676.	5.2	47
71	Retrotransposon promoter of <i>Ruby1</i> controls both light- and cold-induced accumulation of anthocyanins in blood orange. Plant, Cell and Environment, 2019, 42, 3092-3104.	5.7	47
72	A fruit ripening-associated transcription factor CsMADS5 positively regulates carotenoid biosynthesis in citrus. Journal of Experimental Botany, 2021, 72, 3028-3043.	4.8	47

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73	Construction of a SNP-based high-density genetic map for pummelo using RAD sequencing. <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	1.6	46
74	Genome of a citrus rootstock and global DNA demethylation caused by heterografting. <i>Horticulture Research</i> , 2021, 8, 69.	6.3	45
75	Transcriptome profile analysis of flowering molecular processes of early flowering trifoliate orange mutant and the wild-type [<i>Poncirus trifoliata</i> (L.) Raf.] by massively parallel signature sequencing. <i>BMC Genomics</i> , 2011, 12, 63.	2.8	44
76	Integration of Metabolomics and Subcellular Organelle Expression Microarray to Increase Understanding the Organic Acid Changes in Postharvest Citrus Fruit. <i>Journal of Integrative Plant Biology</i> , 2013, 55, 1038-1053.	8.5	44
77	A Comprehensive Analysis of Chromoplast Differentiation Reveals Complex Protein Changes Associated with Plastoglobule Biogenesis and Remodeling of Protein Systems in Sweet Orange Flesh. <i>Plant Physiology</i> , 2015, 168, 1648-1665.	4.8	43
78	Evolutionary dynamics of linc RNA transcription in nine citrus species. <i>Plant Journal</i> , 2019, 98, 912-927.	5.7	43
79	Presence of diverse ratios of lycopene/β-carotene in five pink or red-fleshed citrus cultivars. <i>Scientia Horticulturae</i> , 2006, 108, 181-184.	3.6	42
80	Characterization of DNA Methylation Variations During Fruit Development and Ripening of Sweet Orange. <i>Plant Molecular Biology Reporter</i> , 2015, 33, 1-11.	1.8	42
81	Cit1,2RhaT and two novel CitdGlcTs participate in flavor-related flavonoid metabolism during citrus fruit development. <i>Journal of Experimental Botany</i> , 2019, 70, 2759-2771.	4.8	42
82	Red light-induced kumquat fruit coloration is attributable to increased carotenoid metabolism regulated by FcrNAC22. <i>Journal of Experimental Botany</i> , 2021, 72, 6274-6290.	4.8	42
83	Exploiting BAC-end sequences for the mining, characterization and utility of new short sequences repeat (SSR) markers in Citrus. <i>Molecular Biology Reports</i> , 2012, 39, 5373-5386.	2.3	41
84	miR3954 is a trigger of phase-specific RNA silencing that affects flowering time in citrus. <i>Plant Journal</i> , 2017, 92, 263-275.	5.7	41
85	Genomic basis of high-altitude adaptation in Tibetan <i>Prunus</i> fruit trees. <i>Current Biology</i> , 2021, 31, 3848-3860.e8.	3.9	41
86	Comparative proteomics analysis of differentially accumulated proteins in juice sacs of ponkan (<i>Citrus reticulata</i>) fruit during postharvest cold storage. <i>Postharvest Biology and Technology</i> , 2010, 56, 189-201.	6.0	40
87	Microarray Expression Profiling of Postharvest Ponkan Mandarin (<i>Citrus reticulata</i>) Fruit under Cold Storage Reveals Regulatory Gene Candidates and Implications on Soluble Sugars Metabolism. <i>Journal of Integrative Plant Biology</i> , 2011, 53, 358-374.	8.5	40
88	Transcriptional profiling of genes involved in embryogenic, non-embryogenic calluses and somatic embryogenesis of Valencia sweet orange by SSH-based microarray. <i>Planta</i> , 2012, 236, 1107-1124.	3.2	40
89	Non-targeted metabolomic analysis of orange (<i>Citrus sinensis</i> [L.] Osbeck) wild type and bud mutant fruits by direct analysis in real-time and HPLC-electrospray mass spectrometry. <i>Metabolomics</i> , 2014, 10, 508-523.	3.0	40
90	Effects of phosphorus on fruit soluble sugar and citric acid accumulations in citrus. <i>Plant Physiology and Biochemistry</i> , 2021, 160, 73-81.	5.8	40

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91	Somatic cybrid production via protoplast fusion for citrus improvement. <i>Scientia Horticulturae</i> , 2013, 163, 20-26.	3.6	39
92	Comparative genome analyses reveal sequence features reflecting distinct modes of host-adaptation between dicot and monocot powdery mildew. <i>BMC Genomics</i> , 2018, 19, 705.	2.8	39
93	A NAC transcription factor and its interaction protein hinder abscisic acid biosynthesis by synergistically repressing NCED5 in <i>Citrus reticulata</i> . <i>Journal of Experimental Botany</i> , 2020, 71, 3613-3625.	4.8	39
94	Identification and Comparative Profiling of miRNAs in an Early Flowering Mutant of Trifoliate Orange and Its Wild Type by Genome-Wide Deep Sequencing. <i>PLoS ONE</i> , 2012, 7, e43760.	2.5	38
95	Reproduction in woody perennial Citrus: an update on nucellar embryony and self-incompatibility. <i>Plant Reproduction</i> , 2018, 31, 43-57.	2.2	38
96	The miR399- <i>CsUBC24</i> Module Regulates Reproductive Development and Male Fertility in Citrus. <i>Plant Physiology</i> , 2020, 183, 1681-1695.	4.8	38
97	Production of two mandarin— trifoliate orange hybrid populations via embryo rescue with verification by SSR analysis. <i>Euphytica</i> , 2007, 157, 155-160.	1.2	37
98	Identification and Expression Pattern of a Novel NAM, ATAF, and CUC-Like Gene from <i>Citrus sinensis</i> Osbeck. <i>Plant Molecular Biology Reporter</i> , 2009, 27, 292-297.	1.8	37
99	Distinct Carotenoid and Flavonoid Accumulation in a Spontaneous Mutant of Ponkan (<i>Citrus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock Agricultural and Food Chemistry, 2015, 63, 8601-8614.	5.2	37
100	Genome-scale mRNA and small RNA transcriptomic insights into initiation of citrus apomixis. <i>Journal of Experimental Botany</i> , 2016, 67, 5743-5756.	4.8	36
101	Development of Juglans Regia SSR Markers by Data Mining of the EST Database. <i>Plant Molecular Biology Reporter</i> , 2010, 28, 646-653.	1.8	35
102	Transcriptomic analysis of differentially expressed genes in an orange-pericarp mutant and wild type in pummelo (<i>Citrus grandis</i>). <i>BMC Plant Biology</i> , 2015, 15, 44.	3.6	35
103	The impact of a novel peach gum-derived polysaccharide on postprandial blood glucose control in streptozotocin-induced diabetic mice. <i>International Journal of Biological Macromolecules</i> , 2017, 98, 379-386.	7.5	35
104	Doubled haploid callus lines of Valencia sweet orange recovered from anther culture. <i>Plant Cell, Tissue and Organ Culture</i> , 2011, 104, 415-423.	2.3	34
105	Chemotaxonomic Study of Citrus, Poncirus and Fortunella Genotypes Based on Peel Oil Volatile Compounds - Deciphering the Genetic Origin of Mangshanyegan (<i>Citrus nobilis</i> Lauriro). <i>PLoS ONE</i> , 2013, 8, e58411.	2.5	34
106	Dynamic changes in methylome and transcriptome patterns in response to methyltransferase inhibitor 5-azacytidine treatment in citrus. <i>DNA Research</i> , 2017, 24, 509-522.	3.4	34
107	Fatty acid metabolic flux and lipid peroxidation homeostasis maintain the biomembrane stability to improve citrus fruit storage performance. <i>Food Chemistry</i> , 2019, 292, 314-324.	8.2	33
108	Abnormal Microspore Development Leads to Pollen Abortion in a Seedless Mutant of 'Ougana' Mandarin (<i>Citrus suaveolens</i> Hort. ex Tanaka). <i>Journal of the American Society for Horticultural Science</i> , 2007, 132, 777-782.	1.0	33

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109	Obtaining autotetraploids in vitro at a high frequency in <i>Citrus sinensis</i> . <i>Plant Cell, Tissue and Organ Culture</i> , 2007, 89, 211-216.	2.3	32
110	CgSL2, an S-like RNase gene in 'Zigui shatian' pummelo (<i>Citrus grandis</i> Osbeck), is involved in ovary senescence. <i>Molecular Biology Reports</i> , 2011, 38, 1-8.	2.3	32
111	Ectopic expression of citrus UDP-GLUCOSYL TRANSFERASE gene enhances anthocyanin and proanthocyanidins contents and confers high light tolerance in <i>Arabidopsis</i> . <i>BMC Plant Biology</i> , 2019, 19, 603.	3.6	32
112	Light effect on carotenoids production and expression of carotenogenesis genes in citrus callus of four genotypes. <i>Acta Physiologiae Plantarum</i> , 2011, 33, 2485-2492.	2.1	31
113	Production and molecular characterization of diploid and tetraploid somatic cybrid plants between male sterile Satsuma mandarin and seedy sweet orange cultivars. <i>Plant Cell, Tissue and Organ Culture</i> , 2014, 116, 81-88.	2.3	31
114	Effect of the Citrus Lycopene β -Cyclase Transgene on Carotenoid Metabolism in Transgenic Tomato Fruits. <i>PLoS ONE</i> , 2012, 7, e32221.	2.5	31
115	Production and molecular characterization of potential seedless cybrid plants between pollen sterile Satsuma mandarin and two seedy Citrus cultivars. <i>Plant Cell, Tissue and Organ Culture</i> , 2007, 90, 275-283.	2.3	30
116	Prediction and functional analysis of the sweet orange protein-protein interaction network. <i>BMC Plant Biology</i> , 2014, 14, 213.	3.6	30
117	Isolation and characterization of carotenoid cleavage dioxygenase 4 genes from different citrus species. <i>Molecular Genetics and Genomics</i> , 2015, 290, 1589-1603.	2.1	30
118	Difference of a citrus late-ripening mutant (<i>Citrus sinensis</i>) from its parental line in sugar and acid metabolism at the fruit ripening stage. <i>Science in China Series C: Life Sciences</i> , 2007, 50, 511-517.	1.3	29
119	Self-sterility in the mutant 'Zigui shatian' pummelo (<i>Citrus grandis</i> Osbeck) is due to abnormal post-zygotic embryo development and not self-incompatibility. <i>Plant Cell, Tissue and Organ Culture</i> , 2011, 104, 1-11.	2.3	29
120	Features of citrus terpenoid production as revealed by carotenoid, limonoid and aroma profiles of two pummelos (<i>Citrus maxima</i>) with different flesh color. <i>Journal of the Science of Food and Agriculture</i> , 2015, 95, 111-119.	3.5	29
121	Genome-wide identification and functional analysis of S-RNase involved in the self-incompatibility of citrus. <i>Molecular Genetics and Genomics</i> , 2017, 292, 325-341.	2.1	29
122	Metabolic Mechanisms of Host Species Against Citrus Huanglongbing (Greening Disease). <i>Critical Reviews in Plant Sciences</i> , 2018, 37, 496-511.	5.7	29
123	Regulation of carotenoid and chlorophyll pools in hesperidia, anatomically unique fruits found only in <i>Citrus</i> . <i>Plant Physiology</i> , 2021, 187, 829-845.	4.8	29
124	Evaluation of Codon Biology in Citrus and <i>Poncirus trifoliata</i> Based on Genomic Features and Frame Corrected Expressed Sequence Tags. <i>DNA Research</i> , 2013, 20, 135-150.	3.4	28
125	Illuminating the cells: transient transformation of citrus to study gene functions and organelle activities related to fruit quality. <i>Horticulture Research</i> , 2021, 8, 175.	6.3	28
126	Fragile Sites of 'Valencia' Sweet Orange (<i>Citrus sinensis</i>) Chromosomes Are Related with Active 45s rDNA. <i>PLoS ONE</i> , 2016, 11, e0151512.	2.5	28

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127	Retro-transposon based genetic similarity within the genus <i>Citrus</i> and its relatives. <i>Genetic Resources and Crop Evolution</i> , 2010, 57, 963-972.	1.6	27
128	SLAF-Based Construction of a High-Density Genetic Map and Its Application in QTL Mapping of Carotenoids Content in Citrus Fruit. <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 994-1002.	5.2	27
129	De Novo Transcriptome Assembly of Pummelo and Molecular Marker Development. <i>PLoS ONE</i> , 2015, 10, e0120615.	2.5	26
130	Isolation, Characterization, and Expression Analysis of an SKP1-like Gene from ‘Shatian’ Pummelo (<i>Citrus grandis</i> Osbeck). <i>Plant Molecular Biology Reporter</i> , 2010, 28, 569-577.	1.8	25
131	QTL analysis reveals the effect of CER1-1 and CER1-3 to reduce fruit water loss by increasing cuticular wax alkanes in citrus fruit. <i>Postharvest Biology and Technology</i> , 2022, 185, 111771.	6.0	25
132	Identification, characterization and expression analysis of lineage-specific genes within sweet orange (<i>Citrus sinensis</i>). <i>BMC Genomics</i> , 2015, 16, 995.	2.8	24
133	The Scion/Rootstock Genotypes and Habitats Affect Arbuscular Mycorrhizal Fungal Community in Citrus. <i>Frontiers in Microbiology</i> , 2015, 6, 1372.	3.5	24
134	Isolation and Functional Characterization of a Lycopene β -cyclase Gene Promoter from Citrus. <i>Frontiers in Plant Science</i> , 2016, 7, 1367.	3.6	24
135	Multimics-based dissection of citrus flavonoid metabolism using a <i>Citrus reticulata</i> ‘Poncirus trifoliata’ population. <i>Horticulture Research</i> , 2021, 8, 56.	6.3	24
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161	Lycopene- β -Cyclase Pre-mRNA is Alternatively Spliced in Cara Cara Navel Orange (Citrus sinensis) Tj ETQq1 1 0.784314 rgBT /Overlock 1	2.2	16
162	Cloning of two classes of PR genes and the development of SNAP markers for powdery mildew resistance loci in chestnut rose (<i>Rosa roxburghii</i> Tratt). Molecular Breeding, 2007, 19, 179-191.	2.1	16

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