

Xiuxin Deng

List of Publications by Year in descending order

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250
papers

10,504
citations

34100

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 100 131-144.	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. <i>BMC Plant Biology</i> , 2015, 15, 27.	3.6	53
56	Ethylene activation of carotenoid biosynthesis by a novel transcription factor CsERF061. <i>Journal of Experimental Botany</i> , 2021, 72, 3137-3154.	4.8	53
57	Occurrence of chromosomal variations and plant regeneration from long-term-cultured citrus callus. <i>In Vitro Cellular and Developmental Biology - Plant</i> , 2002, 38, 472-476.	2.1	52
58	Genome-wide analysis of the R2R3-MYB transcription factor gene family in sweet orange (<i>Citrus</i>) 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. <i>Plant and Cell Physiology</i> , 2020, 61, 318-330.	3.1	52
60	Comparative analysis of genetic diversity in Citrus germplasm collection using AFLP, SSAP, SAMPL and SSR markers. <i>Scientia Horticulturae</i> , 2011, 129, 798-803.	3.6	51
61	Genome Wide Characterization of Short Tandem Repeat Markers in Sweet Orange (<i>Citrus sinensis</i>). <i>PLoS ONE</i> , 2014, 9, e104182.	2.5	50
62	Involvement of polyamine biosynthesis in somatic embryogenesis of Valencia sweet orange (<i>Citrus</i>) 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 [<i>Poncirus trifoliata</i> (L.) Raf]. <i>Molecular Biotechnology</i> , 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. <i>Horticulture Research</i> , 2018, 5, 43.	6.3	49
65	Identification of 2,4-D-responsive proteins in embryogenic callus of Valencia sweet orange (<i>Citrus</i>) 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. <i>Nature Plants</i> , 2021, 7, 954-965.	9.3	48
67	Citrus sinensis Annotation Project (CAP): A Comprehensive Database for Sweet Orange Genome. <i>PLoS ONE</i> , 2014, 9, e87723.	2.5	47
68	Comparative study of flavonoid production in lycopene-accumulated and blonde-flesh sweet oranges (<i>Citrus sinensis</i>) during fruit development. <i>Food Chemistry</i> , 2015, 184, 238-246.	8.2	47
69	Effects of exogenous 24-epibrassinolide treatment on postharvest quality and resistance of Satsuma mandarin (<i>Citrus unshiu</i>). <i>Postharvest Biology and Technology</i> , 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>) × Fairchild (<i>Citrus reticulata</i>) Hybrid Population. <i>Journal of Agricultural and Food Chemistry</i> , 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. <i>Plant, Cell and Environment</i> , 2019, 42, 3092-3104.	5.7	47
72	A fruit ripening-associated transcription factor CsMADS5 positively regulates carotenoid biosynthesis in citrus. <i>Journal of Experimental Botany</i> , 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 trifoliolate 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 transition 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 Trifoliolate 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>CsLUC24</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-trifoliolate 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 suavissima</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 <i>in vitro</i> 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 Citrus 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
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160	Concentration and distribution of main bitter compounds in fruit tissues of 'Oroblanco'™ (<i>Citrus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T	3.6	17
161	Lycopene- β -Cyclase Pre-mRNA is Alternatively Spliced in Cara Cara Navel Orange (<i>Citrus sinensis</i>) 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). <i>Molecular Breeding</i> , 2007, 19, 179-191.	2.1	16

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