

Xiuxin Deng

List of Publications by Year in descending order

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Version: 2024-02-01

250
papers

10,504
citations

39113

52
h-index

62345

84
g-index

259
all docs

259
docs citations

259
times ranked

8550
citing authors

#	ARTICLE	IF	CITATIONS
1	CsMYB96 confers resistance to water loss in citrus fruit by simultaneous regulation of water transport and wax biosynthesis. <i>Journal of Experimental Botany</i> , 2022, 73, 953-966.	2.4	20
2	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.	2.9	25
3	Cytological and proteomic evidence reveals the involvement of mitochondria in hypoxia-induced quality degradation in postharvest citrus fruit. <i>Food Chemistry</i> , 2022, 375, 131833.	4.2	9
4	Illustration of the variation in the content of flavanone rutinosides in various citrus germplasms from genetic and enzymatic perspectives. <i>Horticulture Research</i> , 2022, 9, .	2.9	2
5	Variation burst during dedifferentiation and increased CHH-type DNA methylation after 30 years of <i>in vitro</i> culture of sweet orange. <i>Horticulture Research</i> , 2022, 9, .	2.9	2
6	Carotenoid extraction, detection, and analysis in citrus. <i>Methods in Enzymology</i> , 2022, , 179-212.	0.4	11
7	Transcriptome and co-expression network analyses provide insights into fruit shading that enhances carotenoid accumulation in pomelo (<i>Citrus grandis</i>). <i>Horticultural Plant Journal</i> , 2022, 8, 423-434.	2.3	9
8	CitWRKY28 and CitNAC029 promote the synthesis of cuticular wax by activating CitKCS gene expression in citrus fruit. <i>Plant Cell Reports</i> , 2022, 41, 905-920.	2.8	11
9	TRIPTYCHON-LIKE regulates aspects of both fruit flavor and color in citrus. <i>Journal of Experimental Botany</i> , 2022, 73, 3610-3624.	2.4	11
10	MYB308-mediated transcriptional activation of plasma membrane H ⁺ -ATPase 6 promotes iron uptake in citrus. <i>Horticulture Research</i> , 2022, 9, .	2.9	14
11	Genome-wide identification of ovate family in Citrus and functional characterization of CitOFP19. <i>Plant Science</i> , 2022, 321, 111328.	1.7	6
12	Structural variation and parallel evolution of apomixis in citrus during domestication and diversification. <i>National Science Review</i> , 2022, 9, .	4.6	19
13	Chlorophyll retention reduces storability and pathogen defense in a novel citrus brown flavedo mutant. <i>Postharvest Biology and Technology</i> , 2022, 192, 112006.	2.9	5
14	Variations of membrane fatty acids and epicuticular wax metabolism in response to oleocellosis in lemon fruit. <i>Food Chemistry</i> , 2021, 338, 127684.	4.2	15
15	Natural variations of TFIIA ³ gene and LOB1 promoter contribute to citrus canker disease resistance in <i>Atalantia buxifolia</i> . <i>PLoS Genetics</i> , 2021, 17, e1009316.	1.5	14
16	Isolation and comparative proteomic analysis of mitochondria from the pulp of ripening citrus fruit. <i>Horticulture Research</i> , 2021, 8, 31.	2.9	12
17	Regulation of nucellar embryony, a mode of sporophytic apomixis in Citrus resembling somatic embryogenesis. <i>Current Opinion in Plant Biology</i> , 2021, 59, 101984.	3.5	11
18	Ethylene activation of carotenoid biosynthesis by a novel transcription factor CsERF061. <i>Journal of Experimental Botany</i> , 2021, 72, 3137-3154.	2.4	53

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19	A fruit ripening-associated transcription factor CsMADS5 positively regulates carotenoid biosynthesis in citrus. <i>Journal of Experimental Botany</i> , 2021, 72, 3028-3043.	2.4	47
20	LC-MS-Based Profiling Provides New Insights into Apocarotenoid Biosynthesis and Modifications in Citrus Fruits. <i>Journal of Agricultural and Food Chemistry</i> , 2021, 69, 1842-1851.	2.4	12
21	Effects of phosphorus on fruit soluble sugar and citric acid accumulations in citrus. <i>Plant Physiology and Biochemistry</i> , 2021, 160, 73-81.	2.8	40
22	Multimomics-based dissection of citrus flavonoid metabolism using a <i>Citrus reticulata</i> × <i>Poncirus trifoliata</i> population. <i>Horticulture Research</i> , 2021, 8, 56.	2.9	24
23	Genome of a citrus rootstock and global DNA demethylation caused by heterografting. <i>Horticulture Research</i> , 2021, 8, 69.	2.9	45
24	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.	2.3	29
25	Red light-induced kumquat fruit coloration is attributable to increased carotenoid metabolism regulated by FcNAC22. <i>Journal of Experimental Botany</i> , 2021, 72, 6274-6290.	2.4	42
26	Somatic variations led to the selection of acidic and acidless orange cultivars. <i>Nature Plants</i> , 2021, 7, 954-965.	4.7	48
27	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.	2.9	28
28	Transcriptomes and DNA methylomes in apomictic cells delineate nucellar embryogenesis initiation in citrus. <i>DNA Research</i> , 2021, 28, .	1.5	12
29	Citrus transcription factor CsHB5 regulates abscisic acid biosynthetic genes and promotes senescence. <i>Plant Journal</i> , 2021, 108, 151-168.	2.8	15
30	Storage with apple fruit to improve peel color and maintain freshness of Newhall navel orange. <i>Scientia Horticulturae</i> , 2021, 287, 110246.	1.7	6
31	A plant CitPITP1 protein-coding exon sequence serves as a promoter in bacteria. <i>Journal of Biotechnology</i> , 2021, 339, 1-13.	1.9	0
32	Downregulated expression of <i>S2-RNase</i> attenuates self-incompatibility in ‘Guiyou No. 1’ pummelo. <i>Horticulture Research</i> , 2021, 8, 199.	2.9	12
33	Genomic basis of high-altitude adaptation in Tibetan <i>Prunus</i> fruit trees. <i>Current Biology</i> , 2021, 31, 3848-3860.e8.	1.8	41
34	Development of a gRNA-tRNA array of CRISPR/Cas9 in combination with grafting technique to improve gene-editing efficiency of sweet orange. <i>Plant Cell Reports</i> , 2021, 40, 2453-2456.	2.8	4
35	A Citrus Phosphate Starvation Response Factor CsPHL3 Negatively Regulates Carotenoid Metabolism. <i>Plant and Cell Physiology</i> , 2021, 62, 482-493.	1.5	9
36	Molecular signatures between citrus and <i>Candidatus Liberibacter asiaticus</i> . <i>PLoS Pathogens</i> , 2021, 17, e1010071.	2.1	23

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37	Citrus PH4â€œNoemi regulatory complex is involved in proanthocyanidin biosynthesis via a positive feedback loop. <i>Journal of Experimental Botany</i> , 2020, 71, 1306-1321.	2.4	23
38	CsMYB3 and CsRuby1 form an â€œActivator-and-Repressorâ€™™ Loop for the Regulation of Anthocyanin Biosynthesis in Citrus. <i>Plant and Cell Physiology</i> , 2020, 61, 318-330.	1.5	52
39	Building the Synthetic Biology Toolbox with Enzyme Variants to Expand Opportunities for Biofortification of Provitamin A and Other Health-Promoting Carotenoids. <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 12048-12057.	2.4	11
40	Identification of a delayed leaf greening gene from a mutation of pummelo. <i>Science China Life Sciences</i> , 2020, 64, 1165-1173.	2.3	1
41	Assembly of Satsuma mandarin mitochondrial genome and identification of cytoplasmic male sterilityâ€™specific ORFs in a somatic cybrid of pummelo. <i>Tree Genetics and Genomes</i> , 2020, 16, 1.	0.6	6
42	Genome-wide Characterization of cis-acting Elements in the Promoters of Key Carotenoid Pathway Genes from the Main Species of Genus Citrus. <i>Horticultural Plant Journal</i> , 2020, 6, 385-395.	2.3	13
43	The effect of Î²-cyclocitral treatment on the carotenoid content of transgenic Marsh grapefruit (<i>Citrus paradisi</i> Macf.) suspension-cultured cells. <i>Phytochemistry</i> , 2020, 180, 112509.	1.4	7
44	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.	2.4	39
45	The miR399- <i>CsLUBC24</i> Module Regulates Reproductive Development and Male Fertility in Citrus. <i>Plant Physiology</i> , 2020, 183, 1681-1695.	2.3	38
46	CsCYT75B1, a Citrus CYTOCHROME P450 Gene, Is Involved in Accumulation of Antioxidant Flavonoids and Induces Drought Tolerance in Transgenic Arabidopsis. <i>Antioxidants</i> , 2020, 9, 161.	2.2	65
47	Evolution of self-compatibility by a mutant Sm-RNase in citrus. <i>Nature Plants</i> , 2020, 6, 131-142.	4.7	85
48	Domestication and history. , 2020, , 33-55.		7
49	Lipidomic and transcriptomic analysis reveals reallocation of carbon flux from cuticular wax into plastid membrane lipids in a glossy â€œNewhallâ€™ navel orange mutant. <i>Horticulture Research</i> , 2020, 7, 41.	2.9	23
50	Citrus Reproductive Biology from Flowering to Fruiting. <i>Compendium of Plant Genomes</i> , 2020, , 167-176.	0.3	2
51	Genetic Resources of Citrus and Related Genera. <i>Compendium of Plant Genomes</i> , 2020, , 23-31.	0.3	3
52	Endogenous pararetrovirus sequences are widely present in Citrinae genomes. <i>Virus Research</i> , 2019, 262, 48-53.	1.1	15
53	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.	2.8	47
54	Chromosomal characterization of a potential model mini-Citrus (<i>Fortunella hindsii</i>). <i>Tree Genetics and Genomes</i> , 2019, 15, 1.	0.6	4

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55	Phosphoproteomic changes in root cells of <i>Poncirus trifoliata</i> (L.) Raf. induced by <i>Rhizophagus intraradices</i> inoculation. <i>Tree Genetics and Genomes</i> , 2019, 15, 1.	0.6	1
56	Natural Variation in CCD4 Promoter Underpins Species-Specific Evolution of Red Coloration in Citrus Peel. <i>Molecular Plant</i> , 2019, 12, 1294-1307.	3.9	102
57	Investigation of chromoplast ultrastructure and tissue-specific accumulation of carotenoids in citrus flesh. <i>Scientia Horticulturae</i> , 2019, 256, 108547.	1.7	15
58	A <i>Medicago truncatula</i> <i>SWEET</i> transporter implicated in arbuscule maintenance during arbuscular mycorrhizal symbiosis. <i>New Phytologist</i> , 2019, 224, 396-408.	3.5	101
59	Genome sequencing and <i>CRISPR/Cas9</i> gene editing of an early flowering Mini-Citrus (<i>Fortunella hindsii</i>). <i>Plant Biotechnology Journal</i> , 2019, 17, 2199-2210.	4.1	90
60	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.	2.4	42
61	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.	4.2	33
62	Evolutionary dynamics of linc RNA transcription in nine citrus species. <i>Plant Journal</i> , 2019, 98, 912-927.	2.8	43
63	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.	1.6	32
64	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.	2.4	27
65	The Citrus Transcription Factor CsMADS6 Modulates Carotenoid Metabolism by Directly Regulating Carotenogenic Genes. <i>Plant Physiology</i> , 2018, 176, 2657-2676.	2.3	184
66	Reproduction in woody perennial Citrus: an update on nucellar embryony and self-incompatibility. <i>Plant Reproduction</i> , 2018, 31, 43-57.	1.3	38
67	A comprehensive proteomic analysis of elaioplasts from citrus fruits reveals insights into elaioplast biogenesis and function. <i>Horticulture Research</i> , 2018, 5, 6.	2.9	21
68	Immunoblotting Quantification Approach for Identifying Potential Hypoallergenic Citrus Cultivars. <i>Journal of Agricultural and Food Chemistry</i> , 2018, 66, 1964-1973.	2.4	1
69	Metabolic Mechanisms of Host Species Against Citrus Huanglongbing (Greening Disease). <i>Critical Reviews in Plant Sciences</i> , 2018, 37, 496-511.	2.7	29
70	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.	1.2	39
71	Subfunctionalization of the Ruby2-Ruby1 gene cluster during the domestication of citrus. <i>Nature Plants</i> , 2018, 4, 930-941.	4.7	121
72	Development of Species-Specific InDel Markers in Citrus. <i>Plant Molecular Biology Reporter</i> , 2018, 36, 653-662.	1.0	9

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73	Small RNA profiling reveals involvement of microRNA-mediated gene regulation in response to mycorrhizal symbiosis in <i>Poncirus trifoliata</i> L. Raf.. <i>Tree Genetics and Genomes</i> , 2018, 14, 1.	0.6	9
74	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.	2.9	49
75	Comparative transcriptome analysis of <i>Poncirus trifoliata</i> identifies a core set of genes involved in arbuscular mycorrhizal symbiosis. <i>Journal of Experimental Botany</i> , 2018, 69, 5255-5264.	2.4	19
76	Genome of Wild Mandarin and Domestication History of Mandarin. <i>Molecular Plant</i> , 2018, 11, 1024-1037.	3.9	130
77	Largely different carotenogenesis in two pummelo fruits with different flesh colors. <i>PLoS ONE</i> , 2018, 13, e0200320.	1.1	10
78	Diversity of plastids in citrus fruit. <i>Acta Horticulturae</i> , 2018, , 111-116.	0.1	1
79	Ploidy manipulation via cell engineering for citrus improvement facilitated by application of molecular markers. <i>Acta Horticulturae</i> , 2018, , 105-110.	0.1	2
80	Molecular phylogeography and population evolution analysis of <i>Citrus ichangensis</i> (Rutaceae). <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	15
81	GABA Pathway Rate-Limit Citrate Degradation in Postharvest Citrus Fruit Evidence from HB Pummelo (<i>Citrus grandis</i>) × Fairchild (<i>Citrus reticulata</i>) Hybrid Population. <i>Journal of Agricultural and Food Chemistry</i> , 2017, 65, 1669-1676.	2.4	47
82	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.	3.6	35
83	Changes in Anthocyanin Production during Domestication of <i>Citrus</i> . <i>Plant Physiology</i> , 2017, 173, 2225-2242.	2.3	92
84	Comprehensive comparative analysis of volatile compounds in citrus fruits of different species. <i>Food Chemistry</i> , 2017, 230, 316-326.	4.2	117
85	Genomic analyses of primitive, wild and cultivated citrus provide insights into asexual reproduction. <i>Nature Genetics</i> , 2017, 49, 765-772.	9.4	316
86	Data on water consumption in streptozotocin-induced diabetic mice by a novel peach gum-derived polysaccharide. <i>Data in Brief</i> , 2017, 12, 358-360.	0.5	0
87	Genetic diversity and population structure of pummelo (<i>Citrus maxima</i>) germplasm in China. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	16
88	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.	1.5	34
89	Lemon fruits lower the blood uric acid levels in humans and mice. <i>Scientia Horticulturae</i> , 2017, 220, 4-10.	1.7	14
90	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.	1.0	29

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91	Glycemic index, glycemic load, and glycemic response to pomelo in patients with type 2 diabetes. <i>Current Medical Science</i> , 2017, 37, 711-718.	0.7	9
92	Characterization and Metabolic Diversity of Flavonoids in Citrus Species. <i>Scientific Reports</i> , 2017, 7, 10549.	1.6	103
93	An R2R3-MYB 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.	3.5	145
94	miR3954 is a trigger of phase-transitions that affects flowering time in citrus. <i>Plant Journal</i> , 2017, 92, 263-275.	2.8	41
95	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.	4.2	115
96	Repeats in the transcribed regions: comprehensive characterization and comparison of Citrus spp.. <i>Frontiers of Agricultural Science and Engineering</i> , 2017, 4, 421.	0.9	0
97	Isolation and Functional Characterization of a Lycopene β -cyclase Gene Promoter from Citrus. <i>Frontiers in Plant Science</i> , 2016, 7, 1367.	1.7	24
98	Pro-inflammatory effects of a litchi protein extract in murine RAW264.7 macrophages. <i>Horticulture Research</i> , 2016, 3, 16017.	2.9	14
99	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.	4.2	61
100	Genome-scale mRNA and small RNA transcriptomic insights into initiation of citrus apomixis. <i>Journal of Experimental Botany</i> , 2016, 67, 5743-5756.	2.4	36
101	Development and Application of a Multiplex Real-Time PCR Assay as an Indicator of Potential Allergenicity in Citrus Fruits. <i>Journal of Agricultural and Food Chemistry</i> , 2016, 64, 9089-9098.	2.4	4
102	Molecular characterization, critical amino acid identification, and promoter analysis of a lycopene β -cyclase gene from citrus. <i>Tree Genetics and Genomes</i> , 2016, 12, 1.	0.6	18
103	Characterization of a Citrus R2R3-MYB Transcription Factor that Regulates the Flavonol and Hydroxycinnamic Acid Biosynthesis. <i>Scientific Reports</i> , 2016, 6, 25352.	1.6	93
104	Regulation of cuticle formation during fruit development and ripening in 'Newhall' navel orange (<i>Citrus sinensis</i>). <i>Journal of Horticultural Science and Biotechnology</i> , 2016, 137, 131-144.	1.7	100
105	Fragile Sites of 'Valencia' Sweet Orange (<i>Citrus sinensis</i>) Chromosomes Are Related with Active 45s rDNA. <i>PLoS ONE</i> , 2016, 11, e0151512.	1.1	28
106	DEVELOPMENT OF A GLOBAL CONSERVATION STRATEGY FOR CITRUS GENETIC RESOURCES. <i>Acta Horticulturae</i> , 2015, , 75-83.	0.1	1
107	Identification, characterization and expression analysis of lineage-specific genes within sweet orange (<i>Citrus sinensis</i>). <i>BMC Genomics</i> , 2015, 16, 995.	1.2	24
108	Sweating treatment enhances citrus fruit disease resistance by inducing the accumulation of amino acids and salicylic acid-induced resistance pathway. <i>Physiologia Plantarum</i> , 2015, 155, 109-125.	2.6	18

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109	The Scion/Rootstock Genotypes and Habitats Affect Arbuscular Mycorrhizal Fungal Community in Citrus. <i>Frontiers in Microbiology</i> , 2015, 6, 1372.	1.5	24
110	De Novo Transcriptome Assembly of Pummelo and Molecular Marker Development. <i>PLoS ONE</i> , 2015, 10, e0120615.	1.1	26
111	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.	1.7	61
112	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.	2.3	43
113	Genetic diversity and phylogenetic relationships of citron (<i>Citrus medica</i> L.) and its relatives in southwest China. <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	0.6	22
114	Construction of a SNP-based high-density genetic map for pummelo using RAD sequencing. <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	0.6	46
115	Parentage analysis of natural citrus hybrid ‘Zhelong Zhoupigan’™ based on nuclear and chloroplast SSR markers. <i>Scientia Horticulturae</i> , 2015, 186, 24-30.	1.7	7
116	Isolation and characterization of carotenoid cleavage dioxygenase 4 genes from different citrus species. <i>Molecular Genetics and Genomics</i> , 2015, 290, 1589-1603.	1.0	30
117	Concentration and distribution of main bitter compounds in fruit tissues of ‘Oroblanco’™ (<i>Citrus</i>) Tj ETQq1 1 0,784314 rgBT /Ov	1.7	17
118	Content evaluation of 4 furanocoumarin monomers in various citrus germplasms. <i>Food Chemistry</i> , 2015, 187, 75-81.	4.2	19
119	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.	1.6	35
120	Network Analysis of Postharvest Senescence Process in Citrus Fruits Revealed by Transcriptomic and Metabolomic Profiling. <i>Plant Physiology</i> , 2015, 168, 357-376.	2.3	96
121	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.	4.2	47
122	Recovery and characterization of homozygous lines from two sweet orange cultivars via anther culture. <i>Plant Cell, Tissue and Organ Culture</i> , 2015, 123, 633-644.	1.2	20
123	A Single Amino Acid Substitution in an ORANGE Protein Promotes Carotenoid Overaccumulation in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2015, 169, 421-431.	2.3	91
124	Volunteer study and serum protein profiling to understand inflammatory response induced by Satsuma mandarin. <i>Food Research International</i> , 2015, 75, 367-373.	2.9	1
125	Carotenoid accumulation affects redox status, starch metabolism, and flavonoid/anthocyanin accumulation in citrus. <i>BMC Plant Biology</i> , 2015, 15, 27.	1.6	53
126	Distinct Carotenoid and Flavonoid Accumulation in a Spontaneous Mutant of Ponkan (<i>Citrus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 6 Agricultural and Food Chemistry, 2015, 63, 8601-8614.	2.4	37

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127	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.	1.7	29
128	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.	2.9	47
129	Characterization of DNA Methylation Variations During Fruit Development and Ripening of Sweet Orange. <i>Plant Molecular Biology Reporter</i> , 2015, 33, 1-11.	1.0	42
130	Novel polymorphic EST-based microsatellite marker isolation and characterization from <i>Poncirus trifoliata</i> (Rutaceae). <i>Frontiers of Agricultural Science and Engineering</i> , 2015, 2, 60.	0.9	4
131	Characteristics of 'Hongrou Taoye', a Grafted Chimera in Sweet Orange and Satsuma Mandarin. <i>Horticultural Science and Technology</i> , 2015, 33, 390-395.	0.9	0
132	Citrus sinensis Annotation Project (CAP): A Comprehensive Database for Sweet Orange Genome. <i>PLoS ONE</i> , 2014, 9, e87723.	1.1	47
133	Genome-wide analysis of the R2R3-MYB transcription factor gene family in sweet orange (<i>Citrus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 1	1.0	52
134	Transcriptome responses to phosphate deficiency in <i>Poncirus trifoliata</i> (L.) Raf. <i>Acta Physiologiae Plantarum</i> , 2014, 36, 3207-3215.	1.0	7
135	Phosphoproteomic analysis of chromoplasts from sweet orange during fruit ripening. <i>Physiologia Plantarum</i> , 2014, 150, 252-270.	2.6	20
136	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.	1.3	98
137	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.	1.2	31
138	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.	1.4	40
139	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.	2.4	71
140	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.	1.2	63
141	A novel macromolecular extract screened from satsuma with pro-inflammatory effect. <i>Food and Function</i> , 2014, 5, 295-302.	2.1	12
142	Genome-wide comparison of microRNAs and their targeted transcripts among leaf, flower and fruit of sweet orange. <i>BMC Genomics</i> , 2014, 15, 695.	1.2	70
143	Prediction and functional analysis of the sweet orange protein-protein interaction network. <i>BMC Plant Biology</i> , 2014, 14, 213.	1.6	30
144	Isolation and characterization of LEAFY COTYLEDON 1-LIKE gene related to embryogenic competence in <i>Citrus sinensis</i> . <i>Plant Cell, Tissue and Organ Culture</i> , 2014, 119, 1-13.	1.2	23

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145	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.	2.4	129
146	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.	1.8	61
147	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.	1.6	64
148	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.	4.2	101
149	Genome Wide Characterization of Short Tandem Repeat Markers in Sweet Orange (<i>Citrus sinensis</i>). <i>PLoS ONE</i> , 2014, 9, e104182.	1.1	50
150	Recent advances in fruit crop genomics. <i>Frontiers of Agricultural Science and Engineering</i> , 2014, 1, 21.	0.9	2
151	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.	1.6	155
152	Anti-Inflammatory Effect of Auraptene Extracted from Trifoliolate Orange (<i>Poncirus Trifoliolate</i>) on LPS-Stimulated RAW 264.7 Cells. <i>Inflammation</i> , 2013, 36, 1525-1532.	1.7	22
153	Somatic cybrid production via protoplast fusion for citrus improvement. <i>Scientia Horticulturae</i> , 2013, 163, 20-26.	1.7	39
154	Cytological and molecular characterization of three gametoclones of <i>Citrus clementina</i> . <i>BMC Plant Biology</i> , 2013, 13, 129.	1.6	18
155	Transferability, polymorphism and effectiveness for genetic mapping of the Pummelo (<i>Citrus grandis</i>) Tj ETQq1 1 0.784314 rsBT /Ove	1.7	14
156	Identification and Functional Characterization of the Promoter of a Phytoene Synthase from Sweet Orange (<i>Citrus sinensis</i> Osbeck). <i>Plant Molecular Biology Reporter</i> , 2013, 31, 64-74.	1.0	13
157	Two Lycopene β -Cyclases Genes from Sweet Orange (<i>Citrus sinensis</i> L. Osbeck) Encode Enzymes With Different Functional Efficiency During the Conversion of Lycopene-to-Provitamin A. <i>Journal of Integrative Agriculture</i> , 2013, 12, 1731-1747.	1.7	15
158	The draft genome of sweet orange (<i>Citrus sinensis</i>). <i>Nature Genetics</i> , 2013, 45, 59-66.	9.4	837
159	Microsatellite polymorphism is likely involved in phytoene synthase activity in Citrus. <i>Plant Cell, Tissue and Organ Culture</i> , 2013, 113, 449-458.	1.2	5
160	Integration of Metabolomics and Subcellular Organelle Expression Microarray to Increase Understanding the Organic Acid Changes in Post-harvest Citrus Fruit. <i>Journal of Integrative Plant Biology</i> , 2013, 55, 1038-1053.	4.1	44
161	Chemotaxonomic Study of Citrus, <i>Poncirus</i> and <i>Fortunella</i> 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.	1.1	34
162	Genome-wide characterization and expression analysis of genetic variants in sweet orange. <i>Plant Journal</i> , 2013, 75, 954-964.	2.8	22

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163	Evaluation of Codon Biology in Citrus and Poncirus trifoliata Based on Genomic Features and Frame Corrected Expressed Sequence Tags. <i>DNA Research</i> , 2013, 20, 135-150.	1.5	28
164	The Or Gene Enhances Carotenoid Accumulation and Stability During Post-Harvest Storage of Potato Tubers. <i>Molecular Plant</i> , 2012, 5, 339-352.	3.9	120
165	Array-comparative genome hybridization reveals genome variations between a citrus bud mutant and its parental cultivar. <i>Tree Genetics and Genomes</i> , 2012, 8, 1379-1387.	0.6	7
166	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.	2.4	110
167	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.	2.4	100
168	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.	2.4	94
169	Sugars and organic acids changes in pericarp and endocarp tissues of pumelo fruit during postharvest storage. <i>Scientia Horticulturae</i> , 2012, 142, 112-117.	1.7	22
170	Transcriptome changes during fruit development and ripening of sweet orange (<i>Citrus sinensis</i>). <i>BMC Genomics</i> , 2012, 13, 10.	1.2	134
171	Comparative transcript profiling of gene expression between seedless Ponkan mandarin and its seedy wild type during floral organ development by suppression subtractive hybridization and cDNA microarray. <i>BMC Genomics</i> , 2012, 13, 397.	1.2	19
172	A global view of gene activity at the flowering transition phase in precocious trifoliate orange and its wild-type [<i>Poncirus trifoliata</i> (L.) Raf.] by transcriptome and proteome analysis. <i>Gene</i> , 2012, 510, 47-58.	1.0	12
173	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.	1.1	56
174	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.	1.1	38
175	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.	1.6	40
176	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.	1.0	41
177	Generation, functional analysis and utility of Citrus grandis EST from a flower-derived cDNA library. <i>Molecular Biology Reports</i> , 2012, 39, 7221-7235.	1.0	14
178	The photorespiratory pathway is involved in the defense response to powdery mildew infection in chestnut rose. <i>Molecular Biology Reports</i> , 2012, 39, 8187-8195.	1.0	2
179	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.	1.3	49
180	Volatile chemical and carotenoid profiles in watermelons [<i>Citrullus vulgaris</i> (Thunb.) Schrad (Cucurbitaceae)] with different flesh colors. <i>Food Science and Biotechnology</i> , 2012, 21, 531-541.	1.2	68

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182	Comparison of cell wall metabolism in the pulp of three cultivars of "Nanfeng" tangerine differing in mastication trait. <i>Journal of the Science of Food and Agriculture</i> , 2012, 92, 496-502.	1.7	15
183	Effect of the Citrus Lycopene Î²-Cyclase Transgene on Carotenoid Metabolism in Transgenic Tomato Fruits. <i>PLoS ONE</i> , 2012, 7, e32221.	1.1	31
184	Presence of Two Variants of Lycopene Î²-Cyclase Gene in Genomes of Citrus and its Relatives. <i>Biotechnology and Biotechnological Equipment</i> , 2011, 25, 2452-2457.	0.5	3
185	Comparative analysis of genetic diversity in Citrus germplasm collection using AFLP, SSAP, SAMPL and SSR markers. <i>Scientia Horticulturae</i> , 2011, 129, 798-803.	1.7	51
186	Proteomic Comparison Between Leaves from a Red-Flesh Mutant and Its Wild-Type in Sweet Orange. <i>Agricultural Sciences in China</i> , 2011, 10, 1206-1212.	0.6	1
187	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.	4.1	40
188	Molecular cloning and functional characterization of genes associated with flowering in citrus using an early-flowering trifoliolate orange (<i>Poncirus trifoliata</i> L. Raf.) mutant. <i>Plant Molecular Biology</i> , 2011, 76, 187-204.	2.0	19
189	Isolation of a Polygalacturonase Gene from Citrus sinensis Fruit and Its Expression Relative to Fruit Mastication Trait, Fruit Development, and Calcium or Boron Treatments. <i>Plant Molecular Biology Reporter</i> , 2011, 29, 51-59.	1.0	19
190	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.	1.0	32
191	Molecular analysis and expression of a floral organ-relative F-box gene isolated from "Zigui shatian" pummelo (<i>Citrus grandis</i> Osbeck). <i>Molecular Biology Reports</i> , 2011, 38, 4429-4436.	1.0	19
192	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.	1.2	29
193	Doubled haploid callus lines of Valencia sweet orange recovered from anther culture. <i>Plant Cell, Tissue and Organ Culture</i> , 2011, 104, 415-423.	1.2	34
194	Phylogenetic and evolutionary analysis of NBS-encoding genes in Rutaceae fruit crops. <i>Molecular Genetics and Genomics</i> , 2011, 285, 151-161.	1.0	6
195	Carotenoids synthesized in citrus callus of different genotypes. <i>Acta Physiologiae Plantarum</i> , 2011, 33, 745-753.	1.0	14
196	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.	1.0	31
197	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.	1.2	44
198	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.	2.4	56

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199	Identification of 2,4-D-responsive proteins in embryogenic callus of Valencia sweet orange (<i>Citrus</i>) Tj ETQq1 1 0.784314 rgBT /Overlook	1.2	48
200	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.	2.0	67
201	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.	1.0	25
202	Development of <i>Juglans Regia</i> SSR Markers by Data Mining of the EST Database. <i>Plant Molecular Biology Reporter</i> , 2010, 28, 646-653.	1.0	35
203	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.	0.8	27
204	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.	2.9	40
205	Discovery and comparative profiling of microRNAs in a sweet orange red-flesh mutant and its wild type. <i>BMC Genomics</i> , 2010, 11, 246.	1.2	120
206	Cloning and phylogenetic analyses of serine/threonine kinase class defense-related genes in a wild fruit crop 'chestnut rose'. <i>BMC Research Notes</i> , 2010, 3, 202.	0.6	7
207	Physicochemical and molecular analysis of cell wall metabolism between two navel oranges (<i>Citrus</i>) Tj ETQq1 1 0.784314 rgBT /Overlook 1479-1484.	1.7	12
208	Comprehensive Analysis of Expressed Sequence Tags from the Pulp of the Red Mutant 'Cara Cara' Navel Orange (<i>Citrus sinensis</i> Osbeck). <i>Journal of Integrative Plant Biology</i> , 2010, 52, 856-867.	4.1	12
209	Utility of RAPD, ISSR, IRAP and REMAP markers for the genetic analysis of <i>Citrus</i> spp.. <i>Scientia Horticulturae</i> , 2010, 124, 254-261.	1.7	58
210	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.	1.2	69
211	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.	1.0	37
212	Phylogenetic analysis of the citrus Huanglongbing (HLB) bacterium based on the sequences of 16S rDNA and 16S/23S rDNA intergenic regions among isolates in China. <i>European Journal of Plant Pathology</i> , 2009, 124, 495-503.	0.8	18
213	Proteomic analysis of somatic embryogenesis in Valencia sweet orange (<i>Citrus sinensis</i> Osbeck). <i>Plant Cell Reports</i> , 2009, 28, 281-289.	2.8	87
214	Functional characterization of <i>Citrus</i> PSY gene in Hongkong kumquat (<i>Fortunella hindsii</i> Swingle). <i>Plant Cell Reports</i> , 2009, 28, 1737-1746.	2.8	58
215	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.	1.3	59
216	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.	2.4	68

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218	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.	1.7	53
219	Involvement of polyamine biosynthesis in somatic embryogenesis of Valencia sweet orange (<i>Citrus</i>) Tj ETQq1 1 0.784314 rgBT/Overland	1.6	49
220	Construction and characterization of two <i>Citrus</i> BAC libraries and identification of clones containing the phytoene synthase gene. <i>Genome</i> , 2009, 52, 484-489.	0.9	9
221	Somaclonal variation with early juice-sac granulation obtained by inter-specific protoplast fusion in citrus. <i>Journal of Horticultural Science and Biotechnology</i> , 2009, 84, 567-573.	0.9	3
222	Phytoene Synthase Gene Cloning from <i>Citrus sinensis</i> Osbeck cv. Cara Cara and Its Prokaryotic Expression. <i>Agricultural Sciences in China</i> , 2008, 7, 148-156.	0.6	0
223	Genomic Organization, Rapid Evolution and Meiotic Instability of Nucleotide-Binding-Site-Encoding Genes in a New Fruit Crop, "Chestnut Rose". <i>Genetics</i> , 2008, 178, 2081-2091.	1.2	10
224	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.	2.4	185
225	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.	2.8	71
226	Asymmetric somatic hybridization between UV-irradiated <i>Citrus unshiu</i> and <i>C. sinensis</i> : regeneration and characterization of hybrid shoots. <i>Plant Cell Reports</i> , 2007, 26, 1263-1273.	2.8	13
227	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.	1.0	16
228	Obtaining autotetraploids <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.	1.2	32
229	Production and molecular characterization of potential seedless cybrid plants between pollen sterile Satsuma mandarin and two seedy <i>Citrus</i> cultivars. <i>Plant Cell, Tissue and Organ Culture</i> , 2007, 90, 275-283.	1.2	30
230	Production of two mandarin-trifoliolate orange hybrid populations via embryo rescue with verification by SSR analysis. <i>Euphytica</i> , 2007, 157, 155-160.	0.6	37
231	Phylogenetic relationships within <i>Citrus</i> and its related genera as inferred from AFLP markers. <i>Genetic Resources and Crop Evolution</i> , 2007, 54, 429-436.	0.8	74
232	RAPD-based genetic analysis of offsprings from the sexual cross using allotetraploid citrus somatic hybrid as pollen parent. <i>Science in China Series C: Life Sciences</i> , 2007, 50, 367-376.	1.3	0
233	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
234	Abnormal Microspore Development Leads to Pollen Abortion in a Seedless Mutant of "Ougan" Mandarin (<i>Citrus suavissima</i> Hort. ex Tanaka). <i>Journal of the American Society for Horticultural Science</i> , 2007, 132, 777-782.	0.5	33

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236	Presence of diverse ratios of lycopene/ β -carotene in five pink or red-fleshed citrus cultivars. <i>Scientia Horticulturae</i> , 2006, 108, 181-184.	1.7	42
237	Mitochondrial gene expression in stamens is differentially regulated during male gametogenesis in <i>Citrus unshiu</i> . <i>Journal of Horticultural Science and Biotechnology</i> , 2006, 81, 565-569.	0.9	12
238	Construction and Characterization of a cDNA Library from the Pulp of Cara Cara Navel Orange (<i>Citrus sinensis</i> Osbeck). <i>Journal of Integrative Plant Biology</i> , 2006, 48, 315-319.	4.1	6
239	Extraction of High Quality of RNA and Construction of a Suppression Subtractive Hybridization (SSH) Library from Chestnut Rose (<i>Rosa roxburghii</i> Tratt). <i>Biotechnology Letters</i> , 2006, 28, 587-591.	1.1	13
240	Relationship Between Ploidy Variation of Citrus Calli and Competence for Somatic Embryogenesis. <i>Journal of Genetics and Genomics</i> , 2006, 33, 647-654.	0.3	12
241	Cytological and molecular evaluation of strawberry plants recovered from <i>in vitro</i> conservation by slow-growth. <i>Journal of Horticultural Science and Biotechnology</i> , 2005, 80, 588-592.	0.9	3
242	Isolation and Characterization of Copia-like Retrotransposons from 12 Sweet Orange (<i>Citrus sinensis</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	4.1	8
243	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.	1.8	56
244	Lycopene- β -Cyclase Pre-mRNA is Alternatively Spliced in Cara Cara Navel Orange (<i>Citrus sinensis</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.1	16
245	A set of primers for analyzing chloroplast DNA diversity in Citrus and related genera. <i>Tree Physiology</i> , 2005, 25, 661-672.	1.4	76
246	In vitro induction of tetraploid in pomegranate (<i>Punica granatum</i>). <i>Plant Cell, Tissue and Organ Culture</i> , 2003, 75, 241-246.	1.2	101
247	Phylogenetic relationships among citrus and its relatives as revealed by SSR markers. <i>Journal of Genetics and Genomics</i> , 2003, 30, 81-7.	0.3	12
248	Title is missing!. <i>Euphytica</i> , 2002, 125, 13-20.	0.6	22
249	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.	0.9	52
250	Title is missing!. <i>Plant Cell, Tissue and Organ Culture</i> , 1999, 59, 81-87.	1.2	14