

Qiang Xu

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

84
papers

2,955
citations

30
h-index

52
g-index

98
ext. papers

3,963
ext. citations

6.1
avg, IF

5.02
L-index

#	Paper	IF	Citations
84	The draft genome of sweet orange (<i>Citrus sinensis</i>). <i>Nature Genetics</i> , 2013 , 45, 59-66	36.3	630
83	Genomic analyses of primitive, wild and cultivated citrus provide insights into asexual reproduction. <i>Nature Genetics</i> , 2017 , 49, 765-772	36.3	194
82	Discovery and comparative profiling of microRNAs in a sweet orange red-flesh mutant and its wild type. <i>BMC Genomics</i> , 2010 , 11, 246	4.5	115
81	The Or gene enhances carotenoid accumulation and stability during post-harvest storage of potato tubers. <i>Molecular Plant</i> , 2012 , 5, 339-52	14.4	100
80	The Citrus Transcription Factor CsMADS6 Modulates Carotenoid Metabolism by Directly Regulating Carotenogenic Genes. <i>Plant Physiology</i> , 2018 , 176, 2657-2676	6.6	93
79	Genome of Wild Mandarin and Domestication History of Mandarin. <i>Molecular Plant</i> , 2018 , 11, 1024-1037	14.4	75
78	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, 4403-17	7	75
77	An R2R3-MYB transcription factor represses the transformation of β and β -branch carotenoids by negatively regulating expression of CrBCH2 and CrNCED5 in flavedo of Citrus reticulata. <i>New Phytologist</i> , 2017 , 216, 178-192	9.8	72
76	Network analysis of postharvest senescence process in citrus fruits revealed by transcriptomic and metabolomic profiling. <i>Plant Physiology</i> , 2015 , 168, 357-76	6.6	67
75	A Single Amino Acid Substitution in an ORANGE Protein Promotes Carotenoid Overaccumulation in Arabidopsis. <i>Plant Physiology</i> , 2015 , 169, 421-31	6.6	64
74	Changes in Anthocyanin Production during Domestication of. <i>Plant Physiology</i> , 2017 , 173, 2225-2242	6.6	63
73	Subfunctionalization of the Ruby2-Ruby1 gene cluster during the domestication of citrus. <i>Nature Plants</i> , 2018 , 4, 930-941	11.5	61
72	Genome-wide comparison of microRNAs and their targeted transcripts among leaf, flower and fruit of sweet orange. <i>BMC Genomics</i> , 2014 , 15, 695	4.5	60
71	Characterization of a Citrus R2R3-MYB Transcription Factor that Regulates the Flavonol and Hydroxycinnamic Acid Biosynthesis. <i>Scientific Reports</i> , 2016 , 6, 25352	4.9	59
70	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, 5455-70	4.8	54
69	Natural Variation in CCD4 Promoter Underpins Species-Specific Evolution of Red Coloration in Citrus Peel. <i>Molecular Plant</i> , 2019 , 12, 1294-1307	14.4	53
68	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, 5297-309	7	50

67	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	11.6	44
66	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	2.7	44
65	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, 1205-16	3.6	41
64	Functional characterization of Citrus PSY gene in Hongkong kumquat (<i>Fortunella hindsii</i> Swingle). <i>Plant Cell Reports</i> , 2009 , 28, 1737-46	5.1	39
63	Characterization of DNA Methylation Variations During Fruit Development and Ripening of Sweet Orange. <i>Plant Molecular Biology Reporter</i> , 2015 , 33, 1-11	1.7	36
62	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	6.2	36
61	Genome wide characterization of short tandem repeat markers in sweet orange (<i>Citrus sinensis</i>). <i>PLoS ONE</i> , 2014 , 9, e104182	3.7	36
60	Construction of a SNP-based high-density genetic map for pummelo using RAD sequencing. <i>Tree Genetics and Genomes</i> , 2015 , 11, 1	2.1	33
59	Genome-wide analysis of the R2R3-MYB transcription factor gene family in sweet orange (<i>Citrus sinensis</i>). <i>Molecular Biology Reports</i> , 2014 , 41, 6769-85	2.8	33
58	Carotenoid accumulation affects redox status, starch metabolism, and flavonoid/anthocyanin accumulation in citrus. <i>BMC Plant Biology</i> , 2015 , 15, 27	5.3	32
57	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, 1648-65	6.6	30
56	Citrus sinensis annotation project (CAP): a comprehensive database for sweet orange genome. <i>PLoS ONE</i> , 2014 , 9, e87723	3.7	30
55	High-throughput sequencing and degradome analysis reveal altered expression of miRNAs and their targets in a male-sterile cybrid pummelo (<i>Citrus grandis</i>). <i>BMC Genomics</i> , 2016 , 17, 591	4.5	30
54	miR3954 is a trigger of phasiRNAs that affects flowering time in citrus. <i>Plant Journal</i> , 2017 , 92, 263-275	6.9	28
53	CsCYT75B1, a Citrus CYTOCHROME P450 Gene, Is Involved in Accumulation of Antioxidant Flavonoids and Induces Drought Tolerance in Transgenic. <i>Antioxidants</i> , 2020 , 9,	7.1	27
52	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	2.7	27
51	Effect of the citrus lycopene β -cyclase transgene on carotenoid metabolism in transgenic tomato fruits. <i>PLoS ONE</i> , 2012 , 7, e32221	3.7	25
50	Reproduction in woody perennial Citrus: an update on nucellar embryony and self-incompatibility. <i>Plant Reproduction</i> , 2018 , 31, 43-57	3.9	23

49	Plastids and Carotenoid Accumulation. <i>Sub-Cellular Biochemistry</i> , 2016 , 79, 273-93	5.5	23
48	Isolation and characterization of carotenoid cleavage dioxygenase 4 genes from different citrus species. <i>Molecular Genetics and Genomics</i> , 2015 , 290, 1589-603	3.1	22
47	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	4.5	21
46	Isolation and Functional Characterization of a Lycopene β -cyclase Gene Promoter from Citrus. <i>Frontiers in Plant Science</i> , 2016 , 7, 1367	6.2	20
45	Carotenoid Pigment Accumulation in Horticultural Plants. <i>Horticultural Plant Journal</i> , 2020 , 6, 343-360	4.3	18
44	Fragile Sites of 'Valencia' Sweet Orange (<i>Citrus sinensis</i>) Chromosomes Are Related with Active 45s rDNA. <i>PLoS ONE</i> , 2016 , 11, e0151512	3.7	17
43	Metabolic Mechanisms of Host Species Against Citrus Huanglongbing (Greening Disease). <i>Critical Reviews in Plant Sciences</i> , 2018 , 37, 496-511	5.6	17
42	Retrotransposon promoter of Ruby1 controls both light- and cold-induced accumulation of anthocyanins in blood orange. <i>Plant, Cell and Environment</i> , 2019 , 42, 3092-3104	8.4	16
41	Phosphoproteomic analysis of chromoplasts from sweet orange during fruit ripening. <i>Physiologia Plantarum</i> , 2014 , 150, 252-70	4.6	16
40	Identification, characterization and expression analysis of lineage-specific genes within sweet orange (<i>Citrus sinensis</i>). <i>BMC Genomics</i> , 2015 , 16, 995	4.5	15
39	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	4.9	15
38	Identification and characterization of microRNAs from citrus expressed sequence tags. <i>Tree Genetics and Genomes</i> , 2011 , 7, 117-133	2.1	14
37	Ectopic expression of citrus UDP-GLUCOSYL TRANSFERASE gene enhances anthocyanin and proanthocyanidins contents and confers high light tolerance in Arabidopsis. <i>BMC Plant Biology</i> , 2019 , 19, 603	5.3	14
36	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	5.7	14
35	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	2.7	13
34	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	2.1	13
33	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	1.7	13
32	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	3.2	13

31	T-DNA direct repeat and 35S promoter methylation affect transgene expression but do not cause silencing in transgenic sweet orange. <i>Plant Cell, Tissue and Organ Culture</i> , 2011 , 107, 225-232	2.7	13
30	Genome of a citrus rootstock and global DNA demethylation caused by heterografting. <i>Horticulture Research</i> , 2021 , 8, 69	7.7	12
29	Molecular phylogeography and population evolution analysis of Citrus ichangensis (Rutaceae). <i>Tree Genetics and Genomes</i> , 2017 , 13, 1	2.1	11
28	Genetic diversity and population structure of pummelo (Citrus maxima) germplasm in China. <i>Tree Genetics and Genomes</i> , 2017 , 13, 1	2.1	11
27	Identification of differentially expressed microRNAs from a male sterile Ponkan mandarin (Citrus reticulata Blanco) and its fertile wild type by small RNA and degradome sequencing. <i>Tree Genetics and Genomes</i> , 2014 , 10, 1567-1581	2.1	11
26	Evolutionary dynamics of lincRNA transcription in nine citrus species. <i>Plant Journal</i> , 2019 , 98, 912-927	6.9	10
25	Citrus PH4-Noemi regulatory complex is involved in proanthocyanidin biosynthesis via a positive feedback loop. <i>Journal of Experimental Botany</i> , 2020 , 71, 1306-1321	7	10
24	A fruit ripening-associated transcription factor CsMADS5 positively regulates carotenoid biosynthesis in citrus. <i>Journal of Experimental Botany</i> , 2021 , 72, 3028-3043	7	10
23	Genomic insights into citrus domestication and its important agronomic traits. <i>Plant Communications</i> , 2021 , 2, 100138	9	10
22	Comparative analysis of miniature inverted-repeat transposable elements (MITEs) and long terminal repeat (LTR) retrotransposons in six Citrus species. <i>BMC Plant Biology</i> , 2019 , 19, 140	5.3	9
21	Endogenous pararetrovirus sequences are widely present in Citrinae genomes. <i>Virus Research</i> , 2019 , 262, 48-53	6.4	8
20	Regulation of carotenoid and chlorophyll pools in hesperidia, anatomically unique fruits found only in Citrus. <i>Plant Physiology</i> , 2021 , 187, 829-845	6.6	6
19	Natural variations of TFIIA gene and LOB1 promoter contribute to citrus canker disease resistance in Atalantia buxifolia. <i>PLoS Genetics</i> , 2021 , 17, e1009316	6	6
18	Ethylene activation of carotenoid biosynthesis by a novel transcription factor CsERF061. <i>Journal of Experimental Botany</i> , 2021 , 72, 3137-3154	7	6
17	Glycemic index, glycemic load, and glycemic response to pomelo in patients with type 2 diabetes. <i>Current Medical Science</i> , 2017 , 37, 711-718	2.8	5
16	Microsatellite polymorphism is likely involved in phytoene synthase activity in Citrus. <i>Plant Cell, Tissue and Organ Culture</i> , 2013 , 113, 449-458	2.7	5
15	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	4.3	5
14	Somatic variations led to the selection of acidic and acidless orange cultivars. <i>Nature Plants</i> , 2021 , 7, 954-965	11.5	5

13	Genome-wide analysis of the citrus B3 superfamily and their association with somatic embryogenesis. <i>BMC Genomics</i> , 2020 , 21, 305	4.5	5
12	Genomic basis of high-altitude adaptation in Tibetan Prunus fruit trees. <i>Current Biology</i> , 2021 , 31, 3848-3860.e8	3.6	5
11	Detection and application of genome-wide variations in peach for association and genetic relationship analysis. <i>BMC Genetics</i> , 2019 , 20, 101	2.6	4
10	Regulation of nucellar embryony, a mode of sporophytic apomixis in Citrus resembling somatic embryogenesis. <i>Current Opinion in Plant Biology</i> , 2021 , 59, 101984	9.9	3
9	Development of Species-Specific InDel Markers in Citrus. <i>Plant Molecular Biology Reporter</i> , 2018 , 36, 653-662	1.7	3
8	Microbiome and Metagenome Analysis Reveals Huanglongbing Affects the Abundance of Citrus Rhizosphere Bacteria Associated with Resistance and Energy Metabolism. <i>Horticulturae</i> , 2021 , 7, 151	2.5	2
7	A Citrus Phosphate Starvation Response Factor CsPHL3 Negatively Regulates Carotenoid Metabolism. <i>Plant and Cell Physiology</i> , 2021 , 62, 482-493	4.9	2
6	Identification of a delayed leaf greening gene from a mutation of pummelo. <i>Science China Life Sciences</i> , 2021 , 64, 1165-1173	8.5	1
5	Genetic background of the citrus landrace Huarongdao Zhoupigan revealed by simple sequence repeat marker and genomic analyses. <i>Scientia Horticulturae</i> , 2021 , 289, 110456	4.1	1
4	Molecular signatures between citrus and Candidatus Liberibacter asiaticus. <i>PLoS Pathogens</i> , 2021 , 17, e1010071	7.6	1
3	Storage with apple fruit to improve peel color and maintain freshness of Newhall navel orange. <i>Scientia Horticulturae</i> , 2021 , 287, 110246	4.1	0
2	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	5.1	0
1	A plant CitPITP1 protein-coding exon sequence serves as a promoter in bacteria. <i>Journal of Biotechnology</i> , 2021 , 339, 1-13	3.7	0