

Wen-Wu Guo

List of Publications by Year in descending order

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88
papers

3,796
citations

168829

31
h-index

156644

58
g-index

92
all docs

92
docs citations

92
times ranked

3652
citing authors

#	ARTICLE	IF	CITATIONS
1	An efficient transient gene expression system for protein subcellular localization assay and genome editing in citrus protoplasts. <i>Horticultural Plant Journal</i> , 2023, 9, 425-436.	2.3	8
2	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
3	Research on Levitation Force of High Temperature Superconductor Magnetic Levitation Vehicle. , 2022, , .		0
4	miR171 modulates induction of somatic embryogenesis in citrus callus. <i>Plant Cell Reports</i> , 2022, 41, 1403-1415.	2.8	8
5	miR156 regulates somatic embryogenesis by modulating starch accumulation in citrus. <i>Journal of Experimental Botany</i> , 2022, 73, 6170-6185.	2.4	15
6	Structural variation and parallel evolution of apomixis in citrus during domestication and diversification. <i>National Science Review</i> , 2022, 9, .	4.6	19
7	Reduced expression of a subunit gene of sucrose non-fermenting 1 related kinase, PpSnRK1 ² , confers flat fruit abortion in peach by regulating sugar and starch metabolism. <i>BMC Plant Biology</i> , 2021, 21, 88.	1.6	2
8	Genomic analyses provide insights into peach local adaptation and responses to climate change. <i>Genome Research</i> , 2021, 31, 592-606.	2.4	30
9	GRAS transcription factor <i>LOSS OF AXILLARY MERISTEMS</i> is essential for stamen and runner formation in wild strawberry. <i>Plant Physiology</i> , 2021, 186, 1970-1984.	2.3	21
10	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
11	Transcriptomes and DNA methylomes in apomictic cells delineate nucellar embryogenesis initiation in citrus. <i>DNA Research</i> , 2021, 28, .	1.5	12
12	Genomic and transcriptomic analyses of <i>Citrus sinensis</i> varieties provide insights into Valencia orange fruit mastication trait formation. <i>Horticulture Research</i> , 2021, 8, 218.	2.9	10
13	An integrated peach genome structural variation map uncovers genes associated with fruit traits. <i>Genome Biology</i> , 2020, 21, 258.	3.8	77
14	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
15	Assembly of Satsuma mandarin mitochondrial genome and identification of cytoplasmic male sterility-specific ORFs in a somatic cybrid of pummelo. <i>Tree Genetics and Genomes</i> , 2020, 16, 1.	0.6	6
16	Localization and characterization of Citrus centromeres by combining half-tetrad analysis and CenH3-associated sequence profiling. <i>Plant Cell Reports</i> , 2020, 39, 1609-1622.	2.8	7
17	Genome-wide identification and expression profiles of phased siRNAs in a male-sterile somatic cybrid of pummelo (<i>Citrus grandis</i>). <i>Tree Genetics and Genomes</i> , 2020, 16, 1.	0.6	6
18	The miR399- <i>CsUBC24</i> Module Regulates Reproductive Development and Male Fertility in Citrus. <i>Plant Physiology</i> , 2020, 183, 1681-1695.	2.3	38

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19	DR5 is a Suitable System for Studying the Auxin Response in the Poncirus trifoliata-Xanthomonas axonopodis pv. citri Interaction. Horticultural Plant Journal, 2020, 6, 277-283.	2.3	4
20	Evolution of self-compatibility by a mutant Sm-RNase in citrus. Nature Plants, 2020, 6, 131-142.	4.7	85
21	Plant regeneration via protoplast electrofusion in cassava. Journal of Integrative Agriculture, 2020, 19, 632-642.	1.7	6
22	Genome-wide analysis of the citrus B3 superfamily and their association with somatic embryogenesis. BMC Genomics, 2020, 21, 305.	1.2	13
23	Ploidy Manipulation for Citrus Breeding, Genetics, and Genomics. Compendium of Plant Genomes, 2020, , 75-105.	0.3	10
24	Polyploidy remodels fruit metabolism by modifying carbon source utilization and metabolic flux in Ponkan mandarin (Citrus reticulata Blanco). Plant Science, 2019, 289, 110276.	1.7	29
25	Mechanism underlying 2n male and female gamete formation in lemon via cytological and molecular marker analysis. Plant Biotechnology Reports, 2019, 13, 141-149.	0.9	10
26	Fatty acid metabolic flux and lipid peroxidation homeostasis maintain the biomembrane stability to improve citrus fruit storage performance. Food Chemistry, 2019, 292, 314-324.	4.2	33
27	Citrus triploid recovery based on 2x \times 4x crosses via an optimized embryo rescue approach. Scientia Horticulturae, 2019, 252, 104-109.	1.7	12
28	Genomic analyses of an extensive collection of wild and cultivated accessions provide new insights into peach breeding history. Genome Biology, 2019, 20, 36.	3.8	120
29	miR156-SPL modules regulate induction of somatic embryogenesis in citrus callus. Journal of Experimental Botany, 2018, 69, 2979-2993.	2.4	78
30	Overexpression of the CsFUS3 gene encoding a B3 transcription factor promotes somatic embryogenesis in Citrus. Plant Science, 2018, 277, 121-131.	1.7	19
31	Genomic characterization of miR156 and SQUAMOSA promoter binding protein-like genes in sweet orange (Citrus sinensis). Plant Cell, Tissue and Organ Culture, 2017, 130, 103-116.	1.2	24
32	Mitochondrial Genome of Callus Protoplast Has a Role in Mesophyll Protoplast Regeneration in Citrus : Evidence From Transgenic GFP Somatic Homo-Fusion. Horticultural Plant Journal, 2017, 3, 177-182.	2.3	7
33	Metabolic adaptation following genome doubling in citrus doubled diploids revealed by non-targeted metabolomics. Metabolomics, 2017, 13, 1.	1.4	36
34	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> . New Phytologist, 2017, 216, 178-192.	3.5	145
35	High-throughput sequencing and degradome analysis reveal altered expression of miRNAs and their targets in a male-sterile cybrid pummelo (Citrus grandis). BMC Genomics, 2016, 17, 591.	1.2	36
36	Genome-scale mRNA and small RNA transcriptomic insights into initiation of citrus apomixis. Journal of Experimental Botany, 2016, 67, 5743-5756.	2.4	36

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37	Induction of parthenogenetic haploid plants using gamma irradiated pollens in "Hirado Buntan"™ pummelo (<i>Citrus grandis</i> [L.] Osbeck). <i>Scientia Horticulturae</i> , 2016, 207, 233-239.	1.7	12
38	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
39	The Scion/Rootstock Genotypes and Habitats Affect Arbuscular Mycorrhizal Fungal Community in Citrus. <i>Frontiers in Microbiology</i> , 2015, 6, 1372.	1.5	24
40	Cytogenetic and SSR-marker evidence of mixed disomic, tetrasomic, and intermediate inheritance in a citrus allotetraploid somatic hybrid between "Nova"™ tangelo and "HB"™ pummelo. <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	0.6	24
41	Genomewide analysis of small <sc>RNA</sc>s in nonembryogenic and embryogenic tissues of citrus: micro<sc>RNA</sc> and si<sc>RNA</sc>-mediated transcript cleavage involved in somatic embryogenesis. <i>Plant Biotechnology Journal</i> , 2015, 13, 383-394.	4.1	88
42	Genome-wide identification, classification and analysis of HD-ZIP gene family in citrus, and its potential roles in somatic embryogenesis regulation. <i>Gene</i> , 2015, 574, 61-68.	1.0	13
43	Content evaluation of 4 furanocoumarin monomers in various citrus germplasms. <i>Food Chemistry</i> , 2015, 187, 75-81.	4.2	19
44	Comparative metabolic and transcriptional analysis of a doubled diploid and its diploid citrus rootstock (<i>C. junos</i> cv. Ziyang xiangcheng) suggests its potential value for stress resistance improvement. <i>BMC Plant Biology</i> , 2015, 15, 89.	1.6	120
45	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
46	2n megagametophyte formed via SDR contributes to tetraploidization in polyembryonic "Nadorcott"™ tangor crossed by citrus allotetraploids. <i>Plant Cell Reports</i> , 2014, 33, 1641-1650.	2.8	27
47	Maximum parsimony based resolution of inter-species phylogenetic relationships in <i>Citrus</i> L. (<i>Rutaceae</i>) using ITS of rDNA. <i>Biotechnology and Biotechnological Equipment</i> , 2014, 28, 61-67.	0.5	8
48	Identification of differentially expressed microRNAs from a male sterile Ponkan mandarin (<i>Citrus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 3 Genomes, 2014, 10, 1567-1581.	0.6	14
49	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
50	Production of Transgenic Anliucheng Sweet Orange (<i>Citrus sinensis</i> Osbeck) with Xa21 Gene for Potential Canker Resistance. <i>Journal of Integrative Agriculture</i> , 2014, 13, 2370-2377.	1.7	14
51	Citrus somatic hybrid: an alternative system to study rapid structural and epigenetic reorganization in allotetraploid genomes. <i>Plant Cell, Tissue and Organ Culture</i> , 2014, 119, 511-522.	1.2	11
52	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
53	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
54	High efficient transformation of auxin reporter gene into trifoliolate orange via <i>Agrobacterium</i> rhizogenes-mediated co-transformation. <i>Plant Cell, Tissue and Organ Culture</i> , 2014, 118, 137-146.	1.2	12

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55	Somatic cybrid production via protoplast fusion for citrus improvement. <i>Scientia Horticulturae</i> , 2013, 163, 20-26.	1.7	39
56	Cytological and molecular characterization of three gametoclones of <i>Citrus clementina</i> . <i>BMC Plant Biology</i> , 2013, 13, 129.	1.6	18
57	Transferability, polymorphism and effectiveness for genetic mapping of the Pummelo (<i>Citrus grandis</i>) Tj ETQq1 1 0.784314 rgBT /Ove	1.7	14
58	The draft genome of sweet orange (<i>Citrus sinensis</i>). <i>Nature Genetics</i> , 2013, 45, 59-66.	9.4	837
59	Selection and validation of suitable reference genes for mRNA qRT-PCR analysis using somatic embryogenic cultures, floral and vegetative tissues in citrus. <i>Plant Cell, Tissue and Organ Culture</i> , 2013, 113, 469-481.	1.2	37
60	Selection and validation of suitable reference genes for miRNA expression normalization by quantitative RT-PCR in citrus somatic embryogenic and adult tissues. <i>Plant Cell Reports</i> , 2012, 31, 2151-2163.	2.8	68
61	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
62	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
63	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
64	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
65	Estimating transgene copy number in precocious trifoliate orange by TaqMan real-time PCR. <i>Plant Cell, Tissue and Organ Culture</i> , 2012, 109, 363-371.	1.2	19
66	Identification of miRNAs and Their Target Genes Using Deep Sequencing and Degradome Analysis in Trifoliate Orange [<i>Poncirus trifoliate</i> (L.) Raf]. <i>Molecular Biotechnology</i> , 2012, 51, 44-57.	1.3	49
67	Exploitation of SSR, SRAP and CAPS-SNP markers for genetic diversity of <i>Citrus</i> germplasm collection. <i>Scientia Horticulturae</i> , 2011, 128, 220-227.	1.7	78
68	Comparison of expression of three different sub-cellular targeted GFPs in transgenic Valencia sweet orange by confocal laser scanning microscopy. <i>Plant Cell, Tissue and Organ Culture</i> , 2011, 104, 199-207.	1.2	11
69	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
70	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.	1.2	17
71	Identification and characterization of microRNAs from citrus expressed sequence tags. <i>Tree Genetics and Genomes</i> , 2011, 7, 117-133.	0.6	16
72	Stage and tissue-specific modulation of ten conserved miRNAs and their targets during somatic embryogenesis of Valencia sweet orange. <i>Planta</i> , 2011, 233, 495-505.	1.6	112

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73	Effect of ploidy increase on transgene expression: example from Citrus diploid cybrid and allotetraploid somatic hybrid expressing the EGFP gene. <i>Protoplasma</i> , 2011, 248, 531-540.	1.0	2
74	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
75	Production and molecular characterization of two new Citrus somatic hybrids for scion improvement. <i>Acta Physiologiae Plantarum</i> , 2010, 32, 215-221.	1.0	5
76	Cloning, molecular characterization and expression analysis of a SOMATIC EMBRYOGENESIS RECEPTOR-LIKE KINASE gene (CitSERK1-like) in Valencia sweet orange. <i>Acta Physiologiae Plantarum</i> , 2010, 32, 1197-1207.	1.0	22
77	Regeneration and characterization of transgenic kumquat plants containing the Arabidopsis APETALA1 gene. <i>Plant Cell, Tissue and Organ Culture</i> , 2010, 100, 273-281.	1.2	27
78	Proteomic analysis of leaves from a diploid cybrid produced by protoplast fusion between Satsuma mandarin and pummelo. <i>Plant Cell, Tissue and Organ Culture</i> , 2010, 103, 165-174.	1.2	29
79	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
80	Highly efficient transformation of the GFP and MAC12.2 genes into precocious trifoliolate orange (<i>Poncirus trifoliata</i> [L.] Raf), a potential model genotype for functional genomics studies in Citrus. <i>Tree Genetics and Genomes</i> , 2009, 5, 529-537.	0.6	29
81	Cybrid/hybrid plants regenerated from somatic fusions between male sterile Satsuma mandarin and seedy tangelos. <i>Scientia Horticulturae</i> , 2009, 122, 323-327.	1.7	15
82	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.	1.2	30
83	Molecular analysis revealed autotetraploid, diploid and tetraploid cybrid plants regenerated from an interspecific somatic fusion in Citrus. <i>Scientia Horticulturae</i> , 2006, 108, 162-166.	1.7	21
84	GFP expression as an indicator of somatic hybrids between transgenic Satsuma mandarin and calamondin at embryoid stage. <i>Plant Cell, Tissue and Organ Culture</i> , 2006, 87, 245-253.	1.2	11
85	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
86	Protoplast transformation and regeneration of transgenic Valencia sweet orange plants containing a juice quality-related pectin methylesterase gene. <i>Plant Cell Reports</i> , 2005, 24, 482-486.	2.8	65
87	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
88	Somatic hybrid vigor in Citrus: Direct evidence from protoplast fusion of an embryogenic callus line with a transgenic mesophyll parent expressing the GFP gene. <i>Plant Science</i> , 2005, 168, 1541-1545.	1.7	40