Feishi Luan

List of Publications by Year
in descending order

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53
papers

1,426
citations

361413

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docs citations

53
times ranked

929
citing authors

#	ARTICLE	IF	CITATIONS
1	Nucleotide variation in the phytoene synthase (ClPsy1) gene contributes to golden flesh in watermelon (Citrullus lanatus L.). Theoretical and Applied Genetics, 2022, 135, 185-200.	3.6	10
2	Identification of major-effect QTL CmFpl3.1 controlling fruit pedicel length in melon (Cucumis melo) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	3.6	5
3	QTL analysis of floweringâ€related traits by specific length amplified fragment sequencing in melon. Crop Science, 2022, 62, 203-215.	1.8	2
4	CmPMRl and CmPMrs are responsible for resistance to powdery mildew caused by Podosphaera xanthii race 1 in Melon. Theoretical and Applied Genetics, 2022, 135, 1209-1222.	3.6	12
5	Genome-Wide Analysis of the Peroxidase Gene Family and Verification of Lignin Synthesis-Related Genes in Watermelon. International Journal of Molecular Sciences, 2022, 23, 642.	4.1	19
6	CAPS marker-base genetic linkage mapping and QTL analysis for watermelon ovary, fruit and seed-related traits. Euphytica, 2022, 218, 1.	1.2	5
7	Biparental genetic mapping reveals that CmCLAVATA3 (CmCLV3) is responsible for the variation in carpel number in melon (Cucumis melo L.). Theoretical and Applied Genetics, 2022, 135, 1909-1921.	3.6	2
8	Mapping of genetic loci controlling fruit linked morphological traits of melon using developed CAPS markers. Molecular Biology Reports, 2022, 49, 5459-5472.	2.3	9
9	Identification of Candidate Chromosome Region Related to Melon (Cucumis melo L.) Fruit Surface Groove Trait Through Biparental Genetic Mapping and Genome-Wide Association Study. Frontiers in Plant Science, 2022, 13, 828287.	3.6	7
10	BSAâ€seq and quantitative trait locus mapping reveals a major effective QTL for carpel number in watermelon (<scp><i>Citrullus lanatus</i></scp>). Plant Breeding, 2022, 141, 460-470.	1.9	2
11	Development of Whole Genome SNP-CAPS Markers and Preliminary QTL Mapping of Fruit Pedicel Traits in Watermelon. Frontiers in Plant Science, 2022, 13, .	3.6	5
12	Genetic Mapping and QTL Analysis of Stigma Color in Melon (Cucumis melo L.). Frontiers in Plant Science, 2022, 13, .	3.6	7
13	Identification of QTLs linked with watermelon fruit and seed traits using GBS-based high-resolution genetic mapping. Scientia Horticulturae, 2022, 303, 111237.	3.6	8
14	Comparative Transcriptome Analysis Identified Key Pathways and Genes Regulating Differentiated Stigma Color in Melon (Cucumis melo L.). International Journal of Molecular Sciences, 2022, 23, 6721.	4.1	3
15	Identification and Characterization Roles of Phytoene Synthase (PSY) Genes in Watermelon Development. Genes, 2022, 13, 1189.	2.4	4
16	Genetic linkage mapping and QTLs identification for morphology and fruit quality related traits of melon by SNP based CAPS markers. Scientia Horticulturae, 2021, 278, 109849.	3.6	18
17	The complete chloroplast genome sequence of the <i>Sechium edule</i> (Jacq.) Swartz. (Cucurbitaceae). Mitochondrial DNA Part B: Resources, 2021, 6, 97-98.	0.4	4
18	Quantitative trait loci and candidate genes responsible for pale green flesh colour in watermelon (<i>Citrullus lanatus</i>). Plant Breeding, 2021, 140, 349-359.	1.9	15

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19	First report of powdery mildew caused by Podosphaera xanthii race 1 on watermelon in China. Journal of Plant Pathology, 2021, 103, 1029-1029.	1.2	2
20	QTL-seq identifies major quantitative trait loci of stigma color in melon. Horticultural Plant Journal, 2021, 7, 318-326.	5.0	9
21	Genetic architecture of fruit size and shape variation in cucurbits: a comparative perspective. Theoretical and Applied Genetics, 2020, 133, 1-21.	3.6	111
22	Optimized combination methods for exploring and verifying disease-resistant transcription factors in melon. Briefings in Bioinformatics, 2020, 22, .	6.5	0
23	Functional Characterization and in Silico Analysis of Phytoene Synthase Family Genes Responsible for Carotenoid Biosynthesis in Watermelon (Citrullus lanatus L.). Agronomy, 2020, 10, 1077.	3.0	4
24	Editorial: Translational Research for Cucurbit Molecular Breeding: Traits, Markers, and Genes. Frontiers in Plant Science, 2020, 11, 615346.	3.6	1
25	Expression of ClPAP and ClPSY1 in watermelon correlates with chromoplast differentiation, carotenoid accumulation, and flesh color formation. Scientia Horticulturae, 2020, 270, 109437.	3.6	28
26	Detection of putative QTL regions associated with ovary traits in melon using SNP-CAPS markers. Scientia Horticulturae, 2020, 270, 109445.	3.6	14
27	Linkage Mapping and Comparative Transcriptome Analysis of Firmness in Watermelon (Citrullus) Tj ETQq1 1 0.784314 rgBT /Overlock 1	3.6	25
28	Resequencing of 297 melon accessions reveals the genomic history of improvement and loci related to fruit traits in melon. Plant Biotechnology Journal, 2020, 18, 2545-2558.	8.3	51
29	Quantitative Trait Loci for Seed Size Variation in Cucurbits â€“ A Review. Frontiers in Plant Science, 2020, 11, 304.	3.6	30
30	Genome-wide identification, characterization and expression analysis of the TLP gene family in melon (Cucumis melo L.). Genomics, 2020, 112, 2499-2509.	2.9	42
31	Identification of lncRNAs and their regulatory relationships with target genes and corresponding miRNAs in melon response to powdery mildew fungi. Gene, 2020, 735, 144403.	2.2	19
32	Fine Mapping of Lycopene Content and Flesh Color Related Gene and Development of Molecular Markerâ€“Assisted Selection for Flesh Color in Watermelon (Citrullus lanatus). Frontiers in Plant Science, 2019, 10, 1240.	3.6	43
33	Genetic mapping reveals a candidate gene for egusi seed in watermelon. Euphytica, 2019, 215, 1.	1.2	12
34	Transcriptome analysis of differentially expressed genes during anther development stages on male sterility and fertility in Cucumis melo L. line. Gene, 2019, 707, 65-77.	2.2	11
35	QTL mapping for melon (Cucumis melo L.) fruit traits by assembling and utilization of novel SNPs based CAPS markers. Scientia Horticulturae, 2018, 236, 18-29.	3.6	36
36	Comparative transcriptome profiling of genes and pathways related to resistance against powdery mildew in two contrasting melon genotypes. Scientia Horticulturae, 2018, 227, 169-180.	3.6	38

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37	The complete chloroplast genome sequence of the <i>Cucurbita pepo</i> L. (Cucurbitaceae). Mitochondrial DNA Part B: Resources, 2018, 3, 717-718.	0.4	7
38	Comparative transcriptome analysis of two contrasting watermelon genotypes during fruit development and ripening. BMC Genomics, 2017, 18, 3.	2.8	72
39	Mapping of powdery mildew resistance genes in melon (Cucumis melo L.) by bulked segregant analysis. Scientia Horticulturae, 2017, 220, 160-167.	3.6	59
40	The complete chloroplast genome sequence of the <i>Citrullus colocynthis</i> L. (Cucurbitaceae). Mitochondrial DNA Part B: Resources, 2017, 2, 480-482.	0.4	3
41	Development of cleaved amplified polymorphic sequence markers and a CAPS-based genetic linkage map in watermelon (<i>Citrullus lanatus</i> [Thunb.] Matsum. and Nakai) constructed using whole-genome re-sequencing data. Breeding Science, 2016, 66, 244-259.	1.9	39
42	Comparative analysis of single nucleotide polymorphisms in the nuclear, chloroplast, and mitochondrial genomes in identification of phylogenetic association among seven melon (<i>Cucumis melo</i> L.) cultivars. Breeding Science, 2016, 66, 711-719.	1.9	19
43	Development of genome-wide SSR markers in melon with their cross-species transferability analysis and utilization in genetic diversity study. Molecular Breeding, 2016, 36, 1.	2.1	35
44	The complete chloroplast genome sequence of the <i>Citrullus lanatus</i> L. Subsp. Vulgaris (Cucurbitaceae). Mitochondrial DNA Part B: Resources, 2016, 1, 943-944.	0.4	11
45	Construction of a genetic linkage map of watermelon (Citrullus lanatus) using CAPS and SSR markers and QTL analysis for fruit quality traits. Scientia Horticulturae, 2016, 202, 25-31.	3.6	38
46	RNAâ€Seq Transcriptome Profiling Reveals Differentially Expressed Genes Involved in Sex Expression in Melon. Crop Science, 2015, 55, 1686-1695.	1.8	12
47	Mapping of quantitative trait loci for lycopene content and fruit traits in Citrullus lanatus. Euphytica, 2015, 202, 411-426.	1.2	60
48	Nextâ€generation sequencing, <scp>FISH</scp> mapping and syntenyâ€based modeling reveal mechanisms of decreasing dysploidy in <i><scp>C</scp>ucumis</i>. Plant Journal, 2014, 77, 16-30.	5.7	90
49	An improved method of Agrobacterium tumefaciens-mediated genetic transformation system of melon (Cucumis melo L.). Journal of Plant Biochemistry and Biotechnology, 2014, 23, 278-283.	1.7	4
50	Chromosome rearrangements during domestication of cucumber as revealed by highâ€density genetic mapping and draft genome assembly. Plant Journal, 2012, 71, 895-906.	5.7	177
51	Syntenic relationships between cucumber (Cucumis sativus L.) and melon (C. melo L.) chromosomes as revealed by comparative genetic mapping. BMC Genomics, 2011, 12, 396.	2.8	69
52	Performance of melon hybrids derived from parents of diverse geographic Origins. Euphytica, 2010, 173, 1-16.	1.2	25
53	Chinese melon (CucumisÂmelo L.) diversity analyses provide strategies for germplasm curation, genetic improvement, and evidentiary support of domestication patterns. Euphytica, 2008, 164, 445-461.	1.2	93