

Feishi Luan

List of Publications by Year in descending order

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Version: 2024-02-01

53
papers

1,426
citations

361413
20
h-index

345221
36
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53
all docs

53
docs citations

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times ranked

929
citing authors

#	ARTICLE	IF	CITATIONS
1	Chromosome rearrangements during domestication of cucumber as revealed by high-density genetic mapping and draft genome assembly. <i>Plant Journal</i> , 2012, 71, 895-906.	5.7	177
2	Genetic architecture of fruit size and shape variation in cucurbits: a comparative perspective. <i>Theoretical and Applied Genetics</i> , 2020, 133, 1-21.	3.6	111
3	Chinese melon (<i>Cucumis melo</i> L.) diversity analyses provide strategies for germplasm curation, genetic improvement, and evidentiary support of domestication patterns. <i>Euphytica</i> , 2008, 164, 445-461.	1.2	93
4	Next-generation sequencing, FISH mapping and synteny-based modeling reveal mechanisms of decreasing dysploidy in <i>Cucumis</i> . <i>Plant Journal</i> , 2014, 77, 16-30.	5.7	90
5	Comparative transcriptome analysis of two contrasting watermelon genotypes during fruit development and ripening. <i>BMC Genomics</i> , 2017, 18, 3.	2.8	72
6	Syntenic relationships between cucumber (<i>Cucumis sativus</i> L.) and melon (<i>C. melo</i> L.) chromosomes as revealed by comparative genetic mapping. <i>BMC Genomics</i> , 2011, 12, 396.	2.8	69
7	Mapping of quantitative trait loci for lycopene content and fruit traits in <i>Citrullus lanatus</i> . <i>Euphytica</i> , 2015, 202, 411-426.	1.2	60
8	Mapping of powdery mildew resistance genes in melon (<i>Cucumis melo</i> L.) by bulked segregant analysis. <i>Scientia Horticulturae</i> , 2017, 220, 160-167.	3.6	59
9	Resequencing of 297 melon accessions reveals the genomic history of improvement and loci related to fruit traits in melon. <i>Plant Biotechnology Journal</i> , 2020, 18, 2545-2558.	8.3	51
10	Fine Mapping of Lycopene Content and Flesh Color Related Gene and Development of Molecular Marker-Assisted Selection for Flesh Color in Watermelon (<i>Citrullus lanatus</i>). <i>Frontiers in Plant Science</i> , 2019, 10, 1240.	3.6	43
11	Genome-wide identification, characterization and expression analysis of the TLP gene family in melon (<i>Cucumis melo</i> L.). <i>Genomics</i> , 2020, 112, 2499-2509.	2.9	42
12	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. <i>Breeding Science</i> , 2016, 66, 244-259.	1.9	39
13	Construction of a genetic linkage map of watermelon (<i>Citrullus lanatus</i>) using CAPS and SSR markers and QTL analysis for fruit quality traits. <i>Scientia Horticulturae</i> , 2016, 202, 25-31.	3.6	38
14	Comparative transcriptome profiling of genes and pathways related to resistance against powdery mildew in two contrasting melon genotypes. <i>Scientia Horticulturae</i> , 2018, 227, 169-180.	3.6	38
15	QTL mapping for melon (<i>Cucumis melo</i> L.) fruit traits by assembling and utilization of novel SNPs based CAPS markers. <i>Scientia Horticulturae</i> , 2018, 236, 18-29.	3.6	36
16	Development of genome-wide SSR markers in melon with their cross-species transferability analysis and utilization in genetic diversity study. <i>Molecular Breeding</i> , 2016, 36, 1.	2.1	35
17	Quantitative Trait Loci for Seed Size Variation in Cucurbits – A Review. <i>Frontiers in Plant Science</i> , 2020, 11, 304.	3.6	30
18	Expression of CIPAP and CIPSY1 in watermelon correlates with chromoplast differentiation, carotenoid accumulation, and flesh color formation. <i>Scientia Horticulturae</i> , 2020, 270, 109437.	3.6	28

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19	Performance of melon hybrids derived from parents of diverse geographic Origins. <i>Euphytica</i> , 2010, 173, 1-16.	1.2	25
20	Linkage Mapping and Comparative Transcriptome Analysis of Firmness in Watermelon (<i>Citrullus</i>) Tj ETQq0 0 0 rgBT/Overlock, 10 Tf 50 7	3.6	25
21	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. <i>Breeding Science</i> , 2016, 66, 711-719.	1.9	19
22	Identification of lncRNAs and their regulatory relationships with target genes and corresponding miRNAs in melon response to powdery mildew fungi. <i>Gene</i> , 2020, 735, 144403.	2.2	19
23	Genome-Wide Analysis of the Peroxidase Gene Family and Verification of Lignin Synthesis-Related Genes in Watermelon. <i>International Journal of Molecular Sciences</i> , 2022, 23, 642.	4.1	19
24	Genetic linkage mapping and QTLs identification for morphology and fruit quality related traits of melon by SNP based CAPS markers. <i>Scientia Horticulturae</i> , 2021, 278, 109849.	3.6	18
25	Quantitative trait loci and candidate genes responsible for pale green flesh colour in watermelon (<i>Citrullus lanatus</i>). <i>Plant Breeding</i> , 2021, 140, 349-359.	1.9	15
26	Detection of putative QTL regions associated with ovary traits in melon using SNP-CAPS markers. <i>Scientia Horticulturae</i> , 2020, 270, 109445.	3.6	14
27	RNA-Seq Transcriptome Profiling Reveals Differentially Expressed Genes Involved in Sex Expression in Melon. <i>Crop Science</i> , 2015, 55, 1686-1695.	1.8	12
28	Genetic mapping reveals a candidate gene for egusi seed in watermelon. <i>Euphytica</i> , 2019, 215, 1.	1.2	12
29	CmPMR1 and CmPMRs are responsible for resistance to powdery mildew caused by <i>Podosphaera xanthii</i> race 1 in Melon. <i>Theoretical and Applied Genetics</i> , 2022, 135, 1209-1222.	3.6	12
30	The complete chloroplast genome sequence of the <i>Citrullus lanatus</i> L. Subsp. <i>Vulgaris</i> (Cucurbitaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 943-944.	0.4	11
31	Transcriptome analysis of differentially expressed genes during anther development stages on male sterility and fertility in <i>Cucumis melo</i> L. line. <i>Gene</i> , 2019, 707, 65-77.	2.2	11
32	Nucleotide variation in the phytoene synthase (CIPsy1) gene contributes to golden flesh in watermelon (<i>Citrullus lanatus</i> L.). <i>Theoretical and Applied Genetics</i> , 2022, 135, 185-200.	3.6	10
33	QTL-seq identifies major quantitative trait loci of stigma color in melon. <i>Horticultural Plant Journal</i> , 2021, 7, 318-326.	5.0	9
34	Mapping of genetic loci controlling fruit linked morphological traits of melon using developed CAPS markers. <i>Molecular Biology Reports</i> , 2022, 49, 5459-5472.	2.3	9
35	Identification of QTLs linked with watermelon fruit and seed traits using GBS-based high-resolution genetic mapping. <i>Scientia Horticulturae</i> , 2022, 303, 111237.	3.6	8
36	The complete chloroplast genome sequence of the <i>Cucurbita pepo</i> L. (Cucurbitaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 717-718.	0.4	7

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37	Identification of Candidate Chromosome Region Related to Melon (<i>Cucumis melo</i> L.) Fruit Surface Groove Trait Through Biparental Genetic Mapping and Genome-Wide Association Study. <i>Frontiers in Plant Science</i> , 2022, 13, 828287.	3.6	7
38	Genetic Mapping and QTL Analysis of Stigma Color in Melon (<i>Cucumis melo</i> L.). <i>Frontiers in Plant Science</i> , 2022, 13, .	3.6	7
39	Identification of major-effect QTL CmFpl3.1 controlling fruit pedicel length in melon (<i>Cucumis melo</i>) Tj ETQq1 1 0.784314 rgBT /Over	3.6	5
40	CAPS marker-base genetic linkage mapping and QTL analysis for watermelon ovary, fruit and seed-related traits. <i>Euphytica</i> , 2022, 218, 1.	1.2	5
41	Development of Whole Genome SNP-CAPS Markers and Preliminary QTL Mapping of Fruit Pedicel Traits in Watermelon. <i>Frontiers in Plant Science</i> , 2022, 13, .	3.6	5
42	An improved method of <i>Agrobacterium tumefaciens</i> -mediated genetic transformation system of melon (<i>Cucumis melo</i> L.). <i>Journal of Plant Biochemistry and Biotechnology</i> , 2014, 23, 278-283.	1.7	4
43	Functional Characterization and in Silico Analysis of Phytoene Synthase Family Genes Responsible for Carotenoid Biosynthesis in Watermelon (<i>Citrullus lanatus</i> L.). <i>Agronomy</i> , 2020, 10, 1077.	3.0	4
44	The complete chloroplast genome sequence of the <i>Sechium edule</i> (Jacq.) Swartz. (<i>Cucurbitaceae</i>). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 97-98.	0.4	4
45	Identification and Characterization Roles of Phytoene Synthase (PSY) Genes in Watermelon Development. <i>Genes</i> , 2022, 13, 1189.	2.4	4
46	The complete chloroplast genome sequence of the <i>Citrullus colocynthis</i> L. (<i>Cucurbitaceae</i>). <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 480-482.	0.4	3
47	Comparative Transcriptome Analysis Identified Key Pathways and Genes Regulating Differentiated Stigma Color in Melon (<i>Cucumis melo</i> L.). <i>International Journal of Molecular Sciences</i> , 2022, 23, 6721.	4.1	3
48	First report of powdery mildew caused by <i>Podosphaera xanthii</i> race 1 on watermelon in China. <i>Journal of Plant Pathology</i> , 2021, 103, 1029-1029.	1.2	2
49	QTL analysis of flowering-related traits by specific length amplified fragment sequencing in melon. <i>Crop Science</i> , 2022, 62, 203-215.	1.8	2
50	Biparental genetic mapping reveals that CmCLAVATA3 (CmCLV3) is responsible for the variation in carpel number in melon (<i>Cucumis melo</i> L.). <i>Theoretical and Applied Genetics</i> , 2022, 135, 1909-1921.	3.6	2
51	BSA-seq and quantitative trait locus mapping reveals a major effective QTL for carpel number in watermelon (<i>Citrullus lanatus</i>). <i>Plant Breeding</i> , 2022, 141, 460-470.	1.9	2
52	Editorial: Translational Research for Cucurbit Molecular Breeding: Traits, Markers, and Genes. <i>Frontiers in Plant Science</i> , 2020, 11, 615346.	3.6	1
53	Optimized combination methods for exploring and verifying disease-resistant transcription factors in melon. <i>Briefings in Bioinformatics</i> , 2020, 22, .	6.5	0