

Qunfeng Lou

List of Publications by Year in descending order

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Version: 2024-02-01

45
papers

1,128
citations

471509

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32
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docs citations

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times ranked

1053
citing authors

#	ARTICLE	IF	CITATIONS
1	Molecular Research Progress on Xishuangbanna Cucumber (<i>Cucumis sativus</i> L. var. <i>Xishuangbannensis</i>) Tj ETQq1 1 0.784314 19gBT /Overlock 10	3.0	19
2	Long-distance control of the scion by the rootstock under drought stress as revealed by transcriptome sequencing and mobile mRNA identification. Horticulture Research, 2022, 9, .	6.3	15
3	Genome-Wide Identification and Expression Analysis of Heat Shock Protein 70 (HSP70) Gene Family in Pumpkin (<i>Cucurbita moschata</i>) Rootstock under Drought Stress Suggested the Potential Role of these Chaperones in Stress Tolerance. International Journal of Molecular Sciences, 2022, 23, 1918.	4.1	22
4	Genome-Wide Identification of the B-Box Gene Family and Expression Analysis Suggests Their Potential Role in Photoperiod-Mediated β -Carotene Accumulation in the Endocarp of Cucumber (<i>Cucumis sativus</i>) Tj ETQq0 0.4 19gBT /Overlock 10	4.0	19
5	Rapid and visual monitoring of alien sequences using crop wild relatives specific oligo-painting: The case of cucumber chromosome engineering. Plant Science, 2022, 319, 111199.	3.6	1
6	The mutation of C-24 reductase, a key enzyme involved in brassinolide biosynthesis, confers a novel compact plant architecture phenotype to cucumber. Theoretical and Applied Genetics, 2022, 135, 2711-2723.	3.6	5
7	Whole-Genome Sequence of Synthesized Allopolyploids in <i>Cucumis</i> Reveals Insights into the Genome Evolution of Allopolyploidization. Advanced Science, 2021, 8, 2004222.	11.2	24
8	Identification of a putative candidate gene encoding 7-dehydrocholesterol reductase involved in brassinosteroids biosynthesis for compact plant architecture in Cucumber (<i>Cucumis sativus</i> L.). Theoretical and Applied Genetics, 2021, 134, 2023-2034.	3.6	9
9	Chromosome-scale genome assembly of <i>Cucumis hystrix</i> a wild species interspecifically cross-compatible with cultivated cucumber. Horticulture Research, 2021, 8, 40.	6.3	18
10	Complete chloroplast genome sequencing and comparative analysis reveals changes to the chloroplast genome after allopolyploidization in <i>Cucumis</i> . Genome, 2021, 64, 627-638.	2.0	6
11	Reconstruction of ancestral karyotype illuminates chromosome evolution in the genus <i>Cucumis</i> . Plant Journal, 2021, 107, 1243-1259.	5.7	23
12	A SNP Mutation in Homeodomain-DDT (HD-DDT) Transcription Factor Results in Multiple Trichomes (mt) in Cucumber (<i>Cucumis sativus</i> L.). Genes, 2021, 12, 1478.	2.4	2
13	Flexible chromosome painting based on multiplex PCR of oligonucleotides and its application for comparative chromosome analyses in <i>Cucumis</i> . Plant Journal, 2020, 102, 178-186.	5.7	40
14	An irregularly striped rind mutant reveals new insight into the function of PG1 ² in cucumber (<i>Cucumis</i>) Tj ETQq0 0.0 19gBT /Overlock 10	3.6	14
15	Fine Mapping and Transcriptome Analysis of Virescent Leaf Gene v-2 in Cucumber (<i>Cucumis sativus</i> L.). Frontiers in Plant Science, 2020, 11, 570817.	3.6	9
16	Development of alien addition lines from <i>Cucumis hystrix</i> in <i>Cucumis sativus</i> : cytological and molecular marker analyses. Genome, 2020, 63, 629-641.	2.0	1
17	Identification and Expression Analysis of the CsMYB Gene Family in Root Knot Nematode-Resistant and Susceptible Cucumbers. Frontiers in Genetics, 2020, 11, 550677.	2.3	9
18	Global Profiling of lncRNAs Expression Responsive to Allopolyploidization in <i>Cucumis</i> . Genes, 2020, 11, 1500.	2.4	7

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19	Genome-wide analysis of a putative lipid transfer protein LTP_2 gene family reveals CsLTP_2 genes involved in response of cucumber against root-knot nematode (<i>Meloidogyne incognita</i>). <i>Genome</i> , 2020, 63, 225-238.	2.0	11
20	Development and application of oligonucleotide-based chromosome painting for chromosome 4D of <i>Triticum aestivum</i> L.. <i>Chromosome Research</i> , 2020, 28, 171-182.	2.2	21
21	Multi-omics analysis revealed that MAPK signaling and flavonoid metabolic pathway contributed to resistance against <i>Meloidogyne incognita</i> in the introgression line cucumber. <i>Journal of Proteomics</i> , 2020, 220, 103675.	2.4	7
22	Candidate genes underlying the quantitative trait loci for root-knot nematode resistance in a <i>Cucumis hystrix</i> introgression line of cucumber based on population sequencing. <i>Journal of Plant Research</i> , 2019, 132, 813-823.	2.4	13
23	Oligo-painting and GISH reveal meiotic chromosome biases and increased meiotic stability in synthetic allotetraploid <i>Cucumis</i> \tilde{A} - <i>hytivus</i> with dysploid parental karyotypes. <i>BMC Plant Biology</i> , 2019, 19, 471.	3.6	15
24	Genetic mapping of angular leaf spot resistance to <i>Pseudomonas syringae</i> pv. <i>lachrymans</i> in a <i>Cucumis hystrix</i> introgression line of cucumber. <i>Euphytica</i> , 2019, 215, 1.	1.2	5
25	A leaf shape mutant provides insight into PINOID Serine/Threonine Kinase function in cucumber (<i>Cucumis sativus</i>) Tj ETQq1 1 0.784314 rgBT /Overloc	8.5	17
26	Chromosome identification in <i>Cucumis anguria</i> revealed by cross-species single-copy gene FISH. <i>Genome</i> , 2018, 61, 397-404.	2.0	7
27	Allopolyploidization in <i>Cucumis</i> contributes to delayed leaf maturation with repression of redundant homoeologous genes. <i>Plant Journal</i> , 2018, 94, 393-404.	5.7	13
28	Comparative transcriptomics reveals suppressed expression of genes related to auxin and the cell cycle contributes to the resistance of cucumber against <i>Meloidogyne incognita</i> . <i>BMC Genomics</i> , 2018, 19, 583.	2.8	23
29	Fine Mapping of CsVYL, Conferring Virescent Leaf Through the Regulation of Chloroplast Development in Cucumber. <i>Frontiers in Plant Science</i> , 2018, 9, 432.	3.6	38
30	Complete resistance to powdery mildew and partial resistance to downy mildew in a <i>Cucumis hystrix</i> introgression line of cucumber were controlled by a co-localized locus. <i>Theoretical and Applied Genetics</i> , 2018, 131, 2229-2243.	3.6	54
31	Molecular and cytogenetic analyses provide evidence of the introgression of chromosomal segments from the wild <i>Cucumis hystrix</i> into the cultivated cucumber through the bridge of a synthetic allotetraploid. <i>Molecular Breeding</i> , 2017, 37, 1.	2.1	4
32	Identification of all homoeologous chromosomes of newly synthetic allotetraploid <i>Cucumis</i> \tilde{A} - <i>hytivus</i> and its wild parent reveals stable subgenome structure. <i>Chromosoma</i> , 2017, 126, 713-728.	2.2	14
33	Organization and evolution of four differentially amplified tandem repeats in the <i>Cucumis hystrix</i> genome. <i>Planta</i> , 2017, 246, 749-761.	3.2	9
34	Identification of a stable major-effect QTL (Parth 2.1) controlling parthenocarpy in cucumber and associated candidate gene analysis via whole genome re-sequencing. <i>BMC Plant Biology</i> , 2016, 16, 182.	3.6	45
35	The complete chloroplast genome sequence of the wild cucumber <i>Cucumis hystrix</i> Chakr. (<i>Cucumis</i> , cucurbitaceae). <i>Mitochondrial DNA</i> , 2016, 27, 142-144.	0.6	4
36	Chromosomal structures and repetitive sequences divergence in <i>Cucumis</i> species revealed by comparative cytogenetic mapping. <i>BMC Genomics</i> , 2015, 16, 730.	2.8	36

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37	An SNP-based saturated genetic map and QTL analysis of fruit-related traits in cucumber using specific-length amplified fragment (SLAF) sequencing. <i>BMC Genomics</i> , 2014, 15, 1158.	2.8	127
38	Cloning and expression analysis of Cs-TIR1/AFB2: the fruit development-related genes of cucumber (<i>Cucumis sativus</i> L.). <i>Acta Physiologiae Plantarum</i> , 2014, 36, 139-149.	2.1	11
39	Identification and Expression Analysis of D-type Cyclin Genes in Early Developing Fruit of Cucumber (<i>Cucumis sativus</i> L.). <i>Plant Molecular Biology Reporter</i> , 2014, 32, 209-218.	1.8	13
40	Transcriptome Comparison of Global Distinctive Features Between Pollination and Parthenocarpic Fruit Set Reveals Transcriptional Phytohormone Cross-Talk in Cucumber (<i>Cucumis sativus</i> L.). <i>Plant and Cell Physiology</i> , 2014, 55, 1325-1342.	3.1	54
41	Cassava genome from a wild ancestor to cultivated varieties. <i>Nature Communications</i> , 2014, 5, 5110.	12.8	230
42	Single-copy gene-based chromosome painting in cucumber and its application for chromosome rearrangement analysis in <i>Cucumis</i> . <i>Plant Journal</i> , 2014, 78, 169-179.	5.7	41
43	Integration of High-Resolution Physical and Genetic Map Reveals Differential Recombination Frequency between Chromosomes and the Genome Assembling Quality in Cucumber. <i>PLoS ONE</i> , 2013, 8, e62676.	2.5	26
44	Inheritance and mapping of the ore gene controlling the quantity of β -carotene in cucumber (<i>Cucumis</i>) Tj ETQq0 0.0 rgBT /Oygrlock 10	2.1	40
45	Ty1 retrotransposon-based SSAP marker development and its potential in the genetic study of cucurbits. <i>Genome</i> , 2007, 50, 802-810.	2.0	36