

Qunfeng Lou

List of Publications by Year in descending order

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Version: 2024-02-01

45
papers

1,128
citations

471509

17
h-index

414414

32
g-index

45
all docs

45
docs citations

45
times ranked

1053
citing authors

#	ARTICLE	IF	CITATIONS
1	Cassava genome from a wild ancestor to cultivated varieties. <i>Nature Communications</i> , 2014, 5, 5110.	12.8	230
2	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
3	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
4	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
5	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
6	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
7	Inheritance and mapping of the ore gene controlling the quantity of β -carotene in cucumber (<i>Cucumis</i>) Tj ETQq1 1,0,784314,rgBT /Ore	2.1	40
8	Flexible chromosome painting based on multiplex PCR of oligonucleotides and its application for comparative chromosome analyses in <i>Cucumis</i> . <i>Plant Journal</i> , 2020, 102, 178-186.	5.7	40
9	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
10	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
11	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
12	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
13	Whole-Genome Sequence of Synthesized Allopolyploids in <i>Cucumis</i> Reveals Insights into the Genome Evolution of Allopolyploidization. <i>Advanced Science</i> , 2021, 8, 2004222.	11.2	24
14	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
15	Reconstruction of ancestral karyotype illuminates chromosome evolution in the genus <i>Cucumis</i> . <i>Plant Journal</i> , 2021, 107, 1243-1259.	5.7	23
16	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. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1918.	4.1	22
17	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
18	Chromosome-scale genome assembly of <i>Cucumis hystrix</i> a wild species interspecifically cross-compatible with cultivated cucumber. <i>Horticulture Research</i> , 2021, 8, 40.	6.3	18

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19	A leaf shape mutant provides insight into PINOID Serine/Threonine Kinase function in cucumber (<i>Cucumis sativus</i> L.). <i>Journal of Experimental Botany</i> , 2019, 60, 1783-1792.	8.5	17
20	Oligo-painting and GISH reveal meiotic chromosome biases and increased meiotic stability in synthetic allotetraploid <i>Cucumis anguria</i> with dysploid parental karyotypes. <i>BMC Plant Biology</i> , 2019, 19, 471.	3.6	15
21	Long-distance control of the scion by the rootstock under drought stress as revealed by transcriptome sequencing and mobile mRNA identification. <i>Horticulture Research</i> , 2022, 9, .	6.3	15
22	Identification of all homoeologous chromosomes of newly synthetic allotetraploid <i>Cucumis anguria</i> and its wild parent reveals stable subgenome structure. <i>Chromosoma</i> , 2017, 126, 713-728.	2.2	14
23	An irregularly striped rind mutant reveals new insight into the function of PG1 ² in cucumber (<i>Cucumis sativus</i> L.). <i>Journal of Experimental Botany</i> , 2019, 60, 1783-1792.	3.6	14
24	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
25	Allopolyploidization in <i>Cucumis sativus</i> contributes to delayed leaf maturation with repression of redundant homoeologous genes. <i>Plant Journal</i> , 2018, 94, 393-404.	5.7	13
26	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
27	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
28	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
29	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
30	Fine Mapping and Transcriptome Analysis of Virescent Leaf Gene v-2 in Cucumber (<i>Cucumis sativus</i> L.). <i>Frontiers in Plant Science</i> , 2020, 11, 570817.	3.6	9
31	Identification and Expression Analysis of the CsMYB Gene Family in Root Knot Nematode-Resistant and Susceptible Cucumbers. <i>Frontiers in Genetics</i> , 2020, 11, 550677.	2.3	9
32	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.). <i>Theoretical and Applied Genetics</i> , 2021, 134, 2023-2034.	3.6	9
33	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> L.). <i>Journal of Experimental Botany</i> , 2019, 60, 1783-1792.	3.6	9
34	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
35	Global Profiling of lncRNAs Expression Responsive to Allopolyploidization in <i>Cucumis sativus</i> . <i>Genes</i> , 2020, 11, 1500.	2.4	7
36	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

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37	Complete chloroplast genome sequencing and comparative analysis reveals changes to the chloroplast genome after allopolyploidization in <i>Cucumis</i> . <i>Genome</i> , 2021, 64, 627-638.	2.0	6
38	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
39	The mutation of C-24 reductase, a key enzyme involved in brassinolide biosynthesis, confers a novel compact plant architecture phenotype to cucumber. <i>Theoretical and Applied Genetics</i> , 2022, 135, 2711-2723.	3.6	5
40	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
41	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
42	A SNP Mutation in Homeodomain-DDT (HD-DDT) Transcription Factor Results in Multiple Trichomes (mt) in Cucumber (<i>Cucumis sativus</i> L.). <i>Genes</i> , 2021, 12, 1478.	2.4	2
43	Development of alien addition lines from <i>Cucumis hystrix</i> in <i>Cucumis sativus</i> : cytological and molecular marker analyses. <i>Genome</i> , 2020, 63, 629-641.	2.0	1
44	Molecular Research Progress on Xishuangbanna Cucumber (<i>Cucumis sativus</i> L. var. <i>Xishuangbannensis</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T	3.6	1
45	Rapid and visual monitoring of alien sequences using crop wild relatives specific oligo-painting: The case of cucumber chromosome engineering. <i>Plant Science</i> , 2022, 319, 111199.	3.6	1