

Jinfeng Chen

List of Publications by Year in descending order

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72
papers

2,268
citations

304743

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docs citations

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#	ARTICLE	IF	CITATIONS
1	A genomic variation map provides insights into the genetic basis of cucumber domestication and diversity. <i>Nature Genetics</i> , 2013, 45, 1510-1515.	21.4	472
2	Selection of appropriate reference genes for gene expression studies by quantitative real-time polymerase chain reaction in cucumber. <i>Analytical Biochemistry</i> , 2010, 399, 257-261.	2.4	380
3	Molecular mapping reveals structural rearrangements and quantitative trait loci underlying traits with local adaptation in semi-wild Xishuangbanna cucumber (<i>Cucumis sativus</i> L. var.) Tj ETQq1 1 0.784314 rgBT /Overlock 10.0750 687	10.7	687
4	Genome-wide analysis of NBS-encoding disease resistance genes in <i>Cucumis sativus</i> and phylogenetic study of NBS-encoding genes in Cucurbitaceae crops. <i>BMC Genomics</i> , 2013, 14, 109.	2.8	98
5	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
6	Molecularly tagged genes and quantitative trait loci in cucumber with recommendations for QTL nomenclature. <i>Horticulture Research</i> , 2020, 7, 3.	6.3	73
7	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
8	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
9	Cytological diploidization and rapid genome changes of the newly synthesized allotetraploids <i>Cucumis</i> — <i>hytivus</i> . <i>Planta</i> , 2007, 225, 603-614.	3.2	53
10	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
11	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
12	Inheritance and mapping of the ore gene controlling the quantity of β -carotene in cucumber (<i>Cucumis</i>) Tj ETQq0 0.0 rgBT /Overlock 10.0750 40	2.1	40
13	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
14	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
15	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
16	QTL Mapping of Downy Mildew Resistance in an Introgression Line Derived from Interspecific Hybridization Between Cucumber and <i>Cucumis hystrix</i> . <i>Journal of Phytopathology</i> , 2013, 161, 536-543.	1.0	32
17	Genetic mapping of gummy stem blight (<i>Didymella bryoniae</i>) resistance genes in <i>Cucumis sativus</i> - <i>hystrix</i> introgression lines. <i>Euphytica</i> , 2013, 192, 359-369.	1.2	27
18	Changes of cytosine methylation induced by wide hybridization and allopolyploidy in <i>Cucumis</i> . <i>Genome</i> , 2008, 51, 789-799.	2.0	26

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19	Integration of High-Resolution Physical and Genetic Map Reveals Differential Recombination Frequency between Chromosomes and the Genome Assembling Quality in Cucumber. PLoS ONE, 2013, 8, e62676.	2.5	26
20	Retrotransposon- and microsatellite sequence-associated genomic changes in early generations of a newly synthesized allotetraploid Cucumis <i>hytivus</i> Chen & Kirkbride. Plant Molecular Biology, 2011, 77, 225-233.	3.9	25
21	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
22	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> . BMC Genomics, 2018, 19, 583.	2.8	23
23	Reconstruction of ancestral karyotype illuminates chromosome evolution in the genus <i>Cucumis</i> . Plant Journal, 2021, 107, 1243-1259.	5.7	23
24	SHORT HYPOCOTYL 1 Encodes a SMARCA3-like Chromatin Remodeling Factor Regulating Elongation. Plant Physiology, 2016, 172, pp.00501.2016.	4.8	22
25	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
26	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
27	A leaf shape mutant provides insight into PINOID Serine/Threonine Kinase function in cucumber (<i>Cucumis sativus</i>) Tj ETQq1 1 0.784314 rgBT /Overl	8.5	17
28	Oligo-painting and GISH reveal meiotic chromosome biases and increased meiotic stability in synthetic allotetraploid Cucumis <i>hytivus</i> with dysploid parental karyotypes. BMC Plant Biology, 2019, 19, 471.	3.6	15
29	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
30	Identification of all homoeologous chromosomes of newly synthetic allotetraploid Cucumis <i>hytivus</i> and its wild parent reveals stable subgenome structure. Chromosoma, 2017, 126, 713-728.	2.2	14
31	An irregularly striped rind mutant reveals new insight into the function of PG1 ¹² in cucumber (<i>Cucumis</i>) Tj ETQq1 1 0.784314 rgBT /O	3.6	14
32	Identification and Expression Analysis of D-type Cyclin Genes in Early Developing Fruit of Cucumber (<i>Cucumis sativus</i> L.). Plant Molecular Biology Reporter, 2014, 32, 209-218.	1.8	13
33	Allopolyploidization in <i>Cucumis</i> contributes to delayed leaf maturation with repression of redundant homoeologous genes. Plant Journal, 2018, 94, 393-404.	5.7	13
34	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. Journal of Plant Research, 2019, 132, 813-823.	2.4	13
35	Interspecific hybridization in <i>Cucumis</i> leads to the divergence of phenotypes in response to low light and extended photoperiods. Frontiers in Plant Science, 2015, 6, 802.	3.6	12
36	Evaluation and Genetic Analysis of Parthenocarpic Germplasms in Cucumber. Genes, 2022, 13, 225.	2.4	12

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37	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
38	Nuclearâ€“Cytoplasmic Coevolution Analysis of RuBisCO in Synthesized Cucumis Allopolyploid. <i>Genes</i> , 2019, 10, 869.	2.4	11
39	A novel mutation in TFL1 homolog sustaining determinate growth in cucumber (<i>Cucumis sativus</i> L.). <i>Theoretical and Applied Genetics</i> , 2020, 133, 3323-3332.	3.6	11
40	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
41	Genome-Wide Identification, Phylogenetic and Expression Pattern Analysis of GATA Family Genes in Cucumber (<i>Cucumis sativus</i> L.). <i>Plants</i> , 2021, 10, 1626.	3.5	11
42	Direct regeneration of haploid or doubled haploid plantlets in cucumber (<i>Cucumis sativus</i> L.) through ovary culture. <i>Plant Cell, Tissue and Organ Culture</i> , 2020, 142, 253-268.	2.3	10
43	Genetic and Transcriptomic Analysis Reveal the Molecular Basis of Photoperiod-Regulated Flowering in Xishuangbanna Cucumber (<i>Cucumis sativus</i> L. var. xishuangbannensis Qi et Yuan). <i>Genes</i> , 2021, 12, 1064.	2.4	10
44	Mapping of fruit apex shape related QTLs across multi-genetic backgrounds in cucumber (<i>Cucumis</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	3.0	10
45	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
46	Transcriptome analysis of callus from melon. <i>Gene</i> , 2019, 684, 131-138.	2.2	9
47	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
48	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
49	Genome-Wide Characterization of HSP90 Gene Family in Cucumber and Their Potential Roles in Response to Abiotic and Biotic Stresses. <i>Frontiers in Genetics</i> , 2021, 12, 584886.	2.3	9
50	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
51	Persistence and Protection of Mitochondrial DNA in the Generative Cell of Cucumber is Consistent with its Paternal Transmission. <i>Plant and Cell Physiology</i> , 2015, 56, pcv140.	3.1	8
52	De novo transcriptome sequencing of pakchoi (<i>Brassica rapa</i> L. <i>chinensis</i>) reveals the key genes related to the response of heat stress. <i>Acta Physiologiae Plantarum</i> , 2016, 38, 1.	2.1	8
53	Comparative Cyto-molecular Analysis of Repetitive DNA Provides Insights into the Differential Genome Structure and Evolution of Five <i>Cucumis</i> Species. <i>Horticultural Plant Journal</i> , 2019, 5, 192-204.	5.0	8
54	Genome-Wide Identification of the B-Box Gene Family and Expression Analysis Suggests Their Potential Role in Photoperiod-Mediated Î²-Carotene Accumulation in the Endocarp of Cucumber (<i>Cucumis sativus</i>) Tj ETQq0 0.0 rgBT /Overlock 10	2.0	8

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55	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
56	Global Profiling of lncRNAs Expression Responsive to Allopolyploidization in <i>Cucumis</i> . <i>Genes</i> , 2020, 11, 1500.	2.4	7
57	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
58	Morphological, anatomical and photosynthetic consequences of artificial allopolyploidization in <i>Cucumis</i> . <i>Euphytica</i> , 2021, 217, 1.	1.2	6
59	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
60	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
61	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
62	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
63	Rare maternal and biparental transmission of the cucumber mitochondrial DNA reveals sorting of polymorphisms among progenies. <i>Theoretical and Applied Genetics</i> , 2019, 132, 1223-1233.	3.6	4
64	Genome-Wide Identification and Expression Analyses of CONSTANS-Like Family Genes in Cucumber (<i>Cucumis sativus</i> L.). <i>Journal of Plant Growth Regulation</i> , 2022, 41, 1627-1641.	5.1	4
65	Molecular Dissection Unveiling Dwarfing Effects of Plant Growth Retardants on Pomegranate. <i>Frontiers in Plant Science</i> , 2022, 13, 866193.	3.6	4
66	Characterization of the mitochondrial genome of <i>Cucumis hystrix</i> and comparison with other cucurbit crops. <i>Gene</i> , 2022, 823, 146342.	2.2	3
67	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
68	Transcriptome analysis of ovary culture-induced embryogenesis in cucumber (<i>Cucumis</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 222 Td	2.0	2
69	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
70	GENETIC VARIATION ANALYSIS OF THE NEWLY SYNTHESIZED ALLOTETRAPLOIDS CUCUMIS HYTIVUS USING RETROTRANSPOSON-BASED SSAP MARKERS. <i>Acta Horticulturae</i> , 2010, , 567-572.	0.2	1
71	Molecular Research Progress on Xishuangbanna Cucumber (<i>Cucumis sativus</i> L. var. <i>Xishuangbannensis</i>) Tj ETQq1 1 0.784314 rgBT /Over	3.0	1
72	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