

Jinfeng Chen

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4466748/publications.pdf>

Version: 2024-02-01

72
papers

2,268
citations

304743

22
h-index

233421

45
g-index

75
all docs

75
docs citations

75
times ranked

2117
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	Evaluation and Genetic Analysis of Parthenocarpic Germplasms in Cucumber. <i>Genes</i> , 2022, 13, 225.	2.4	12
3	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
4	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
5	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
6	Molecular Dissection Unveiling Dwarfing Effects of Plant Growth Retardants on Pomegranate. <i>Frontiers in Plant Science</i> , 2022, 13, 866193.	3.6	4
7	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 ETQq1 1 0.784314 rgBT /Ov	3.0	1
8	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
9	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
10	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	5.0	10
11	Morphological, anatomical and photosynthetic consequences of artificial allopolyploidization in <i>Cucumis</i> . <i>Euphytica</i> , 2021, 217, 1.	1.2	6
12	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
13	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
14	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
15	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
16	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
17	Reconstruction of ancestral karyotype illuminates chromosome evolution in the genus <i>Cucumis</i> . <i>Plant Journal</i> , 2021, 107, 1243-1259.	5.7	23
18	Genetic and Transcriptomic Analysis Reveal the Molecular Basis of Photoperiod-Regulated Flowering in Xishuangbanna Cucumber (<i>Cucumis sativus</i> L. var. <i>xishuangbannensis</i> Qi et Yuan). <i>Genes</i> , 2021, 12, 1064.	2.4	10

#	ARTICLE	IF	CITATIONS
19	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
20	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
21	Transcriptome analysis of ovary culture-induced embryogenesis in cucumber (<i>Cucumis</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf	2.0	2
22	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
23	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 /Ove	3.6	14
24	Molecularly tagged genes and quantitative trait loci in cucumber with recommendations for QTL nomenclature. <i>Horticulture Research</i> , 2020, 7, 3.	6.3	73
25	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
26	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
27	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
28	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
29	Global Profiling of lncRNAs Expression Responsive to Allopolyploidization in <i>Cucumis</i> . <i>Genes</i> , 2020, 11, 1500.	2.4	7
30	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
31	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
32	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
33	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
34	Oligo-painting and GISH reveal meiotic chromosome biases and increased meiotic stability in synthetic allotetraploid <i>Cucumis</i> Å–hystivus with dysploid parental karyotypes. <i>BMC Plant Biology</i> , 2019, 19, 471.	3.6	15
35	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
36	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

#	ARTICLE	IF	CITATIONS
37	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
38	Nuclear–Cytoplasmic Coevolution Analysis of RuBisCO in Synthesized Cucumis Allopolyploid. <i>Genes</i> , 2019, 10, 869.	2.4	11
39	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
40	Transcriptome analysis of callus from melon. <i>Gene</i> , 2019, 684, 131-138.	2.2	9
41	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
42	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
43	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
44	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
45	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
46	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
47	Identification of all homoeologous chromosomes of newly synthetic allotetraploid <i>Cucumis</i> <i>hytivus</i> and its wild parent reveals stable subgenome structure. <i>Chromosoma</i> , 2017, 126, 713-728.	2.2	14
48	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
49	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
50	SHORT HYPOCOTYL 1 Encodes a SMARCA3-like Chromatin Remodeling Factor Regulating Elongation. <i>Plant Physiology</i> , 2016, 172, pp.00501.2016.	4.8	22
51	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
52	The complete chloroplast genome sequence of the wild cucumber <i>Cucumis hystrix</i> Chakr. (<i>Cucumis</i> , <i>cucurbitaceae</i>). <i>Mitochondrial DNA</i> , 2016, 27, 142-144.	0.6	4
53	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
54	Interspecific hybridization in <i>Cucumis</i> leads to the divergence of phenotypes in response to low light and extended photoperiods. <i>Frontiers in Plant Science</i> , 2015, 6, 802.	3.6	12

#	ARTICLE	IF	CITATIONS
55	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
56	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 ETQq0 0 0 rgBT /Overlock 106Tf 50 6977d (xish)	1.0	1
57	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
58	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
59	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
60	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
61	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
62	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
63	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
64	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
65	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
66	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
67	Inheritance and mapping of the ore gene controlling the quantity of Î²-carotene in cucumber (<i>Cucumis</i>) Tj ETQq1 1,0,784314 rgBT /O 2.1 46	2.1	46
68	Retrotransposon- and microsatellite sequence-associated genomic changes in early generations of a newly synthesized allotetraploid <i>Cucumis</i> . Ahytivus Chen & Kirkbride. <i>Plant Molecular Biology</i> , 2011, 77, 225-233.	3.9	25
69	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
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	Changes of cytosine methylation induced by wide hybridization and allopolyploidy in <i>Cucumis</i> . <i>Genome</i> , 2008, 51, 789-799.	2.0	26
72	Cytological diploidization and rapid genome changes of the newly synthesized allotetraploids <i>Cucumis</i> . Ahytivus. <i>Planta</i> , 2007, 225, 603-614.	3.2	53