

Junsong Pan

List of Publications by Year in descending order

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Version: 2024-02-01

47
papers

1,546
citations

361413
20
h-index

315739
38
g-index

52
all docs

52
docs citations

52
times ranked

1360
citing authors

#	ARTICLE	IF	CITATIONS
1	QTL Mapping for Disease Resistance in Cucumber. <i>Compendium of Plant Genomes</i> , 2022, , 81-92.	0.5	1
2	Detection and characterization of <i>Aspergillus tubingensis</i> causing leaf rot disease in pak choi in China. <i>Canadian Journal of Plant Pathology</i> , 2022, 44, 702-708.	1.4	0
3	Study of micro-trichome (mict) reveals novel connections between transcriptional regulation of multicellular trichome development and specific metabolism in cucumber. <i>Horticulture Research</i> , 2021, 8, 21.	6.3	15
4	Mapping and identification of CsSh5.1, a gene encoding a xyloglucan galactosyltransferase required for hypocotyl elongation in cucumber (<i>Cucumis sativus</i> L.). <i>Theoretical and Applied Genetics</i> , 2021, 134, 979-991.	3.6	4
5	CsUFO is involved in the formation of flowers and tendrils in cucumber. <i>Theoretical and Applied Genetics</i> , 2021, 134, 2141-2150.	3.6	11
6	A positive feedback loop mediated by <i>CsERF31</i> initiates female cucumber flower development. <i>Plant Physiology</i> , 2021, 186, 1088-1100.	4.8	11
7	A SNP of HD-ZIP I transcription factor leads to distortion of trichome morphology in cucumber (<i>Cucumis sativus</i> L.). <i>BMC Plant Biology</i> , 2021, 21, 182.	3.6	11
8	<i>TERMINAL FLOWER</i> 1 and <i>TERMINAL FLOWER</i> 1d respond to temperature and photoperiod signals to inhibit determinate growth in cucumber. <i>Plant, Cell and Environment</i> , 2021, 44, 2580-2592.	5.7	5
9	Genome-Wide Identification, Classification and Expression Analysis of the MYB Transcription Factor Family in Petunia. <i>International Journal of Molecular Sciences</i> , 2021, 22, 4838.	4.1	18
10	A Mutation in CsYL2.1 Encoding a Plastid Isoform of Triose Phosphate Isomerase Leads to Yellow Leaf 2.1 (yl2.1) in Cucumber (<i>Cucumis Sativus</i> L.). <i>International Journal of Molecular Sciences</i> , 2021, 22, 322.	4.1	32
11	Molecularly tagged genes and quantitative trait loci in cucumber with recommendations for QTL nomenclature. <i>Horticulture Research</i> , 2020, 7, 3.	6.3	73
12	Genome-Wide Identification and Characterization of the TCP Gene Family in Cucumber (<i>Cucumis</i>) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50</i>	2.4	16
13	The HD-ZIP IV transcription factor Tril regulates fruit spine density through gene dosage effects in cucumber. <i>Journal of Experimental Botany</i> , 2020, 71, 6297-6310.	4.8	18
14	Comprehensive Genomic Analysis and Expression Profiling of the C2H2 Zinc Finger Protein Family under Abiotic Stresses in Cucumber (<i>Cucumis sativus</i> L.). <i>Genes</i> , 2020, 11, 171.	2.4	20
15	STAYGREEN, STAY HEALTHY: a loss-of-susceptibility mutation in the <i>STAYGREEN</i> gene provides durable, broad-spectrum disease resistances for over 50 years of US cucumber production. <i>New Phytologist</i> , 2019, 221, 415-430.	7.3	72
16	Cucumber CsTRY Negatively Regulates Anthocyanin Biosynthesis and Trichome Formation When Expressed in Tobacco. <i>Frontiers in Plant Science</i> , 2019, 10, 1232.	3.6	8
17	Deep Learning-Based Segmentation and Quantification of Cucumber Powdery Mildew Using Convolutional Neural Network. <i>Frontiers in Plant Science</i> , 2019, 10, 155.	3.6	146
18	Mapping and identification of CsUp, a gene encoding an Auxilin-like protein, as a putative candidate gene for the upward-pedicel mutation (up) in cucumber. <i>BMC Plant Biology</i> , 2019, 19, 157.	3.6	7

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19	STAYGREEN (CsSGR) is a candidate for the anthracnose (<i>Colletotrichum orbiculare</i>) resistance locus <i>cla</i> in Gy14 cucumber. <i>Theoretical and Applied Genetics</i> , 2018, 131, 1577-1587.	3.6	21
20	Efficient Transposition of the Retrotransposon <i>Tnt1</i> in Cucumber (<i>Cucumis sativus</i> L.). <i>Horticultural Plant Journal</i> , 2018, 4, 111-116.	5.0	2
21	Identification and mapping of <i>ts</i> (tender spines), a gene involved in soft spine development in <i>Cucumis sativus</i> . <i>Theoretical and Applied Genetics</i> , 2018, 131, 1-12.	3.6	38
22	GLABROUS (CmGL) encodes a HD-ZIP IV transcription factor playing roles in multicellular trichome initiation in melon. <i>Theoretical and Applied Genetics</i> , 2018, 131, 569-579.	3.6	17
23	Photoexcited CRYPTOCHROME 1 Interacts Directly with G-Protein β^2 Subunit AGB1 to Regulate the DNA-Binding Activity of HY5 and Photomorphogenesis in Arabidopsis. <i>Molecular Plant</i> , 2018, 11, 1248-1263.	8.3	46
24	Identification and fine mapping of molecular markers closely linked to fruit spines size <i>ss</i> gene in cucumber (<i>Cucumis sativus</i> L.). <i>Euphytica</i> , 2018, 214, 1.	1.2	6
25	Differential Gene Expression Caused by the F and M Loci Provides Insight Into Ethylene-Mediated Female Flower Differentiation in Cucumber. <i>Frontiers in Plant Science</i> , 2018, 9, 1091.	3.6	30
26	Asynchronous meiosis in <i>Cucumis hystrix</i> cucumber synthetic tetraploids resulting in low male fertility. <i>Crop Journal</i> , 2016, 4, 275-279.	5.2	5
27	Identification and mapping of <i>Tril</i> , a homeodomain-leucine zipper gene involved in multicellular trichome initiation in <i>Cucumis sativus</i> . <i>Theoretical and Applied Genetics</i> , 2016, 129, 305-316.	3.6	77
28	Expression analysis of dihydroflavonol 4-reductase genes in <i>Petunia hybrida</i> . <i>Genetics and Molecular Research</i> , 2015, 14, 5010-5021.	0.2	8
29	Loss-of-Function Mutations in <i>CsMLO1</i> Confer Durable Powdery Mildew Resistance in Cucumber (<i>Cucumis sativus</i> L.). <i>Frontiers in Plant Science</i> , 2015, 6, 1155.	3.6	65
30	Genome-Wide Mapping of Structural Variations Reveals a Copy Number Variant That Determines Reproductive Morphology in Cucumber. <i>Plant Cell</i> , 2015, 27, 1595-1604.	6.6	125
31	Identification and fine mapping of <i>pm5.1</i> : a recessive gene for powdery mildew resistance in cucumber (<i>Cucumis sativus</i> L.). <i>Molecular Breeding</i> , 2015, 35, 1.	2.1	46
32	Transcriptome profiling of trichome-less reveals genes associated with multicellular trichome development in <i>Cucumis sativus</i> . <i>Molecular Genetics and Genomics</i> , 2015, 290, 2007-2018.	2.1	25
33	Ectopic Expression of <i>CsCTR1</i> , a Cucumber CTR-Like Gene, Attenuates Constitutive Ethylene Signaling in an Arabidopsis <i>ctr1-1</i> Mutant and Expression Pattern Analysis of <i>CsCTR1</i> in Cucumber (<i>Cucumis sativus</i>). <i>International Journal of Molecular Sciences</i> , 2014, 15, 16331-16350.	4.1	11
34	Tuberculate fruit gene <i>Tu</i> encodes a C ₂ H ₂ zinc finger protein that is required for the warty fruit phenotype in cucumber (<i>Cucumis sativus</i> L.). <i>Plant Journal</i> , 2014, 78, 1034-1046.	5.7	83
35	High-resolution mapping of the dull fruit skin gene <i>D</i> in cucumber (<i>Cucumis sativus</i> L.). <i>Molecular Breeding</i> , 2014, 33, 15-22.	2.1	37
36	Fine mapping of the uniform immature fruit color gene <i>u</i> in cucumber (<i>Cucumis sativus</i> L.). <i>Euphytica</i> , 2014, 196, 341-348.	1.2	38

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37	Molecular cloning and functional characterization of dihydroflavonol-4-reductase gene from <i>Calibrachoa hybrida</i> . <i>Scientia Horticulturae</i> , 2014, 165, 398-403.	3.6	15
38	A putative positive feedback regulation mechanism in CsACS2 expression suggests a modified model for sex determination in cucumber (<i>Cucumis sativus</i> L.). <i>Journal of Experimental Botany</i> , 2012, 63, 4475-4484.	4.8	77
39	Genetic relationship analyses of oil-bearing roses in China using matK sequences. <i>Scientia Horticulturae</i> , 2012, 137, 121-124.	3.6	6
40	Identification and mapping of molecular markers linked to the tuberculate fruit gene in the cucumber (<i>Cucumis sativus</i> L.). <i>Theoretical and Applied Genetics</i> , 2010, 120, 645-654.	3.6	71
41	Molecular Isolation of the <i>M</i> Gene Suggests That a Conserved-Residue Conversion Induces the Formation of Bisexual Flowers in Cucumber Plants. <i>Genetics</i> , 2009, 182, 1381-1385.	2.9	139
42	Development and fine mapping of three co-dominant SCAR markers linked to the M/m gene in the cucumber plant (<i>Cucumis sativus</i> L.). <i>Theoretical and Applied Genetics</i> , 2008, 117, 1253-1260.	3.6	35
43	Quantitative trait locus analysis of lateral branch-related traits in cucumber (<i>Cucumis sativus</i> L.) using recombinant inbred lines. <i>Science in China Series C: Life Sciences</i> , 2008, 51, 833-841.	1.3	7
44	QTL molecular marker location of powdery mildew resistance in cucumber (<i>Cucumis sativus</i> L.). <i>Science in China Series C: Life Sciences</i> , 2008, 51, 1003-1008.	1.3	12
45	Reporter-based screen for <i>Arabidopsis</i> mutants compromised in nonhost resistance. <i>Science Bulletin</i> , 2008, 53, 1027-1034.	9.0	3
46	Construction of a BAC library from cucumber (<i>Cucumis sativus</i> L.) and identification of linkage group specific clones. <i>Progress in Natural Science: Materials International</i> , 2008, 18, 143-147.	4.4	4
47	Construction of a cucumber genetic linkage map with SRAP markers and location of the genes for lateral branch traits. <i>Science in China Series C: Life Sciences</i> , 2005, 48, 213-220.	1.3	27