

Sanwen Huang

List of Publications by Year in descending order

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Version: 2024-02-01

128
papers

21,879
citations

20817

60
h-index

15266

126
g-index

136
all docs

136
docs citations

136
times ranked

15785
citing authors

#	ARTICLE	IF	CITATIONS
1	Deletion of a cyclin-dependent protein kinase inhibitor, CsSMR1, leads to dwarf and determinate growth in cucumber (<i>Cucumis sativus</i> L.). <i>Theoretical and Applied Genetics</i> , 2022, 135, 915-927.	3.6	10
2	<i>In vivo</i> maternal haploid induction in tomato. <i>Plant Biotechnology Journal</i> , 2022, 20, 250-252.	8.3	44
3	Removal of lycopene substrate inhibition enables high carotenoid productivity in <i>Yarrowia lipolytica</i> . <i>Nature Communications</i> , 2022, 13, 572.	12.8	70
4	Targeted creation of new mutants with compact plant architecture using CRISPR/Cas9 genome editing by an optimized genetic transformation procedure in cucurbit plants. <i>Horticulture Research</i> , 2022, 9, .	6.3	36
5	Graph-based pan-genome reveals structural and sequence variations related to agronomic traits and domestication in cucumber. <i>Nature Communications</i> , 2022, 13, 682.	12.8	59
6	The multi-omics basis of potato heterosis. <i>Journal of Integrative Plant Biology</i> , 2022, 64, 671-687.	8.5	22
7	The integrated genomics of crop domestication and breeding. <i>Cell</i> , 2022, 185, 2828-2839.	28.9	47
8	Genome evolution and diversity of wild and cultivated potatoes. <i>Nature</i> , 2022, 606, 535-541.	27.8	125
9	Graph pangenome captures missing heritability and empowers tomato breeding. <i>Nature</i> , 2022, 606, 527-534.	27.8	131
10	Genome architecture and tetrasomic inheritance of autotetraploid potato. <i>Molecular Plant</i> , 2022, 15, 1211-1226.	8.3	33
11	Natural variations in <i>SISOS1</i> contribute to the loss of salt tolerance during tomato domestication. <i>Plant Biotechnology Journal</i> , 2021, 19, 20-22.	8.3	43
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	Genomic analyses provide insights into peach local adaptation and responses to climate change. <i>Genome Research</i> , 2021, 31, 592-606.	5.5	30
14	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
15	Domestication of Crop Metabolomes: Desired and Unintended Consequences. <i>Trends in Plant Science</i> , 2021, 26, 650-661.	8.8	60
16	A nonS-locus F-box gene breaks self-incompatibility in diploid potatoes. <i>Nature Communications</i> , 2021, 12, 4142.	12.8	42
17	Genome design of hybrid potato. <i>Cell</i> , 2021, 184, 3873-3883.e12.	28.9	112
18	The <i>Taxus</i> genome provides insights into paclitaxel biosynthesis. <i>Nature Plants</i> , 2021, 7, 1026-1036.	9.3	103

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19	Enhanced chemoselectivity of a plant cytochrome P450 through protein engineering of surface and catalytic residues. <i>ABIOTECH</i> , 2021, 2, 215-225.	3.9	4
20	Gain-of-function of the 1-aminocyclopropane-1-carboxylate synthase gene <i>ACS1G</i> induces female flower development in cucumber gynoecey. <i>Plant Cell</i> , 2021, 33, 306-321.	6.6	31
21	Targeting pathway expression to subcellular organelles improves astaxanthin synthesis in <i>Yarrowia lipolytica</i> . <i>Metabolic Engineering</i> , 2021, 68, 152-161.	7.0	63
22	Genome-wide Target Mapping Shows Histone Deacetylase Complex1 Regulates Cell Proliferation in Cucumber Fruit. <i>Plant Physiology</i> , 2020, 182, 167-184.	4.8	47
23	A high-throughput BAC end analysis protocol (<i>BAC</i> -anchor) for profiling genome assembly and physical mapping. <i>Plant Biotechnology Journal</i> , 2020, 18, 364-372.	8.3	6
24	Domestication and breeding changed tomato fruit transcriptome. <i>Journal of Integrative Agriculture</i> , 2020, 19, 120-132.	3.5	18
25	Metabolomics should be deployed in the identification and characterization of gene-edited crops. <i>Plant Journal</i> , 2020, 102, 897-902.	5.7	30
26	<i>FLOWERING LOCUS T</i> Improves Cucumber Adaptation to Higher Latitudes. <i>Plant Physiology</i> , 2020, 182, 908-918.	4.8	30
27	Engineering Plant Cytochrome P450s for Enhanced Synthesis of Natural Products: Past Achievements and Future Perspectives. <i>Plant Communications</i> , 2020, 1, 100012.	7.7	29
28	The genomic architecture of the sex-determining region and sex-related metabolic variation in <i>Ginkgo biloba</i> . <i>Plant Journal</i> , 2020, 104, 1399-1409.	5.7	26
29	Haplotype-resolved genome analyses of a heterozygous diploid potato. <i>Nature Genetics</i> , 2020, 52, 1018-1023.	21.4	134
30	Regulation of plant architecture by a new histone acetyltransferase targeting gene bodies. <i>Nature Plants</i> , 2020, 6, 809-822.	9.3	33
31	Genetic dissection of climacteric fruit ripening in a melon population segregating for ripening behavior. <i>Horticulture Research</i> , 2020, 7, 187.	6.3	29
32	Loss of salt tolerance during tomato domestication conferred by variation in a Na ⁺ /K ⁺ transporter. <i>EMBO Journal</i> , 2020, 39, e103256.	7.8	112
33	The mutation of a PECTATE LYASE-LIKE gene is responsible for the Yellow Margin phenotype in potato. <i>Theoretical and Applied Genetics</i> , 2020, 133, 1123-1131.	3.6	7
34	Resequencing of 414 cultivated and wild watermelon accessions identifies selection for fruit quality traits. <i>Nature Genetics</i> , 2019, 51, 1616-1623.	21.4	226
35	A comprehensive genome variation map of melon identifies multiple domestication events and loci influencing agronomic traits. <i>Nature Genetics</i> , 2019, 51, 1607-1615.	21.4	153
36	The wax gourd genomes offer insights into the genetic diversity and ancestral cucurbit karyotype. <i>Nature Communications</i> , 2019, 10, 5158.	12.8	94

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37	A structural and data-driven approach to engineering a plant cytochrome P450 enzyme. <i>Science China Life Sciences</i> , 2019, 62, 873-882.	4.9	18
38	A chromosome-scale genome assembly of cucumber (<i>Cucumis sativus</i> L.). <i>GigaScience</i> , 2019, 8, .	6.4	138
39	The tomato pan-genome uncovers new genes and a rare allele regulating fruit flavor. <i>Nature Genetics</i> , 2019, 51, 1044-1051.	21.4	441
40	Next-Gen Approaches to Flavor-Related Metabolism. <i>Annual Review of Plant Biology</i> , 2019, 70, 187-212.	18.7	36
41	Genetic Regulation of Ethylene Dosage for Cucumber Fruit Elongation. <i>Plant Cell</i> , 2019, 31, 1063-1076.	6.6	85
42	Meta-analysis of genome-wide association studies provides insights into genetic control of tomato flavor. <i>Nature Communications</i> , 2019, 10, 1534.	12.8	91
43	The genetic basis of inbreeding depression in potato. <i>Nature Genetics</i> , 2019, 51, 374-378.	21.4	110
44	Multi-omics data-driven investigations of metabolic diversity of plant triterpenoids. <i>Plant Journal</i> , 2019, 97, 101-111.	5.7	50
45	Cucurbit Genomics Database (CuGenDB): a central portal for comparative and functional genomics of cucurbit crops. <i>Nucleic Acids Research</i> , 2019, 47, D1128-D1136.	14.5	177
46	Acquisition of deleterious mutations during potato polyploidization. <i>Journal of Integrative Plant Biology</i> , 2019, 61, 7-11.	8.5	30
47	Rewiring of the Fruit Metabolome in Tomato Breeding. <i>Cell</i> , 2018, 172, 249-261.e12.	28.9	606
48	An Overlooked Paleotetraploidization in Cucurbitaceae. <i>Molecular Biology and Evolution</i> , 2018, 35, 16-26.	8.9	89
49	Genome analysis of <i>Taraxacum kok-saghyz</i> Rodin provides new insights into rubber biosynthesis. <i>National Science Review</i> , 2018, 5, 78-87.	9.5	90
50	An EMS mutant library for cucumber. <i>Journal of Integrative Agriculture</i> , 2018, 17, 1612-1619.	3.5	17
51	The chicken gut metagenome and the modulatory effects of plant-derived benzylisoquinoline alkaloids. <i>Microbiome</i> , 2018, 6, 211.	11.1	204
52	Genetic analysis and identification of a candidate gene associated with in vitro regeneration ability of cucumber. <i>Theoretical and Applied Genetics</i> , 2018, 131, 2663-2675.	3.6	11
53	A High-Density EST-SSR-Based Genetic Map and QTL Analysis of Dwarf Trait in <i>Cucurbita pepo</i> L.. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3140.	4.1	19
54	Resequencing of 243 diploid cotton accessions based on an updated A genome identifies the genetic basis of key agronomic traits. <i>Nature Genetics</i> , 2018, 50, 796-802.	21.4	401

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55	Generation of self-compatible diploid potato by knockout of S-RNase. <i>Nature Plants</i> , 2018, 4, 651-654.	9.3	152
56	A chemical genetic roadmap to improved tomato flavor. <i>Science</i> , 2017, 355, 391-394.	12.6	561
57	Developmentally Regulated Glucosylation of Bitter Triterpenoid in Cucumber by the UDP-Glucosyltransferase UGT73AM3. <i>Molecular Plant</i> , 2017, 10, 1000-1003.	8.3	16
58	The Genome of Medicinal Plant <i>Macleaya cordata</i> Provides New Insights into Benzylisoquinoline Alkaloids Metabolism. <i>Molecular Plant</i> , 2017, 10, 975-989.	8.3	116
59	Draft genome of spinach and transcriptome diversity of 120 <i>Spinacia</i> accessions. <i>Nature Communications</i> , 2017, 8, 15275.	12.8	156
60	Mutation in a novel gene <i>SMALL AND CORDATE LEAF 1</i> affects leaf morphology in cucumber. <i>Journal of Integrative Plant Biology</i> , 2017, 59, 736-741.	8.5	7
61	Changing Ploidy as a Strategy: The Irish Potato Famine Pathogen Shifts Ploidy in Relation to Its Sexuality. <i>Molecular Plant-Microbe Interactions</i> , 2017, 30, 45-52.	2.6	58
62	Engineering Non-transgenic Gynoecious Cucumber Using an Improved Transformation Protocol and Optimized CRISPR/Cas9 System. <i>Molecular Plant</i> , 2017, 10, 1575-1578.	8.3	159
63	CsAP3: A Cucumber Homolog to Arabidopsis APETALA3 with Novel Characteristics. <i>Frontiers in Plant Science</i> , 2016, 07, 1181.	3.6	34
64	An ACC Oxidase Gene Essential for Cucumber Carpel Development. <i>Molecular Plant</i> , 2016, 9, 1315-1327.	8.3	108
65	Integrative Analyses of Nontargeted Volatile Profiling and Transcriptome Data Provide Molecular Insight into VOC Diversity in Cucumber Plants (<i>Cucumis sativus</i>). <i>Plant Physiology</i> , 2016, 172, 603-618.	4.8	99
66	CsWRKY46, a WRKY transcription factor from cucumber, confers cold resistance in transgenic-plant by regulating a set of cold-stress responsive genes in an ABA-dependent manner. <i>Plant Physiology and Biochemistry</i> , 2016, 108, 478-487.	5.8	126
67	Convergence and divergence of bitterness biosynthesis and regulation in Cucurbitaceae. <i>Nature Plants</i> , 2016, 2, 16183.	9.3	188
68	SSR Analysis of Genetic Diversity Among 192 Diploid Potato Cultivars. <i>Horticultural Plant Journal</i> , 2016, 2, 163-171.	5.0	19
69	New insights into substrate folding preference of plant OSCs. <i>Science Bulletin</i> , 2016, 61, 1407-1412.	9.0	14
70	An exon skipping in a <i>SEPALLATA</i> -like gene is associated with perturbed floral and fruits development in cucumber. <i>Journal of Integrative Plant Biology</i> , 2016, 58, 766-771.	8.5	17
71	A proposed regulatory framework for genome-edited crops. <i>Nature Genetics</i> , 2016, 48, 109-111.	21.4	184
72	A CsYcf54 variant conferring light green coloration in cucumber. <i>Euphytica</i> , 2016, 208, 509-517.	1.2	47

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73	Domestication selected for deceleration of the circadian clock in cultivated tomato. <i>Nature Genetics</i> , 2016, 48, 89-93.	21.4	165
74	A Truncated F-Box Protein Confers the Dwarfism in Cucumber. <i>Journal of Genetics and Genomics</i> , 2016, 43, 223-226.	3.9	27
75	A major quantitative trait locus conferring subgynoecy in cucumber. <i>Theoretical and Applied Genetics</i> , 2016, 129, 97-104.	3.6	17
76	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
77	A Sequencing-Based Linkage Map of Cucumber. <i>Molecular Plant</i> , 2015, 8, 961-963.	8.3	28
78	An <i>ACCUMULATION AND REPLICATION OF CHLOROPLASTS 5</i> gene mutation confers light green peel in cucumber. <i>Journal of Integrative Plant Biology</i> , 2015, 57, 936-942.	8.5	53
79	A Rare SNP Identified a TCP Transcription Factor Essential for Tendril Development in Cucumber. <i>Molecular Plant</i> , 2015, 8, 1795-1808.	8.3	58
80	Single Nucleus Genome Sequencing Reveals High Similarity among Nuclei of an Endomycorrhizal Fungus. <i>PLoS Genetics</i> , 2014, 10, e1004078.	3.5	238
81	Biosynthesis, regulation, and domestication of bitterness in cucumber. <i>Science</i> , 2014, 346, 1084-1088.	12.6	388
82	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
83	Genomic analyses provide insights into the history of tomato breeding. <i>Nature Genetics</i> , 2014, 46, 1220-1226.	21.4	801
84	QTL-seq identifies an early flowering QTL located near Flowering Locus T in cucumber. <i>Theoretical and Applied Genetics</i> , 2014, 127, 1491-1499.	3.6	267
85	A high-resolution cucumber cytogenetic map integrated with the genome assembly. <i>BMC Genomics</i> , 2013, 14, 461.	2.8	33
86	A 1,681-locus consensus genetic map of cultivated cucumber including 67 NB-LRR resistance gene homolog and ten gene loci. <i>BMC Plant Biology</i> , 2013, 13, 53.	3.6	58
87	Fine mapping of the Ph-3 gene conferring resistance to late blight (<i>Phytophthora infestans</i>) in tomato. <i>Theoretical and Applied Genetics</i> , 2013, 126, 2643-2653.	3.6	52
88	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
89	The draft genome of watermelon (<i>Citrullus lanatus</i>) and resequencing of 20 diverse accessions. <i>Nature Genetics</i> , 2013, 45, 51-58.	21.4	731
90	The potato <i>R10</i> resistance specificity to late blight is conferred by both a single dominant <i>R</i> gene and quantitative trait loci. <i>Plant Breeding</i> , 2013, 132, 407-412.	1.9	7

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91	Characterization and expression profiling of cucumber kinesin genes during early fruit development: revealing the roles of kinesins in exponential cell production and enlargement in cucumber fruit. <i>Journal of Experimental Botany</i> , 2013, 64, 4541-4557.	4.8	59
92	Construction of Reference Chromosome-Scale Pseudomolecules for Potato: Integrating the Potato Genome with Genetic and Physical Maps. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 2031-2047.	1.8	244
93	Localization of a New Gene for Bitterness in Cucumber. <i>Journal of Heredity</i> , 2013, 104, 134-139.	2.4	37
94	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
95	The tomato genome sequence provides insights into fleshy fruit evolution. <i>Nature</i> , 2012, 485, 635-641.	27.8	2,860
96	Genetic Diversity and Population Structure of Cucumber (<i>Cucumis sativus</i> L.). <i>PLoS ONE</i> , 2012, 7, e46919.	2.5	123
97	Comparison of the distribution of the repetitive DNA sequences in three variants of <i>Cucumis sativus</i> reveals their phylogenetic relationships. <i>Journal of Genetics and Genomics</i> , 2011, 38, 39-45.	3.9	28
98	Genome sequence and analysis of the tuber crop potato. <i>Nature</i> , 2011, 475, 189-195.	27.8	1,912
99	An integrated molecular cytogenetic map of <i>Cucumis sativus</i> L. chromosome 2. <i>BMC Genetics</i> , 2011, 12, 18.	2.7	25
100	The genome of the mesopolyploid crop species <i>Brassica rapa</i> . <i>Nature Genetics</i> , 2011, 43, 1035-1039.	21.4	1,893
101	A linkage map of cultivated cucumber (<i>Cucumis sativus</i> L.) with 248 microsatellite marker loci and seven genes for horticulturally important traits. <i>Euphytica</i> , 2011, 182, 167-176.	1.2	91
102	Fine genetic mapping localizes cucumber scab resistance gene <i>Ccu</i> into an R gene cluster. <i>Theoretical and Applied Genetics</i> , 2011, 122, 795-803.	3.6	43
103	Genome-wide analysis of WRKY gene family in <i>Cucumis sativus</i> . <i>BMC Genomics</i> , 2011, 12, 471.	2.8	236
104	RNA-Seq improves annotation of protein-coding genes in the cucumber genome. <i>BMC Genomics</i> , 2011, 12, 540.	2.8	232
105	Cloning and Characterization of <i>R3b</i> ; Members of the <i>R3</i> Superfamily of Late Blight Resistance Genes Show Sequence and Functional Divergence. <i>Molecular Plant-Microbe Interactions</i> , 2011, 24, 1132-1142.	2.6	113
106	Cucumber Genomics. , 2011, , 335-352.		0
107	Transcriptome sequencing and comparative analysis of cucumber flowers with different sex types. <i>BMC Genomics</i> , 2010, 11, 384.	2.8	161
108	Genome-wide characterization of simple sequence repeats in cucumber (<i>Cucumis sativus</i> L.). <i>BMC Genomics</i> , 2010, 11, 569.	2.8	316

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109	Inducible Positive Mutant Screening System to Unveil the Signaling Pathway of Late Blight Resistance. <i>Journal of Integrative Plant Biology</i> , 2010, 52, 476-484.	8.5	9
110	LATEST ADVANCES IN WATERMELON GENOMICS. <i>Acta Horticulturae</i> , 2010, , 599-606.	0.2	1
111	An Extended Intervarietal Microsatellite Linkage Map of Cucumber, <i>Cucumis sativus</i> L.. <i>Hortscience: A Publication of the American Society for Horticultural Science</i> , 2010, 45, 882-886.	1.0	24
112	Genetic Mapping of the Scab Resistance Gene in Cucumber. <i>Journal of the American Society for Horticultural Science</i> , 2010, 135, 53-58.	1.0	31
113	A Snapshot of the Emerging Tomato Genome Sequence. <i>Plant Genome</i> , 2009, 2, .	2.8	73
114	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
115	Centromere repositioning in cucurbit species: Implication of the genomic impact from centromere activation and inactivation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 14937-14941.	7.1	90
116	Sequencing the Potato Genome: Outline and First Results to Come from the Elucidation of the Sequence of the World's Third Most Important Food Crop. <i>American Journal of Potato Research</i> , 2009, 86, 417-429.	0.9	87
117	The genome of the cucumber, <i>Cucumis sativus</i> L.. <i>Nature Genetics</i> , 2009, 41, 1275-1281.	21.4	1,317
118	An Integrated Genetic and Cytogenetic Map of the Cucumber Genome. <i>PLoS ONE</i> , 2009, 4, e5795.	2.5	232
119	ALLELIC DIVERSITY OF THE POPULATION OF PHYTOPHTHORA INFESTANS IN CHINA. <i>Acta Horticulturae</i> , 2009, , 123-128.	0.2	0
120	Genetic association of ETHYLENE-INSENSITIVE3-like sequence with the sex-determining M locus in cucumber (<i>Cucumis sativus</i> L.). <i>Theoretical and Applied Genetics</i> , 2008, 117, 927-933.	3.6	39
121	Distribution of the tandem repeat sequences and karyotyping in cucumber (&i>Cucumis sativus) Tj ETQq1 1 0,784314 rgBT /Ove	1.1	86
122	Comparative genomics enabled the isolation of the R3a late blight resistance gene in potato. <i>Plant Journal</i> , 2005, 42, 251-261.	5.7	355
123	An ancestral oomycete locus contains late blight avirulence gene Avr3a, encoding a protein that is recognized in the host cytoplasm. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 7766-7771.	7.1	414
124	An Accurate In Vitro Assay for High-Throughput Disease Testing of Phytophthora infestans in Potato. <i>Plant Disease</i> , 2005, 89, 1263-1267.	1.4	30
125	QTL analysis of fertility restoration in cytoplasmic male sterile pepper. <i>Theoretical and Applied Genetics</i> , 2004, 109, 1058-1063.	3.6	69
126	The R3 Resistance to Phytophthora infestans in Potato is Conferred by Two Closely Linked R Genes with Distinct Specificities. <i>Molecular Plant-Microbe Interactions</i> , 2004, 17, 428-435.	2.6	121

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127	Development of pepper SSR markers from sequence databases. Euphytica, 2001, 117, 163-167.	1.2	34
128	Title is missing!. Euphytica, 2000, 112, 267-273.	1.2	14