

# Sanwen Huang

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6485680/publications.pdf>

Version: 2024-02-01

128  
papers

21,879  
citations

20759

60  
h-index

15218

126  
g-index

136  
all docs

136  
docs citations

136  
times ranked

15785  
citing authors

#	ARTICLE	IF	CITATIONS
1	The tomato genome sequence provides insights into fleshy fruit evolution. <i>Nature</i> , 2012, 485, 635-641.	13.7	2,860
2	Genome sequence and analysis of the tuber crop potato. <i>Nature</i> , 2011, 475, 189-195.	13.7	1,912
3	The genome of the mesopolyploid crop species <i>Brassica rapa</i> . <i>Nature Genetics</i> , 2011, 43, 1035-1039.	9.4	1,893
4	The genome of the cucumber, <i>Cucumis sativus</i> L. <i>Nature Genetics</i> , 2009, 41, 1275-1281.	9.4	1,317
5	Genomic analyses provide insights into the history of tomato breeding. <i>Nature Genetics</i> , 2014, 46, 1220-1226.	9.4	801
6	The draft genome of watermelon ( <i>Citrullus lanatus</i> ) and resequencing of 20 diverse accessions. <i>Nature Genetics</i> , 2013, 45, 51-58.	9.4	731
7	Rewiring of the Fruit Metabolome in Tomato Breeding. <i>Cell</i> , 2018, 172, 249-261.e12.	13.5	606
8	A chemical genetic roadmap to improved tomato flavor. <i>Science</i> , 2017, 355, 391-394.	6.0	561
9	A genomic variation map provides insights into the genetic basis of cucumber domestication and diversity. <i>Nature Genetics</i> , 2013, 45, 1510-1515.	9.4	472
10	The tomato pan-genome uncovers new genes and a rare allele regulating fruit flavor. <i>Nature Genetics</i> , 2019, 51, 1044-1051.	9.4	441
11	An ancestral oomycete locus contains late blight avirulence gene <i>Avr3a</i> , 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.	3.3	414
12	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.	9.4	401
13	Biosynthesis, regulation, and domestication of bitterness in cucumber. <i>Science</i> , 2014, 346, 1084-1088.	6.0	388
14	Comparative genomics enabled the isolation of the <i>R3a</i> late blight resistance gene in potato. <i>Plant Journal</i> , 2005, 42, 251-261.	2.8	355
15	Genome-wide characterization of simple sequence repeats in cucumber ( <i>Cucumis sativus</i> L.). <i>BMC Genomics</i> , 2010, 11, 569.	1.2	316
16	QTL-seq identifies an early flowering QTL located near Flowering Locus T in cucumber. <i>Theoretical and Applied Genetics</i> , 2014, 127, 1491-1499.	1.8	267
17	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.	0.8	244
18	Single Nucleus Genome Sequencing Reveals High Similarity among Nuclei of an Endomycorrhizal Fungus. <i>PLoS Genetics</i> , 2014, 10, e1004078.	1.5	238

#	ARTICLE	IF	CITATIONS
19	Genome-wide analysis of WRKY gene family in <i>Cucumis sativus</i> . <i>BMC Genomics</i> , 2011, 12, 471.	1.2	236
20	An Integrated Genetic and Cytogenetic Map of the Cucumber Genome. <i>PLoS ONE</i> , 2009, 4, e5795.	1.1	232
21	RNA-Seq improves annotation of protein-coding genes in the cucumber genome. <i>BMC Genomics</i> , 2011, 12, 540.	1.2	232
22	Resequencing of 414 cultivated and wild watermelon accessions identifies selection for fruit quality traits. <i>Nature Genetics</i> , 2019, 51, 1616-1623.	9.4	226
23	The chicken gut metagenome and the modulatory effects of plant-derived benzylisoquinoline alkaloids. <i>Microbiome</i> , 2018, 6, 211.	4.9	204
24	Convergence and divergence of bitterness biosynthesis and regulation in Cucurbitaceae. <i>Nature Plants</i> , 2016, 2, 16183.	4.7	188
25	A proposed regulatory framework for genome-edited crops. <i>Nature Genetics</i> , 2016, 48, 109-111.	9.4	184
26	Cucurbit Genomics Database (CuGenDB): a central portal for comparative and functional genomics of cucurbit crops. <i>Nucleic Acids Research</i> , 2019, 47, D1128-D1136.	6.5	177
27	Domestication selected for deceleration of the circadian clock in cultivated tomato. <i>Nature Genetics</i> , 2016, 48, 89-93.	9.4	165
28	Transcriptome sequencing and comparative analysis of cucumber flowers with different sex types. <i>BMC Genomics</i> , 2010, 11, 384.	1.2	161
29	Engineering Non-transgenic Gynoecious Cucumber Using an Improved Transformation Protocol and Optimized CRISPR/Cas9 System. <i>Molecular Plant</i> , 2017, 10, 1575-1578.	3.9	159
30	Draft genome of spinach and transcriptome diversity of 120 <i>Spinacia</i> accessions. <i>Nature Communications</i> , 2017, 8, 15275.	5.8	156
31	A comprehensive genome variation map of melon identifies multiple domestication events and loci influencing agronomic traits. <i>Nature Genetics</i> , 2019, 51, 1607-1615.	9.4	153
32	Generation of self-compatible diploid potato by knockout of S-RNase. <i>Nature Plants</i> , 2018, 4, 651-654.	4.7	152
33	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.	1.2	139
34	A chromosome-scale genome assembly of cucumber ( <i>Cucumis sativus</i> L.). <i>GigaScience</i> , 2019, 8, .	3.3	138
35	Haplotype-resolved genome analyses of a heterozygous diploid potato. <i>Nature Genetics</i> , 2020, 52, 1018-1023.	9.4	134
36	Graph pangenome captures missing heritability and empowers tomato breeding. <i>Nature</i> , 2022, 606, 527-534.	13.7	131

#	ARTICLE	IF	CITATIONS
37	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.	2.8	126
38	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.	3.1	125
39	Genome evolution and diversity of wild and cultivated potatoes. <i>Nature</i> , 2022, 606, 535-541.	13.7	125
40	Genetic Diversity and Population Structure of Cucumber ( <i>Cucumis sativus</i> L.). <i>PLoS ONE</i> , 2012, 7, e46919.	1.1	123
41	The R3 Resistance to <i>Phytophthora infestans</i> in Potato is Conferred by Two Closely Linked R Genes with Distinct Specificities. <i>Molecular Plant-Microbe Interactions</i> , 2004, 17, 428-435.	1.4	121
42	The Genome of Medicinal Plant <i>Macleaya cordata</i> Provides New Insights into Benzylisoquinoline Alkaloids Metabolism. <i>Molecular Plant</i> , 2017, 10, 975-989.	3.9	116
43	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.	1.4	113
44	Loss of salt tolerance during tomato domestication conferred by variation in a Na <sup>+</sup> /K <sup>+</sup> transporter. <i>EMBO Journal</i> , 2020, 39, e103256.	3.5	112
45	Genome design of hybrid potato. <i>Cell</i> , 2021, 184, 3873-3883.e12.	13.5	112
46	The genetic basis of inbreeding depression in potato. <i>Nature Genetics</i> , 2019, 51, 374-378.	9.4	110
47	An ACC Oxidase Gene Essential for Cucumber Carpel Development. <i>Molecular Plant</i> , 2016, 9, 1315-1327.	3.9	108
48	The <i>Taxus</i> genome provides insights into paclitaxel biosynthesis. <i>Nature Plants</i> , 2021, 7, 1026-1036.	4.7	103
49	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.	2.3	99
50	The wax gourd genomes offer insights into the genetic diversity and ancestral cucurbit karyotype. <i>Nature Communications</i> , 2019, 10, 5158.	5.8	94
51	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.	0.6	91
52	Meta-analysis of genome-wide association studies provides insights into genetic control of tomato flavor. <i>Nature Communications</i> , 2019, 10, 1534.	5.8	91
53	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.	3.3	90
54	Genome analysis of <i>Taraxacum kok-saghyz</i> Rodin provides new insights into rubber biosynthesis. <i>National Science Review</i> , 2018, 5, 78-87.	4.6	90

#	ARTICLE	IF	CITATIONS
55	An Overlooked Paleotetraploidization in Cucurbitaceae. <i>Molecular Biology and Evolution</i> , 2018, 35, 16-26.	3.5	89
56	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.	0.5	87
57	Genetic Regulation of Ethylene Dosage for Cucumber Fruit Elongation. <i>Plant Cell</i> , 2019, 31, 1063-1076.	3.1	85
58	A Snapshot of the Emerging Tomato Genome Sequence. <i>Plant Genome</i> , 2009, 2, .	1.6	73
59	Removal of lycopene substrate inhibition enables high carotenoid productivity in <i>Yarrowia lipolytica</i> . <i>Nature Communications</i> , 2022, 13, 572.	5.8	70
60	QTL analysis of fertility restoration in cytoplasmic male sterile pepper. <i>Theoretical and Applied Genetics</i> , 2004, 109, 1058-1063.	1.8	69
61	Distribution of the tandem repeat sequences and karyotyping in cucumber (&#x26;#x26;Cucumis sativus) Tj ETQq1 1 0,784314 rgBT /Overl	0.6	66
62	Targeting pathway expression to subcellular organelles improves astaxanthin synthesis in <i>Yarrowia lipolytica</i> . <i>Metabolic Engineering</i> , 2021, 68, 152-161.	3.6	63
63	Domestication of Crop Metabolomes: Desired and Unintended Consequences. <i>Trends in Plant Science</i> , 2021, 26, 650-661.	4.3	60
64	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.	2.4	59
65	Graph-based pan-genome reveals structural and sequence variations related to agronomic traits and domestication in cucumber. <i>Nature Communications</i> , 2022, 13, 682.	5.8	59
66	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.	1.6	58
67	A Rare SNP Identified a TCP Transcription Factor Essential for Tendril Development in Cucumber. <i>Molecular Plant</i> , 2015, 8, 1795-1808.	3.9	58
68	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.	1.4	58
69	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.	1.5	54
70	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.	4.1	53
71	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.	1.8	52
72	Multi-omics data-driven investigations of metabolic diversity of plant triterpenoids. <i>Plant Journal</i> , 2019, 97, 101-111.	2.8	50

#	ARTICLE	IF	CITATIONS
73	A CsYcf54 variant conferring light green coloration in cucumber. <i>Euphytica</i> , 2016, 208, 509-517.	0.6	47
74	Genome-wide Target Mapping Shows Histone Deacetylase Complex1 Regulates Cell Proliferation in Cucumber Fruit. <i>Plant Physiology</i> , 2020, 182, 167-184.	2.3	47
75	The integrated genomics of crop domestication and breeding. <i>Cell</i> , 2022, 185, 2828-2839.	13.5	47
76	<i>in vivo</i> maternal haploid induction in tomato. <i>Plant Biotechnology Journal</i> , 2022, 20, 250-252.	4.1	44
77	Fine genetic mapping localizes cucumber scab resistance gene Ccu into an R gene cluster. <i>Theoretical and Applied Genetics</i> , 2011, 122, 795-803.	1.8	43
78	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.	4.1	43
79	A nonS-locus F-box gene breaks self-incompatibility in diploid potatoes. <i>Nature Communications</i> , 2021, 12, 4142.	5.8	42
80	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.	1.8	39
81	Localization of a New Gene for Bitterness in Cucumber. <i>Journal of Heredity</i> , 2013, 104, 134-139.	1.0	37
82	Next-Gen Approaches to Flavor-Related Metabolism. <i>Annual Review of Plant Biology</i> , 2019, 70, 187-212.	8.6	36
83	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, .	2.9	36
84	Development of pepper SSR markers from sequence databases. <i>Euphytica</i> , 2001, 117, 163-167.	0.6	34
85	CsAP3: A Cucumber Homolog to Arabidopsis APETALA3 with Novel Characteristics. <i>Frontiers in Plant Science</i> , 2016, 07, 1181.	1.7	34
86	A high-resolution cucumber cytogenetic map integrated with the genome assembly. <i>BMC Genomics</i> , 2013, 14, 461.	1.2	33
87	Regulation of plant architecture by a new histone acetyltransferase targeting gene bodies. <i>Nature Plants</i> , 2020, 6, 809-822.	4.7	33
88	Genome architecture and tetrasomic inheritance of autotetraploid potato. <i>Molecular Plant</i> , 2022, 15, 1211-1226.	3.9	33
89	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.	3.1	31
90	Genetic Mapping of the Scab Resistance Gene in Cucumber. <i>Journal of the American Society for Horticultural Science</i> , 2010, 135, 53-58.	0.5	31

#	ARTICLE	IF	CITATIONS
91	An Accurate In Vitro Assay for High-Throughput Disease Testing of <i>Phytophthora infestans</i> in Potato. <i>Plant Disease</i> , 2005, 89, 1263-1267.	0.7	30
92	Acquisition of deleterious mutations during potato polyploidization. <i>Journal of Integrative Plant Biology</i> , 2019, 61, 7-11.	4.1	30
93	Metabolomics should be deployed in the identification and characterization of gene-edited crops. <i>Plant Journal</i> , 2020, 102, 897-902.	2.8	30
94	<i>FLOWERING LOCUS T</i> Improves Cucumber Adaptation to Higher Latitudes. <i>Plant Physiology</i> , 2020, 182, 908-918.	2.3	30
95	Genomic analyses provide insights into peach local adaptation and responses to climate change. <i>Genome Research</i> , 2021, 31, 592-606.	2.4	30
96	Engineering Plant Cytochrome P450s for Enhanced Synthesis of Natural Products: Past Achievements and Future Perspectives. <i>Plant Communications</i> , 2020, 1, 100012.	3.6	29
97	Genetic dissection of climacteric fruit ripening in a melon population segregating for ripening behavior. <i>Horticulture Research</i> , 2020, 7, 187.	2.9	29
98	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.	1.7	28
99	A Sequencing-Based Linkage Map of Cucumber. <i>Molecular Plant</i> , 2015, 8, 961-963.	3.9	28
100	A Truncated F-Box Protein Confers the Dwarfism in Cucumber. <i>Journal of Genetics and Genomics</i> , 2016, 43, 223-226.	1.7	27
101	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.	2.8	26
102	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.	1.1	26
103	An integrated molecular cytogenetic map of <i>Cucumis sativus</i> L. chromosome 2. <i>BMC Genetics</i> , 2011, 12, 18.	2.7	25
104	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.	5.6	24
105	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.	0.5	24
106	The multi-omics basis of potato heterosis. <i>Journal of Integrative Plant Biology</i> , 2022, 64, 671-687.	4.1	22
107	SSR Analysis of Genetic Diversity Among 192 Diploid Potato Cultivars. <i>Horticultural Plant Journal</i> , 2016, 2, 163-171.	2.3	19
108	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.	1.8	19

#	ARTICLE	IF	CITATIONS
109	A structural and data-driven approach to engineering a plant cytochrome P450 enzyme. <i>Science China Life Sciences</i> , 2019, 62, 873-882.	2.3	18
110	Domestication and breeding changed tomato fruit transcriptome. <i>Journal of Integrative Agriculture</i> , 2020, 19, 120-132.	1.7	18
111	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.	2.9	18
112	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.	4.1	17
113	A major quantitative trait locus conferring subgynoecey in cucumber. <i>Theoretical and Applied Genetics</i> , 2016, 129, 97-104.	1.8	17
114	An EMS mutant library for cucumber. <i>Journal of Integrative Agriculture</i> , 2018, 17, 1612-1619.	1.7	17
115	Developmentally Regulated Glucosylation of Bitter Triterpenoid in Cucumber by the UDP-Glucosyltransferase UGT73AM3. <i>Molecular Plant</i> , 2017, 10, 1000-1003.	3.9	16
116	Title is missing!. <i>Euphytica</i> , 2000, 112, 267-273.	0.6	14
117	New insights into substrate folding preference of plant OSCs. <i>Science Bulletin</i> , 2016, 61, 1407-1412.	4.3	14
118	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.	1.8	11
119	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.	1.8	10
120	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.	4.1	9
121	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.	1.0	7
122	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.	4.1	7
123	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.	1.8	7
124	A high-throughput BAC end analysis protocol (BAC-anchor) for profiling genome assembly and physical mapping. <i>Plant Biotechnology Journal</i> , 2020, 18, 364-372.	4.1	6
125	Enhanced chemoselectivity of a plant cytochrome P450 through protein engineering of surface and catalytic residues. <i>ABIOTECH</i> , 2021, 2, 215-225.	1.8	4
126	LATEST ADVANCES IN WATERMELON GENOMICS. <i>Acta Horticulturae</i> , 2010, , 599-606.	0.1	1



#	ARTICLE	IF	CITATIONS
127	ALLELIC DIVERSITY OF THE POPULATION OF PHYTOPHTHORA INFESTANS IN CHINA. Acta Horticulturae, 2009, , 123-128.	0.1	0
128	Cucumber Genomics. , 2011, , 335-352.		0