

# Jinsheng Lai

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2013607/publications.pdf>

Version: 2024-02-01

76  
papers

8,043  
citations

71061

41  
h-index

66879

78  
g-index

79  
all docs

79  
docs citations

79  
times ranked

8402  
citing authors

#	ARTICLE	IF	CITATIONS
1	The RppC-AvrRppC NLR-effector interaction mediates the resistance to southern corn rust in maize. <i>Molecular Plant</i> , 2022, 15, 904-912.	3.9	31
2	DNA demethylation affects imprinted gene expression in maize endosperm. <i>Genome Biology</i> , 2022, 23, 77.	3.8	20
3	Maize PPR278 Functions in Mitochondrial RNA Splicing and Editing. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3035.	1.8	6
4	<i>ENB1</i> encodes a cellulose synthase 5 that directs synthesis of cell wall ingrowths in maize basal endosperm transfer cells. <i>Plant Cell</i> , 2022, 34, 1054-1074.	3.1	13
5	The transcription factor <i>bZIP68</i> negatively regulates cold tolerance in maize. <i>Plant Cell</i> , 2022, 34, 2833-2851.	3.1	42
6	The transcription factor ZmMYB69 represses lignin biosynthesis by activating <i>ZmMYB31/42</i> expression in maize. <i>Plant Physiology</i> , 2022, 189, 1916-1919.	2.3	11
7	Large-scale reconstruction of chromatin structures of maize temperate and tropical inbred lines. <i>Journal of Experimental Botany</i> , 2021, 72, 3582-3596.	2.4	5
8	Metabolomics-driven gene mining and genetic improvement of tolerance to salt-induced osmotic stress in maize. <i>New Phytologist</i> , 2021, 230, 2355-2370.	3.5	46
9	MP3RNA-seq: Massively parallel 3' end RNA sequencing for high-throughput gene expression profiling and genotyping. <i>Journal of Integrative Plant Biology</i> , 2021, 63, 1227-1239.	4.1	4
10	Cotyledons facilitate the adaptation of early-maturing soybean varieties to high-latitude long-day environments. <i>Plant, Cell and Environment</i> , 2021, 44, 2551-2564.	2.8	15
11	Programmable RNA editing with compact CRISPR-Cas13 systems from uncultivated microbes. <i>Nature Methods</i> , 2021, 18, 499-506.	9.0	182
12	Large-scale translome profiling annotates the functional genome and reveals the key role of genic 3' untranslated regions in translomic variation in plants. <i>Plant Communications</i> , 2021, 2, 100181.	3.6	15
13	Megabase-scale presence-absence variation with <i>Tripsacum</i> origin was under selection during maize domestication and adaptation. <i>Genome Biology</i> , 2021, 22, 237.	3.8	21
14	HITAC-seq enables high-throughput cost-effective sequencing of plasmids and DNA fragments with identity. <i>Journal of Genetics and Genomics</i> , 2021, 48, 671-680.	1.7	2
15	ZmCTLP1 is required for the maintenance of lipid homeostasis and the basal endosperm transfer layer in maize kernels. <i>New Phytologist</i> , 2021, 232, 2384-2399.	3.5	9
16	<i>Miniature Seed6</i> , encoding an endoplasmic reticulum signal peptidase, is critical in seed development. <i>Plant Physiology</i> , 2021, 185, 985-1001.	2.3	8
17	Loss-of-function alleles of ZmPLD3 cause haploid induction in maize. <i>Nature Plants</i> , 2021, 7, 1579-1588.	4.7	52
18	Genome-wide identification and analysis of heterotic loci in three maize hybrids. <i>Plant Biotechnology Journal</i> , 2020, 18, 185-194.	4.1	39

#	ARTICLE	IF	CITATIONS
19	Evolution and Domestication Footprints Uncovered from the Genomes of Coix. <i>Molecular Plant</i> , 2020, 13, 295-308.	3.9	35
20	Maize <i>WI5</i> encodes an endo- $\beta$ -1,4-xylanase required for secondary cell wall synthesis and water transport in xylem. <i>Journal of Integrative Plant Biology</i> , 2020, 62, 1607-1624.	4.1	11
21	A Large Transposon Insertion in the <i>stiff1</i> Promoter Increases Stalk Strength in Maize. <i>Plant Cell</i> , 2020, 32, 152-165.	3.1	40
22	Genome-wide selection and genetic improvement during modern maize breeding. <i>Nature Genetics</i> , 2020, 52, 565-571.	9.4	146
23	A barley stripe mosaic virus-based guide RNA delivery system for targeted mutagenesis in wheat and maize. <i>Molecular Plant Pathology</i> , 2019, 20, 1463-1474.	2.0	91
24	Chromosome conformation capture resolved near complete genome assembly of broomcorn millet. <i>Nature Communications</i> , 2019, 10, 464.	5.8	81
25	Mutation of ZmDMP enhances haploid induction in maize. <i>Nature Plants</i> , 2019, 5, 575-580.	4.7	149
26	Long-range interactions between proximal and distal regulatory regions in maize. <i>Nature Communications</i> , 2019, 10, 2633.	5.8	79
27	High Temporal-Resolution Transcriptome Landscape of Early Maize Seed Development. <i>Plant Cell</i> , 2019, 31, 974-992.	3.1	141
28	A HAK family Na <sup>+</sup> transporter confers natural variation of salt tolerance in maize. <i>Nature Plants</i> , 2019, 5, 1297-1308.	4.7	136
29	Characterization of maize translational responses to sugarcane mosaic virus infection. <i>Virus Research</i> , 2019, 259, 97-107.	1.1	11
30	OS1 functions in the allocation of nutrients between the endosperm and embryo in maize seeds. <i>Journal of Integrative Plant Biology</i> , 2019, 61, 706-727.	4.1	15
31	Construction of the third-generation <i>Zea mays</i> haplotype map. <i>GigaScience</i> , 2018, 7, 1-12.	3.3	191
32	Effects of drought stress and water recovery on physiological responses and gene expression in maize seedlings. <i>BMC Plant Biology</i> , 2018, 18, 68.	1.6	116
33	<i>Defective Kernel 39</i> encodes a PPR protein required for seed development in maize. <i>Journal of Integrative Plant Biology</i> , 2018, 60, 45-64.	4.1	54
34	Sequential gene activation and gene imprinting during early embryo development in maize. <i>Plant Journal</i> , 2018, 93, 445-459.	2.8	18
35	A retrotransposon in an HKT1 family sodium transporter causes variation of leaf Na <sup>+</sup> exclusion and salt tolerance in maize. <i>New Phytologist</i> , 2018, 217, 1161-1176.	3.5	229
36	Extensive intraspecific gene order and gene structural variations between Mo17 and other maize genomes. <i>Nature Genetics</i> , 2018, 50, 1289-1295.	9.4	335

#	ARTICLE	IF	CITATIONS
37	Identification and Fine-Mapping of a Major Maize Leaf Width QTL in a Re-sequenced Large Recombinant Inbred Lines Population. <i>Frontiers in Plant Science</i> , 2018, 9, 101.	1.7	21
38	Identification of minor effect QTLs for plant architecture related traits using super high density genotyping and large recombinant inbred population in maize ( <i>Zea mays</i> ). <i>BMC Plant Biology</i> , 2018, 18, 17.	1.6	33
39	Parent-of-origin-dependent nucleosome organization correlates with genomic imprinting in maize. <i>Genome Research</i> , 2018, 28, 1020-1028.	2.4	5
40	A 4-bp Insertion at ZmPLA1 Encoding a Putative Phospholipase A Generates Haploid Induction in Maize. <i>Molecular Plant</i> , 2017, 10, 520-522.	3.9	219
41	Holotrichia oblita Midgut Proteins That Bind to Bacillus thuringiensis Cry8-Like Toxin and Assembly of the H. oblita Midgut Tissue Transcriptome. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	10
42	Genome-wide Nucleosome Occupancy and Organization Modulates the Plasticity of Gene Transcriptional Status in Maize. <i>Molecular Plant</i> , 2017, 10, 962-974.	3.9	16
43	Highly interwoven communities of a gene regulatory network unveil topologically important genes for maize seed development. <i>Plant Journal</i> , 2017, 92, 1143-1156.	2.8	20
44	Dynamic and Antagonistic Allele-Specific Epigenetic Modifications Controlling the Expression of Imprinted Genes in Maize Endosperm. <i>Molecular Plant</i> , 2017, 10, 442-455.	3.9	38
45	The coupled effect of nucleosome organization on gene transcription level and transcriptional plasticity. <i>Nucleus</i> , 2017, 8, 605-612.	0.6	6
46	The second subunit of DNA-polymerase delta is required for genomic stability and epigenetic regulation. <i>Plant Physiology</i> , 2016, 171, pp.01976.2015.	2.3	15
47	Gene duplication confers enhanced expression of 27-kDa $\beta$ -zein for endosperm modification in quality protein maize. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 4964-4969.	3.3	67
48	Genetic dissection of maize seedling root system architecture traits using an ultra-high density bin map and a recombinant inbred line population. <i>Journal of Integrative Plant Biology</i> , 2016, 58, 266-279.	4.1	48
49	DNA methylation signature of intergenic region involves in nucleosome remodeler DDM1-mediated repression of aberrant gene transcriptional read-through. <i>Journal of Genetics and Genomics</i> , 2016, 43, 513-523.	1.7	16
50	The Genetic Basis of Haploid Induction in Maize Identified with a Novel Genome-Wide Association Method. <i>Genetics</i> , 2016, 202, 1267-1276.	1.2	61
51	Efficiency and Inheritance of Targeted Mutagenesis in Maize Using CRISPR-Cas9. <i>Journal of Genetics and Genomics</i> , 2016, 43, 25-36.	1.7	171
52	Ribosome profiling reveals dynamic translational landscape in maize seedlings under drought stress. <i>Plant Journal</i> , 2015, 84, 1206-1218.	2.8	162
53	Methyl-CpG-Binding Domain Protein MBD7 Is Required for Active DNA Demethylation in Arabidopsis. <i>Plant Physiology</i> , 2015, 167, 905-914.	2.3	51
54	Patterns of genomic changes with crop domestication and breeding. <i>Current Opinion in Plant Biology</i> , 2015, 24, 47-53.	3.5	83

#	ARTICLE	IF	CITATIONS
55	Genome-Wide Identification of VQ Motif-Containing Proteins and their Expression Profiles Under Abiotic Stresses in Maize. <i>Frontiers in Plant Science</i> , 2015, 6, 1177.	1.7	59
56	Dynamic Transcriptome Landscape of Maize Embryo and Endosperm Development. <i>Plant Physiology</i> , 2014, 166, 252-264.	2.3	274
57	Specific adaptation of <i>Ustilagoidea virens</i> in occupying host florets revealed by comparative and functional genomics. <i>Nature Communications</i> , 2014, 5, 3849.	5.8	202
58	Genome-wide high resolution parental-specific DNA and histone methylation maps uncover patterns of imprinting regulation in maize. <i>Genome Research</i> , 2014, 24, 167-176.	2.4	140
59	<i>REPRESSOR OF SILENCING5</i> Encodes a Member of the Small Heat Shock Protein Family and Is Required for DNA Demethylation in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2014, 26, 2660-2675.	3.1	42
60	Metabolic map of mature maize kernels. <i>Metabolomics</i> , 2014, 10, 775-787.	1.4	55
61	An ultra-high density bin-map for rapid QTL mapping for tassel and ear architecture in a large F2 maize population. <i>BMC Genomics</i> , 2014, 15, 433.	1.2	151
62	Combined linkage and association mapping reveals candidates for <i>Scmv1</i> , a major locus involved in resistance to sugarcane mosaic virus (SCMV) in maize. <i>BMC Plant Biology</i> , 2013, 13, 162.	1.6	68
63	Genome-wide Transcription Factor Gene Prediction and their Expressional Tissue-specificities in Maize. <i>Journal of Integrative Plant Biology</i> , 2012, 54, 616-630.	4.1	82
64	Characterization, fine mapping and expression profiling of <i>Ragged leaves1</i> in maize. <i>Theoretical and Applied Genetics</i> , 2012, 125, 1125-1135.	1.8	7
65	Genome-wide genetic changes during modern breeding of maize. <i>Nature Genetics</i> , 2012, 44, 812-815.	9.4	352
66	Maize HapMap2 identifies extant variation from a genome in flux. <i>Nature Genetics</i> , 2012, 44, 803-807.	9.4	577
67	Comparative population genomics of maize domestication and improvement. <i>Nature Genetics</i> , 2012, 44, 808-811.	9.4	816
68	Identification and Fine Mapping of <i>rhm1</i> Locus for Resistance to Southern Corn Leaf Blight in Maize. <i>Journal of Integrative Plant Biology</i> , 2012, 54, 321-329.	4.1	19
69	Identification of genetic factors affecting plant density response through QTL mapping of yield component traits in maize ( <i>Zea mays</i> L.). <i>Euphytica</i> , 2011, 182, 409.	0.6	33
70	Extensive, clustered parental imprinting of protein-coding and noncoding RNAs in developing maize endosperm. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 20042-20047.	3.3	162
71	Identification of an Active New <i>Mutator</i> Transposable Element in Maize. <i>G3: Genes, Genomes, Genetics</i> , 2011, 1, 293-302.	0.8	46
72	Genome-wide patterns of genetic variation among elite maize inbred lines. <i>Nature Genetics</i> , 2010, 42, 1027-1030.	9.4	439

#	ARTICLE	IF	CITATIONS
73	Steady-state transposon mutagenesis in inbred maize. <i>Plant Journal</i> , 2005, 44, 52-61.	2.8	234
74	Gene movement by Helitron transposons contributes to the haplotype variability of maize. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 9068-9073.	3.3	244
75	Close Split of Sorghum and Maize Genome Progenitors. <i>Genome Research</i> , 2004, 14, 1916-1923.	2.4	443
76	Characterization of the Maize Endosperm Transcriptome and Its Comparison to the Rice Genome. <i>Genome Research</i> , 2004, 14, 1932-1937.	2.4	80