

# Chuanqing Sun

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4114526/publications.pdf>

Version: 2024-02-01

64  
papers

4,017  
citations

109321

35  
h-index

123424

61  
g-index

64  
all docs

64  
docs citations

64  
times ranked

3593  
citing authors

#	ARTICLE	IF	CITATIONS
1	Polyamine oxidase 3 is involved in salt tolerance at the germination stage in rice. <i>Journal of Genetics and Genomics</i> , 2022, 49, 458-468.	3.9	11
2	The genetic control of glabrous glume during African rice domestication. <i>Journal of Genetics and Genomics</i> , 2022, , .	3.9	1
3	Convergent selection of a WD40 protein that enhances grain yield in maize and rice. <i>Science</i> , 2022, 375, eabg7985.	12.6	110
4	<i>TAC4</i> controls tiller angle by regulating the endogenous auxin content and distribution in rice. <i>Plant Biotechnology Journal</i> , 2021, 19, 64-73.	8.3	38
5	<i>HIGH-TILLERING AND DWARF 12</i> modulates photosynthesis and plant architecture by affecting carotenoid biosynthesis in rice. <i>Journal of Experimental Botany</i> , 2021, 72, 1212-1224.	4.8	21
6	A gain-of-function mutation of OsMAPK6 leads to long grain in rice. <i>Crop Journal</i> , 2021, 9, 1481-1481.	5.2	1
7	What happened during domestication of wild to cultivated rice. <i>Crop Journal</i> , 2021, 9, 564-576.	5.2	19
8	An Agrobacterium-mediated non-antibiotic selection-based transformation system for rice ( <i>Oryza</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 Cellular and Developmental Biology - Plant, 2021, 57, 786-795.	2.1	3
9	The lipid transfer protein OsLTPL159 is involved in cold tolerance at the early seedling stage in rice. <i>Plant Biotechnology Journal</i> , 2020, 18, 756-769.	8.3	47
10	Whole-genome <i>de novo</i> assemblies reveal extensive structural variations and dynamic organelle-to-nucleus DNA transfers in African and Asian rice. <i>Plant Journal</i> , 2020, 104, 596-612.	5.7	19
11	A common wild rice-derived BOC1 allele reduces callus browning in indica rice transformation. <i>Nature Communications</i> , 2020, 11, 443.	12.8	43
12	Identification of microRNAs responding to cold stress in Dongxiang common wild rice. <i>Genome</i> , 2019, 62, 635-642.	2.0	12
13	Natural Variations at TIG1 Encoding a TCP Transcription Factor Contribute to Plant Architecture Domestication in Rice. <i>Molecular Plant</i> , 2019, 12, 1075-1089.	8.3	70
14	Identification of an active miniature inverted repeat transposable element <i>mJing</i> in rice. <i>Plant Journal</i> , 2019, 98, 639-653.	5.7	11
15	<i>ESA1</i> Is Involved in Embryo Sac Abortion in Interspecific Hybrid Progeny of Rice. <i>Plant Physiology</i> , 2019, 180, 356-366.	4.8	18
16	Identification of QTLs related to cadmium tolerance from wild rice ( <i>Oryza nivara</i> ) using a high-density genetic map for a set of introgression lines. <i>Euphytica</i> , 2019, 215, 1.	1.2	6
17	The APETALA2-Like Transcription Factor SUPERNUMERARY BRACT Controls Rice Seed Shattering and Seed Size. <i>Plant Cell</i> , 2019, 31, 17-36.	6.6	93
18	The domestication of plant architecture in African rice. <i>Plant Journal</i> , 2018, 94, 661-669.	5.7	39

#	ARTICLE	IF	CITATIONS
19	Deletions linked to PROG1 gene participate in plant architecture domestication in Asian and African rice. <i>Nature Communications</i> , 2018, 9, 4157.	12.8	63
20	Variation in the regulatory region of <i>FZP</i> causes increases in secondary inflorescence branching and grain yield in rice domestication. <i>Plant Journal</i> , 2018, 96, 716-733.	5.7	65
21	Genetic control of seed shattering during African rice domestication. <i>Nature Plants</i> , 2018, 4, 331-337.	9.3	55
22	A single-nucleotide polymorphism causes smaller grain size and loss of seed shattering during African rice domestication. <i>Nature Plants</i> , 2017, 3, 17064.	9.3	133
23	Emergence of a Novel Chimeric Gene Underlying Grain Number in Rice. <i>Genetics</i> , 2017, 205, 993-1002.	2.9	15
24	NOG1 increases grain production in rice. <i>Nature Communications</i> , 2017, 8, 1497.	12.8	111
25	Integrated RNA Sequencing and QTL Mapping to Identify Candidate Genes from <i>Oryza rufipogon</i> Associated with Salt Tolerance at the Seedling Stage. <i>Frontiers in Plant Science</i> , 2017, 8, 1427.	3.6	59
26	Evaluation of ORYZA2000 for Simulating Rice Growth of Different Genotypes at Two Latitudes. <i>Agronomy Journal</i> , 2017, 109, 2613-2629.	1.8	8
27	<i>GAD1</i> Encodes a Secreted Peptide That Regulates Grain Number, Grain Length, and Awn Development in Rice Domestication. <i>Plant Cell</i> , 2016, 28, 2453-2463.	6.6	115
28	Genomic structure analysis of a set of <i>Oryza nivara</i> introgression lines and identification of yield-associated QTLs using whole-genome resequencing. <i>Scientific Reports</i> , 2016, 6, 27425.	3.3	45
29	RLS3, a protein with AAA+ domain localized in chloroplast, sustains leaf longevity in rice. <i>Journal of Integrative Plant Biology</i> , 2016, 58, 971-982.	8.5	18
30	<i>NARROW AND ROLLED LEAF 2</i> regulates leaf shape, male fertility, and seed size in rice. <i>Journal of Integrative Plant Biology</i> , 2016, 58, 983-996.	8.5	53
31	Quantitative evaluation of influence of PROSTRATE GROWTH 1 gene on rice canopy structure based on three-dimensional structure model. <i>Field Crops Research</i> , 2016, 194, 65-74.	5.1	10
32	<i>CLUSTERED PRIMARY BRANCH 1</i> , a new allele of <i>DWARF 11</i> , controls panicle architecture and seed size in rice. <i>Plant Biotechnology Journal</i> , 2016, 14, 377-386.	8.3	101
33	<i>PAY 1</i> improves plant architecture and enhances grain yield in rice. <i>Plant Journal</i> , 2015, 83, 528-536.	5.7	87
34	Identification of Quantitative Trait Locus for Seed Dormancy and Expression Analysis of Four Dormancy-Related Genes in Sorghum. <i>Tropical Plant Biology</i> , 2015, 8, 9-18.	1.9	4
35	<i>LABA1</i> , a Domestication Gene Associated with Long, Barbed Awns in Wild Rice. <i>Plant Cell</i> , 2015, 27, 1875-1888.	6.6	178
36	<i>TOND1</i> confers tolerance to nitrogen deficiency in rice. <i>Plant Journal</i> , 2015, 81, 367-376.	5.7	57

#	ARTICLE	IF	CITATIONS
37	Molecular Evolution of the Sorghum Maturity Gene Ma3. PLoS ONE, 2015, 10, e0124435.	2.5	6
38	Global gene expression analysis of a rice high-tillering dwarf mutant. Genes and Genomics, 2014, 36, 485-496.	1.4	0
39	<sc><i>GS</i></sc> <i>6</i>, A Member of the <sc>GRAS</sc> Gene Family, Negatively Regulates Grain Size in Rice. Journal of Integrative Plant Biology, 2013, 55, 938-949.	8.5	99
40	Identification of heat-sensitive QTL derived from common wild rice ( <i>Oryza rufipogon</i> Griff.). Plant Science, 2013, 201-202, 121-127.	3.6	26
41	Identification and characterization of <i>Os<sc>EBS</sc></i>, a gene involved in enhanced plant biomass and spikelet number in rice. Plant Biotechnology Journal, 2013, 11, 1044-1057.	8.3	23
42	Genetic control of inflorescence architecture during rice domestication. Nature Communications, 2013, 4, 2200.	12.8	134
43	Molecular Evolution of the TAC1 Gene from Rice ( <i>Oryza sativa</i> L.). Journal of Genetics and Genomics, 2012, 39, 551-560.	3.9	44
44	<i>LHD1</i>, an Allele of <i>DTH8</i>/<i>Ghd8</i>, Controls Late Heading Date in Common Wild Rice (<i>Oryza rufipogon</i>)<sup>F</sup>. Journal of Integrative Plant Biology, 2012, 54, 790-799.	8.5	72
45	TH1, a DUF640 domain-like gene controls lemma and palea development in rice. Plant Molecular Biology, 2012, 78, 351-359.	3.9	50
46	Characterization of a novel high-tillering dwarf 3 mutant in rice. Journal of Genetics and Genomics, 2011, 38, 411-418.	3.9	21
47	Identification of quantitative trait loci associated with salt tolerance at seedling stage from <i>Oryza rufipogon</i> . Journal of Genetics and Genomics, 2011, 38, 593-601.	3.9	72
48	Identification of heterotic loci associated with yield-related traits in Chinese common wild rice ( <i>Oryza rufipogon</i> Griff.). Plant Science, 2011, 181, 14-22.	3.6	33
49	Analysis of QTLs for yield-related traits in Yuanjiang common wild rice ( <i>Oryza rufipogon</i> Griff.). Journal of Genetics and Genomics, 2010, 37, 147-157.	3.9	71
50	The Effect of the Crosstalk between Photoperiod and Temperature on the Heading-Date in Rice. PLoS ONE, 2009, 4, e5891.	2.5	57
51	Isolation and characterization of conserved non-coding sequences among rice ( <i>Oryza sativa</i> L.) paralogous regions. Molecular Genetics and Genomics, 2009, 281, 11-18.	2.1	9
52	Patterns of nucleotide diversity in wild and cultivated rice. Plant Systematics and Evolution, 2009, 281, 97-106.	0.9	13
53	Genetic Identification of Quantitative Trait Loci for Contents of Mineral Nutrients in Rice Grain. Journal of Integrative Plant Biology, 2009, 51, 84-92.	8.5	209
54	Additive and Overdominant Effects Resulting from Epistatic Loci Are the Primary Genetic Basis of Heterosis in Rice. Journal of Integrative Plant Biology, 2009, 51, 393-408.	8.5	51

#	ARTICLE	IF	CITATIONS
55	Construction of the physical map of the <i>gpa7</i> locus reveals that a large segment was deleted during rice domestication. <i>Plant Cell Reports</i> , 2008, 27, 1087-1092.	5.6	2
56	Construction of a bacterial artificial chromosome (BAC) library of common wild rice ( <i>Oryza</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 707 T Biotechnology Letters, 2008, 30, 555-561.	2.2	8
57	Control of a key transition from prostrate to erect growth in rice domestication. <i>Nature Genetics</i> , 2008, 40, 1360-1364.	21.4	411
58	Quantitative trait loci underlying domestication- and yield-related traits in an <i>Oryza sativa</i> — <i>Oryza rufipogon</i> advanced backcross population. <i>Genome</i> , 2008, 51, 692-704.	2.0	38
59	<i>TAC1</i> , a major quantitative trait locus controlling tiller angle in rice. <i>Plant Journal</i> , 2007, 52, 891-898.	5.7	281
60	Development of <i>Oryza rufipogon</i> and <i>O. sativa</i> Introgression Lines and Assessment for Yield-related Quantitative Trait Loci. <i>Journal of Integrative Plant Biology</i> , 2007, 49, 871-884.	8.5	84
61	Origin of seed shattering in rice ( <i>Oryza sativa</i> L.). <i>Planta</i> , 2007, 226, 11-20.	3.2	215
62	Identification of a Drought Tolerant Introgression Line Derived from Dongxiang Common Wild Rice ( <i>O. rufipogon</i> Griff.). <i>Plant Molecular Biology</i> , 2006, 62, 247-259.	3.9	140
63	Haplotype variation in structure and expression of a gene cluster associated with a quantitative trait locus for improved yield in rice. <i>Genome Research</i> , 2006, 16, 618-626.	5.5	105
64	Utilization of Diverse Rice Ecotypes in Heterosis Breeding.. <i>Breeding Science</i> , 2002, 52, 107-113.	1.9	4