

Chengzhi Liang

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1875108/publications.pdf>

Version: 2024-02-01

41
papers

7,739
citations

236925

25
h-index

289244

40
g-index

42
all docs

42
docs citations

42
times ranked

9818
citing authors

#	ARTICLE	IF	CITATIONS
1	Omics-based interdisciplinarity is accelerating plant breeding. <i>Current Opinion in Plant Biology</i> , 2022, 66, 102167.	7.1	26
2	Extensive sequence divergence between the reference genomes of <i>Taraxacum kok-saghyz</i> and <i>Taraxacum mongolicum</i> . <i>Science China Life Sciences</i> , 2022, 65, 515-528.	4.9	26
3	A chromosome-level genome assembly of the wild rice <i>Oryza rufipogon</i> facilitates tracing the origins of Asian cultivated rice. <i>Science China Life Sciences</i> , 2021, 64, 282-293.	4.9	24
4	A route to de novo domestication of wild allotetraploid rice. <i>Cell</i> , 2021, 184, 1156-1170.e14.	28.9	259
5	Forecasting rice latitude adaptation through a daylength-sensing-based environment adaptation simulator. <i>Nature Food</i> , 2021, 2, 348-362.	14.0	16
6	Pan-genome analysis of 33 genetically diverse rice accessions reveals hidden genomic variations. <i>Cell</i> , 2021, 184, 3542-3558.e16.	28.9	237
7	<i>Oryza</i> pan-genomics: A new foundation for future rice research and improvement. <i>Crop Journal</i> , 2021, 9, 622-632.	5.2	7
8	Long-read genome assembly and genetic architecture of fruit shape in the bottle gourd. <i>Plant Journal</i> , 2021, 107, 956-968.	5.7	23
9	A backbone parent contributes core genomic architecture to pedigree breeding of early-season indica rice. <i>Journal of Genetics and Genomics</i> , 2021, 48, 1040-1043.	3.9	3
10	Identification and fine mapping of qPBR10-1, a novel locus controlling panicle blast resistance in Pigm-containing P/TGMS line. <i>Molecular Breeding</i> , 2021, 41, 1.	2.1	2
11	MBKbase for rice: an integrated omics knowledgebase for molecular breeding in rice. <i>Nucleic Acids Research</i> , 2020, 48, D1085-D1092.	14.5	50
12	Evolution and Domestication Footprints Uncovered from the Genomes of Coix. <i>Molecular Plant</i> , 2020, 13, 295-308.	8.3	35
13	The Chromosome-Level Genome Sequence of the Autotetraploid Alfalfa and Resequencing of Core Germplasm Provide Genomic Resources for Alfalfa Research. <i>Molecular Plant</i> , 2020, 13, 1250-1261.	8.3	120
14	Genomic atlases of introgression and differentiation reveal breeding footprints in Chinese cultivated rice. <i>Journal of Genetics and Genomics</i> , 2020, 47, 637-649.	3.9	17
15	Pan-Genome of Wild and Cultivated Soybeans. <i>Cell</i> , 2020, 182, 162-176.e13.	28.9	508
16	Analysis of genetic architecture and favorable allele usage of agronomic traits in a large collection of Chinese rice accessions. <i>Science China Life Sciences</i> , 2020, 63, 1688-1702.	4.9	41
17	Systematic discovery of novel and valuable plant gene modules by large-scale RNA-seq samples. <i>Bioinformatics</i> , 2019, 35, 361-364.	4.1	6
18	Update soybean Zhonghuang 13 genome to a golden reference. <i>Science China Life Sciences</i> , 2019, 62, 1257-1260.	4.9	65

#	ARTICLE	IF	CITATIONS
19	Genome structure and evolution of <i>Antirrhinum majus</i> L. <i>Nature Plants</i> , 2019, 5, 174-183.	9.3	85
20	Cytosine, but not adenine, base editors induce genome-wide off-target mutations in rice. <i>Science</i> , 2019, 364, 292-295.	12.6	491
21	Assembly of chromosome-scale contigs by efficiently resolving repetitive sequences with long reads. <i>Nature Communications</i> , 2019, 10, 5360.	12.8	62
22	Dissecting the genetic basis of heavy panicle hybrid rice uncovered <i>Gn1a</i> and <i>GS3</i> as key genes. <i>Theoretical and Applied Genetics</i> , 2018, 131, 1391-1403.	3.6	17
23	Identification of Genes Related to Cold Tolerance and a Functional Allele That Confers Cold Tolerance. <i>Plant Physiology</i> , 2018, 177, 1108-1123.	4.8	68
24	De novo genome assembly of <i>Oryza granulata</i> reveals rapid genome expansion and adaptive evolution. <i>Communications Biology</i> , 2018, 1, 84.	4.4	24
25	Extensive intraspecific gene order and gene structural variations between Mo17 and other maize genomes. <i>Nature Genetics</i> , 2018, 50, 1289-1295.	21.4	335
26	Transcriptomics analyses reveal the molecular roadmap and long non-coding RNA landscape of sperm cell lineage development. <i>Plant Journal</i> , 2018, 96, 421-437.	5.7	15
27	Genome sequence of the progenitor of wheat A subgenome <i>Triticum urartu</i> . <i>Nature</i> , 2018, 557, 424-428.	27.8	354
28	NetMiner-an ensemble pipeline for building genome-wide and high-quality gene co-expression network using massive-scale RNA-seq samples. <i>PLoS ONE</i> , 2018, 13, e0192613.	2.5	41
29	Sequencing and de novo assembly of a near complete indica rice genome. <i>Nature Communications</i> , 2017, 8, 15324.	12.8	246
30	Development and Evaluation of Near-Isogenic Lines with Different Blast Resistance Alleles at the <i>Piz</i> Locus in <i>japonica</i> Rice from the Lower Region of the Yangtze River, China. <i>Plant Disease</i> , 2017, 101, 1283-1291.	1.4	11
31	The Tartary Buckwheat Genome Provides Insights into Rutin Biosynthesis and Abiotic Stress Tolerance. <i>Molecular Plant</i> , 2017, 10, 1224-1237.	8.3	254
32	Melatonin Regulates Root Architecture by Modulating Auxin Response in Rice. <i>Frontiers in Plant Science</i> , 2017, 8, 134.	3.6	134
33	Gene expression analysis and SNP/InDel discovery to investigate yield heterosis of two rubber tree F1 hybrids. <i>Scientific Reports</i> , 2016, 6, 24984.	3.3	30
34	Effects of drought and salt-stresses on gene expression in <i>Caragana korshinskii</i> seedlings revealed by RNA-seq. <i>BMC Genomics</i> , 2016, 17, 200.	2.8	47
35	Integrated analysis of phenome, genome, and transcriptome of hybrid rice uncovered multiple heterosis-related loci for yield increase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E6026-E6035.	7.1	126
36	Development of near-isogenic lines with different alleles of <i>Piz</i> locus and analysis of their breeding effect under Yangdao 6 background. <i>Molecular Breeding</i> , 2016, 36, 1.	2.1	22

#	ARTICLE	IF	CITATIONS
37	Improving of Rice Blast Resistances in Japonica by Pyramiding Major R Genes. <i>Frontiers in Plant Science</i> , 2016, 7, 1918.	3.6	62
38	Whole-genome sequencing of <i>Oryza brachyantha</i> reveals mechanisms underlying <i>Oryza</i> genome evolution. <i>Nature Communications</i> , 2013, 4, 1595.	12.8	190
39	Evidence-based gene predictions in plant genomes. <i>Genome Research</i> , 2009, 19, 1912-1923.	5.5	44
40	The B73 Maize Genome: Complexity, Diversity, and Dynamics. <i>Science</i> , 2009, 326, 1112-1115.	12.6	3,612
41	A Catalog of Structural and Gene Copy Number Variations of Cultivated Rice. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1