

Jianwei Zhang

List of Publications by Year in descending order

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42
papers

7,980
citations

186209

28
h-index

243529

44
g-index

50
all docs

50
docs citations

50
times ranked

10277
citing authors

#	ARTICLE	IF	CITATIONS
1	The B73 Maize Genome: Complexity, Diversity, and Dynamics. <i>Science</i> , 2009, 326, 1112-1115.	6.0	3,612
2	Genomic variation in 3,010 diverse accessions of Asian cultivated rice. <i>Nature</i> , 2018, 557, 43-49.	13.7	1,091
3	Genomes of 13 domesticated and wild rice relatives highlight genetic conservation, turnover and innovation across the genus <i>Oryza</i> . <i>Nature Genetics</i> , 2018, 50, 285-296.	9.4	413
4	Genome-Wide Prediction of Highly Specific Guide RNA Spacers for CRISPR-Cas9-Mediated Genome Editing in Model Plants and Major Crops. <i>Molecular Plant</i> , 2014, 7, 923-926.	3.9	277
5	Extensive sequence divergence between the reference genomes of two elite <i>indica</i> rice varieties Zhenshan 97 and Minghui 63. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E5163-71.	3.3	211
6	RMD: a rice mutant database for functional analysis of the rice genome. <i>Nucleic Acids Research</i> , 2006, 34, D745-D748.	6.5	200
7	Identification and analysis of adenine N6-methylation sites in the rice genome. <i>Nature Plants</i> , 2018, 4, 554-563.	4.7	177
8	Expression Profiles of 10,422 Genes at Early Stage of Low Nitrogen Stress in Rice Assayed using a cDNA Microarray. <i>Plant Molecular Biology</i> , 2006, 60, 617-631.	2.0	167
9	A single-nucleotide polymorphism causes smaller grain size and loss of seed shattering during African rice domestication. <i>Nature Plants</i> , 2017, 3, 17064.	4.7	133
10	Two gap-free reference genomes and a global view of the centromere architecture in rice. <i>Molecular Plant</i> , 2021, 14, 1757-1767.	3.9	133
11	Rapid evolution of protein diversity by de novo origination in <i>Oryza</i> . <i>Nature Ecology and Evolution</i> , 2019, 3, 679-690.	3.4	121
12	Non-random distribution of T-DNA insertions at various levels of the genome hierarchy as revealed by analyzing 13,804 T-DNA flanking sequences from an enhancer-trap mutant library. <i>Plant Journal</i> , 2007, 49, 947-959.	2.8	107
13	Heterosis and polymorphisms of gene expression in an elite rice hybrid as revealed by a microarray analysis of 9198 unique ESTs. <i>Plant Molecular Biology</i> , 2006, 62, 579-591.	2.0	104
14	The Physical and Genetic Framework of the Maize B73 Genome. <i>PLoS Genetics</i> , 2009, 5, e1000715.	1.5	95
15	Young inversion with multiple linked QTLs under selection in a hybrid zone. <i>Nature Ecology and Evolution</i> , 2017, 1, 119.	3.4	94
16	Aflatoxin-free transgenic maize using host-induced gene silencing. <i>Science Advances</i> , 2017, 3, e1602382.	4.7	88
17	RiTE database: a resource database for genus-wide rice genomics and evolutionary biology. <i>BMC Genomics</i> , 2015, 16, 538.	1.2	86
18	A platinum standard pan-genome resource that represents the population structure of Asian rice. <i>Scientific Data</i> , 2020, 7, 113.	2.4	86

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19	Genome-wide association mapping of date palm fruit traits. <i>Nature Communications</i> , 2019, 10, 4680.	5.8	75
20	ABC transporter mis-splicing associated with resistance to Bt toxin Cry2Ab in laboratory- and field-selected pink bollworm. <i>Scientific Reports</i> , 2018, 8, 13531.	1.6	66
21	A chromosome-scale assembly of allotetraploid <i>Brassica juncea</i> (AABB) elucidates comparative architecture of the A and B genomes. <i>Plant Biotechnology Journal</i> , 2021, 19, 602-614.	4.1	62
22	CRISPR-PLANT v2: an online resource for highly specific guide RNA spacers based on improved off-target analysis. <i>Plant Biotechnology Journal</i> , 2019, 17, 5-8.	4.1	60
23	The chromosome-scale reference genome of safflower (<i>Carthamus tinctorius</i>) provides insights into linoleic acid and flavonoid biosynthesis. <i>Plant Biotechnology Journal</i> , 2021, 19, 1725-1742.	4.1	60
24	Genetic control of seed shattering during African rice domestication. <i>Nature Plants</i> , 2018, 4, 331-337.	4.7	55
25	Features of the expressed sequences revealed by a large-scale analysis of ESTs from a normalized cDNA library of the elite indica rice cultivar Minghui 63. <i>Plant Journal</i> , 2005, 42, 772-780.	2.8	39
26	Detailed Analysis of a Contiguous 22-Mb Region of the Maize Genome. <i>PLoS Genetics</i> , 2009, 5, e1000728.	1.5	39
27	Building two indica rice reference genomes with PacBio long-read and Illumina paired-end sequencing data. <i>Scientific Data</i> , 2016, 3, 160076.	2.4	34
28	Establishment of a patterned GAL4-VP16 transactivation system for discovering gene function in rice. <i>Plant Journal</i> , 2006, 46, 1059-1072.	2.8	33
29	Rice Information GateWay: A Comprehensive Bioinformatics Platform for Indica Rice Genomes. <i>Molecular Plant</i> , 2018, 11, 505-507.	3.9	33
30	Sequencing and comparative analyses of <i>Aegilops tauschii</i> chromosome arm 3DS reveal rapid evolution of Triticeae genomes. <i>Journal of Genetics and Genomics</i> , 2017, 44, 51-61.	1.7	25
31	Conservation and Purifying Selection of Transcribed Genes Located in a Rice Centromere. <i>Plant Cell</i> , 2011, 23, 2821-2830.	3.1	22
32	Genome puzzle master (GPM): an integrated pipeline for building and editing pseudomolecules from fragmented sequences. <i>Bioinformatics</i> , 2016, 32, 3058-3064.	1.8	22
33	Development of species diagnostic SNP markers for quality control genotyping in four rice (<i>Oryza L.</i>) species. <i>Molecular Breeding</i> , 2018, 38, 131.	1.0	22
34	Isolation and annotation of 10828 putative full length cDNAs from indica rice. <i>Science in China Series C: Life Sciences</i> , 2005, 48, 445.	1.3	17
35	Evolution and diversity of the wild rice <i>Oryza officinalis</i> complex, across continents genome types, and ploidy levels. <i>Genome Biology and Evolution</i> , 2020, 12, 413-428.	1.1	17
36	DNA methylation changes facilitated evolution of genes derived from Mutator-like transposable elements. <i>Genome Biology</i> , 2016, 17, 92.	3.8	14

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37	Single feature polymorphisms between two rice cultivars detected using a median polish method. <i>Theoretical and Applied Genetics</i> , 2009, 119, 151-164.	1.8	13
38	Identification of Novel Stress-responsive Transcription Factor Genes in Rice by cDNA Array Analysis. <i>Journal of Integrative Plant Biology</i> , 2006, 48, 1216-1224.	4.1	10
39	Global Genomic Diversity of <i>Oryza sativa</i> Varieties Revealed by Comparative Physical Mapping. <i>Genetics</i> , 2014, 196, 937-949.	1.2	10
40	Phasing analysis of the transcriptome and epigenome in a rice hybrid reveals the inheritance and difference in DNA methylation and allelic transcription regulation. <i>Plant Communications</i> , 2021, 2, 100185.	3.6	10
41	Genome assembly of the JD17 soybean provides a new reference genome for comparative genomics. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	7
42	Full-Length Transcriptome Sequencing Reveals Alternative Splicing and lncRNA Regulation during Nodule Development in <i>Glycine max</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 7371.	1.8	6