

Jianzhong Wu

List of Publications by Year in descending order

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Version: 2024-02-01

91
papers

12,103
citations

70961

41
h-index

48187

88
g-index

92
all docs

92
docs citations

92
times ranked

11835
citing authors

#	ARTICLE	IF	CITATIONS
1	Shifting the limits in wheat research and breeding using a fully annotated reference genome. <i>Science</i> , 2018, 361, .	6.0	2,424
2	Improvement of the <i>Oryza sativa</i> Nipponbare reference genome using next generation sequence and optical map data. <i>Rice</i> , 2013, 6, 4.	1.7	1,777
3	Control of root system architecture by DEEPER ROOTING 1 increases rice yield under drought conditions. <i>Nature Genetics</i> , 2013, 45, 1097-1102.	9.4	1,134
4	The ethylene response factors SNORKEL1 and SNORKEL2 allow rice to adapt to deep water. <i>Nature</i> , 2009, 460, 1026-1030.	13.7	840
5	The genome sequence and structure of rice chromosome 1. <i>Nature</i> , 2002, 420, 312-316.	13.7	519
6	Multiple wheat genomes reveal global variation in modern breeding. <i>Nature</i> , 2020, 588, 277-283.	13.7	513
7	Two Adjacent Nucleotide-Binding Site-“Leucine-Rich Repeat Class Genes Are Required to Confer <i>Pikm</i> -Specific Rice Blast Resistance. <i>Genetics</i> , 2008, 180, 2267-2276.	1.2	330
8	The Rice Annotation Project Database (RAP-DB): 2008 update. <i>Nucleic Acids Research</i> , 2007, 36, D1028-D1033.	6.5	295
9	A Comprehensive Rice Transcript Map Containing 6591 Expressed Sequence Tag Sites. <i>Plant Cell</i> , 2002, 14, 525-535.	3.1	260
10	Ethylene-gibberellin signaling underlies adaptation of rice to periodic flooding. <i>Science</i> , 2018, 361, 181-186.	6.0	188
11	A natural variant of NAL1, selected in high-yield rice breeding programs, pleiotropically increases photosynthesis rate. <i>Scientific Reports</i> , 2013, 3, 2149.	1.6	181
12	Artificial selection for a green revolution gene during <i>japonica</i> rice domestication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 11034-11039.	3.3	179
13	A Causal Gene for Seed Dormancy on Wheat Chromosome 4A Encodes a MAP Kinase Kinase. <i>Current Biology</i> , 2016, 26, 782-787.	1.8	152
14	Genetic control of inflorescence architecture during rice domestication. <i>Nature Communications</i> , 2013, 4, 2200.	5.8	134
15	Root angle modifications by the <i>DRO1</i> homolog improve rice yields in saline paddy fields. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 21242-21250.	3.3	134
16	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
17	The isolation of Pi1, an allele at the <i>Pik</i> locus which confers broad spectrum resistance to rice blast. <i>Theoretical and Applied Genetics</i> , 2012, 125, 1047-1055.	1.8	129
18	Mitochondrial gene in the nuclear genome induces reproductive barrier in rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 1494-1499.	3.3	128

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19	Physical maps and recombination frequency of six rice chromosomes. <i>Plant Journal</i> , 2003, 36, 720-730.	2.8	126
20	Composition and Structure of the Centromeric Region of Rice Chromosome 8[W]. <i>Plant Cell</i> , 2004, 16, 967-976.	3.1	122
21	Localization of anchor loci representing five hundred annotated rice genes to wheat chromosomes using PLUG markers. <i>Theoretical and Applied Genetics</i> , 2009, 118, 499-514.	1.8	116
22	Gain of deleterious function causes an autoimmune response and Batesonâ€“Dobzhanskyâ€“Muller incompatibility in rice. <i>Molecular Genetics and Genomics</i> , 2010, 283, 305-315.	1.0	103
23	Genome-Wide Transcriptome Analysis Reveals that Cadmium Stress Signaling Controls the Expression of Genes in Drought Stress Signal Pathways in Rice. <i>PLoS ONE</i> , 2014, 9, e96946.	1.1	102
24	Antagonistic regulation of the gibberellic acid response during stem growth in rice. <i>Nature</i> , 2020, 584, 109-114.	13.7	98
25	Natural Variation of the RICE FLOWERING LOCUS T 1 Contributes to Flowering Time Divergence in Rice. <i>PLoS ONE</i> , 2013, 8, e75959.	1.1	94
26	Loss of function at <i>RAE2</i> , a previously unidentified EPFL, is required for awnlessness in cultivated Asian rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 8969-8974.	3.3	94
27	Mitogen-Activated Protein Kinase Kinase 3 Regulates Seed Dormancy in Barley. <i>Current Biology</i> , 2016, 26, 775-781.	1.8	85
28	Massive parallel sequencing of mRNA in identification of unannotated salinity stress-inducible transcripts in rice (<i>Oryza sativa</i> L.). <i>BMC Genomics</i> , 2010, 11, 683.	1.2	76
29	Construction of Pseudomolecule Sequences of the aus Rice Cultivar Kasalath for Comparative Genomics of Asian Cultivated Rice. <i>DNA Research</i> , 2014, 21, 397-405.	1.5	74
30	Independent Domestication of Asian Rice Followed by Gene Flow from japonica to indica. <i>Molecular Biology and Evolution</i> , 2012, 29, 1471-1479.	3.5	70
31	Uncovering of major genetic factors generating naturally occurring variation in heading date among Asian rice cultivars. <i>Theoretical and Applied Genetics</i> , 2011, 122, 1199-1210.	1.8	65
32	Population Genomic Analysis and De Novo Assembly Reveal the Origin of Weedy Rice as an Evolutionary Game. <i>Molecular Plant</i> , 2019, 12, 632-647.	3.9	61
33	Sequencing and characterization of telomere and subtelomere regions on rice chromosomes 1S, 2S, 2L, 6L, 7S, 7L and 8S. <i>Plant Journal</i> , 2006, 46, 206-217.	2.8	60
34	Diversity in the complexity of phosphate starvation transcriptomes among rice cultivars based on RNA-Seq profiles. <i>Plant Molecular Biology</i> , 2013, 83, 523-537.	2.0	59
35	Genomics Approach to Abscisic Acid- and Gibberellin-responsive Genes in Rice. <i>DNA Research</i> , 2003, 10, 249-261.	1.5	57
36	Characterization of a mini core collection of Japanese wheat varieties using single-nucleotide polymorphisms generated by genotyping-by-sequencing. <i>Breeding Science</i> , 2016, 66, 213-225.	0.9	57

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37	Physical Mapping of Duplicated Genomic Regions of Two Chromosome Ends in Rice. <i>Genetics</i> , 1998, 150, 1595-1603.	1.2	57
38	Multiple introgression events surrounding the Hd1 flowering-time gene in cultivated rice, <i>Oryza sativa</i> L.. <i>Molecular Genetics and Genomics</i> , 2010, 284, 137-146.	1.0	51
39	A physical map with yeast artificial chromosome (YAC) clones covering 63% of the 12 rice chromosomes. <i>Genome</i> , 2001, 44, 32-37.	0.9	50
40	<i>Hd18</i> , Encoding Histone Acetylase Related to Arabidopsis FLOWERING LOCUS D, is Involved in the Control of Flowering Time in Rice. <i>Plant and Cell Physiology</i> , 2016, 57, 1828-1838.	1.5	47
41	mRNA-Seq Reveals a Comprehensive Transcriptome Profile of Rice under Phosphate Stress. <i>Rice</i> , 2011, 4, 50-65.	1.7	45
42	Next-Generation Survey Sequencing and the Molecular Organization of Wheat Chromosome 6B. <i>DNA Research</i> , 2014, 21, 103-114.	1.5	45
43	Random sheared fosmid library as a new genomic tool to accelerate complete finishing of rice (<i>Oryza</i>) Tj ETQq1 1 0.784314 rgBT /Overlapped euchromatic portions of the genome. <i>Theoretical and Applied Genetics</i> , 2005, 111, 1596-1607.	1.8	36
44	The Sorghum Gene for Leaf Color Changes upon Wounding (<i>P</i>) Encodes a Flavanone 4-Reductase in the 3-Deoxyanthocyanidin Biosynthesis Pathway. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 1439-1447.	0.8	36
45	Duplication and Loss of Function of Genes Encoding RNA Polymerase III Subunit C4 Causes Hybrid Incompatibility in Rice. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2565-2575.	0.8	36
46	Genomic adaptation of flowering-time genes during the expansion of rice cultivation area. <i>Plant Journal</i> , 2018, 94, 895-909.	2.8	35
47	Positional cloning of ds1, the target leaf spot resistance gene against <i>Bipolaris sorghicola</i> in sorghum. <i>Theoretical and Applied Genetics</i> , 2011, 123, 131-142.	1.8	32
48	Improvement of barley genome annotations by deciphering the Haruna Nijo genome. <i>DNA Research</i> , 2016, 23, dsv033.	1.5	32
49	Convergent Loss of Awn in Two Cultivated Rice Species <i>Oryza sativa</i> and <i>Oryza glaberrima</i> Is Caused by Mutations in Different Loci. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 2267-2274.	0.8	31
50	Characterization of the rice blast resistance gene <i>Pik</i> cloned from Kanto51. <i>Molecular Breeding</i> , 2012, 30, 485-494.	1.0	30
51	The Nipponbare genome and the next-generation of rice genomics research in Japan. <i>Rice</i> , 2016, 9, 33.	1.7	29
52	End Sequencing and Chromosomal <i>in silico</i> Mapping of BAC Clones Derived from an <i>indica</i> Rice Cultivar, Kasalath. <i>Breeding Science</i> , 2004, 54, 273-279.	0.9	29
53	Distinct evolutionary patterns of <i>Oryza glaberrima</i> deciphered by genome sequencing and comparative analysis. <i>Plant Journal</i> , 2011, 66, 796-805.	2.8	28
54	Structure, transcription and post-transcriptional regulation of the bread wheat orthologs of the barley cleistogamy gene <i>Cly1</i> . <i>Theoretical and Applied Genetics</i> , 2013, 126, 1273-1283.	1.8	27

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55	miR172 downregulates the translation of cleistogamy 1 in barley. <i>Annals of Botany</i> , 2018, 122, 251-265.	1.4	25
56	Genome-wide indel markers shared by diverse Asian rice cultivars compared to Japanese rice cultivar "Koshihikari". <i>Breeding Science</i> , 2015, 65, 249-256.	0.9	24
57	Genomic organization of 57 ribosomal protein genes in rice (<i>Oryza sativa</i> L.) through RFLP mapping. <i>Genome</i> , 1995, 38, 1189-1200.	0.9	23
58	Fine Mapping of HWC2, a Complementary Hybrid Weakness Gene, and Haplotype Analysis Around the Locus in Rice. <i>Rice</i> , 2009, 2, 93-103.	1.7	22
59	Comparative analysis of complete orthologous centromeres from two subspecies of rice reveals rapid variation of centromere organization and structure. <i>Plant Journal</i> , 2009, 60, 805-819.	2.8	22
60	Expression level of a flavonoid 3-hydroxylase gene determines pathogen-induced color variation in sorghum. <i>BMC Research Notes</i> , 2014, 7, 761.	0.6	22
61	An Epiallele at <i>cly1</i> Affects the Expression of Floret Closing (Cleistogamy) in Barley. <i>Genetics</i> , 2015, 199, 95-104.	1.2	22
62	Evolutionary dynamics and impacts of chromosome regions carrying R-gene clusters in rice. <i>Scientific Reports</i> , 2020, 10, 872.	1.6	22
63	Sequence comparison of distal and proximal ribosomal DNA arrays in rice (<i>Oryza sativa</i> L.) chromosome 9S and analysis of their flanking regions. <i>Theoretical and Applied Genetics</i> , 2006, 113, 419-428.	1.8	18
64	Identification and Mapping of Expressed Genes, Simple Sequence Repeats and Transposable Elements in Centromeric Regions of Rice Chromosomes. <i>DNA Research</i> , 2006, 13, 267-274.	1.5	18
65	DaizuBase, an integrated soybean genome database including BAC-based physical maps. <i>Breeding Science</i> , 2012, 61, 661-664.	0.9	18
66	A high-resolution physical map integrating an anchored chromosome with the BAC physical maps of wheat chromosome 6B. <i>BMC Genomics</i> , 2015, 16, 595.	1.2	18
67	Chromosome-Specific Distribution of Nucleotide Substitutions in Telomeric Repeats of Rice (<i>Oryza</i>) Tj ETQq1 1 0.784314 rgBT /Overl 3.5 17		
68	Structural features of two major nucleolar organizer regions (NORs), <i>NorB1</i> and <i>NorB2</i> , and chromosome-specific rRNA gene expression in wheat. <i>Plant Journal</i> , 2018, 96, 1148-1159.	2.8	17
69	Sequence differences in the seed dormancy gene <i>Qsd1</i> among various wheat genomes. <i>BMC Genomics</i> , 2017, 18, 497.	1.2	16
70	Asymmetric Distribution of Gene Expression in the Centromeric Region of Rice Chromosome 5. <i>Frontiers in Plant Science</i> , 2011, 2, 16.	1.7	15
71	Investigation of the Genetic Diversity of a Rice Core Collection of Japanese Landraces using Whole-Genome Sequencing. <i>Plant and Cell Physiology</i> , 2021, 61, 2087-2096.	1.5	15
72	A fine physical map of the rice chromosome 5. <i>Molecular Genetics and Genomics</i> , 2005, 274, 337-345.	1.0	14

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73	A BAC physical map of <i>aus</i> rice cultivar <i>Kasalath</i> TM , and the map-based genomic sequence of <i>Kasalath</i> TM chromosome 1. <i>Plant Journal</i> , 2013, 76, 699-708.	2.8	13
74	SNORKEL Genes Relating to Flood Tolerance Were Pseudogenized in Normal Cultivated Rice. <i>Plants</i> , 2022, 11, 376.	1.6	13
75	Characterization of chromosome ends on the basis of the structure of TrsA subtelomeric repeats in rice (<i>Oryza sativa</i> L.). <i>Molecular Genetics and Genomics</i> , 2008, 280, 19-24.	1.0	12
76	Molecular and Evolutionary Analysis of the Hd6 Photoperiod Sensitivity Gene Within Genus <i>Oryza</i> . <i>Rice</i> , 2009, 2, 56-66.	1.7	11
77	Haplotype diversity and molecular evolution of the rice <i>Pikm</i> locus for blast resistance. <i>Journal of General Plant Pathology</i> , 2010, 76, 37-42.	0.6	9
78	Development in Rice Genome Research Based on Accurate Genome Sequence. <i>International Journal of Plant Genomics</i> , 2008, 2008, 1-9.	2.2	8
79	Multiple Wheat Genomes Reveal Novel Gli-2 Sublocus Location and Variation of Celiac Disease Epitopes in Duplicated \pm -Gliadin Genes. <i>Frontiers in Plant Science</i> , 2021, 12, 715985.	1.7	7
80	Comparative Analysis of Rice Genome Sequence to Understand the Molecular Basis of Genome Evolution. <i>Rice</i> , 2008, 1, 119-126.	1.7	6
81	Composition and Structure of Rice Centromeres and Telomeres. , 2018, , 37-52.		6
82	Domain Unknown Function DUF1668-Containing Genes in Multiple Lineages Are Responsible for F1 Pollen Sterility in Rice. <i>Frontiers in Plant Science</i> , 2020, 11, 632420.	1.7	6
83	bex-db: Bioinformatics workbench for comprehensive analysis of barley-expressed genes. <i>Breeding Science</i> , 2013, 63, 430-434.	0.9	5
84	Rice Genomics: Current Status of Genome Sequencing. <i>Novartis Foundation Symposium</i> , 2001, 236, 28-45.	1.2	4
85	Characterization of Chromosomal Ends on the Basis of Chromosome-Specific Telomere Variants and Subtelomeric Repeats in Rice (<i>Oryza sativa</i> L.). , 2014, , 187-194.		4
86	The Rice Genome Sequence as an Indispensable Tool for Crop Improvement. <i>Biotechnology in Agriculture and Forestry</i> , 2008, , 3-12.	0.2	2
87	Completion of Rice Genome Sequencing. <i>Japan Agricultural Research Quarterly</i> , 2006, 40, 99-105.	0.1	1
88	Reference Genome Sequencing and Advances in Genomic Resources in Common Wheatâ€“Chromosome 6B Project in Japan. <i>Japan Agricultural Research Quarterly</i> , 2021, 55, 285-294.	0.1	1
89	Fine mapping of <i>Rf5</i> region for a sorghum fertility restorer gene and microsynteny analysis across grass species. <i>Breeding Science</i> , 2022, 72, 141-149.	0.9	1
90	Rice Genetics and Genomics Information as the Ultimate Tool for Rice Improvement. , 2007, , 475-485.		0

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91	Sequencing of Wheat Chromosome 6B: Toward Functional Genomics. , 2015, , 111-116.		0