

Jianzhong Wu

List of Publications by Year in descending order

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91
papers

12,103
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71102

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88
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all docs

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docs citations

92
times ranked

11835
citing authors

#	ARTICLE	IF	CITATIONS
1	SNORKEL Genes Relating to Flood Tolerance Were Pseudogenized in Normal Cultivated Rice. <i>Plants</i> , 2022, 11, 376.	3.5	13
2	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.	1.9	1
3	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.	3.1	15
4	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.	3.6	7
5	Reference Genome Sequencing and Advances in Genomic Resources in Common Wheat—“Chromosome 6B Project in Japan. <i>Japan Agricultural Research Quarterly</i> , 2021, 55, 285-294.	0.4	1
6	Antagonistic regulation of the gibberellic acid response during stem growth in rice. <i>Nature</i> , 2020, 584, 109-114.	27.8	98
7	Multiple wheat genomes reveal global variation in modern breeding. <i>Nature</i> , 2020, 588, 277-283.	27.8	513
8	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.	7.1	134
9	Evolutionary dynamics and impacts of chromosome regions carrying R-gene clusters in rice. <i>Scientific Reports</i> , 2020, 10, 872.	3.3	22
10	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.	3.6	6
11	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.	8.3	61
12	Composition and Structure of Rice Centromeres and Telomeres. , 2018, , 37-52.		6
13	Genomic adaptation of flowering-time genes during the expansion of rice cultivation area. <i>Plant Journal</i> , 2018, 94, 895-909.	5.7	35
14	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.	5.7	17
15	miR172 downregulates the translation of cleistogamy 1 in barley. <i>Annals of Botany</i> , 2018, 122, 251-265.	2.9	25
16	Ethylene-gibberellin signaling underlies adaptation of rice to periodic flooding. <i>Science</i> , 2018, 361, 181-186.	12.6	188
17	Shifting the limits in wheat research and breeding using a fully annotated reference genome. <i>Science</i> , 2018, 361, .	12.6	2,424
18	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

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19	Duplication and Loss of Function of Genes Encoding RNA Polymerase III Subunit C4 Causes Hybrid Incompatibility in Rice. G3: Genes, Genomes, Genetics, 2017, 7, 2565-2575.	1.8	36
20	Sequence differences in the seed dormancy gene Qsd1 among various wheat genomes. BMC Genomics, 2017, 18, 497.	2.8	16
21	Improvement of barley genome annotations by deciphering the Haruna Nijo genome. DNA Research, 2016, 23, dsv033.	3.4	32
22	Characterization of a mini core collection of Japanese wheat varieties using single-nucleotide polymorphisms generated by genotyping-by-sequencing. Breeding Science, 2016, 66, 213-225.	1.9	57
23	The Sorghum Gene for Leaf Color Changes upon Wounding (<i>PtGL3</i>) Encodes a Flavanone 4-Reductase in the 3-Deoxyanthocyanidin Biosynthesis Pathway. G3: Genes, Genomes, Genetics, 2016, 6, 1439-1447.	1.8	36
24	Loss of function at <i>RAE2</i> , a previously unidentified EPFL, is required for awnlessness in cultivated Asian rice. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 8969-8974.	7.1	94
25	The Nipponbare genome and the next-generation of rice genomics research in Japan. Rice, 2016, 9, 33.	4.0	29
26	<i>Hd18</i> , Encoding Histone Acetylase Related to Arabidopsis FLOWERING LOCUS D, is Involved in the Control of Flowering Time in Rice. Plant and Cell Physiology, 2016, 57, 1828-1838.	3.1	47
27	A Causal Gene for Seed Dormancy on Wheat Chromosome 4A Encodes a MAP Kinase Kinase. Current Biology, 2016, 26, 782-787.	3.9	152
28	Mitogen-Activated Protein Kinase Kinase 3 Regulates Seed Dormancy in Barley. Current Biology, 2016, 26, 775-781.	3.9	85
29	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. G3: Genes, Genomes, Genetics, 2015, 5, 2267-2274.	1.8	31
30	An Epiallele at <i>cly1</i> Affects the Expression of Floret Closing (Cleistogamy) in Barley. Genetics, 2015, 199, 95-104.	2.9	22
31	A high-resolution physical map integrating an anchored chromosome with the BAC physical maps of wheat chromosome 6B. BMC Genomics, 2015, 16, 595.	2.8	18
32	Genome-wide indel markers shared by diverse Asian rice cultivars compared to Japanese rice cultivar 'Koshihikari'. Breeding Science, 2015, 65, 249-256.	1.9	24
33	Sequencing of Wheat Chromosome 6B: Toward Functional Genomics. , 2015, , 111-116.		0
34	Genome-Wide Transcriptome Analysis Reveals that Cadmium Stress Signaling Controls the Expression of Genes in Drought Stress Signal Pathways in Rice. PLoS ONE, 2014, 9, e96946.	2.5	102
35	Expression level of a flavonoid 3-hydroxylase gene determines pathogen-induced color variation in sorghum. BMC Research Notes, 2014, 7, 761.	1.4	22
36	Construction of Pseudomolecule Sequences of the aus Rice Cultivar Kasalath for Comparative Genomics of Asian Cultivated Rice. DNA Research, 2014, 21, 397-405.	3.4	74

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37	Next-Generation Survey Sequencing and the Molecular Organization of Wheat Chromosome 6B. DNA Research, 2014, 21, 103-114.	3.4	45
38	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
39	Diversity in the complexity of phosphate starvation transcriptomes among rice cultivars based on RNA-Seq profiles. Plant Molecular Biology, 2013, 83, 523-537.	3.9	59
40	Control of root system architecture by DEEPER ROOTING 1 increases rice yield under drought conditions. Nature Genetics, 2013, 45, 1097-1102.	21.4	1,134
41	Structure, transcription and post-transcriptional regulation of the bread wheat orthologs of the barley cleistogamy gene <i>Cly1</i> . Theoretical and Applied Genetics, 2013, 126, 1273-1283.	3.6	27
42	Improvement of the <i>Oryza sativa</i> Nipponbare reference genome using next generation sequence and optical map data. Rice, 2013, 6, 4.	4.0	1,777
43	A <i>BAC</i> 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. Plant Journal, 2013, 76, 699-708.	5.7	13
44	bex-db: Bioinformatics workbench for comprehensive analysis of barley-expressed genes. Breeding Science, 2013, 63, 430-434.	1.9	5
45	Genetic control of inflorescence architecture during rice domestication. Nature Communications, 2013, 4, 2200.	12.8	134
46	A natural variant of <i>NAL1</i> , selected in high-yield rice breeding programs, pleiotropically increases photosynthesis rate. Scientific Reports, 2013, 3, 2149.	3.3	181
47	Natural Variation of the <i>RICE FLOWERING LOCUS T 1</i> Contributes to Flowering Time Divergence in Rice. PLoS ONE, 2013, 8, e75959.	2.5	94
48	DaizuBase, an integrated soybean genome database including <i>BAC</i> -based physical maps. Breeding Science, 2012, 61, 661-664.	1.9	18
49	Independent Domestication of Asian Rice Followed by Gene Flow from japonica to indica. Molecular Biology and Evolution, 2012, 29, 1471-1479.	8.9	70
50	The isolation of <i>Pi1</i> , an allele at the <i>Pik</i> locus which confers broad spectrum resistance to rice blast. Theoretical and Applied Genetics, 2012, 125, 1047-1055.	3.6	129
51	Characterization of the rice blast resistance gene <i>Pik</i> cloned from Kanto51. Molecular Breeding, 2012, 30, 485-494.	2.1	30
52	Artificial selection for a green revolution gene during <i>japonica</i> rice domestication. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 11034-11039.	7.1	179
53	Asymmetric Distribution of Gene Expression in the Centromeric Region of Rice Chromosome 5. Frontiers in Plant Science, 2011, 2, 16.	3.6	15
54	Distinct evolutionary patterns of <i>Oryza glaberrima</i> deciphered by genome sequencing and comparative analysis. Plant Journal, 2011, 66, 796-805.	5.7	28

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55	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.	3.6	65
56	Positional cloning of <i>ds1</i> , the target leaf spot resistance gene against <i>Bipolaris sorghicola</i> in sorghum. <i>Theoretical and Applied Genetics</i> , 2011, 123, 131-142.	3.6	32
57	mRNA-Seq Reveals a Comprehensive Transcriptome Profile of Rice under Phosphate Stress. <i>Rice</i> , 2011, 4, 50-65.	4.0	45
58	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.	2.1	103
59	Multiple introgression events surrounding the <i>Hd1</i> flowering-time gene in cultivated rice, <i>Oryza sativa</i> L.. <i>Molecular Genetics and Genomics</i> , 2010, 284, 137-146.	2.1	51
60	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.	1.0	9
61	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.	2.8	76
62	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.	7.1	128
63	Molecular and Evolutionary Analysis of the <i>Hd6</i> Photoperiod Sensitivity Gene Within Genus <i>Oryza</i> . <i>Rice</i> , 2009, 2, 56-66.	4.0	11
64	Fine Mapping of <i>HWC2</i> , a Complementary Hybrid Weakness Gene, and Haplotype Analysis Around the Locus in Rice. <i>Rice</i> , 2009, 2, 93-103.	4.0	22
65	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.	3.6	116
66	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.	5.7	22
67	The ethylene response factors <i>SNORKEL1</i> and <i>SNORKEL2</i> allow rice to adapt to deep water. <i>Nature</i> , 2009, 460, 1026-1030.	27.8	840
68	Comparative Analysis of Rice Genome Sequence to Understand the Molecular Basis of Genome Evolution. <i>Rice</i> , 2008, 1, 119-126.	4.0	6
69	Characterization of chromosome ends on the basis of the structure of <i>TrsA</i> subtelomeric repeats in rice (<i>Oryza sativa</i> L.). <i>Molecular Genetics and Genomics</i> , 2008, 280, 19-24.	2.1	12
70	The Rice Genome Sequence as an Indispensable Tool for Crop Improvement. <i>Biotechnology in Agriculture and Forestry</i> , 2008, , 3-12.	0.2	2
71	Two Adjacent Nucleotide-Binding Siteâ€“Leucine-Rich Repeat Class Genes Are Required to Confer <i>Pikm</i> -Specific Rice Blast Resistance. <i>Genetics</i> , 2008, 180, 2267-2276.	2.9	330
72	Development in Rice Genome Research Based on Accurate Genome Sequence. <i>International Journal of Plant Genomics</i> , 2008, 2008, 1-9.	2.2	8

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73	The Rice Annotation Project Database (RAP-DB): 2008 update. Nucleic Acids Research, 2007, 36, D1028-D1033.	14.5	295
74	Chromosome-Specific Distribution of Nucleotide Substitutions in Telomeric Repeats of Rice (<i>Oryza</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	8.9	17
75	Rice Genetics and Genomics Information as the Ultimate Tool for Rice Improvement. , 2007, , 475-485.		0
76	Sequencing and characterization of telomere and subtelomere regions on rice chromosomes 1S, 2S, 2L, 6L, 7S, 7L and 8S. Plant Journal, 2006, 46, 206-217.	5.7	60
77	Sequence comparison of distal and proximal ribosomal DNA arrays in rice (<i>Oryza sativa</i> L.) chromosome 9S and analysis of their flanking regions. Theoretical and Applied Genetics, 2006, 113, 419-428.	3.6	18
78	Identification and Mapping of Expressed Genes, Simple Sequence Repeats and Transposable Elements in Centromeric Regions of Rice Chromosomes. DNA Research, 2006, 13, 267-274.	3.4	18
79	Completion of Rice Genome Sequencing. Japan Agricultural Research Quarterly, 2006, 40, 99-105.	0.4	1
80	Random sheared fosmid library as a new genomic tool to accelerate complete finishing of rice (<i>Oryza</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 euchromatic portions of the genome. Theoretical and Applied Genetics, 2005, 111, 1596-1607.	3.6	36
81	A fine physical map of the rice chromosome 5. Molecular Genetics and Genomics, 2005, 274, 337-345.	2.1	14
82	Composition and Structure of the Centromeric Region of Rice Chromosome 8[W]. Plant Cell, 2004, 16, 967-976.	6.6	122
83	End Sequencing and Chromosomal <i>in silico</i> Mapping of BAC Clones Derived from an <i>indica</i> Rice Cultivar, Kasalath. Breeding Science, 2004, 54, 273-279.	1.9	29
84	Physical maps and recombination frequency of six rice chromosomes. Plant Journal, 2003, 36, 720-730.	5.7	126
85	Genomics Approach to Absciscic Acid- and Gibberellin-responsive Genes in Rice. DNA Research, 2003, 10, 249-261.	3.4	57
86	A Comprehensive Rice Transcript Map Containing 6591 Expressed Sequence Tag Sites. Plant Cell, 2002, 14, 525-535.	6.6	260
87	The genome sequence and structure of rice chromosome 1. Nature, 2002, 420, 312-316.	27.8	519
88	A physical map with yeast artificial chromosome (YAC) clones covering 63% of the 12 rice chromosomes. Genome, 2001, 44, 32-37.	2.0	50
89	Rice Genomics: Current Status of Genome Sequencing. Novartis Foundation Symposium, 2001, 236, 28-45.	1.1	4
90	Physical Mapping of Duplicated Genomic Regions of Two Chromosome Ends in Rice. Genetics, 1998, 150, 1595-1603.	2.9	57

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91	Genomic organization of 57 ribosomal protein genes in rice (<i>Oryza sativa</i>L.) through RFLP mapping. Genome, 1995, 38, 1189-1200.	2.0	23